



Full wwPDB EM Validation Report ⓘ

Mar 22, 2026 – 10:36 AM UTC

PDB ID : 4AQ9 / pdb_00004aq9
EMDB ID : EMD-2072
Title : Gating movement in acetylcholine receptor analysed by time- resolved electron cryo-microscopy (open class)
Authors : Unwin, N.; Fujiyoshi, Y.
Deposited on : 2012-04-13
Resolution : 6.20 Å(reported)
Based on initial model : 2BG9

This is a Full wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

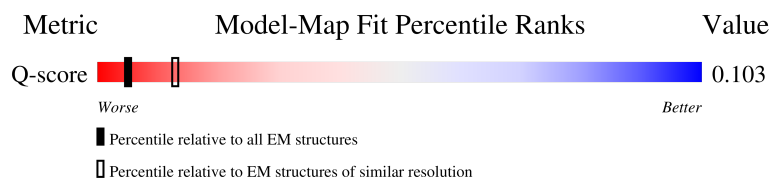
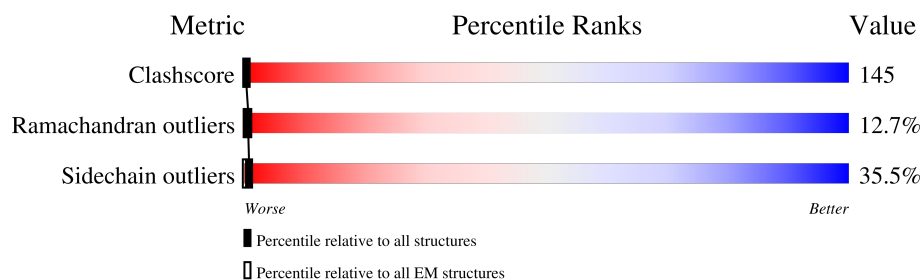
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.20 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	537 (5.70 - 6.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	461	25% 12% 33% 34% 20%
1	D	461	21% 15% 31% 33% 20%
2	B	493	25% 13% 29% 31% 25%
3	C	522	25% 13% 26% 30% 29%

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Mol	Chain	Length	Quality of chain
4	E	488	19% 15% 27% 33% 24%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14924 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 ACETYLCHOLINE RECEPTOR SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	370	Total	C	N	O	S	0	0
			2991	1954	478	540	19		
1	D	370	Total	C	N	O	S	0	0
			2991	1954	478	540	19		

- Molecule 2 is a protein called ACETYLCHOLINE RECEPTOR BETA SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	370	Total	C	N	O	S	0	0
			2972	1938	465	554	15		

- Molecule 3 is a protein called ACETYLCHOLINE RECEPTOR DELTA SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	370	Total	C	N	O	S	0	1
			2983	1944	489	536	14		

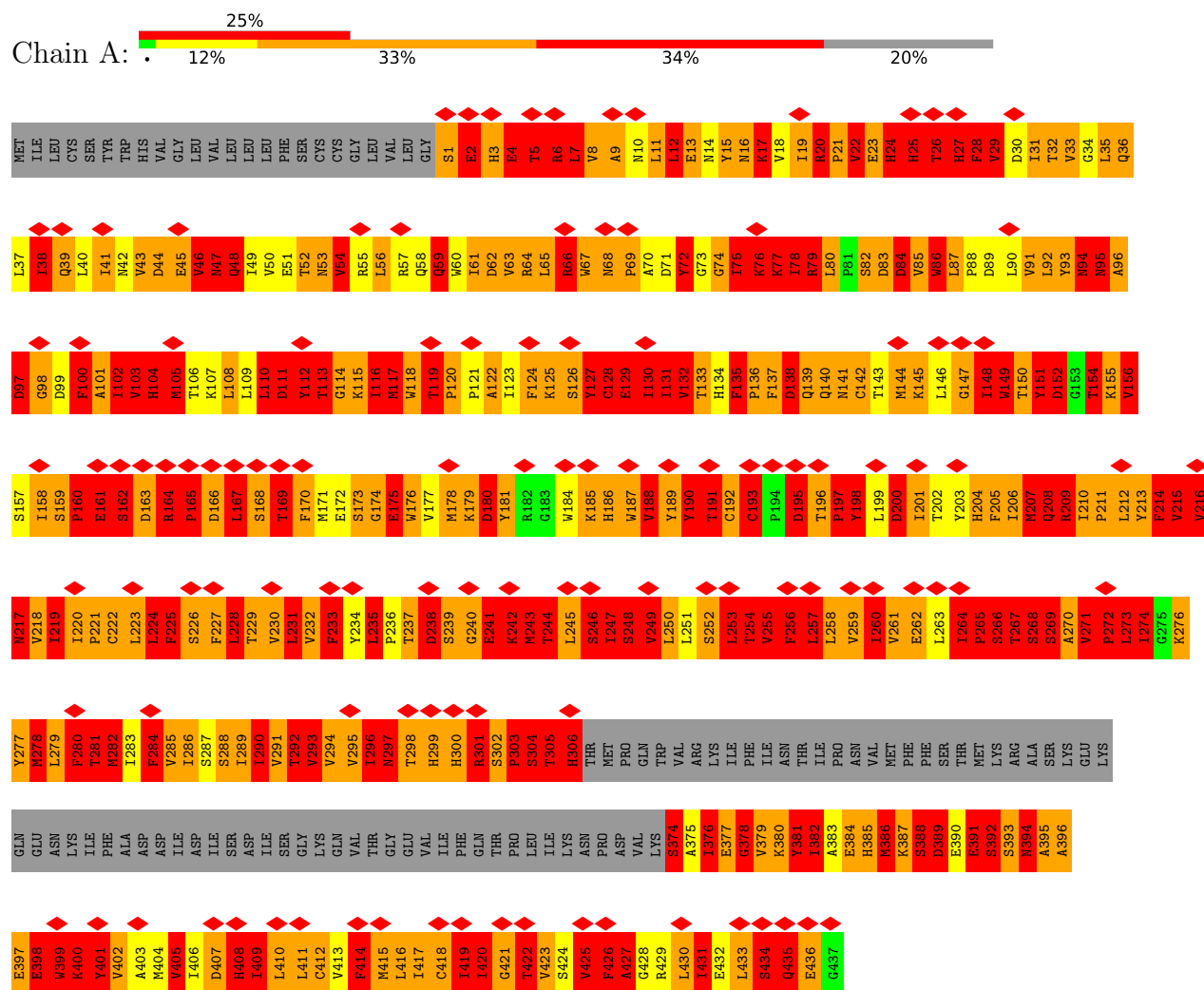
- Molecule 4 is a protein called ACETYLCHOLINE RECEPTOR GAMMA SUBUNIT.

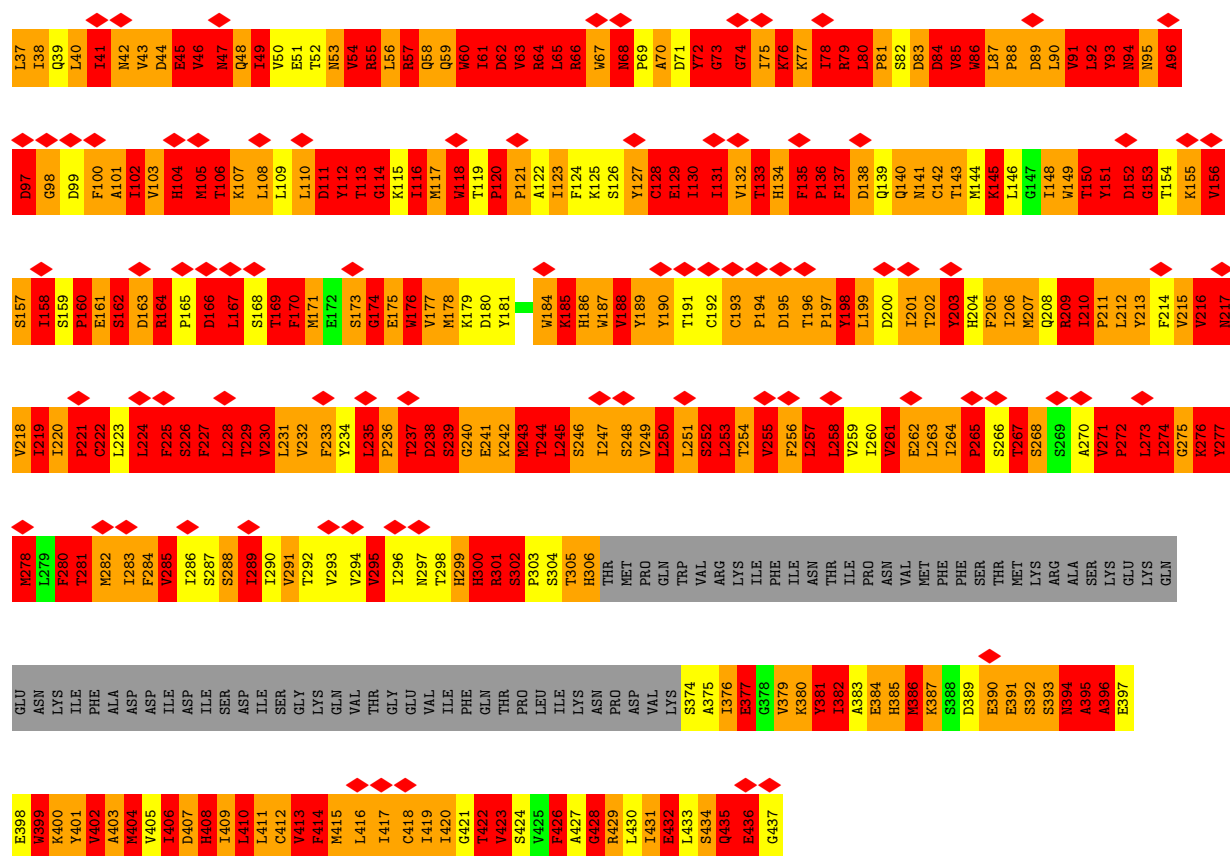
Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	371	Total	C	N	O	S	0	1
			2987	1948	478	551	10		

3 Residue-property plots

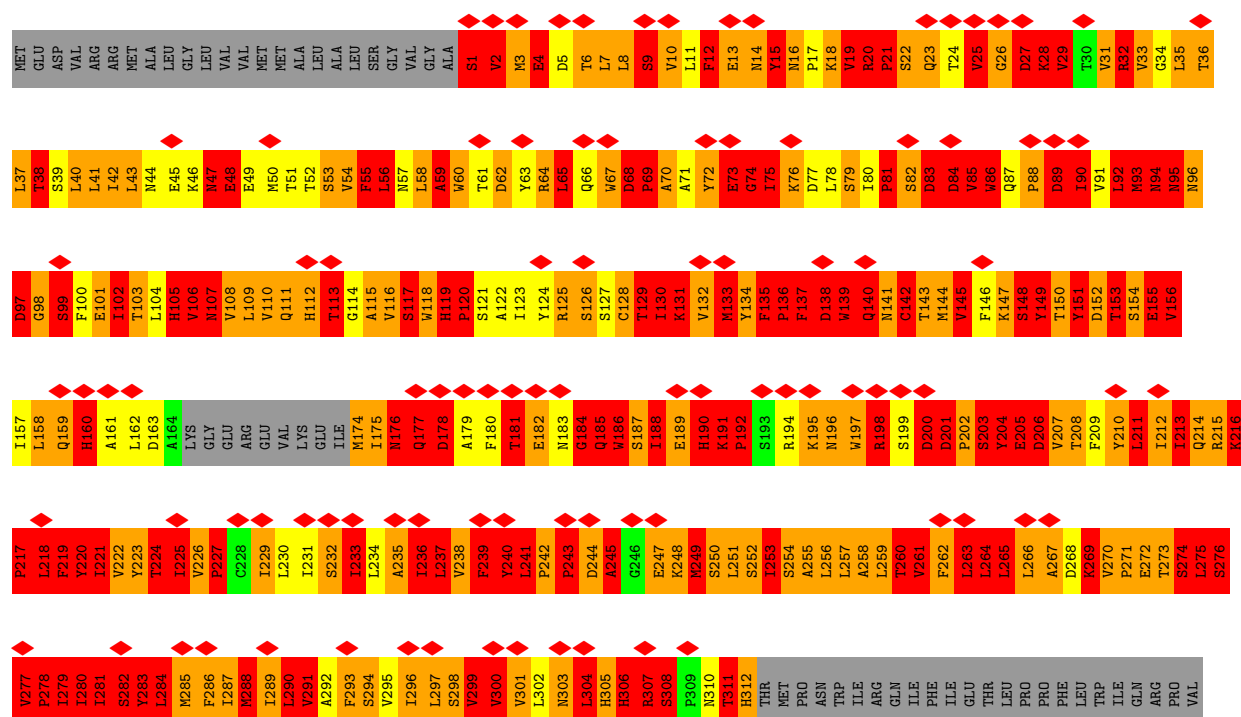
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

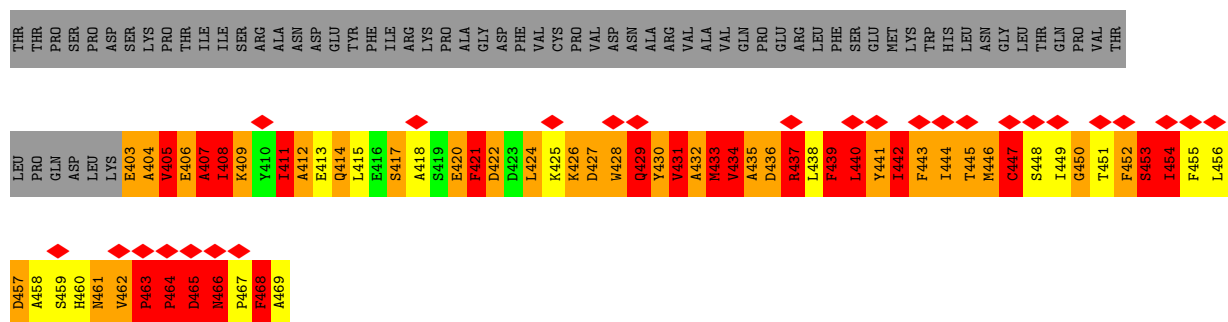
• Molecule 1: ACETYLCHOLINE RECEPTOR SUBUNIT ALPHA



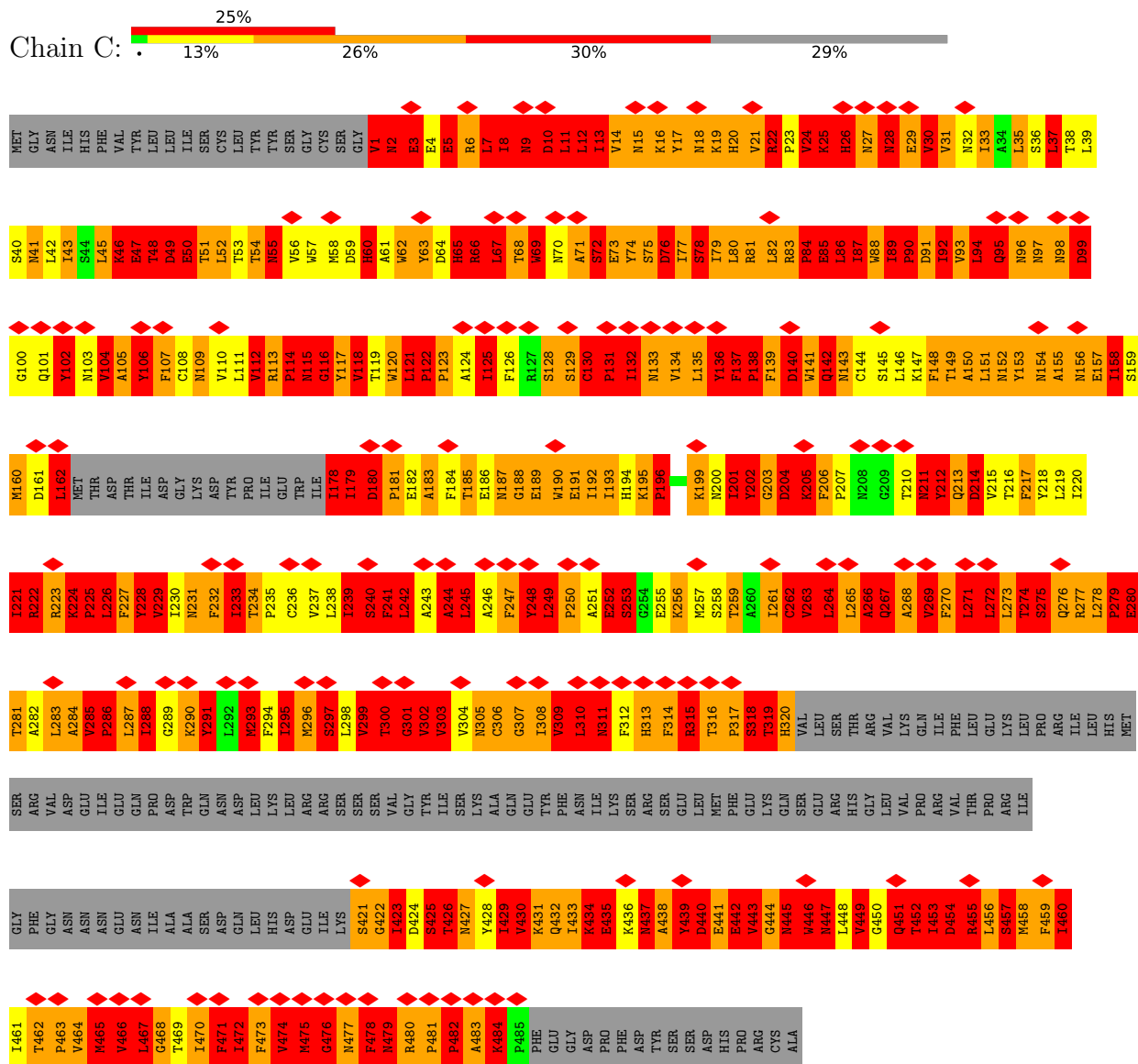


• Molecule 2: ACETYLCHOLINE RECEPTOR BETA SUBUNIT





● Molecule 3: ACETYLCHOLINE RECEPTOR DELTA SUBUNIT



● Molecule 4: ACETYLCHOLINE RECEPTOR GAMMA SUBUNIT



GLY	ASP	PRO	ARG	LYS	TYR	VAL	PRO	F421	I422	A423	K424	S425	T426	K427	E428	Q429	N430	D431	S432	G433	S434	E435	N436	E437	N438	K439	V440	I441	I442	G443	K444	V445	I446	D447	K448	A449	C450	F451	W452	I453	A454	L455	L456	L457	F458	S459	L460	G461	T462	L463	A464	I465	F466	L467	T468	G469	H470	L471	N472	Q473	V474	P475	E476	F477	PRO	PHE	PRO
								GLU	GLU	TYR	ILE	LEU	LYS	LYS	PRO	ARG	GLU	GLU	GLN	LYS	ASP	GLU	ARG	HIS	GLY	LEU	LYS	HIS	LEU	ARG	VAL	ASN	LYS	MET	THR	SER	ASP	ILE	ASP	GLY	THR	THR	VAL	ASP	LEU	TYR	LYS	ASP	LEU	ALA	ASN	PHE	ALA	PRO	GLU	ILE	LYS	S414	C415	V416	E417	A418	C419	P475	E476	F477	PRO
								F241	L242	P243	A244	Q245	A246	G247	G248	Q249	K250	C251	T252	L253	S254	I255	S256	V257	L258	L259	A260	Q261	T262	I263	F264	L265	F266	L267	I268	A269	Q270	K271	I272	P273	E274	T275	S276	L277	N278	V279	P280	L281	I282	G283	K284	Y285	L286	T287	F288	V289	M290	F291	V292	S293	L294	V295	I296	V297	T298	N299	C300
								G181	E182	W183	I184	I185	I186	H187	R188	F189	A190	K191	N192	M193	Y194	M195	Q197	L198	T199	K200	D201	D202	I203	D204	F205	Q206	E207	I208	I209	F210	T211	L212	I213	I214	Q215	R216	K217	P218	L219	F220	Y221	I222	I223	N224	I225	I226	A227	P228	C229	V230	L231	I232	S233	S234	L235	V236	V237	L238	V239	Y240	
								A121	I122	Y123	R124	S125	T126	C127	P128	I129	A130	V131	T132	Y133	F134	P135	F136	D137	W138	Q139	N140	C141	S142	L143	V144	F145	R146	S147	Q148	T149	Y150	M151	A152	H153	E154	Y155	N156	L157	D158	Q159	S160	A161	E162	E163	G164	GLU	VAL	VAL	GLU	TRP	ILE	HIS	I172	D173	P174	E175	D176	F177	T178	E179	N180
								D61	Y62	R63	L64	S65	W66	W67	T68	S69	E70	K71	E72	G73	I74	D75	L76	V77	R78	I79	P80	S81	K82	L83	L84	W85	L86	P87	D88	W89	V90	L91	S92	N93	N94	Y95	D96	G97	Q98	F99	E100	V101	A102	Y103	Y104	A105	M106	V107	L108	V109	Y110	N111	D112	G113	W114	L115	Y116	W117	L118	P119	P120

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	Not provided	
Resolution determination method	Not provided	
CTF correction method	EACH TUBE IMAGE	Depositor
Microscope	JEOL 3000SFF	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	38500	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	5.148	Depositor
Minimum map value	-3.483	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1	Depositor
Map size (Å)	128.0, 128.0, 168.0	wwPDB
Map dimensions	128, 128, 168	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

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	2.16	53/3069 (1.7%)	3.32	520/4186 (12.4%)
1	D	2.20	62/3069 (2.0%)	3.37	551/4186 (13.2%)
2	B	2.20	68/3048 (2.2%)	3.34	559/4162 (13.4%)
3	C	2.17	60/3059 (2.0%)	3.36	542/4175 (13.0%)
4	E	2.17	74/3057 (2.4%)	3.39	548/4174 (13.1%)
All	All	2.18	317/15302 (2.1%)	3.35	2720/20883 (13.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	6	122
1	D	5	120
2	B	11	128
3	C	5	120
4	E	9	118
All	All	36	608

All (317) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	129	THR	C-N	-17.79	1.12	1.34
1	D	208	GLN	C-N	16.06	1.56	1.33
2	B	159	GLN	C-N	9.56	1.49	1.33
2	B	144	MET	C-N	9.55	1.46	1.33
2	B	225	ILE	CA-CB	9.52	1.66	1.54
4	E	311	PRO	N-CD	8.99	1.60	1.47
1	A	180	ASP	C-O	-8.82	1.12	1.24
4	E	77	VAL	CA-CB	-8.58	1.46	1.55
1	A	282	MET	SD-CE	8.49	2.00	1.79
4	E	182	GLU	C-N	8.40	1.46	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	206	ASP	C-N	8.39	1.44	1.33
2	B	137	PHE	C-N	-7.93	1.23	1.33
3	C	139	PHE	C-N	-7.85	1.23	1.33
3	C	88	TRP	C-N	-7.85	1.25	1.33
4	E	416	VAL	CA-CB	7.78	1.65	1.54
1	D	176	TRP	C-N	7.69	1.44	1.33
3	C	30	VAL	C-N	7.68	1.43	1.33
1	D	97	ASP	C-O	7.64	1.33	1.24
1	A	409	ILE	CA-CB	7.63	1.64	1.54
3	C	191	GLU	C-N	-7.51	1.26	1.33
1	D	58	GLN	C-N	-7.48	1.24	1.33
3	C	31	VAL	CA-CB	7.44	1.62	1.54
1	D	176	TRP	NE1-CE2	-7.44	1.29	1.37
3	C	265	LEU	C-N	7.37	1.43	1.33
1	D	104	HIS	CB-CG	7.37	1.60	1.50
1	D	140	GLN	C-N	-7.35	1.22	1.33
3	C	275	SER	C-N	-7.35	1.23	1.33
2	B	99	SER	C-N	7.32	1.43	1.33
3	C	125	ILE	N-CA	7.26	1.54	1.46
1	D	158	ILE	CA-CB	7.22	1.66	1.54
1	D	156	VAL	CA-CB	7.21	1.65	1.54
1	D	163	ASP	N-CA	-7.12	1.37	1.46
1	D	211	PRO	C-N	-7.10	1.23	1.33
3	C	428	TYR	N-CA	-7.01	1.38	1.46
1	D	271	VAL	CA-C	7.00	1.60	1.52
1	D	379	VAL	CA-CB	-7.00	1.45	1.54
1	A	122	ALA	C-N	-6.99	1.24	1.33
3	C	139	PHE	C-O	6.98	1.32	1.24
2	B	16	ASN	N-CA	-6.97	1.39	1.46
3	C	33	ILE	CA-C	6.96	1.60	1.52
4	E	141	CYS	CA-CB	6.94	1.62	1.53
4	E	306	VAL	C-N	-6.94	1.24	1.33
1	A	419	ILE	CA-CB	6.93	1.63	1.54
4	E	39	LEU	C-N	-6.91	1.24	1.33
4	E	34	LEU	C-N	-6.84	1.23	1.33
3	C	97	ASN	C-O	6.81	1.33	1.23
1	D	376	ILE	CA-C	6.78	1.61	1.52
1	A	126	SER	C-N	-6.77	1.24	1.33
3	C	244	ALA	N-CA	-6.70	1.38	1.46
2	B	143	THR	CA-CB	6.68	1.62	1.53
4	E	144	VAL	C-O	-6.65	1.17	1.24
2	B	226	VAL	C-O	-6.62	1.19	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	126	THR	C-N	-6.60	1.19	1.33
4	E	209	ILE	CA-CB	6.59	1.62	1.54
2	B	90	ILE	C-N	6.58	1.42	1.33
4	E	432	SER	C-O	-6.54	1.15	1.24
1	A	209	ARG	C-N	6.51	1.40	1.33
4	E	138	TRP	NE1-CE2	-6.51	1.30	1.37
1	A	132	VAL	CA-C	6.44	1.60	1.52
2	B	444	ILE	CA-CB	6.44	1.61	1.54
3	C	227	PHE	C-N	6.44	1.41	1.33
1	D	85	VAL	CA-CB	6.43	1.62	1.54
3	C	430	VAL	CA-CB	6.42	1.62	1.54
4	E	224	ASN	C-O	-6.36	1.16	1.24
3	C	279	PRO	CA-CB	-6.35	1.44	1.53
3	C	27	ASN	CA-CB	6.34	1.61	1.53
4	E	55	ILE	CA-CB	6.33	1.63	1.54
3	C	480	ARG	C-N	6.28	1.40	1.33
1	A	435	GLN	N-CA	-6.28	1.39	1.46
1	D	158	ILE	CA-C	6.27	1.60	1.52
1	D	27	HIS	CE1-NE2	6.26	1.38	1.32
2	B	213	ILE	CA-CB	6.24	1.61	1.54
4	E	465	ILE	CA-CB	6.21	1.62	1.54
1	D	68	ASN	CA-C	6.21	1.60	1.52
1	A	91	VAL	C-O	-6.19	1.16	1.24
2	B	304	LEU	N-CA	6.17	1.53	1.46
4	E	87	PRO	C-O	6.16	1.30	1.23
2	B	405	VAL	N-CA	-6.15	1.39	1.46
1	A	262	GLU	C-O	-6.13	1.16	1.24
1	D	55	ARG	NE-CZ	6.13	1.39	1.33
4	E	60	ASN	C-N	-6.12	1.25	1.33
4	E	457	LEU	C-O	-6.11	1.17	1.24
2	B	181	THR	CA-CB	6.09	1.61	1.53
1	D	426	PHE	N-CA	-6.09	1.38	1.46
4	E	287	ILE	CA-CB	6.09	1.62	1.54
1	D	267	THR	CA-C	6.09	1.60	1.52
2	B	253	ILE	CA-CB	6.07	1.63	1.54
1	A	143	THR	C-N	6.06	1.41	1.33
4	E	280	PRO	C-N	6.04	1.41	1.33
4	E	35	THR	C-N	-6.03	1.25	1.33
1	A	209	ARG	NE-CZ	6.03	1.39	1.33
1	D	237	THR	CA-CB	6.02	1.63	1.53
2	B	278	PRO	CA-C	6.02	1.58	1.52
2	B	287	ILE	CA-CB	6.02	1.63	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	24	LEU	N-CA	-6.01	1.39	1.46
1	A	41	ILE	C-O	6.00	1.29	1.23
4	E	220	PHE	C-N	6.00	1.42	1.33
1	A	132	VAL	N-CA	-5.99	1.38	1.46
1	D	103	VAL	CA-CB	5.99	1.63	1.54
1	A	156	VAL	CA-CB	5.97	1.62	1.54
2	B	145	VAL	C-O	-5.95	1.17	1.24
1	D	203	TYR	N-CA	-5.95	1.38	1.45
4	E	77	VAL	C-O	-5.94	1.16	1.23
1	D	250	LEU	N-CA	-5.94	1.39	1.46
3	C	47	GLU	CA-C	-5.94	1.46	1.53
1	D	143	THR	CA-CB	5.93	1.61	1.53
1	D	18	VAL	CA-CB	5.91	1.61	1.54
1	A	54	VAL	CA-CB	5.90	1.62	1.54
2	B	459	SER	C-O	-5.90	1.17	1.24
1	D	419	ILE	CA-CB	5.89	1.63	1.54
4	E	205	PHE	N-CA	-5.89	1.39	1.46
1	A	136	PRO	C-N	-5.88	1.26	1.33
4	E	133	TYR	CA-C	5.87	1.60	1.52
1	D	263	LEU	N-CA	-5.86	1.38	1.46
3	C	125	ILE	C-O	5.86	1.30	1.23
1	A	28	PHE	CA-C	5.85	1.60	1.52
1	D	410	LEU	N-CA	-5.84	1.39	1.46
1	A	305	THR	CA-CB	5.83	1.62	1.54
3	C	460	ILE	CA-C	-5.83	1.46	1.52
1	A	169	THR	CA-CB	5.81	1.59	1.53
4	E	153	HIS	CE1-NE2	5.81	1.38	1.32
3	C	315	ARG	CA-C	5.80	1.60	1.52
2	B	305	HIS	CA-C	-5.78	1.46	1.53
2	B	420	GLU	CA-C	5.78	1.60	1.52
3	C	291	TYR	C-O	5.77	1.30	1.24
2	B	134	TYR	N-CA	5.77	1.52	1.46
2	B	199	SER	C-O	5.77	1.31	1.24
1	A	27	HIS	CE1-NE2	5.76	1.38	1.32
4	E	190	ALA	N-CA	5.75	1.53	1.46
3	C	465	MET	CA-C	-5.73	1.44	1.52
1	D	72	TYR	CA-CB	5.72	1.62	1.53
1	A	165	PRO	CA-C	5.71	1.59	1.52
1	D	243	MET	SD-CE	-5.71	1.65	1.79
2	B	225	ILE	N-CA	5.70	1.53	1.46
2	B	265	LEU	N-CA	5.69	1.53	1.46
1	D	7	LEU	C-O	-5.69	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	429	ILE	CA-CB	5.68	1.60	1.54
2	B	458	ALA	C-O	5.68	1.30	1.24
3	C	76	ASP	C-N	-5.67	1.25	1.33
2	B	412	ALA	CA-C	-5.67	1.45	1.52
2	B	36	THR	CA-CB	5.64	1.60	1.53
2	B	285	MET	C-O	-5.64	1.17	1.24
4	E	259	LEU	C-O	-5.64	1.17	1.24
3	C	191	GLU	CA-C	5.64	1.58	1.52
1	A	247	ILE	CA-CB	5.63	1.62	1.54
3	C	242	LEU	CA-C	5.63	1.59	1.52
2	B	133	MET	C-N	-5.63	1.24	1.34
4	E	312	ASN	C-O	5.62	1.29	1.24
2	B	157	ILE	C-O	5.61	1.29	1.24
1	D	429	ARG	N-CA	-5.61	1.39	1.46
1	D	143	THR	CA-C	-5.61	1.45	1.52
1	D	86	TRP	CA-CB	5.61	1.60	1.52
3	C	285	VAL	CA-C	5.60	1.58	1.52
4	E	211	PHE	CA-C	5.60	1.60	1.52
2	B	302	LEU	N-CA	-5.59	1.39	1.46
4	E	258	LEU	CA-C	-5.59	1.45	1.52
4	E	421	PHE	C-O	5.59	1.30	1.24
1	A	148	ILE	CA-C	5.58	1.59	1.52
1	A	292	THR	CA-C	-5.58	1.45	1.52
4	E	268	ILE	CA-CB	5.58	1.62	1.54
2	B	194	ARG	CA-C	5.58	1.59	1.52
2	B	154	SER	CA-C	5.57	1.60	1.52
1	D	408	HIS	C-N	5.57	1.40	1.34
4	E	153	HIS	CG-CD2	5.57	1.42	1.35
3	C	94	LEU	CA-C	5.57	1.59	1.53
4	E	57	ILE	CA-CB	5.57	1.60	1.54
2	B	124	TYR	N-CA	5.56	1.52	1.46
1	A	211	PRO	CA-C	5.56	1.59	1.52
4	E	178	THR	CA-CB	5.55	1.61	1.53
3	C	266	ALA	CA-C	5.54	1.59	1.52
4	E	465	ILE	C-O	-5.54	1.17	1.24
3	C	130	CYS	C-N	5.54	1.46	1.33
1	A	379	VAL	CA-C	-5.54	1.45	1.52
4	E	452	TRP	C-N	-5.53	1.27	1.33
1	D	391	GLU	C-O	-5.53	1.17	1.24
4	E	54	TRP	N-CA	-5.53	1.39	1.46
3	C	122	PRO	C-O	5.53	1.30	1.24
2	B	48	GLU	C-O	-5.52	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	216	LYS	CA-C	-5.52	1.47	1.52
4	E	187	HIS	ND1-CE1	5.50	1.38	1.32
1	D	86	TRP	CA-C	5.49	1.59	1.52
2	B	296	ILE	CA-CB	5.49	1.62	1.54
3	C	13	ILE	CA-C	5.49	1.59	1.52
1	A	299	HIS	CG-ND1	-5.49	1.32	1.38
1	D	291	VAL	CA-CB	5.49	1.61	1.54
2	B	462	VAL	N-CA	-5.48	1.39	1.46
3	C	291	TYR	C-N	-5.47	1.26	1.33
4	E	260	ALA	N-CA	-5.47	1.39	1.46
1	A	280	PHE	N-CA	5.46	1.52	1.46
1	A	205	PHE	C-O	-5.46	1.17	1.24
4	E	257	VAL	CA-CB	5.45	1.61	1.54
3	C	295	ILE	CA-CB	-5.45	1.47	1.54
1	D	145	LYS	N-CA	5.45	1.52	1.46
1	D	164	ARG	N-CA	5.45	1.52	1.45
3	C	117	TYR	CA-CB	5.44	1.62	1.53
2	B	54	VAL	CA-CB	-5.44	1.47	1.54
1	A	43	VAL	N-CA	-5.43	1.39	1.46
3	C	241	PHE	C-O	-5.43	1.17	1.24
1	A	136	PRO	N-CA	-5.43	1.40	1.47
2	B	276	SER	C-N	-5.43	1.27	1.33
4	E	194	TYR	N-CA	5.43	1.52	1.45
4	E	194	TYR	C-N	5.42	1.40	1.33
3	C	464	VAL	CA-C	-5.42	1.45	1.52
1	A	401	TYR	C-O	-5.41	1.17	1.23
3	C	183	ALA	CA-CB	-5.41	1.46	1.53
3	C	464	VAL	C-O	-5.41	1.17	1.24
1	D	25	HIS	CG-CD2	5.40	1.41	1.35
3	C	228	TYR	CA-C	5.40	1.59	1.52
1	D	164	ARG	CA-C	5.40	1.57	1.52
4	E	312	ASN	N-CA	5.39	1.52	1.46
4	E	183	TRP	CA-C	-5.39	1.46	1.53
1	D	295	VAL	N-CA	5.39	1.52	1.46
4	E	230	VAL	CA-C	-5.39	1.46	1.52
4	E	206	GLN	N-CA	-5.39	1.39	1.46
4	E	306	VAL	N-CA	-5.38	1.40	1.46
4	E	269	ALA	N-CA	-5.38	1.39	1.46
3	C	27	ASN	N-CA	5.37	1.53	1.46
3	C	5	GLU	N-CA	-5.37	1.39	1.46
1	D	251	LEU	CA-C	5.36	1.59	1.52
1	D	55	ARG	CA-CB	5.36	1.59	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	269	LYS	N-CA	-5.36	1.40	1.46
1	A	130	ILE	CA-CB	5.35	1.61	1.54
2	B	139	TRP	C-O	-5.34	1.17	1.24
4	E	108	LEU	CA-C	5.34	1.59	1.52
2	B	38	THR	CA-C	5.34	1.59	1.52
1	D	96	ALA	N-CA	5.33	1.53	1.46
2	B	160	HIS	ND1-CE1	-5.33	1.27	1.32
2	B	210	TYR	CA-C	5.33	1.59	1.52
4	E	151	ASN	CA-C	5.33	1.58	1.52
1	D	27	HIS	ND1-CE1	-5.32	1.27	1.32
1	A	103	VAL	N-CA	-5.30	1.39	1.46
1	D	248	SER	C-N	-5.30	1.27	1.33
1	A	248	SER	C-O	-5.30	1.17	1.24
1	D	297	ASN	N-CA	5.30	1.52	1.46
1	A	209	ARG	C-O	-5.29	1.16	1.24
4	E	307	SER	C-O	-5.29	1.17	1.23
3	C	87	ILE	CA-C	-5.29	1.46	1.52
1	D	299	HIS	CG-ND1	5.28	1.44	1.38
2	B	130	ILE	N-CA	-5.28	1.39	1.46
1	A	238	ASP	CA-C	5.27	1.59	1.52
2	B	160	HIS	N-CA	5.27	1.51	1.46
1	A	46	VAL	C-O	-5.26	1.17	1.24
2	B	112	HIS	CE1-NE2	-5.26	1.27	1.32
2	B	68	ASP	CA-C	5.26	1.59	1.52
2	B	128	CYS	CA-C	5.25	1.59	1.52
1	A	163	ASP	N-CA	-5.25	1.39	1.46
2	B	119	HIS	CD2-NE2	5.25	1.43	1.37
4	E	124	ARG	CA-C	-5.24	1.46	1.52
3	C	299	VAL	C-O	-5.24	1.17	1.24
2	B	220	TYR	N-CA	5.24	1.53	1.45
2	B	252	SER	C-N	-5.23	1.27	1.34
4	E	189	PRO	N-CA	-5.23	1.41	1.46
3	C	103	ASN	C-N	5.22	1.40	1.33
1	A	381	TYR	N-CA	-5.22	1.39	1.46
1	D	232	VAL	N-CA	5.22	1.52	1.46
2	B	197	TRP	N-CA	-5.22	1.38	1.46
4	E	239	VAL	CA-CB	5.20	1.61	1.54
3	C	51	THR	C-O	-5.19	1.18	1.24
3	C	477	ASN	CA-CB	5.19	1.62	1.53
2	B	126	SER	C-N	-5.19	1.26	1.33
4	E	52	ASN	CA-CB	5.18	1.59	1.52
3	C	112	VAL	C-O	-5.18	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	23	THR	C-O	5.18	1.29	1.23
4	E	426	THR	N-CA	5.18	1.52	1.46
4	E	272	VAL	N-CA	-5.17	1.40	1.46
1	A	117	MET	SD-CE	5.17	1.92	1.79
2	B	443	PHE	C-O	-5.17	1.18	1.24
3	C	280	GLU	C-O	5.17	1.30	1.24
1	D	229	THR	CA-C	-5.17	1.45	1.52
3	C	320	HIS	CE1-NE2	5.16	1.37	1.32
3	C	151	LEU	C-O	5.15	1.30	1.24
2	B	216	LYS	N-CA	5.15	1.52	1.46
4	E	204	ASP	N-CA	-5.15	1.39	1.46
4	E	312	ASN	CA-C	-5.15	1.46	1.52
2	B	221	ILE	CA-C	5.14	1.59	1.52
1	D	62	ASP	CA-C	-5.14	1.47	1.53
2	B	221	ILE	C-O	5.12	1.30	1.24
1	D	277	TYR	N-CA	-5.12	1.39	1.46
2	B	264	LEU	C-O	5.12	1.29	1.24
3	C	90	PRO	C-O	5.12	1.30	1.24
1	A	25	HIS	CE1-NE2	5.12	1.37	1.32
1	A	62	ASP	N-CA	-5.12	1.40	1.46
4	E	155	VAL	CA-C	5.12	1.58	1.52
2	B	233	ILE	C-O	-5.11	1.18	1.24
1	D	116	ILE	CA-CB	-5.10	1.47	1.54
3	C	481	PRO	CA-C	5.10	1.56	1.52
1	A	431	ILE	N-CA	-5.10	1.40	1.46
2	B	270	VAL	N-CA	5.10	1.52	1.46
1	D	188	VAL	CA-C	5.09	1.58	1.52
4	E	476	GLU	C-N	-5.09	1.26	1.33
1	A	376	ILE	N-CA	-5.09	1.40	1.46
4	E	289	VAL	CA-CB	5.09	1.59	1.54
1	A	104	HIS	CA-CB	5.09	1.61	1.53
3	C	93	VAL	CA-CB	-5.08	1.48	1.54
3	C	190	TRP	N-CA	5.08	1.51	1.45
1	D	245	LEU	N-CA	-5.08	1.40	1.46
2	B	226	VAL	CA-CB	5.07	1.57	1.54
4	E	75	ASP	CA-C	5.07	1.59	1.52
3	C	84	PRO	C-O	5.06	1.30	1.24
1	A	288	SER	CA-C	-5.06	1.46	1.52
1	D	187	TRP	C-N	-5.06	1.27	1.33
4	E	470	HIS	CG-ND1	5.06	1.43	1.38
1	A	204	HIS	CA-CB	-5.05	1.45	1.53
4	E	69	SER	C-N	5.05	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	67	TRP	N-CA	5.05	1.51	1.45
1	A	161	GLU	CA-C	5.04	1.59	1.52
1	A	293	VAL	N-CA	-5.04	1.40	1.46
3	C	80	LEU	N-CA	5.03	1.52	1.45
3	C	226	LEU	CA-C	-5.03	1.45	1.52
1	D	289	ILE	CA-CB	5.03	1.60	1.54
4	E	209	ILE	N-CA	5.03	1.52	1.46
1	A	102	ILE	CA-CB	-5.02	1.47	1.54
4	E	181	GLY	C-N	-5.01	1.25	1.33
1	D	61	ILE	CA-C	-5.01	1.46	1.52
4	E	265	LEU	C-N	-5.01	1.27	1.33
4	E	203	ILE	C-O	-5.01	1.18	1.24
2	B	16	ASN	CA-C	5.00	1.58	1.52

All (2720) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	140	GLN	OE1-CD-NE2	-20.07	102.53	122.60
4	E	98	GLN	OE1-CD-NE2	-18.71	103.89	122.60
1	A	20	ARG	CA-C-O	-17.45	106.41	119.32
1	D	251	LEU	O-C-N	15.13	138.16	122.12
4	E	238	LEU	N-CA-C	-14.67	90.92	112.04
3	C	265	LEU	O-C-N	14.56	137.55	122.12
1	A	101	ALA	CA-C-N	14.14	147.42	121.97
1	A	101	ALA	C-N-CA	14.14	147.42	121.97
1	D	95	ASN	CA-CB-CG	13.98	126.58	112.60
3	C	474	VAL	O-C-N	-13.78	107.57	121.90
4	E	445	VAL	N-CA-C	13.55	124.32	110.23
2	B	94	ASN	CA-C-N	13.51	147.34	121.54
2	B	94	ASN	C-N-CA	13.51	147.34	121.54
4	E	305	ASN	CA-C-N	13.43	137.84	121.85
4	E	305	ASN	C-N-CA	13.43	137.84	121.85
1	A	394	ASN	CA-CB-CG	13.30	125.90	112.60
3	C	313	HIS	CA-CB-CG	13.15	126.95	113.80
2	B	204	TYR	CA-C-O	-13.09	105.81	120.60
4	E	220	PHE	CA-C-O	13.09	134.03	119.24
4	E	310	THR	CA-C-N	13.06	132.82	119.24
4	E	310	THR	C-N-CA	13.06	132.82	119.24
2	B	463	PRO	N-CA-C	13.04	126.61	110.70
2	B	176	ASN	OD1-CG-ND2	12.99	135.59	122.60
1	D	230	VAL	N-CA-C	-12.85	97.74	110.72
3	C	30	VAL	O-C-N	-12.84	106.51	122.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	135	PHE	O-C-N	12.81	136.06	121.32
3	C	101	GLN	OE1-CD-NE2	-12.80	109.80	122.60
4	E	5	ARG	CD-NE-CZ	12.80	142.32	124.40
4	E	219	LEU	O-C-N	12.74	137.75	123.22
4	E	214	ILE	CA-C-N	12.71	142.35	120.87
4	E	214	ILE	C-N-CA	12.71	142.35	120.87
1	D	95	ASN	OD1-CG-ND2	-12.50	110.10	122.60
3	C	443	VAL	CA-C-N	12.45	133.76	119.94
3	C	443	VAL	C-N-CA	12.45	133.76	119.94
1	A	8	VAL	N-CA-C	12.39	123.37	110.36
4	E	215	GLN	CG-CD-NE2	12.33	134.90	116.40
3	C	460	ILE	N-CA-C	-12.32	101.88	111.62
4	E	260	ALA	CA-C-N	12.31	145.06	121.54
4	E	260	ALA	C-N-CA	12.31	145.06	121.54
3	C	130	CYS	CA-C-N	12.18	135.07	119.84
3	C	130	CYS	C-N-CA	12.18	135.07	119.84
2	B	211	LEU	CA-C-O	-12.18	107.69	120.84
1	A	52	THR	CA-C-N	12.12	140.22	122.41
1	A	52	THR	C-N-CA	12.12	140.22	122.41
4	E	261	GLN	OE1-CD-NE2	-12.11	110.49	122.60
3	C	481	PRO	N-CA-C	12.08	125.43	110.70
4	E	3	GLU	CA-C-N	11.98	133.00	119.94
4	E	3	GLU	C-N-CA	11.98	133.00	119.94
1	A	174	GLY	CA-C-N	11.93	144.32	121.54
1	A	174	GLY	C-N-CA	11.93	144.32	121.54
3	C	268	ALA	O-C-N	-11.90	108.58	122.15
4	E	1	ASN	OD1-CG-ND2	-11.86	110.74	122.60
3	C	92	ILE	O-C-N	11.86	137.39	122.57
1	D	18	VAL	CB-CA-C	-11.81	96.85	111.97
1	A	393	SER	CA-C-O	-11.72	108.36	120.90
4	E	472	ASN	N-CA-C	-11.65	99.59	114.04
3	C	437	ASN	OD1-CG-ND2	11.60	134.20	122.60
3	C	243	ALA	O-C-N	11.55	134.37	122.12
3	C	473	PHE	N-CA-C	-11.43	95.58	112.04
1	A	67	TRP	N-CA-C	11.38	124.91	108.86
1	A	234	TYR	N-CA-C	11.35	123.21	111.07
1	D	381	TYR	CA-C-O	-11.31	106.44	119.79
2	B	19	VAL	CA-C-N	11.30	139.47	121.17
2	B	19	VAL	C-N-CA	11.30	139.47	121.17
3	C	308	ILE	N-CA-C	-11.29	99.87	110.82
4	E	67	ASN	CA-C-N	11.23	143.00	121.54
4	E	67	ASN	C-N-CA	11.23	143.00	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	209	ARG	NE-CZ-NH2	11.21	129.29	119.20
2	B	141	ASN	CA-CB-CG	11.20	123.80	112.60
1	A	195	ASP	CA-CB-CG	11.20	123.80	112.60
3	C	306	CYS	N-CA-C	-11.11	99.86	113.41
4	E	178	THR	N-CA-C	11.06	126.45	109.96
1	D	13	GLU	CA-C-O	-11.03	109.42	121.00
1	A	269	SER	CA-C-N	11.01	139.47	122.29
1	A	269	SER	C-N-CA	11.01	139.47	122.29
2	B	301	VAL	N-CA-C	-11.01	99.39	110.62
1	A	267	THR	N-CA-CB	10.99	126.54	110.06
3	C	426	THR	CA-C-O	-10.96	109.17	120.90
1	A	28	PHE	CA-C-N	-10.95	108.89	123.12
1	A	28	PHE	C-N-CA	-10.95	108.89	123.12
4	E	25	ASP	CA-CB-CG	10.91	123.51	112.60
1	A	388	SER	N-CA-C	10.91	122.86	110.97
1	A	414	PHE	CA-C-N	10.91	134.90	120.28
1	A	414	PHE	C-N-CA	10.91	134.90	120.28
1	D	7	LEU	CA-C-O	-10.90	109.45	120.89
3	C	30	VAL	CA-C-O	10.88	134.39	120.78
2	B	445	THR	O-C-N	10.88	133.34	122.03
2	B	5	ASP	CA-C-N	10.87	138.49	120.88
2	B	5	ASP	C-N-CA	10.87	138.49	120.88
3	C	223	ARG	NE-CZ-NH2	10.85	128.96	119.20
3	C	142	GLN	CA-C-N	10.78	138.64	122.47
3	C	142	GLN	C-N-CA	10.78	138.64	122.47
1	A	407	ASP	O-C-N	-10.73	110.75	122.12
2	B	32	ARG	CD-NE-CZ	10.72	139.41	124.40
3	C	109	ASN	CA-C-O	-10.68	108.75	120.92
2	B	468	PHE	CA-CB-CG	10.68	124.47	113.80
4	E	66	TRP	CD2-CE2-CZ2	10.68	133.08	122.40
4	E	77	VAL	O-C-N	10.66	132.24	122.97
4	E	436	ASN	CA-CB-CG	10.63	123.23	112.60
4	E	17	ARG	NE-CZ-NH2	-10.61	109.65	119.20
3	C	287	LEU	CA-C-O	-10.56	108.60	120.54
2	B	307	ARG	N-CA-C	10.56	133.29	110.80
1	A	225	PHE	N-CA-C	-10.54	98.95	112.23
1	D	85	VAL	N-CA-C	10.49	123.48	109.21
2	B	241	LEU	O-C-N	-10.46	112.11	120.38
1	A	20	ARG	O-C-N	10.46	130.98	121.35
1	A	248	SER	O-C-N	-10.45	108.69	122.59
3	C	9	ASN	N-CA-C	-10.44	101.04	113.88
2	B	117	SER	CA-C-O	-10.42	109.11	120.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	62	ASP	CA-CB-CG	10.41	123.01	112.60
1	A	9	ALA	N-CA-C	10.39	122.36	111.14
3	C	202	TYR	N-CA-C	10.36	127.13	108.48
1	D	132	VAL	CA-C-O	10.31	132.64	119.85
1	A	10	ASN	CA-C-N	10.30	134.44	120.44
1	A	10	ASN	C-N-CA	10.30	134.44	120.44
3	C	203	GLY	CA-C-O	-10.29	111.55	120.92
1	D	295	VAL	N-CA-C	10.28	122.33	110.62
4	E	205	PHE	CA-CB-CG	-10.27	103.53	113.80
4	E	107	VAL	CA-C-O	-10.27	109.91	121.92
1	A	101	ALA	O-C-N	10.26	135.26	123.05
4	E	155	VAL	CA-C-O	-10.26	110.40	121.28
1	D	252	SER	CA-C-N	10.25	135.03	120.79
1	D	252	SER	C-N-CA	10.25	135.03	120.79
1	D	166	ASP	CA-CB-CG	10.24	122.84	112.60
1	D	411	LEU	CA-C-N	10.20	137.41	121.19
1	D	411	LEU	C-N-CA	10.20	137.41	121.19
1	D	167	LEU	CA-C-N	10.16	136.06	120.82
1	D	167	LEU	C-N-CA	10.16	136.06	120.82
2	B	119	HIS	CA-CB-CG	10.16	123.96	113.80
2	B	25	VAL	O-C-N	-10.14	109.89	122.57
1	A	200	ASP	CA-C-N	10.13	136.40	122.01
1	A	200	ASP	C-N-CA	10.13	136.40	122.01
1	A	140	GLN	OE1-CD-NE2	-10.11	112.49	122.60
3	C	22	ARG	NE-CZ-NH2	10.10	128.29	119.20
2	B	306	HIS	CA-CB-CG	-10.10	103.70	113.80
1	D	136	PRO	CB-CA-C	10.10	128.22	111.56
2	B	434	VAL	CB-CA-C	-10.06	98.89	111.87
1	A	159	SER	O-C-N	10.06	132.89	121.32
1	D	414	PHE	N-CA-C	-10.05	100.41	111.36
2	B	417	SER	CA-C-O	-10.03	110.17	120.90
2	B	240	TYR	CA-C-N	10.02	132.20	119.78
2	B	240	TYR	C-N-CA	10.02	132.20	119.78
1	A	268	SER	CA-C-O	10.01	132.09	121.07
2	B	69	PRO	N-CA-C	9.97	129.94	113.78
1	D	8	VAL	N-CA-CB	9.96	121.56	110.51
1	A	383	ALA	CA-C-N	9.95	133.61	120.28
1	A	383	ALA	C-N-CA	9.95	133.61	120.28
3	C	158	ILE	CA-C-O	-9.95	109.99	120.64
1	D	55	ARG	O-C-N	-9.91	111.04	122.93
4	E	63	ARG	NE-CZ-NH1	9.89	131.39	121.50
3	C	129	SER	N-CA-CB	9.88	121.71	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	389	ASP	N-CA-C	9.87	123.28	111.33
4	E	26	HIS	CA-C-O	-9.87	110.26	120.32
4	E	146	ARG	O-C-N	-9.85	109.49	122.59
2	B	90	ILE	CA-C-O	9.82	133.05	120.78
3	C	244	ALA	O-C-N	-9.81	110.97	122.15
1	D	198	TYR	CA-C-O	-9.80	110.82	121.99
2	B	431	VAL	N-CA-C	9.76	126.07	112.50
3	C	266	ALA	N-CA-CB	9.75	124.12	109.98
1	D	376	ILE	CA-C-N	9.74	135.44	120.82
1	D	376	ILE	C-N-CA	9.74	135.44	120.82
1	A	168	SER	CA-C-O	9.74	130.74	120.42
1	A	170	PHE	CA-CB-CG	9.72	123.52	113.80
1	D	141	ASN	OD1-CG-ND2	-9.71	112.89	122.60
4	E	136	PHE	CA-C-N	9.69	135.38	122.30
4	E	136	PHE	C-N-CA	9.69	135.38	122.30
4	E	252	THR	N-CA-CB	9.69	124.12	110.07
3	C	20	HIS	CA-CB-CG	-9.67	104.13	113.80
1	D	58	GLN	OE1-CD-NE2	-9.66	112.94	122.60
4	E	437	GLU	CA-C-O	-9.65	110.11	120.92
4	E	118	LEU	CA-C-N	9.65	130.32	120.38
4	E	118	LEU	C-N-CA	9.65	130.32	120.38
3	C	446	TRP	CA-C-N	9.64	134.97	120.31
3	C	446	TRP	C-N-CA	9.64	134.97	120.31
1	A	389	ASP	O-C-N	-9.63	111.91	122.12
3	C	97	ASN	CA-C-O	-9.62	110.16	121.32
1	A	399	TRP	CA-C-N	9.61	136.75	120.71
1	A	399	TRP	C-N-CA	9.61	136.75	120.71
3	C	286	PRO	O-C-N	-9.61	112.34	123.10
3	C	428	TYR	O-C-N	-9.60	111.72	122.09
1	A	67	TRP	CA-C-O	-9.58	110.77	121.40
1	D	251	LEU	CA-C-O	-9.57	110.29	120.63
4	E	292	VAL	O-C-N	9.56	131.15	121.87
1	D	231	LEU	O-C-N	9.55	132.40	122.09
1	D	380	LYS	N-CA-C	-9.54	100.75	111.71
1	D	213	TYR	O-C-N	9.53	133.74	122.20
1	A	242	LYS	CA-C-N	9.52	132.81	120.44
1	A	242	LYS	C-N-CA	9.52	132.81	120.44
3	C	158	ILE	N-CA-C	9.52	121.31	108.27
1	A	170	PHE	CA-C-O	-9.52	110.49	121.72
3	C	425	SER	CA-C-O	-9.52	110.83	120.82
3	C	291	TYR	CA-C-O	-9.52	110.37	120.55
3	C	122	PRO	CA-C-N	9.50	131.71	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	122	PRO	C-N-CA	9.50	131.71	119.84
3	C	425	SER	CA-C-N	9.50	133.36	120.54
3	C	425	SER	C-N-CA	9.50	133.36	120.54
1	A	21	PRO	O-C-N	9.49	135.45	122.64
4	E	456	LEU	CA-C-N	9.47	133.32	120.44
4	E	456	LEU	C-N-CA	9.47	133.32	120.44
1	A	48	GLN	OE1-CD-NE2	-9.47	113.13	122.60
1	D	111	ASP	CA-C-O	-9.46	110.74	120.77
1	D	82	SER	N-CA-C	9.45	121.66	111.36
1	A	208	GLN	OE1-CD-NE2	-9.45	113.15	122.60
2	B	288	MET	CA-C-N	9.44	132.78	120.60
2	B	288	MET	C-N-CA	9.44	132.78	120.60
2	B	462	VAL	CB-CA-C	9.43	128.53	111.36
3	C	468	GLY	N-CA-C	-9.43	101.41	112.73
3	C	426	THR	O-C-N	-9.42	112.29	122.09
1	D	89	ASP	N-CA-CB	9.42	124.14	110.58
2	B	215	ARG	CB-CA-C	9.41	126.32	111.73
1	A	295	VAL	N-CA-C	-9.40	100.49	110.36
4	E	15	ASP	CA-C-O	9.40	130.20	120.24
2	B	14	ASN	CA-CB-CG	-9.39	103.21	112.60
1	A	300	HIS	CA-CB-CG	-9.38	104.42	113.80
2	B	458	ALA	CA-C-O	-9.36	111.17	121.00
4	E	225	ILE	CA-C-N	9.37	132.36	120.56
4	E	225	ILE	C-N-CA	9.37	132.36	120.56
4	E	442	ILE	N-CA-CB	9.36	122.33	111.66
1	A	258	LEU	CA-C-N	9.35	133.27	120.46
1	A	258	LEU	C-N-CA	9.35	133.27	120.46
2	B	224	THR	N-CA-C	-9.35	100.19	111.69
1	A	419	ILE	CA-C-O	-9.34	109.10	120.78
2	B	280	ILE	N-CA-CB	9.34	126.64	111.23
4	E	285	TYR	CA-C-O	9.32	130.59	120.24
2	B	118	TRP	CB-CA-C	9.32	124.50	110.14
1	A	394	ASN	OD1-CG-ND2	-9.32	113.28	122.60
1	A	254	THR	N-CA-C	-9.30	101.02	111.71
3	C	228	TYR	CA-C-O	-9.28	111.26	121.00
1	D	211	PRO	CA-C-O	-9.28	103.71	120.60
1	A	276	LYS	CA-C-N	9.27	133.45	120.29
1	A	276	LYS	C-N-CA	9.27	133.45	120.29
1	A	20	ARG	CA-C-N	9.23	131.38	119.84
1	A	20	ARG	C-N-CA	9.23	131.38	119.84
4	E	63	ARG	NH1-CZ-NH2	-9.23	107.30	119.30
1	A	209	ARG	N-CA-C	9.22	125.48	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	246	ALA	CA-C-O	-9.22	110.59	120.92
1	A	129	GLU	CA-C-O	-9.21	107.33	120.51
2	B	84	ASP	N-CA-C	9.21	124.07	113.01
1	D	49	ILE	CA-C-O	-9.21	110.15	120.84
1	D	233	PHE	CA-C-N	9.21	133.60	120.79
1	D	233	PHE	C-N-CA	9.21	133.60	120.79
1	D	250	LEU	CB-CA-C	9.20	126.25	110.79
1	A	135	PHE	O-C-N	9.18	131.87	121.32
4	E	251	CYS	CA-C-N	9.16	132.90	120.44
4	E	251	CYS	C-N-CA	9.16	132.90	120.44
2	B	463	PRO	O-C-N	-9.16	110.65	121.46
1	A	411	LEU	CA-C-N	9.15	133.51	120.79
1	A	411	LEU	C-N-CA	9.15	133.51	120.79
3	C	89	ILE	N-CA-C	9.15	118.16	107.73
2	B	205	GLU	N-CA-C	9.14	130.26	110.80
1	D	61	ILE	CA-C-O	9.13	131.26	121.67
1	D	14	ASN	OD1-CG-ND2	-9.13	113.47	122.60
1	A	277	TYR	CA-C-O	9.12	130.09	120.42
3	C	182	GLU	N-CA-C	-9.10	101.33	111.07
1	D	84	ASP	CA-C-N	9.08	135.32	121.71
1	D	84	ASP	C-N-CA	9.08	135.32	121.71
2	B	20	ARG	NH1-CZ-NH2	9.05	131.06	119.30
3	C	185	THR	N-CA-CB	9.04	124.42	109.60
1	A	86	TRP	CE2-CD2-CE3	9.02	127.82	118.80
1	D	209	ARG	CA-C-N	9.00	138.78	122.13
1	D	209	ARG	C-N-CA	9.00	138.78	122.13
1	D	160	PRO	O-C-N	8.99	133.83	123.04
1	D	419	ILE	CA-C-O	-8.99	110.48	120.46
4	E	5	ARG	NE-CZ-NH2	8.98	127.28	119.20
4	E	29	ASP	CA-C-N	8.98	134.25	122.93
4	E	29	ASP	C-N-CA	8.98	134.25	122.93
3	C	434	LYS	CA-C-N	8.98	132.50	120.65
3	C	434	LYS	C-N-CA	8.98	132.50	120.65
1	A	249	VAL	N-CA-CB	8.97	126.03	111.23
3	C	115	ASN	CA-CB-CG	-8.97	103.63	112.60
1	A	217	ASN	CA-CB-CG	-8.96	103.64	112.60
1	D	155	LYS	N-CA-C	8.93	124.56	112.68
1	D	266	SER	CA-C-O	-8.93	111.00	120.55
2	B	85	VAL	O-C-N	8.92	131.76	123.19
3	C	432	GLN	OE1-CD-NE2	8.92	131.52	122.60
1	D	294	VAL	CA-C-O	-8.92	111.75	121.29
2	B	177	GLN	CA-C-N	8.91	133.18	120.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	177	GLN	C-N-CA	8.91	133.18	120.79
2	B	183	ASN	OD1-CG-ND2	-8.91	113.69	122.60
4	E	303	VAL	N-CA-CB	8.91	120.97	110.55
2	B	144	MET	CA-C-N	-8.90	111.00	123.11
2	B	144	MET	C-N-CA	-8.90	111.00	123.11
2	B	99	SER	O-C-N	-8.90	110.75	122.59
2	B	218	LEU	CA-C-O	-8.89	111.43	121.39
3	C	122	PRO	N-CA-C	8.89	121.55	110.70
4	E	132	THR	CA-C-N	8.89	138.52	121.54
4	E	132	THR	C-N-CA	8.89	138.52	121.54
3	C	13	ILE	CA-C-N	8.89	137.97	121.97
3	C	13	ILE	C-N-CA	8.89	137.97	121.97
1	D	414	PHE	O-C-N	-8.88	112.03	122.15
3	C	225	PRO	O-C-N	8.87	133.64	122.91
4	E	118	LEU	N-CA-C	8.86	129.40	109.81
2	B	303	ASN	CA-CB-CG	8.86	121.46	112.60
3	C	435	GLU	CA-C-O	-8.85	111.71	121.00
4	E	151	ASN	CA-C-N	8.85	138.44	121.54
4	E	151	ASN	C-N-CA	8.85	138.44	121.54
1	D	67	TRP	N-CA-C	8.85	122.86	109.41
3	C	136	TYR	CA-CB-CG	8.84	129.81	113.90
4	E	416	VAL	O-C-N	-8.83	111.53	122.57
2	B	291	VAL	CA-C-N	8.83	132.99	120.28
2	B	291	VAL	C-N-CA	8.83	132.99	120.28
3	C	31	VAL	CA-C-N	8.83	138.40	121.54
3	C	31	VAL	C-N-CA	8.83	138.40	121.54
1	D	62	ASP	CB-CA-C	8.82	122.98	111.42
1	D	281	THR	CA-C-O	-8.82	111.10	120.63
2	B	292	ALA	CA-C-O	-8.80	110.16	120.10
1	A	128	CYS	N-CA-C	8.79	122.79	108.99
4	E	46	GLU	CA-C-N	8.78	138.31	121.54
4	E	46	GLU	C-N-CA	8.78	138.31	121.54
3	C	295	ILE	O-C-N	8.77	133.53	122.57
4	E	89	VAL	N-CA-C	8.77	121.65	109.55
4	E	80	PRO	CA-C-O	-8.77	111.39	121.56
1	D	302	SER	N-CA-C	8.75	121.41	109.24
1	A	164	ARG	NE-CZ-NH1	-8.75	112.75	121.50
1	D	295	VAL	CA-C-O	-8.74	111.96	121.05
3	C	250	PRO	CA-C-N	8.74	135.04	120.88
3	C	250	PRO	C-N-CA	8.74	135.04	120.88
1	A	163	ASP	CA-CB-CG	8.74	121.34	112.60
2	B	198	ARG	CA-C-N	8.74	136.43	121.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	198	ARG	C-N-CA	8.74	136.43	121.14
4	E	189	PRO	CB-CA-C	8.74	123.93	110.21
4	E	176	ASP	CA-C-N	8.74	133.12	120.71
4	E	176	ASP	C-N-CA	8.74	133.12	120.71
1	D	22	VAL	CA-C-N	-8.73	110.69	123.00
1	D	22	VAL	C-N-CA	-8.73	110.69	123.00
1	D	408	HIS	ND1-CE1-NE2	-8.73	99.67	108.40
3	C	453	ILE	O-C-N	-8.72	111.67	122.57
1	D	92	LEU	CA-C-O	-8.70	111.83	122.36
3	C	222	ARG	O-C-N	-8.70	111.02	122.59
2	B	135	PHE	CA-C-N	-8.70	110.30	120.13
2	B	135	PHE	C-N-CA	-8.70	110.30	120.13
4	E	260	ALA	O-C-N	-8.70	112.70	122.09
2	B	3	MET	CA-C-N	8.70	132.88	120.79
2	B	3	MET	C-N-CA	8.70	132.88	120.79
4	E	61	ASP	O-C-N	-8.68	112.03	123.14
1	D	406	ILE	CB-CA-C	8.66	124.17	112.22
1	A	220	ILE	O-C-N	8.66	130.97	121.10
1	A	289	ILE	N-CA-C	8.65	118.55	110.42
1	D	431	ILE	CA-C-O	-8.65	111.95	120.95
4	E	72	GLU	O-C-N	-8.65	110.43	122.37
4	E	113	GLY	CA-C-N	-8.65	110.00	122.19
4	E	113	GLY	C-N-CA	-8.65	110.00	122.19
1	A	88	PRO	CA-C-O	8.64	131.13	121.36
4	E	303	VAL	CA-C-O	-8.64	112.01	121.17
3	C	69	TRP	CA-C-O	-8.64	111.35	121.46
2	B	94	ASN	OD1-CG-ND2	-8.62	113.98	122.60
2	B	201	ASP	CA-CB-CG	-8.59	104.01	112.60
1	A	79	ARG	NE-CZ-NH2	8.57	126.92	119.20
3	C	245	LEU	N-CA-C	-8.57	100.53	112.45
1	A	274	ILE	CA-CB-CG2	8.56	125.06	110.50
4	E	430	ASN	OD1-CG-ND2	-8.56	114.04	122.60
1	A	405	VAL	O-C-N	-8.56	113.84	122.23
3	C	312	PHE	CA-CB-CG	8.56	122.36	113.80
2	B	417	SER	O-C-N	8.54	130.98	122.09
3	C	311	ASN	CA-C-O	-8.53	111.41	120.63
1	A	66	ARG	CA-C-O	-8.52	111.61	121.16
2	B	154	SER	CA-C-O	-8.52	108.32	120.51
1	A	22	VAL	N-CA-CB	8.52	122.46	112.15
4	E	30	VAL	N-CA-C	8.51	120.53	108.36
2	B	408	ILE	CA-C-N	8.51	132.61	120.79
2	B	408	ILE	C-N-CA	8.51	132.61	120.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	VAL	N-CA-C	8.50	122.26	109.17
1	D	408	HIS	N-CA-CB	8.49	123.38	110.30
2	B	85	VAL	CA-C-O	-8.49	112.98	120.96
2	B	261	VAL	N-CA-C	-8.49	100.94	110.62
4	E	236	VAL	CA-C-O	-8.48	109.35	119.36
4	E	183	TRP	CG-CD2-CE3	8.48	142.38	133.90
2	B	220	TYR	CA-CB-CG	8.46	129.14	113.90
3	C	79	ILE	CA-C-O	-8.45	110.21	120.78
2	B	205	GLU	CA-C-N	8.45	137.68	121.54
2	B	205	GLU	C-N-CA	8.45	137.68	121.54
2	B	272	GLU	O-C-N	-8.45	112.33	122.22
4	E	177	PHE	CA-CB-CG	8.45	122.25	113.80
1	D	68	ASN	OD1-CG-ND2	-8.44	114.16	122.60
2	B	404	ALA	CA-C-N	8.43	131.19	120.56
2	B	404	ALA	C-N-CA	8.43	131.19	120.56
3	C	449	VAL	O-C-N	-8.43	112.03	122.57
1	A	140	GLN	CG-CD-NE2	8.43	129.04	116.40
1	A	99	ASP	CA-C-N	8.43	134.70	121.56
1	A	99	ASP	C-N-CA	8.43	134.70	121.56
1	D	229	THR	CA-C-N	8.41	132.37	120.42
1	D	229	THR	C-N-CA	8.41	132.37	120.42
1	D	67	TRP	CA-C-O	-8.41	111.83	121.58
4	E	244	ALA	N-CA-CB	8.41	122.20	110.01
1	D	429	ARG	N-CA-C	8.40	120.06	111.07
1	A	38	ILE	CA-C-O	-8.40	112.22	120.95
1	A	77	LYS	CA-C-O	-8.40	111.28	121.36
1	A	415	MET	O-C-N	8.39	131.01	122.12
3	C	447	ASN	CA-C-O	8.38	129.61	119.97
3	C	75	SER	CA-C-O	-8.38	111.86	121.07
2	B	445	THR	CA-C-O	-8.37	112.21	121.00
3	C	139	PHE	CA-CB-CG	8.37	122.17	113.80
4	E	439	TRP	NE1-CE2-CD2	8.37	118.28	107.40
1	A	11	LEU	N-CA-C	8.36	120.17	111.14
3	C	138	PRO	O-C-N	-8.35	111.37	122.64
3	C	221	ILE	CA-C-N	8.35	137.48	121.54
3	C	221	ILE	C-N-CA	8.35	137.48	121.54
2	B	73	GLU	CA-C-O	8.33	128.83	119.41
1	D	16	ASN	CA-CB-CG	8.33	120.93	112.60
3	C	422	GLY	O-C-N	-8.32	112.23	122.71
1	A	148	ILE	O-C-N	-8.32	112.17	122.57
4	E	65	SER	N-CA-C	-8.32	99.04	110.35
3	C	228	TYR	CA-CB-CG	8.31	128.87	113.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	122	ILE	CA-C-O	-8.31	111.67	120.57
4	E	67	ASN	CA-CB-CG	8.31	120.91	112.60
2	B	93	MET	CA-C-O	-8.31	108.63	120.51
4	E	69	SER	N-CA-C	8.30	123.41	113.28
3	C	138	PRO	CA-C-N	8.30	132.50	120.38
3	C	138	PRO	C-N-CA	8.30	132.50	120.38
1	D	128	CYS	O-C-N	-8.29	111.75	122.78
4	E	126	THR	N-CA-C	8.30	124.92	109.24
2	B	74	GLY	CA-C-N	8.29	136.89	121.97
2	B	74	GLY	C-N-CA	8.29	136.89	121.97
1	D	151	TYR	CA-CB-CG	8.29	128.81	113.90
4	E	415	CYS	CA-C-N	8.28	136.88	121.97
4	E	415	CYS	C-N-CA	8.28	136.88	121.97
2	B	85	VAL	CB-CA-C	-8.27	99.07	111.80
3	C	118	VAL	O-C-N	-8.27	114.35	123.03
3	C	426	THR	N-CA-CB	8.27	122.26	109.94
3	C	113	ARG	CA-C-N	8.26	130.17	119.84
3	C	113	ARG	C-N-CA	8.26	130.17	119.84
3	C	211	ASN	CA-CB-CG	8.26	120.86	112.60
3	C	104	VAL	CA-CB-CG1	8.25	124.43	110.40
2	B	83	ASP	O-C-N	-8.25	111.62	122.59
3	C	224	LYS	N-CA-CB	8.24	125.03	110.37
4	E	164	GLY	CA-C-O	8.24	138.10	120.80
3	C	86	LEU	CB-CA-C	8.23	121.35	111.22
2	B	434	VAL	O-C-N	-8.23	113.14	121.94
1	A	136	PRO	CB-CA-C	8.22	125.13	111.56
4	E	268	ILE	N-CA-C	-8.22	102.86	111.58
1	D	195	ASP	CA-CB-CG	8.22	120.82	112.60
4	E	23	THR	O-C-N	-8.21	115.08	123.29
4	E	255	ILE	CB-CA-C	-8.21	101.27	112.02
1	D	395	ALA	N-CA-C	-8.20	101.25	111.75
2	B	72	TYR	CA-CB-CG	8.19	128.64	113.90
4	E	470	HIS	N-CA-C	8.19	120.12	111.03
3	C	63	TYR	N-CA-C	8.19	122.16	109.96
3	C	66	ARG	NE-CZ-NH2	-8.19	111.83	119.20
2	B	292	ALA	O-C-N	8.18	131.79	122.22
1	D	160	PRO	N-CA-C	-8.18	98.94	111.13
1	A	415	MET	N-CA-C	-8.18	102.36	111.28
4	E	420	ASN	CA-C-N	8.18	132.16	120.79
4	E	420	ASN	C-N-CA	8.18	132.16	120.79
1	D	23	GLU	O-C-N	-8.18	113.78	123.27
1	A	186	HIS	CA-CB-CG	8.17	121.97	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	190	TYR	N-CA-C	8.16	122.93	109.95
1	D	61	ILE	O-C-N	-8.16	113.98	123.04
2	B	203	SER	N-CA-C	8.16	122.26	110.10
1	A	187	TRP	CA-C-O	-8.15	111.84	120.40
3	C	79	ILE	CB-CA-C	-8.15	97.93	111.29
3	C	270	PHE	CA-C-N	8.15	131.54	120.54
3	C	270	PHE	C-N-CA	8.15	131.54	120.54
4	E	281	LEU	O-C-N	-8.15	114.12	123.33
4	E	220	PHE	CA-CB-CG	8.14	121.94	113.80
1	A	235	LEU	CA-C-N	8.13	130.01	119.84
1	A	235	LEU	C-N-CA	8.13	130.01	119.84
2	B	140	GLN	O-C-N	-8.12	111.79	122.59
1	D	35	LEU	CA-C-O	-8.11	111.72	121.28
4	E	243	PRO	O-C-N	-8.11	111.70	122.64
2	B	142	CYS	CA-C-N	8.10	134.38	123.05
2	B	142	CYS	C-N-CA	8.10	134.38	123.05
3	C	152	ASN	N-CA-C	8.09	124.72	111.37
3	C	191	GLU	CA-C-N	8.08	135.34	122.33
3	C	191	GLU	C-N-CA	8.08	135.34	122.33
3	C	271	LEU	CA-C-O	8.08	129.55	120.90
1	A	169	THR	CA-C-O	-8.07	107.53	122.62
2	B	311	THR	O-C-N	8.07	130.48	122.09
2	B	441	TYR	N-CA-C	-8.07	102.06	112.23
1	D	188	VAL	CA-C-N	8.07	132.96	121.42
1	D	188	VAL	C-N-CA	8.07	132.96	121.42
1	A	290	ILE	CA-C-N	8.06	130.78	120.70
1	A	290	ILE	C-N-CA	8.06	130.78	120.70
2	B	190	HIS	CE1-NE2-CD2	8.06	117.06	109.00
4	E	65	SER	CA-C-O	-8.06	113.00	121.55
4	E	97	GLY	O-C-N	-8.06	112.22	122.70
1	D	186	HIS	O-C-N	8.06	130.66	123.41
4	E	109	VAL	O-C-N	8.05	132.52	123.10
2	B	44	ASN	O-C-N	8.05	132.50	122.84
1	A	392	SER	CA-C-O	8.05	132.02	120.51
3	C	444	GLY	CA-C-N	8.05	132.54	120.31
3	C	444	GLY	C-N-CA	8.05	132.54	120.31
1	A	379	VAL	CB-CA-C	-8.05	101.46	112.24
1	A	273	LEU	CA-C-O	-8.04	111.41	120.66
2	B	446	MET	CA-C-O	-8.04	110.72	119.97
4	E	122	ILE	N-CA-C	-8.04	96.87	108.36
1	D	60	TRP	CA-C-O	-8.04	112.71	121.31
1	A	102	ILE	CA-C-N	8.03	136.43	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	102	ILE	C-N-CA	8.03	136.43	121.97
1	D	431	ILE	O-C-N	8.03	129.66	121.87
1	D	26	THR	CA-C-N	8.02	136.85	121.54
1	D	26	THR	C-N-CA	8.02	136.85	121.54
3	C	476	GLY	O-C-N	-8.01	114.50	122.19
2	B	458	ALA	CA-C-N	8.00	131.34	120.38
2	B	458	ALA	C-N-CA	8.00	131.34	120.38
4	E	282	ILE	CA-C-O	-8.00	112.34	120.90
2	B	274	SER	N-CA-C	-8.00	102.62	112.38
1	D	297	ASN	N-CA-C	-8.00	102.52	111.07
1	D	408	HIS	CA-CB-CG	8.00	121.80	113.80
1	D	103	VAL	CB-CA-C	-7.98	101.88	111.94
1	D	176	TRP	CB-CG-CD1	7.98	138.87	126.90
3	C	86	LEU	CA-C-N	7.98	136.34	121.97
3	C	86	LEU	C-N-CA	7.98	136.34	121.97
3	C	459	PHE	CA-C-N	7.98	131.62	123.16
3	C	459	PHE	C-N-CA	7.98	131.62	123.16
1	D	164	ARG	NE-CZ-NH1	7.98	129.48	121.50
4	E	203	ILE	N-CA-C	-7.97	92.76	109.34
2	B	213	ILE	N-CA-C	7.97	120.40	109.80
2	B	161	ALA	O-C-N	-7.96	112.00	122.59
1	D	265	PRO	CA-N-CD	-7.96	100.86	112.00
1	D	300	HIS	CA-CB-CG	-7.96	105.84	113.80
4	E	134	PHE	CA-C-N	-7.96	109.89	119.84
4	E	134	PHE	C-N-CA	-7.96	109.89	119.84
3	C	87	ILE	N-CA-CB	7.95	124.35	111.23
1	D	87	LEU	CA-C-N	7.95	128.42	119.83
1	D	87	LEU	C-N-CA	7.95	128.42	119.83
1	D	164	ARG	O-C-N	-7.95	116.24	121.88
2	B	182	GLU	O-C-N	7.95	131.52	122.22
1	D	112	TYR	O-C-N	7.94	131.78	122.17
2	B	132	VAL	CA-C-N	7.93	135.55	122.62
2	B	132	VAL	C-N-CA	7.93	135.55	122.62
2	B	136	PRO	CA-C-O	-7.93	111.69	120.97
1	D	27	HIS	CB-CG-CD2	7.93	141.51	131.20
4	E	292	VAL	N-CA-CB	7.92	121.32	110.54
2	B	258	ALA	O-C-N	-7.92	113.91	122.07
4	E	114	SER	CA-C-N	-7.92	110.55	122.74
4	E	114	SER	C-N-CA	-7.92	110.55	122.74
4	E	299	ASN	N-CA-C	-7.92	102.88	112.54
2	B	305	HIS	CA-C-O	-7.91	112.58	120.89
2	B	306	HIS	N-CA-C	7.91	127.66	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	73	GLY	CA-C-O	-7.91	111.62	120.09
1	D	306	HIS	CA-CB-CG	7.91	121.71	113.80
2	B	131	LYS	O-C-N	-7.91	112.08	122.59
1	D	94	ASN	CA-CB-CG	7.91	120.50	112.60
3	C	195	LYS	CA-C-N	7.90	127.86	120.03
3	C	195	LYS	C-N-CA	7.90	127.86	120.03
3	C	69	TRP	N-CA-CB	7.90	124.00	111.20
1	D	26	THR	N-CA-C	7.90	121.25	110.35
4	E	189	PRO	O-C-N	-7.89	112.48	123.05
4	E	268	ILE	CB-CA-C	-7.89	102.00	111.94
3	C	76	ASP	CA-C-N	7.89	136.17	121.97
3	C	76	ASP	C-N-CA	7.89	136.17	121.97
3	C	306	CYS	CA-C-N	7.89	130.28	120.34
3	C	306	CYS	C-N-CA	7.89	130.28	120.34
1	D	205	PHE	CA-C-N	-7.88	112.61	123.10
1	D	205	PHE	C-N-CA	-7.88	112.61	123.10
1	A	109	LEU	O-C-N	7.88	132.53	123.31
1	D	94	ASN	N-CA-CB	7.88	123.81	110.49
1	D	8	VAL	N-CA-C	7.88	118.63	110.36
2	B	44	ASN	N-CA-C	-7.88	91.50	107.41
4	E	100	GLU	CA-C-N	7.87	136.13	121.97
4	E	100	GLU	C-N-CA	7.87	136.13	121.97
1	D	14	ASN	CA-CB-CG	7.87	120.47	112.60
4	E	172	ILE	N-CA-CB	7.87	124.87	111.50
2	B	428	TRP	CB-CG-CD2	7.84	137.77	126.80
1	A	44	ASP	N-CA-CB	7.83	123.07	110.77
3	C	62	TRP	CA-C-N	7.83	132.61	121.02
3	C	62	TRP	C-N-CA	7.83	132.61	121.02
3	C	447	ASN	OD1-CG-ND2	-7.83	114.77	122.60
4	E	71	TYR	CG-CD1-CE1	7.83	132.94	121.20
1	D	171	MET	CA-C-O	-7.83	109.32	120.51
4	E	138	TRP	CE2-CD2-CE3	7.83	126.63	118.80
1	D	389	ASP	N-CA-C	-7.83	102.34	111.03
1	A	89	ASP	CB-CA-C	-7.82	100.85	111.88
1	D	140	GLN	CG-CD-NE2	7.82	128.14	116.40
4	E	82	GLU	CB-CG-CD	7.82	125.90	112.60
2	B	187	SER	CA-C-N	7.82	136.05	121.97
2	B	187	SER	C-N-CA	7.82	136.05	121.97
2	B	265	LEU	CA-C-N	7.81	131.79	120.38
2	B	265	LEU	C-N-CA	7.81	131.79	120.38
2	B	215	ARG	N-CA-C	7.81	121.79	107.73
4	E	266	PHE	N-CA-CB	7.81	121.78	110.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	460	HIS	N-CA-C	7.80	120.68	111.71
1	D	102	ILE	N-CA-CB	7.80	124.11	111.23
3	C	204	ASP	CA-C-N	7.80	136.44	121.54
3	C	204	ASP	C-N-CA	7.80	136.44	121.54
4	E	451	PHE	CA-CB-CG	7.80	121.60	113.80
1	A	280	PHE	N-CA-C	-7.79	102.48	110.97
4	E	60	ASN	OD1-CG-ND2	-7.79	114.81	122.60
4	E	126	THR	N-CA-CB	7.79	124.27	110.79
4	E	78	ARG	NE-CZ-NH1	-7.79	113.71	121.50
3	C	233	ILE	N-CA-C	-7.79	101.37	112.35
1	D	61	ILE	N-CA-C	7.79	121.80	108.95
1	D	258	LEU	N-CA-CB	7.79	121.54	109.94
3	C	270	PHE	CA-CB-CG	-7.78	106.02	113.80
2	B	303	ASN	N-CA-CB	7.78	121.56	110.12
4	E	28	ILE	O-C-N	-7.78	114.67	122.76
1	A	278	MET	CA-C-O	-7.78	111.03	119.97
1	A	302	SER	N-CA-C	7.75	119.41	109.72
4	E	24	LEU	N-CA-C	7.75	121.33	112.57
1	A	297	ASN	O-C-N	7.75	131.54	122.17
1	D	230	VAL	O-C-N	-7.74	113.85	121.83
4	E	19	LYS	CB-CA-C	7.74	121.57	109.42
4	E	195	ASN	CA-CB-CG	7.74	120.34	112.60
4	E	266	PHE	O-C-N	7.74	130.32	122.12
1	A	59	GLN	OE1-CD-NE2	7.74	130.34	122.60
1	D	127	TYR	O-C-N	-7.74	114.31	123.28
4	E	263	ILE	CB-CA-C	-7.74	100.76	112.05
1	D	188	VAL	CA-C-O	-7.73	112.39	120.51
1	A	212	LEU	N-CA-C	7.73	127.26	110.80
1	A	97	ASP	O-C-N	-7.72	112.32	122.59
1	A	213	TYR	O-C-N	-7.72	113.75	122.09
1	A	244	THR	CA-C-O	-7.71	110.69	119.79
1	D	402	VAL	N-CA-C	7.71	122.62	112.98
1	A	47	ASN	CA-C-N	7.71	136.26	121.54
1	A	47	ASN	C-N-CA	7.71	136.26	121.54
3	C	105	ALA	CA-C-N	7.70	133.83	123.05
3	C	105	ALA	C-N-CA	7.70	133.83	123.05
1	D	81	PRO	N-CA-C	-7.69	99.88	111.57
2	B	128	CYS	CA-C-N	7.69	136.23	121.54
2	B	128	CYS	C-N-CA	7.69	136.23	121.54
4	E	473	GLN	CA-C-O	-7.69	109.97	119.28
2	B	308	SER	CA-C-O	-7.68	110.72	119.32
1	D	64	ARG	CD-NE-CZ	7.68	135.15	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	297	LEU	CA-C-N	7.68	131.19	120.29
2	B	297	LEU	C-N-CA	7.68	131.19	120.29
4	E	151	ASN	OD1-CG-ND2	7.68	130.28	122.60
3	C	439	TYR	CA-C-N	7.67	136.20	121.54
3	C	439	TYR	C-N-CA	7.67	136.20	121.54
1	A	149	TRP	CB-CA-C	7.67	125.69	110.42
4	E	77	VAL	CA-C-N	7.67	135.04	123.23
4	E	77	VAL	C-N-CA	7.67	135.04	123.23
2	B	466	ASN	N-CA-C	7.66	126.75	109.81
3	C	246	ALA	CA-C-N	7.66	131.95	120.31
3	C	246	ALA	C-N-CA	7.66	131.95	120.31
1	D	256	PHE	N-CA-C	7.65	120.29	111.11
4	E	234	SER	N-CA-C	-7.65	102.59	112.23
4	E	280	PRO	O-C-N	-7.65	112.32	122.64
2	B	15	TYR	CA-C-N	7.64	133.59	122.66
2	B	15	TYR	C-N-CA	7.64	133.59	122.66
1	D	79	ARG	NH1-CZ-NH2	7.64	129.24	119.30
2	B	414	GLN	N-CA-C	7.64	119.39	111.14
4	E	205	PHE	N-CA-CB	7.64	123.15	110.47
1	A	434	SER	CA-C-N	7.64	131.02	120.63
1	A	434	SER	C-N-CA	7.64	131.02	120.63
3	C	271	LEU	O-C-N	-7.63	114.15	122.09
2	B	271	PRO	O-C-N	7.63	131.76	122.23
1	D	385	HIS	N-CA-C	-7.62	102.91	111.14
4	E	124	ARG	O-C-N	7.62	131.64	123.03
1	A	47	ASN	O-C-N	-7.62	111.98	122.19
3	C	141	TRP	CA-C-N	7.61	136.08	121.54
3	C	141	TRP	C-N-CA	7.61	136.08	121.54
1	D	104	HIS	ND1-CG-CD2	7.61	113.71	106.10
1	D	379	VAL	CB-CA-C	-7.61	101.87	112.14
2	B	140	GLN	CA-C-N	7.61	135.45	122.37
2	B	140	GLN	C-N-CA	7.61	135.45	122.37
1	D	134	HIS	ND1-CG-CD2	7.61	113.71	106.10
3	C	440	ASP	CA-CB-CG	7.61	120.21	112.60
1	D	112	TYR	CA-C-N	7.60	136.06	121.54
1	D	112	TYR	C-N-CA	7.60	136.06	121.54
1	D	66	ARG	NE-CZ-NH1	-7.59	113.91	121.50
1	D	112	TYR	N-CA-C	-7.59	102.14	111.40
2	B	307	ARG	NE-CZ-NH1	-7.59	113.91	121.50
4	E	106	ASN	O-C-N	7.59	132.23	122.97
1	A	190	TYR	N-CA-C	7.58	121.90	110.14
3	C	151	LEU	N-CA-C	7.58	123.81	111.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	97	ASP	CA-CB-CG	7.58	120.18	112.60
4	E	12	GLY	O-C-N	7.58	132.56	122.70
1	D	248	SER	CA-C-O	-7.58	109.67	120.51
4	E	175	GLU	O-C-N	7.58	131.59	122.27
4	E	17	ARG	NH1-CZ-NH2	7.57	129.14	119.30
1	D	417	ILE	CA-C-N	7.57	130.42	120.28
1	D	417	ILE	C-N-CA	7.57	130.42	120.28
4	E	67	ASN	CA-C-O	-7.57	109.69	120.51
4	E	70	GLU	CA-C-O	-7.57	109.69	120.51
4	E	456	LEU	CA-C-O	-7.57	112.46	120.63
1	A	3	HIS	CA-C-N	7.56	135.98	121.54
1	A	3	HIS	C-N-CA	7.56	135.98	121.54
3	C	123	PRO	CA-N-CD	-7.55	101.42	112.00
2	B	118	TRP	CA-C-N	7.55	140.23	121.80
2	B	118	TRP	C-N-CA	7.55	140.23	121.80
2	B	214	GLN	O-C-N	-7.54	114.44	123.27
3	C	70	ASN	CA-CB-CG	7.54	120.14	112.60
1	D	240	GLY	CA-C-O	-7.54	113.41	120.80
2	B	446	MET	N-CA-C	7.54	120.56	111.82
1	A	408	HIS	CB-CG-ND1	7.53	134.00	122.70
1	D	157	SER	O-C-N	-7.53	114.18	123.44
4	E	47	GLU	CA-C-O	-7.51	109.77	120.51
3	C	141	TRP	CB-CG-CD1	7.51	138.16	126.90
1	D	99	ASP	N-CA-CB	7.51	121.12	109.48
4	E	261	GLN	O-C-N	7.51	132.57	122.59
4	E	437	GLU	O-C-N	7.51	130.74	122.11
2	B	298	SER	O-C-N	7.50	130.70	122.15
1	D	173	SER	N-CA-C	-7.50	102.36	113.61
1	D	104	HIS	CB-CG-ND1	-7.50	111.45	122.70
3	C	156	ASN	CA-CB-CG	7.49	120.09	112.60
3	C	312	PHE	CA-C-O	7.48	128.03	119.27
4	E	215	GLN	OE1-CD-NE2	-7.48	115.12	122.60
2	B	8	LEU	CA-C-N	7.48	133.37	120.58
2	B	8	LEU	C-N-CA	7.48	133.37	120.58
1	D	57	ARG	CD-NE-CZ	7.48	134.87	124.40
4	E	152	ALA	N-CA-C	7.48	126.73	110.80
1	D	221	PRO	N-CA-CB	-7.47	96.42	103.52
4	E	8	GLU	N-CA-C	7.47	120.31	111.71
4	E	252	THR	O-C-N	-7.47	114.02	122.09
4	E	417	GLU	O-C-N	-7.46	112.23	122.46
1	A	162	SER	N-CA-C	7.46	126.69	110.80
2	B	155	GLU	CA-C-O	-7.46	112.54	121.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	222	ARG	NH1-CZ-NH2	-7.46	109.60	119.30
3	C	275	SER	O-C-N	-7.46	112.17	122.46
2	B	200	ASP	CA-CB-CG	-7.46	105.14	112.60
1	D	41	ILE	O-C-N	7.46	129.22	121.91
4	E	25	ASP	N-CA-CB	7.46	121.17	110.88
1	D	26	THR	N-CA-CB	7.45	120.67	110.38
2	B	259	LEU	O-C-N	7.45	130.01	122.12
1	D	299	HIS	CB-CA-C	7.45	122.57	110.88
4	E	68	THR	N-CA-CB	7.45	123.08	110.49
1	D	153	GLY	O-C-N	-7.45	113.02	122.70
1	A	29	VAL	O-C-N	-7.45	114.39	123.10
4	E	79	ILE	N-CA-CB	7.44	121.63	111.21
3	C	139	PHE	CA-C-O	-7.43	111.88	120.20
1	D	58	GLN	CG-CD-NE2	7.43	127.54	116.40
3	C	423	ILE	O-C-N	-7.42	114.37	121.87
1	A	427	ALA	O-C-N	-7.42	114.25	122.12
2	B	4	GLU	CA-C-O	-7.42	112.91	121.07
1	D	62	ASP	O-C-N	-7.42	115.02	123.40
1	D	211	PRO	CB-CA-C	-7.42	99.32	111.56
1	D	288	SER	CA-C-N	-7.42	111.67	120.72
1	D	288	SER	C-N-CA	-7.42	111.67	120.72
2	B	94	ASN	CA-CB-CG	7.41	120.01	112.60
4	E	61	ASP	CA-CB-CG	7.41	120.01	112.60
3	C	300	THR	CA-C-N	7.41	135.93	121.41
3	C	300	THR	C-N-CA	7.41	135.93	121.41
3	C	101	GLN	O-C-N	7.40	132.13	122.95
2	B	454	ILE	N-CA-C	-7.40	103.25	110.72
1	D	57	ARG	NE-CZ-NH2	7.39	125.86	119.20
1	D	379	VAL	O-C-N	-7.39	114.70	121.87
1	D	285	VAL	CA-CB-CG1	7.39	122.96	110.40
3	C	26	HIS	CA-CB-CG	-7.38	106.42	113.80
3	C	307	GLY	N-CA-C	-7.38	102.79	113.86
1	D	97	ASP	CA-CB-CG	7.38	119.98	112.60
4	E	81	SER	N-CA-CB	-7.37	99.32	110.01
1	D	114	GLY	CA-C-O	-7.37	107.75	120.57
1	A	82	SER	CA-C-N	7.37	135.61	121.54
1	A	82	SER	C-N-CA	7.37	135.61	121.54
1	A	196	THR	CA-C-N	7.36	127.53	120.31
1	A	196	THR	C-N-CA	7.36	127.53	120.31
2	B	126	SER	O-C-N	-7.36	113.24	123.11
1	D	76	LYS	CA-C-N	7.36	134.79	123.23
1	D	76	LYS	C-N-CA	7.36	134.79	123.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	186	TRP	CH2-CZ2-CE2	7.35	127.06	117.50
1	A	272	PRO	O-C-N	-7.34	115.25	123.03
3	C	435	GLU	N-CA-C	-7.34	102.97	110.97
4	E	11	LEU	O-C-N	-7.34	112.33	122.46
4	E	128	PRO	O-C-N	-7.34	112.73	122.64
1	D	49	ILE	CB-CA-C	-7.34	100.64	110.98
1	A	299	HIS	CA-CB-CG	7.33	121.13	113.80
2	B	119	HIS	CA-C-O	-7.33	110.12	120.16
4	E	267	LEU	O-C-N	-7.33	112.86	122.39
3	C	453	ILE	CA-C-N	7.32	131.80	120.82
3	C	453	ILE	C-N-CA	7.32	131.80	120.82
3	C	283	LEU	O-C-N	-7.32	112.86	122.59
3	C	454	ASP	N-CA-CB	7.32	121.70	109.78
1	D	274	ILE	N-CA-CB	7.32	118.94	110.82
1	A	422	THR	O-C-N	-7.31	114.37	122.12
1	D	436	GLU	CA-C-O	-7.31	110.05	120.51
4	E	60	ASN	CB-CG-ND2	7.30	127.36	116.40
4	E	246	ALA	N-CA-C	7.30	126.35	110.80
3	C	88	TRP	CA-C-O	-7.30	112.31	120.70
3	C	71	ALA	O-C-N	-7.29	112.89	122.59
2	B	278	PRO	CA-C-O	-7.29	113.00	122.19
1	A	190	TYR	CB-CG-CD2	-7.29	109.87	120.80
1	D	57	ARG	CA-C-O	-7.28	110.09	120.51
4	E	59	TRP	O-C-N	-7.28	116.42	123.26
4	E	29	ASP	CA-C-O	7.28	128.11	120.54
1	D	85	VAL	CB-CA-C	-7.27	101.01	111.34
3	C	479	ASN	CA-C-O	-7.27	110.60	119.18
1	A	397	GLU	CA-C-N	-7.27	109.26	120.31
1	A	397	GLU	C-N-CA	-7.27	109.26	120.31
1	A	82	SER	CA-C-O	7.27	130.90	120.51
1	D	301	ARG	CA-C-O	-7.27	110.12	120.51
1	D	386	MET	CA-C-O	-7.26	112.79	120.63
4	E	309	ARG	N-CA-C	7.25	126.25	110.80
1	D	185	LYS	O-C-N	7.25	131.57	122.65
1	A	177	VAL	CG1-CB-CG2	7.25	126.74	110.80
2	B	10	VAL	O-C-N	-7.25	113.51	122.57
2	B	60	TRP	N-CA-C	-7.24	99.33	108.45
3	C	10	ASP	CA-CB-CG	-7.24	105.36	112.60
3	C	60	HIS	CA-CB-CG	-7.24	106.56	113.80
3	C	443	VAL	CA-C-O	-7.23	111.74	120.78
2	B	113	THR	O-C-N	7.23	133.10	121.53
1	A	257	LEU	O-C-N	-7.22	114.47	122.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	263	VAL	CA-C-O	-7.22	113.52	121.17
2	B	216	LYS	CA-C-O	7.21	130.52	120.64
1	D	130	ILE	O-C-N	7.21	131.59	122.57
1	D	134	HIS	CA-C-O	-7.20	113.26	120.82
1	D	14	ASN	CA-C-O	-7.19	112.80	122.44
2	B	407	ALA	O-C-N	-7.19	112.69	122.33
1	D	413	VAL	O-C-N	-7.19	115.01	122.20
2	B	307	ARG	O-C-N	-7.19	113.03	122.59
3	C	134	VAL	CA-C-N	7.19	133.08	122.08
3	C	134	VAL	C-N-CA	7.19	133.08	122.08
1	D	382	ILE	N-CA-C	-7.19	103.46	110.72
4	E	470	HIS	CB-CA-C	-7.18	99.82	110.95
2	B	21	PRO	CA-N-CD	-7.18	101.95	112.00
1	D	237	THR	N-CA-CB	7.18	120.75	110.13
3	C	287	LEU	O-C-N	7.17	131.40	123.22
1	A	299	HIS	O-C-N	7.17	130.36	122.11
1	A	161	GLU	CA-C-O	-7.17	110.10	119.06
4	E	156	ASN	CA-C-O	-7.15	111.61	119.98
4	E	439	TRP	CA-C-N	7.15	130.14	120.77
4	E	439	TRP	C-N-CA	7.15	130.14	120.77
1	A	119	THR	CA-C-O	-7.15	112.00	120.87
1	D	139	GLN	N-CA-C	7.15	126.03	110.80
3	C	426	THR	CB-CA-C	-7.15	99.38	110.81
1	A	394	ASN	N-CA-CB	7.14	121.86	109.72
1	D	10	ASN	CA-C-N	7.14	130.16	120.38
1	D	10	ASN	C-N-CA	7.14	130.16	120.38
2	B	153	THR	O-C-N	-7.14	113.09	122.59
2	B	224	THR	O-C-N	-7.14	112.95	122.23
4	E	274	GLU	O-C-N	7.14	130.32	122.11
2	B	233	ILE	CA-C-N	7.14	130.56	120.28
2	B	233	ILE	C-N-CA	7.14	130.56	120.28
1	D	55	ARG	NE-CZ-NH1	-7.14	114.36	121.50
1	D	168	SER	N-CA-CB	7.13	121.41	109.78
2	B	156	VAL	CB-CA-C	-7.13	99.60	111.29
2	B	460	HIS	CA-CB-CG	7.12	120.92	113.80
2	B	99	SER	CA-C-N	7.12	132.83	123.00
2	B	99	SER	C-N-CA	7.12	132.83	123.00
3	C	288	ILE	CA-C-O	-7.12	111.88	120.78
1	D	390	GLU	CA-C-O	-7.12	113.28	120.90
3	C	192	ILE	N-CA-C	7.11	117.47	107.37
2	B	194	ARG	NE-CZ-NH2	7.10	125.59	119.20
3	C	6	ARG	CA-C-O	-7.10	112.97	120.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	226	SER	CA-C-O	7.10	128.17	119.79
3	C	457	SER	CA-C-O	-7.10	112.36	120.24
2	B	61	THR	CA-C-O	7.10	128.82	120.66
2	B	38	THR	CA-C-O	-7.09	110.20	120.13
3	C	247	PHE	N-CA-C	7.09	120.05	111.82
3	C	423	ILE	CA-C-O	7.09	128.16	120.57
3	C	72	SER	O-C-N	-7.09	113.16	122.59
3	C	19	LYS	N-CA-CB	7.09	122.16	110.39
3	C	103	ASN	O-C-N	7.09	131.73	123.30
2	B	185	GLN	CA-C-O	-7.08	110.38	120.51
1	A	427	ALA	CA-C-N	7.08	135.29	121.41
1	A	427	ALA	C-N-CA	7.08	135.29	121.41
4	E	452	TRP	CG-CD2-CE3	7.08	140.98	133.90
1	A	86	TRP	CD2-CE3-CZ3	-7.08	109.40	118.60
3	C	269	VAL	CA-C-O	7.07	128.11	120.47
1	D	131	ILE	CA-C-N	7.07	132.38	120.64
1	D	131	ILE	C-N-CA	7.07	132.38	120.64
2	B	261	VAL	CA-C-N	7.07	130.62	120.79
2	B	261	VAL	C-N-CA	7.07	130.62	120.79
1	A	391	GLU	CB-CA-C	7.07	124.49	110.42
1	A	6	ARG	NE-CZ-NH2	7.07	125.56	119.20
2	B	256	LEU	CA-C-O	-7.07	112.93	120.42
3	C	150	ALA	CA-C-N	7.07	132.43	121.19
3	C	150	ALA	C-N-CA	7.07	132.43	121.19
4	E	451	PHE	CA-C-O	7.07	127.59	119.18
1	A	14	ASN	OD1-CG-ND2	7.07	129.67	122.60
1	D	184	TRP	CA-CB-CG	7.07	127.02	113.60
4	E	119	PRO	CA-C-N	-7.07	111.01	119.84
4	E	119	PRO	C-N-CA	-7.07	111.01	119.84
2	B	35	LEU	N-CA-CB	7.06	121.64	110.55
2	B	56	LEU	O-C-N	-7.06	113.08	122.19
1	D	86	TRP	CA-C-O	-7.06	113.67	121.58
1	D	428	GLY	CA-C-N	7.06	129.62	120.44
1	D	428	GLY	C-N-CA	7.06	129.62	120.44
4	E	465	ILE	N-CA-CB	7.06	119.30	110.47
1	A	408	HIS	O-C-N	-7.06	114.64	122.12
2	B	55	PHE	CA-C-O	-7.06	113.08	120.70
1	D	227	PHE	N-CA-C	-7.06	103.67	111.36
1	A	119	THR	N-CA-C	7.05	122.58	110.02
4	E	75	ASP	CA-CB-CG	7.04	119.64	112.60
4	E	133	TYR	CA-C-N	7.04	138.99	121.80
4	E	133	TYR	C-N-CA	7.04	138.99	121.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	14	ASN	O-C-N	-7.04	112.36	122.36
4	E	15	ASP	CA-C-N	7.04	134.99	121.54
4	E	15	ASP	C-N-CA	7.04	134.99	121.54
4	E	23	THR	CA-C-N	7.04	133.67	122.83
4	E	23	THR	C-N-CA	7.04	133.67	122.83
1	A	303	PRO	CA-N-CD	-7.03	102.15	112.00
2	B	453	SER	CA-C-N	7.03	130.40	120.42
2	B	453	SER	C-N-CA	7.03	130.40	120.42
4	E	257	VAL	CA-C-O	-7.03	112.00	120.78
1	D	410	LEU	N-CA-CB	7.02	120.66	110.20
4	E	138	TRP	CD2-CE3-CZ3	-7.01	109.48	118.60
1	D	134	HIS	N-CA-C	7.01	118.57	111.07
1	A	425	VAL	CA-C-O	-7.00	113.67	120.95
4	E	420	ASN	CA-C-O	-7.00	113.12	120.55
4	E	99	PHE	CA-C-N	-7.00	113.12	122.99
4	E	99	PHE	C-N-CA	-7.00	113.12	122.99
4	E	131	VAL	CA-CB-CG1	7.00	122.30	110.40
4	E	173	ASP	CA-CB-CG	-7.00	105.60	112.60
2	B	216	LYS	O-C-N	-6.99	115.00	121.36
1	D	379	VAL	N-CA-C	6.99	117.75	110.62
1	D	99	ASP	CA-CB-CG	6.99	119.59	112.60
1	D	237	THR	O-C-N	6.99	130.62	122.17
1	A	305	THR	OG1-CB-CG2	6.97	123.25	109.30
4	E	229	CYS	O-C-N	-6.97	112.75	122.37
1	D	272	PRO	N-CA-C	6.97	122.02	111.14
1	A	64	ARG	NE-CZ-NH2	6.97	125.47	119.20
2	B	119	HIS	CA-C-N	-6.97	111.13	119.84
2	B	119	HIS	C-N-CA	-6.97	111.13	119.84
1	D	289	ILE	CB-CA-C	-6.97	102.88	111.87
3	C	455	ARG	NE-CZ-NH1	6.97	128.47	121.50
1	A	98	GLY	O-C-N	-6.96	113.65	122.70
1	D	118	TRP	O-C-N	6.96	131.89	123.26
1	D	245	LEU	CA-C-O	-6.95	113.52	120.82
1	A	231	LEU	CA-C-O	-6.95	113.52	120.82
1	A	176	TRP	CA-CB-CG	6.95	126.80	113.60
1	A	301	ARG	N-CA-C	6.95	125.60	110.80
1	D	262	GLU	O-C-N	6.95	129.48	122.12
1	D	273	LEU	O-C-N	-6.94	115.22	123.27
1	A	420	ILE	CA-C-O	-6.93	112.11	120.78
3	C	104	VAL	O-C-N	6.93	131.24	122.57
4	E	62	TYR	CG-CD1-CE1	6.93	131.60	121.20
4	E	81	SER	CA-C-N	6.93	134.78	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	81	SER	C-N-CA	6.93	134.78	121.54
3	C	65	HIS	CB-CG-CD2	6.93	140.20	131.20
1	A	5	THR	O-C-N	-6.92	114.94	122.07
4	E	138	TRP	CA-C-N	6.92	130.64	120.95
4	E	138	TRP	C-N-CA	6.92	130.64	120.95
1	A	17	LYS	CA-C-N	6.92	130.29	120.53
1	A	17	LYS	C-N-CA	6.92	130.29	120.53
4	E	293	SER	O-C-N	-6.92	114.26	122.15
1	A	137	PHE	CA-C-O	6.92	127.86	119.49
1	D	406	ILE	N-CA-CB	-6.92	100.21	110.58
2	B	241	LEU	CA-C-N	6.90	127.49	120.38
2	B	241	LEU	C-N-CA	6.90	127.49	120.38
1	A	167	LEU	CA-C-O	-6.90	110.64	120.51
4	E	136	PHE	CB-CA-C	6.90	120.66	109.07
4	E	196	TRP	CD2-CE3-CZ3	-6.90	109.63	118.60
3	C	454	ASP	CA-C-O	-6.90	113.19	120.92
3	C	441	GLU	CA-C-N	6.90	129.52	120.28
3	C	441	GLU	C-N-CA	6.90	129.52	120.28
4	E	430	ASN	N-CA-CB	-6.90	99.95	110.16
4	E	70	GLU	CB-CG-CD	6.89	124.32	112.60
2	B	201	ASP	N-CA-C	6.89	120.42	109.40
1	D	58	GLN	CA-C-O	-6.89	113.10	121.36
3	C	133	ASN	CA-CB-CG	6.88	119.48	112.60
1	A	416	LEU	CA-C-O	6.88	127.84	120.55
1	D	284	PHE	CB-CA-C	-6.88	97.90	110.63
2	B	195	LYS	CA-C-O	-6.88	112.90	120.81
4	E	73	GLY	CA-C-N	6.88	134.35	121.97
4	E	73	GLY	C-N-CA	6.88	134.35	121.97
3	C	140	ASP	CA-CB-CG	6.88	119.47	112.60
3	C	447	ASN	O-C-N	-6.88	113.81	122.27
2	B	443	PHE	CA-CB-CG	6.87	120.67	113.80
3	C	46	LYS	N-CA-C	-6.87	97.15	108.76
3	C	109	ASN	O-C-N	6.86	131.46	122.95
1	A	30	ASP	CB-CA-C	-6.86	99.32	110.77
1	A	257	LEU	CA-C-N	6.85	132.08	121.19
1	A	257	LEU	C-N-CA	6.85	132.08	121.19
2	B	13	GLU	N-CA-C	-6.85	104.56	113.12
2	B	215	ARG	NH1-CZ-NH2	-6.85	110.40	119.30
1	D	222	CYS	CB-CA-C	6.85	122.16	110.86
4	E	152	ALA	CA-C-N	6.84	134.73	121.18
4	E	152	ALA	C-N-CA	6.84	134.73	121.18
3	C	239	ILE	CA-C-O	-6.84	112.23	120.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	448	LYS	N-CA-CB	-6.84	99.33	110.14
3	C	114	PRO	CA-CB-CG	-6.84	91.51	104.50
2	B	441	TYR	CG-CD2-CE2	-6.84	110.94	121.20
3	C	422	GLY	CA-C-O	6.84	127.52	119.45
1	D	105	MET	O-C-N	-6.84	111.02	122.03
3	C	285	VAL	CA-C-O	-6.83	110.79	119.95
1	D	211	PRO	O-C-N	6.83	131.87	122.64
4	E	313	THR	N-CA-CB	6.83	122.45	110.42
1	A	218	VAL	O-C-N	-6.83	114.90	121.94
1	A	213	TYR	CA-C-O	6.83	127.73	120.70
4	E	177	PHE	N-CA-C	-6.83	100.33	110.23
1	D	277	TYR	N-CA-C	6.83	125.34	110.80
2	B	468	PHE	N-CA-CB	6.83	122.02	110.49
3	C	190	TRP	O-C-N	6.83	131.03	122.43
4	E	259	LEU	CA-C-O	6.83	127.99	120.82
4	E	228	PRO	CB-CA-C	-6.82	101.67	113.20
4	E	474	VAL	N-CA-CB	6.82	120.76	111.21
1	A	175	GLU	O-C-N	-6.82	113.52	122.59
1	D	280	PHE	CG-CD1-CE1	6.82	132.29	120.70
2	B	89	ASP	O-C-N	-6.81	113.53	122.59
2	B	444	ILE	CA-C-N	6.81	129.64	120.65
2	B	444	ILE	C-N-CA	6.81	129.64	120.65
1	D	102	ILE	CA-CB-CG1	6.81	121.97	110.40
4	E	148	GLN	O-C-N	-6.81	113.54	122.59
1	A	424	SER	CA-C-O	6.80	127.76	120.55
1	A	188	VAL	N-CA-CB	6.80	122.45	111.23
2	B	312	HIS	CA-CB-CG	6.80	120.60	113.80
2	B	455	PHE	CZ-CE2-CD2	6.79	132.22	120.00
1	A	80	LEU	CA-C-N	-6.79	113.69	120.21
1	A	80	LEU	C-N-CA	-6.79	113.69	120.21
2	B	190	HIS	CG-CD2-NE2	-6.79	100.41	107.20
1	A	256	PHE	CA-C-O	-6.79	113.61	121.07
2	B	213	ILE	CB-CA-C	-6.79	101.92	111.28
4	E	297	VAL	CB-CA-C	-6.79	100.16	111.29
3	C	464	VAL	N-CA-CB	6.78	119.76	110.54
3	C	446	TRP	O-C-N	6.78	129.91	122.11
3	C	32	ASN	OD1-CG-ND2	-6.78	115.82	122.60
1	A	185	LYS	N-CA-C	6.78	119.27	110.53
1	A	424	SER	N-CA-C	6.78	118.67	111.28
2	B	16	ASN	CB-CA-C	6.78	119.15	110.34
4	E	93	ASN	CA-C-N	-6.78	111.27	122.79
4	E	93	ASN	C-N-CA	-6.78	111.27	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	136	PHE	CA-CB-CG	6.78	120.58	113.80
2	B	270	VAL	CA-CB-CG2	6.77	121.91	110.40
1	D	130	ILE	CB-CG1-CD1	6.77	128.02	113.80
4	E	244	ALA	N-CA-C	6.77	118.31	111.07
4	E	151	ASN	N-CA-C	6.77	119.44	108.41
2	B	300	VAL	N-CA-CB	6.77	118.47	110.55
3	C	22	ARG	NH1-CZ-NH2	-6.77	110.50	119.30
3	C	132	ILE	CA-CB-CG2	6.76	122.00	110.50
1	A	27	HIS	CG-CD2-NE2	6.76	113.96	107.20
2	B	445	THR	CB-CA-C	-6.76	100.55	110.96
3	C	28	ASN	CA-CB-CG	6.76	119.36	112.60
3	C	426	THR	N-CA-C	6.76	119.22	111.11
1	A	240	GLY	O-C-N	-6.76	113.92	122.70
3	C	90	PRO	CA-C-N	-6.76	113.98	123.03
3	C	90	PRO	C-N-CA	-6.76	113.98	123.03
1	D	5	THR	O-C-N	-6.76	114.45	122.15
1	D	408	HIS	CE1-NE2-CD2	6.76	115.76	109.00
1	D	248	SER	N-CA-CB	6.75	121.91	110.49
3	C	75	SER	N-CA-C	6.75	119.25	111.02
2	B	256	LEU	N-CA-C	6.75	118.71	111.36
3	C	316	THR	N-CA-CB	6.75	120.68	110.02
1	D	134	HIS	CB-CG-CD2	-6.74	122.44	131.20
4	E	299	ASN	CA-CB-CG	6.74	119.34	112.60
2	B	180	PHE	N-CA-C	-6.74	100.46	110.23
3	C	300	THR	CA-C-O	-6.74	110.87	120.51
4	E	450	CYS	CA-C-N	-6.74	109.53	122.06
4	E	450	CYS	C-N-CA	-6.74	109.53	122.06
1	A	233	PHE	CA-C-N	6.74	129.20	120.44
1	A	233	PHE	C-N-CA	6.74	129.20	120.44
1	D	385	HIS	CA-C-N	6.74	129.61	120.38
1	D	385	HIS	C-N-CA	6.74	129.61	120.38
4	E	470	HIS	N-CA-CB	6.73	119.75	109.98
1	D	102	ILE	CB-CG1-CD1	6.73	127.94	113.80
3	C	438	ALA	N-CA-C	-6.73	104.89	113.23
3	C	137	PHE	CA-CB-CG	-6.72	107.08	113.80
1	A	197	PRO	O-C-N	-6.72	114.94	123.14
2	B	218	LEU	N-CA-CB	6.72	121.68	110.53
1	A	12	LEU	CB-CA-C	-6.71	100.34	110.88
2	B	35	LEU	CD1-CG-CD2	6.71	125.57	110.80
1	D	257	LEU	O-C-N	-6.71	113.33	122.33
1	A	248	SER	CB-CA-C	6.71	123.77	110.42
1	D	301	ARG	N-CA-C	6.71	125.08	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	70	ALA	N-CA-C	6.70	121.68	112.90
1	A	64	ARG	CD-NE-CZ	6.70	133.78	124.40
2	B	64	ARG	CB-CG-CD	6.70	126.70	111.30
1	D	27	HIS	N-CA-C	6.70	125.06	110.80
1	A	259	VAL	N-CA-CB	6.69	119.64	110.54
1	D	22	VAL	O-C-N	6.69	130.98	122.61
1	D	118	TRP	CB-CA-C	6.69	119.71	110.34
3	C	225	PRO	CA-C-O	-6.69	113.59	121.95
1	D	11	LEU	O-C-N	-6.69	115.03	122.12
1	A	23	GLU	O-C-N	6.69	131.51	122.82
1	D	394	ASN	CA-C-O	-6.68	113.47	120.55
3	C	427	ASN	OD1-CG-ND2	6.67	129.28	122.60
1	D	143	THR	CA-C-N	-6.67	113.38	122.86
1	D	143	THR	C-N-CA	-6.67	113.38	122.86
4	E	110	TYR	N-CA-CB	6.67	121.77	110.49
4	E	296	ILE	CB-CA-C	-6.67	103.13	112.14
3	C	31	VAL	N-CA-CB	-6.67	103.41	111.21
1	D	88	PRO	CA-C-O	-6.66	114.10	121.23
2	B	17	PRO	O-C-N	6.65	129.37	122.18
1	D	205	PHE	CA-CB-CG	6.65	120.45	113.80
3	C	37	LEU	N-CA-C	6.64	119.35	108.52
1	D	209	ARG	NH1-CZ-NH2	-6.64	110.66	119.30
1	D	385	HIS	CG-CD2-NE2	6.64	113.84	107.20
1	A	395	ALA	N-CA-C	6.64	119.34	111.71
3	C	156	ASN	CB-CA-C	6.63	122.05	110.64
3	C	297	SER	O-C-N	6.63	131.31	122.43
1	D	41	ILE	N-CA-CB	6.63	118.31	110.55
1	A	68	ASN	CA-C-N	6.63	128.12	119.84
1	A	68	ASN	C-N-CA	6.63	128.12	119.84
4	E	86	LEU	CA-C-O	6.63	125.75	119.72
2	B	457	ASP	CA-CB-CG	6.62	119.22	112.60
1	A	169	THR	CA-CB-OG1	-6.62	99.68	109.60
2	B	62	ASP	O-C-N	-6.62	114.79	123.13
1	D	106	THR	CA-CB-CG2	6.62	121.75	110.50
3	C	31	VAL	CA-C-O	-6.61	113.39	120.59
1	A	375	ALA	CA-C-N	6.61	129.80	120.42
1	A	375	ALA	C-N-CA	6.61	129.80	120.42
2	B	182	GLU	CA-C-N	6.61	129.42	120.44
2	B	182	GLU	C-N-CA	6.61	129.42	120.44
3	C	196	PRO	CA-C-O	-6.61	113.62	122.08
1	D	393	SER	O-C-N	-6.61	115.16	122.03
3	C	247	PHE	CD1-CG-CD2	6.60	128.50	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	25	HIS	O-C-N	6.60	131.37	122.59
3	C	304	VAL	N-CA-C	-6.60	103.43	110.36
2	B	263	LEU	CD1-CG-CD2	6.60	125.31	110.80
3	C	69	TRP	CE2-CD2-CE3	-6.60	112.20	118.80
4	E	93	ASN	N-CA-C	6.60	120.54	112.23
2	B	149	TYR	CA-C-N	6.60	134.14	121.54
2	B	149	TYR	C-N-CA	6.60	134.14	121.54
2	B	176	ASN	O-C-N	-6.60	114.40	122.25
3	C	7	LEU	N-CA-C	6.59	118.55	111.36
4	E	98	GLN	CG-CD-OE1	6.59	133.99	120.80
2	B	16	ASN	CA-C-N	6.59	126.10	119.24
2	B	16	ASN	C-N-CA	6.59	126.10	119.24
1	A	272	PRO	N-CA-C	6.59	120.84	110.50
1	D	156	VAL	CA-C-O	-6.59	113.51	120.76
1	D	225	PHE	CA-C-O	6.59	127.54	119.11
4	E	439	TRP	CE2-CD2-CG	-6.59	99.30	107.20
1	D	151	TYR	CB-CG-CD1	6.59	130.68	120.80
1	A	168	SER	O-C-N	-6.58	114.64	122.15
3	C	252	GLU	O-C-N	-6.58	113.83	122.59
4	E	13	ASP	CA-CB-CG	6.58	119.18	112.60
4	E	438	ASN	OD1-CG-ND2	6.58	129.18	122.60
1	A	200	ASP	N-CA-C	6.58	120.00	108.75
2	B	206	ASP	N-CA-C	6.58	124.81	110.80
2	B	289	ILE	CA-C-N	6.58	129.75	120.28
2	B	289	ILE	C-N-CA	6.58	129.75	120.28
1	A	38	ILE	O-C-N	6.58	128.25	121.87
2	B	140	GLN	CA-C-O	-6.57	111.11	120.51
4	E	96	ASP	N-CA-C	-6.57	106.21	114.56
1	A	15	TYR	CG-CD2-CE2	-6.57	111.34	121.20
1	A	374	SER	O-C-N	-6.57	112.48	123.00
4	E	267	LEU	N-CA-C	-6.57	104.36	112.38
3	C	73	GLU	CB-CG-CD	6.57	123.77	112.60
3	C	37	LEU	N-CA-CB	6.56	120.86	110.55
2	B	141	ASN	OD1-CG-ND2	-6.56	116.04	122.60
1	D	196	THR	CA-C-O	-6.56	111.17	120.16
1	D	415	MET	N-CA-C	-6.56	103.62	111.69
4	E	98	GLN	CA-C-O	-6.56	111.13	120.51
3	C	191	GLU	O-C-N	6.56	131.67	123.28
3	C	95	GLN	CA-CB-CG	6.55	127.21	114.10
3	C	102	TYR	O-C-N	-6.55	115.77	123.11
4	E	26	HIS	CA-CB-CG	-6.55	107.25	113.80
3	C	425	SER	N-CA-CB	6.55	119.50	110.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	413	GLU	CA-C-N	6.55	129.34	120.44
2	B	413	GLU	C-N-CA	6.55	129.34	120.44
3	C	15	ASN	CA-CB-CG	6.54	119.14	112.60
1	D	20	ARG	N-CA-C	-6.54	101.83	110.40
2	B	112	HIS	CA-CB-CG	-6.54	107.26	113.80
3	C	93	VAL	CA-C-O	-6.54	113.52	120.39
3	C	69	TRP	CD2-CE2-CZ2	6.54	128.94	122.40
1	D	73	GLY	CA-C-N	6.53	134.21	121.41
1	D	73	GLY	C-N-CA	6.53	134.21	121.41
4	E	422	ILE	O-C-N	-6.53	115.10	121.83
2	B	88	PRO	CA-C-N	6.53	134.01	121.54
2	B	88	PRO	C-N-CA	6.53	134.01	121.54
2	B	306	HIS	N-CA-CB	6.53	121.53	110.49
3	C	303	VAL	CA-C-N	6.53	129.02	120.60
3	C	303	VAL	C-N-CA	6.53	129.02	120.60
1	D	45	GLU	O-C-N	-6.53	113.90	122.59
2	B	238	VAL	CA-C-O	-6.53	110.98	119.53
2	B	452	PHE	CA-CB-CG	-6.53	107.28	113.80
2	B	420	GLU	N-CA-CB	6.52	119.92	110.20
3	C	249	LEU	O-C-N	6.52	128.82	121.32
1	D	150	THR	N-CA-C	6.52	120.24	112.93
4	E	34	LEU	O-C-N	6.52	131.32	123.36
2	B	20	ARG	NE-CZ-NH1	-6.52	114.98	121.50
2	B	183	ASN	O-C-N	-6.52	115.05	122.09
2	B	274	SER	CA-C-O	-6.52	111.60	119.49
3	C	316	THR	CA-CB-OG1	6.52	119.37	109.60
4	E	200	LYS	N-CA-C	6.52	124.68	110.80
1	D	27	HIS	CE1-NE2-CD2	-6.51	102.48	109.00
3	C	421	SER	CA-C-O	-6.51	109.73	120.80
1	A	149	TRP	O-C-N	-6.51	113.93	122.59
1	A	190	TYR	CA-C-O	-6.51	113.68	121.56
1	D	138	ASP	CA-C-O	-6.51	111.94	119.56
1	D	284	PHE	CB-CG-CD1	6.51	131.77	120.70
2	B	461	ASN	CA-C-O	-6.51	111.99	119.60
2	B	220	TYR	CZ-CE2-CD2	6.50	131.31	119.60
1	D	86	TRP	NE1-CE2-CZ2	6.50	139.86	130.10
1	A	39	GLN	OE1-CD-NE2	6.50	129.10	122.60
2	B	468	PHE	CG-CD1-CE1	6.50	131.76	120.70
4	E	105	ALA	CA-C-O	-6.50	113.34	120.30
4	E	112	ASP	CA-CB-CG	-6.50	106.10	112.60
1	A	393	SER	O-C-N	6.50	128.85	122.09
3	C	291	TYR	CA-C-N	6.50	131.09	120.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	291	TYR	C-N-CA	6.50	131.09	120.63
2	B	427	ASP	N-CA-CB	6.50	119.67	110.12
1	D	248	SER	O-C-N	6.49	131.23	122.59
1	A	192	CYS	CA-C-N	6.49	133.97	122.48
1	A	192	CYS	C-N-CA	6.49	133.97	122.48
1	D	277	TYR	CD1-CG-CD2	6.49	127.83	118.10
2	B	460	HIS	ND1-CE1-NE2	6.49	114.89	108.40
3	C	114	PRO	CB-CA-C	-6.49	100.86	111.56
3	C	31	VAL	CB-CA-C	-6.48	102.10	110.98
1	A	260	ILE	CA-C-N	6.48	130.71	120.47
1	A	260	ILE	C-N-CA	6.48	130.71	120.47
1	A	229	THR	N-CA-C	-6.48	103.33	111.11
3	C	447	ASN	CB-CG-OD1	6.48	133.76	120.80
4	E	215	GLN	N-CA-C	6.48	118.92	110.43
3	C	5	GLU	CA-C-N	6.48	130.54	120.82
3	C	5	GLU	C-N-CA	6.48	130.54	120.82
1	D	79	ARG	NE-CZ-NH1	-6.48	115.02	121.50
3	C	96	ASN	CA-C-O	-6.48	111.61	119.32
1	D	53	ASN	CA-CB-CG	-6.47	106.13	112.60
2	B	428	TRP	CB-CA-C	6.47	121.53	110.79
1	D	198	TYR	N-CA-CB	-6.47	101.52	110.38
1	A	256	PHE	N-CA-CB	6.47	119.65	109.82
1	D	187	TRP	CA-C-O	-6.47	113.85	120.71
2	B	71	ALA	CA-C-N	6.47	133.65	121.81
2	B	71	ALA	C-N-CA	6.47	133.65	121.81
2	B	257	LEU	CA-C-O	6.46	128.16	120.92
3	C	63	TYR	CA-CB-CG	6.46	125.53	113.90
4	E	87	PRO	N-CA-CB	-6.46	98.00	103.36
2	B	307	ARG	CD-NE-CZ	-6.46	115.36	124.40
2	B	192	PRO	N-CD-CG	-6.45	93.52	103.20
2	B	424	LEU	O-C-N	6.45	130.98	122.33
3	C	313	HIS	CB-CG-CD2	6.45	139.59	131.20
1	A	7	LEU	CA-C-N	6.45	128.92	120.60
1	A	7	LEU	C-N-CA	6.45	128.92	120.60
2	B	200	ASP	CA-C-N	6.45	135.47	122.70
2	B	200	ASP	C-N-CA	6.45	135.47	122.70
2	B	145	VAL	N-CA-C	6.45	116.91	107.37
2	B	459	SER	N-CA-C	6.45	119.13	111.33
1	A	209	ARG	NH1-CZ-NH2	-6.45	110.92	119.30
1	A	301	ARG	CA-C-O	-6.45	111.29	120.51
2	B	150	THR	CA-C-N	6.45	131.00	122.30
2	B	150	THR	C-N-CA	6.45	131.00	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	68	ASN	CA-CB-CG	6.45	119.05	112.60
1	D	250	LEU	O-C-N	-6.44	114.38	122.17
4	E	247	GLY	CA-C-O	6.44	129.44	122.03
4	E	420	ASN	OD1-CG-ND2	-6.44	116.16	122.60
2	B	291	VAL	CA-C-O	-6.43	113.72	121.18
2	B	454	ILE	O-C-N	-6.43	115.20	121.83
4	E	459	SER	O-C-N	-6.43	115.44	122.07
1	A	86	TRP	CG-CD2-CE3	-6.43	127.47	133.90
2	B	9	SER	O-C-N	-6.43	113.87	122.23
2	B	156	VAL	O-C-N	-6.43	114.53	122.57
3	C	320	HIS	CB-CG-ND1	6.43	132.35	122.70
4	E	421	PHE	CA-CB-CG	6.43	120.23	113.80
1	D	432	GLU	CA-C-O	-6.43	111.53	119.18
1	A	268	SER	O-C-N	-6.43	115.20	122.08
3	C	231	ASN	CA-CB-CG	6.42	119.02	112.60
4	E	148	GLN	N-CA-CB	6.42	121.34	110.49
1	A	219	ILE	N-CA-C	6.42	121.13	111.89
1	A	400	LYS	N-CA-CB	6.42	119.63	110.13
3	C	270	PHE	CA-C-O	-6.42	113.62	120.42
1	A	398	GLU	CA-C-N	6.42	130.96	120.63
1	A	398	GLU	C-N-CA	6.42	130.96	120.63
3	C	262	CYS	CA-C-O	-6.41	113.74	120.92
3	C	455	ARG	N-CA-CB	6.41	121.33	110.49
1	D	271	VAL	CA-C-N	6.41	126.36	119.76
1	D	271	VAL	C-N-CA	6.41	126.36	119.76
3	C	26	HIS	CG-CD2-NE2	-6.41	100.79	107.20
4	E	66	TRP	CA-CB-CG	6.41	125.78	113.60
2	B	197	TRP	CA-C-O	-6.41	113.63	121.89
1	A	122	ALA	CA-C-N	6.40	133.50	121.97
1	A	122	ALA	C-N-CA	6.40	133.50	121.97
1	A	104	HIS	CA-CB-CG	-6.40	107.40	113.80
1	A	257	LEU	CB-CA-C	-6.40	99.81	110.68
1	D	297	ASN	OD1-CG-ND2	6.40	129.00	122.60
4	E	137	ASP	O-C-N	-6.40	115.78	123.13
1	A	284	PHE	N-CA-C	6.39	117.91	111.07
2	B	178	ASP	CA-CB-CG	6.39	119.00	112.60
2	B	290	LEU	CA-C-O	-6.39	112.88	120.10
1	D	300	HIS	ND1-CG-CD2	6.39	112.50	106.10
1	D	403	ALA	CA-C-N	6.39	135.61	121.80
1	D	403	ALA	C-N-CA	6.39	135.61	121.80
3	C	81	ARG	N-CA-C	6.39	120.05	110.14
1	A	219	ILE	CA-C-O	-6.39	112.30	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	135	PHE	CA-C-O	-6.39	111.41	120.16
3	C	79	ILE	N-CA-CB	6.39	121.77	111.23
3	C	483	ALA	CA-C-N	6.39	133.20	121.70
3	C	483	ALA	C-N-CA	6.39	133.20	121.70
1	D	140	GLN	O-C-N	-6.38	116.33	123.48
1	A	229	THR	CB-CA-C	6.38	121.02	110.81
1	A	383	ALA	O-C-N	-6.38	114.45	122.17
3	C	442	GLU	N-CA-C	6.38	118.24	111.28
1	A	179	LYS	N-CA-C	-6.38	105.39	113.43
2	B	185	GLN	CG-CD-NE2	6.38	125.97	116.40
3	C	439	TYR	CA-C-O	-6.38	113.16	120.24
3	C	225	PRO	CA-N-CD	-6.38	103.07	112.00
1	A	382	ILE	CA-C-O	-6.37	113.59	120.47
2	B	409	LYS	CA-C-N	6.37	133.71	121.54
2	B	409	LYS	C-N-CA	6.37	133.71	121.54
1	A	272	PRO	N-CA-CB	6.37	108.39	103.30
4	E	21	ALA	O-C-N	6.37	131.53	123.12
4	E	242	LEU	CA-C-O	-6.37	111.44	120.16
2	B	234	LEU	N-CA-C	-6.37	104.39	111.71
1	D	13	GLU	O-C-N	6.37	128.65	122.03
1	D	137	PHE	CA-CB-CG	6.36	120.16	113.80
2	B	263	LEU	O-C-N	6.36	131.24	122.46
1	D	176	TRP	CA-CB-CG	6.36	125.68	113.60
1	D	389	ASP	CA-C-O	6.36	127.45	120.90
3	C	24	VAL	N-CA-C	-6.35	106.14	112.17
3	C	462	THR	CA-CB-CG2	6.35	121.30	110.50
4	E	425	SER	CA-C-O	-6.35	113.69	120.42
1	A	2	GLU	N-CA-CB	6.35	121.22	110.49
2	B	67	TRP	CD2-CE2-CZ2	-6.34	116.06	122.40
1	D	155	LYS	CA-C-O	6.34	129.01	120.13
1	D	120	PRO	CB-CA-C	-6.34	103.18	110.92
3	C	109	ASN	CA-CB-CG	-6.34	106.26	112.60
1	A	197	PRO	N-CA-C	6.34	121.20	111.57
1	A	377	GLU	N-CA-C	6.34	119.00	111.33
2	B	178	ASP	O-C-N	-6.34	115.30	122.08
4	E	154	GLU	CB-CG-CD	-6.34	101.82	112.60
4	E	11	LEU	CA-C-O	6.34	127.29	119.05
4	E	309	ARG	NE-CZ-NH2	6.34	124.90	119.20
3	C	429	ILE	N-CA-CB	-6.33	103.49	110.51
1	A	59	GLN	CA-C-O	-6.33	113.96	121.11
2	B	160	HIS	CA-CB-CG	6.33	120.12	113.80
3	C	214	ASP	N-CA-C	6.33	118.69	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	199	LEU	CA-C-O	-6.32	113.82	121.28
4	E	272	VAL	N-CA-C	6.32	122.54	108.88
4	E	425	SER	N-CA-C	6.32	118.25	111.36
3	C	104	VAL	CA-C-N	6.32	132.69	122.14
3	C	104	VAL	C-N-CA	6.32	132.69	122.14
1	A	147	GLY	CA-C-O	-6.31	115.43	121.87
1	A	151	TYR	CA-CB-CG	6.31	125.26	113.90
1	D	189	TYR	O-C-N	-6.31	115.56	123.01
1	D	162	SER	O-C-N	6.31	130.99	122.59
4	E	303	VAL	N-CA-C	-6.31	104.36	110.42
2	B	460	HIS	CA-C-O	6.31	127.23	120.10
3	C	444	GLY	O-C-N	-6.31	116.13	122.18
1	D	14	ASN	O-C-N	6.31	130.93	122.61
2	B	458	ALA	N-CA-C	-6.30	104.10	110.97
1	A	211	PRO	CB-CA-C	6.30	119.09	111.46
4	E	99	PHE	O-C-N	6.30	130.30	122.86
4	E	131	VAL	O-C-N	-6.30	114.69	122.57
1	A	429	ARG	NH1-CZ-NH2	6.30	127.49	119.30
3	C	49	ASP	O-C-N	-6.30	114.78	122.34
1	A	102	ILE	CA-C-O	-6.30	112.91	120.78
1	A	412	CYS	O-C-N	6.30	128.82	122.08
2	B	278	PRO	CB-CA-C	-6.30	100.32	110.21
2	B	77	ASP	CA-CB-CG	6.29	118.89	112.60
3	C	212	TYR	CA-C-O	6.29	129.51	120.51
3	C	290	LYS	CA-C-O	6.29	127.99	121.07
1	A	79	ARG	N-CA-C	6.29	119.12	107.99
3	C	128	SER	CA-C-N	6.29	131.42	122.24
3	C	128	SER	C-N-CA	6.29	131.42	122.24
4	E	230	VAL	N-CA-CB	6.28	118.18	110.64
2	B	277	VAL	CB-CA-C	6.28	122.79	111.36
2	B	156	VAL	CA-CB-CG1	-6.28	99.73	110.40
3	C	234	THR	CA-C-N	6.28	127.68	119.84
3	C	234	THR	C-N-CA	6.28	127.68	119.84
4	E	21	ALA	CA-C-O	-6.28	113.81	120.40
1	D	137	PHE	CG-CD1-CE1	6.27	131.37	120.70
1	D	176	TRP	CB-CG-CD2	-6.27	118.02	126.80
4	E	193	ASN	N-CA-C	6.27	117.39	108.74
2	B	69	PRO	O-C-N	-6.27	115.41	122.18
1	D	237	THR	CA-CB-OG1	6.27	119.00	109.60
1	A	402	VAL	CA-C-N	6.26	133.00	122.79
1	A	402	VAL	C-N-CA	6.26	133.00	122.79
1	D	83	ASP	N-CA-C	6.26	124.14	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	201	ILE	CA-C-O	-6.26	114.64	121.28
1	A	281	THR	O-C-N	-6.26	114.89	122.22
3	C	28	ASN	O-C-N	-6.26	114.26	122.59
3	C	55	ASN	OD1-CG-ND2	6.26	128.86	122.60
4	E	117	TRP	O-C-N	-6.26	115.74	123.44
4	E	177	PHE	CD1-CG-CD2	-6.26	109.21	118.60
3	C	93	VAL	O-C-N	6.26	130.02	123.26
1	D	160	PRO	CA-C-O	-6.26	113.89	122.15
4	E	154	GLU	O-C-N	-6.26	114.46	121.84
1	A	147	GLY	CA-C-N	6.25	133.23	121.97
1	A	147	GLY	C-N-CA	6.25	133.23	121.97
3	C	84	PRO	N-CA-C	6.25	125.36	112.47
4	E	161	ALA	N-CA-CB	6.25	121.06	110.49
2	B	18	LYS	N-CA-C	6.25	120.51	113.01
3	C	157	GLU	CA-C-N	6.25	132.33	122.33
3	C	157	GLU	C-N-CA	6.25	132.33	122.33
1	D	6	ARG	NH1-CZ-NH2	-6.25	111.17	119.30
3	C	244	ALA	CA-C-O	-6.25	113.80	120.42
1	D	278	MET	CA-C-N	6.25	129.50	120.38
1	D	278	MET	C-N-CA	6.25	129.50	120.38
4	E	80	PRO	CA-C-N	6.25	128.56	120.44
4	E	80	PRO	C-N-CA	6.25	128.56	120.44
4	E	221	TYR	CA-C-O	-6.25	112.38	120.00
2	B	12	PHE	CD1-CG-CD2	-6.25	109.23	118.60
3	C	422	GLY	N-CA-C	6.24	122.40	114.66
1	A	195	ASP	N-CA-C	6.24	118.77	110.53
3	C	1	VAL	CA-C-N	6.24	133.46	121.54
3	C	1	VAL	C-N-CA	6.24	133.46	121.54
2	B	424	LEU	CA-C-O	-6.24	112.43	119.79
3	C	74	TYR	CA-C-N	6.24	129.46	120.79
3	C	74	TYR	C-N-CA	6.24	129.46	120.79
4	E	288	PHE	N-CA-C	-6.24	104.56	111.36
4	E	444	LYS	N-CA-C	-6.24	104.02	111.69
2	B	95	ASN	N-CA-CB	6.23	121.02	110.49
2	B	139	TRP	CH2-CZ2-CE2	6.23	125.60	117.50
4	E	94	ASN	N-CA-C	6.23	121.22	112.93
4	E	462	THR	CA-CB-CG2	6.23	121.09	110.50
4	E	157	LEU	CA-C-O	-6.23	113.93	121.28
2	B	407	ALA	CA-C-N	6.23	128.53	120.56
2	B	407	ALA	C-N-CA	6.23	128.53	120.56
1	D	377	GLU	OE1-CD-OE2	6.23	137.84	122.90
3	C	318	SER	O-C-N	-6.22	114.04	122.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	148	GLN	CA-C-O	6.22	129.41	120.51
4	E	220	PHE	CB-CA-C	6.22	119.11	109.03
3	C	245	LEU	CA-C-N	6.22	130.15	120.82
3	C	245	LEU	C-N-CA	6.22	130.15	120.82
4	E	224	ASN	CA-C-O	6.22	127.13	120.10
1	A	133	THR	O-C-N	-6.22	114.88	122.34
4	E	176	ASP	CA-CB-CG	-6.22	106.38	112.60
1	D	379	VAL	CA-C-O	6.21	127.41	120.95
4	E	10	LEU	CA-C-O	-6.21	111.74	119.38
1	D	194	PRO	CA-C-N	6.21	134.55	122.07
1	D	194	PRO	C-N-CA	6.21	134.55	122.07
4	E	85	TRP	CE3-CZ3-CH2	-6.21	113.03	121.10
4	E	116	TYR	N-CA-CB	-6.21	100.02	111.13
3	C	467	LEU	O-C-N	-6.21	115.33	122.03
4	E	43	ASN	N-CA-CB	6.21	120.95	110.46
4	E	183	TRP	O-C-N	-6.20	115.38	122.20
1	A	412	CYS	N-CA-CB	6.20	119.25	109.82
1	D	100	PHE	CA-CB-CG	6.20	120.00	113.80
3	C	28	ASN	CB-CG-ND2	6.20	125.70	116.40
3	C	12	LEU	O-C-N	-6.20	114.35	122.59
1	A	165	PRO	CB-CA-C	-6.20	101.86	111.40
3	C	84	PRO	O-C-N	-6.20	114.28	122.64
3	C	142	GLN	CG-CD-NE2	6.19	125.69	116.40
3	C	20	HIS	CG-CD2-NE2	6.19	113.39	107.20
1	A	299	HIS	CA-C-O	-6.19	113.99	120.92
3	C	35	LEU	O-C-N	-6.19	115.35	123.21
4	E	261	GLN	CB-CG-CD	6.18	123.11	112.60
3	C	459	PHE	O-C-N	6.18	132.36	122.42
1	D	418	CYS	N-CA-C	-6.18	104.55	111.28
3	C	67	LEU	O-C-N	-6.17	113.64	122.41
4	E	71	TYR	CZ-CE2-CD2	6.17	130.71	119.60
1	D	394	ASN	N-CA-C	-6.17	104.56	111.28
4	E	13	ASP	N-CA-C	6.17	123.94	110.80
2	B	63	TYR	CA-C-O	6.17	127.20	119.12
2	B	196	ASN	CB-CG-OD1	6.16	133.13	120.80
1	D	306	HIS	ND1-CE1-NE2	-6.16	102.24	108.40
3	C	48	THR	CA-C-N	-6.16	112.79	122.65
3	C	48	THR	C-N-CA	-6.16	112.79	122.65
3	C	187	ASN	CA-C-N	6.16	126.96	120.43
3	C	187	ASN	C-N-CA	6.16	126.96	120.43
1	D	230	VAL	CA-C-O	6.16	127.38	120.85
1	D	65	LEU	O-C-N	-6.16	114.64	122.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	95	VAL	CA-C-N	6.16	131.50	122.08
4	E	95	VAL	C-N-CA	6.16	131.50	122.08
2	B	97	ASP	CA-C-O	-6.15	111.71	120.51
3	C	191	GLU	CA-C-O	-6.15	112.69	120.20
1	D	24	HIS	CB-CA-C	6.15	122.66	110.42
2	B	213	ILE	CA-C-N	6.15	131.44	122.77
2	B	213	ILE	C-N-CA	6.15	131.44	122.77
3	C	281	THR	O-C-N	6.15	130.38	122.39
1	D	115	LYS	CA-C-O	-6.15	115.10	120.88
4	E	4	GLY	O-C-N	-6.15	116.29	122.19
2	B	112	HIS	N-CA-C	6.14	117.67	110.97
4	E	105	ALA	CA-C-N	6.14	129.56	120.90
4	E	105	ALA	C-N-CA	6.14	129.56	120.90
4	E	107	VAL	O-C-N	6.14	129.15	122.76
1	A	101	ALA	N-CA-CB	6.14	120.50	110.37
1	A	188	VAL	CA-C-O	6.14	128.45	120.78
1	D	435	GLN	CA-C-O	-6.14	111.73	120.51
1	A	209	ARG	CA-C-N	6.13	133.48	122.13
1	A	209	ARG	C-N-CA	6.13	133.48	122.13
4	E	303	VAL	CA-C-N	-6.13	112.06	120.28
4	E	303	VAL	C-N-CA	-6.13	112.06	120.28
4	E	457	LEU	CA-C-O	6.13	127.02	120.70
4	E	16	LYS	N-CA-C	6.13	123.86	110.80
4	E	239	VAL	N-CA-CB	6.13	121.34	111.23
2	B	293	PHE	N-CA-C	6.13	117.65	110.97
1	D	152	ASP	N-CA-CB	-6.12	101.14	110.45
1	A	299	HIS	CE1-NE2-CD2	-6.12	102.88	109.00
2	B	427	ASP	CA-C-N	6.12	128.49	120.28
2	B	427	ASP	C-N-CA	6.12	128.49	120.28
1	D	160	PRO	CA-N-CD	-6.12	103.43	112.00
3	C	25	LYS	O-C-N	6.12	132.42	122.20
3	C	303	VAL	N-CA-CB	6.12	121.33	111.23
1	A	237	THR	CA-C-N	6.12	133.51	121.58
1	A	237	THR	C-N-CA	6.12	133.51	121.58
3	C	48	THR	N-CA-CB	6.12	119.75	109.78
1	A	386	MET	CA-C-O	-6.12	112.57	119.79
4	E	260	ALA	N-CA-C	6.12	117.74	111.14
1	A	161	GLU	CB-CA-C	6.11	120.03	109.15
3	C	211	ASN	CA-C-N	6.11	133.22	121.54
3	C	211	ASN	C-N-CA	6.11	133.22	121.54
2	B	105	HIS	ND1-CE1-NE2	-6.11	102.29	108.40
3	C	48	THR	CB-CA-C	6.11	120.89	110.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	41	SER	CA-C-N	-6.11	113.91	123.13
4	E	41	SER	C-N-CA	-6.11	113.91	123.13
3	C	83	ARG	CA-C-N	6.11	127.47	119.84
3	C	83	ARG	C-N-CA	6.11	127.47	119.84
1	D	88	PRO	CB-CA-C	-6.11	103.94	111.64
4	E	476	GLU	N-CA-CB	6.11	120.88	110.50
2	B	273	THR	CA-C-N	6.11	130.37	120.60
2	B	273	THR	C-N-CA	6.11	130.37	120.60
1	A	422	THR	CA-CB-CG2	6.10	120.87	110.50
2	B	175	ILE	N-CA-CB	6.10	121.29	111.23
1	D	72	TYR	N-CA-C	-6.09	103.98	112.45
2	B	455	PHE	CG-CD1-CE1	6.09	131.06	120.70
1	A	27	HIS	CA-CB-CG	6.09	119.89	113.80
2	B	9	SER	N-CA-C	6.09	119.18	111.69
2	B	427	ASP	CA-CB-CG	6.09	118.69	112.60
3	C	272	LEU	CA-C-O	-6.09	114.43	120.70
3	C	13	ILE	CA-C-O	-6.08	113.17	120.78
3	C	3	GLU	CA-C-O	-6.08	114.48	121.54
2	B	280	ILE	N-CA-C	6.08	121.99	109.34
1	D	27	HIS	O-C-N	6.08	130.68	122.59
1	D	280	PHE	CD1-CE1-CZ	-6.08	109.06	120.00
3	C	8	ILE	CA-CB-CG2	-6.08	100.17	110.50
4	E	119	PRO	CB-CA-C	-6.08	103.50	110.92
4	E	414	SER	CA-C-N	6.08	129.55	120.31
4	E	414	SER	C-N-CA	6.08	129.55	120.31
2	B	141	ASN	N-CA-CB	6.07	122.00	111.13
4	E	162	GLU	CA-C-N	6.07	133.14	121.54
4	E	162	GLU	C-N-CA	6.07	133.14	121.54
1	A	3	HIS	ND1-CG-CD2	6.07	112.17	106.10
1	A	152	ASP	CA-C-O	-6.07	111.83	120.51
2	B	108	VAL	O-C-N	6.07	129.44	122.82
3	C	313	HIS	ND1-CG-CD2	-6.07	100.03	106.10
3	C	443	VAL	N-CA-CB	6.07	121.24	111.23
2	B	226	VAL	CG1-CB-CG2	6.07	124.14	110.80
1	D	63	VAL	CB-CA-C	-6.07	101.34	111.29
1	D	112	TYR	CA-C-O	-6.06	114.06	120.55
4	E	287	ILE	CA-C-O	-6.06	113.92	120.47
1	A	18	VAL	CA-C-N	-6.06	112.57	120.63
1	A	18	VAL	C-N-CA	-6.06	112.57	120.63
3	C	246	ALA	O-C-N	6.06	129.08	122.11
2	B	101	GLU	CA-C-N	6.06	132.88	121.97
2	B	101	GLU	C-N-CA	6.06	132.88	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	261	VAL	CA-CB-CG1	6.06	120.70	110.40
4	E	68	THR	O-C-N	-6.06	114.53	122.59
3	C	22	ARG	CG-CD-NE	-6.06	98.68	112.00
1	A	7	LEU	N-CA-CB	6.05	120.72	110.49
4	E	196	TRP	CB-CG-CD1	-6.05	117.82	126.90
4	E	185	ILE	CA-C-N	-6.05	112.55	121.99
4	E	185	ILE	C-N-CA	-6.05	112.55	121.99
1	A	84	ASP	CA-CB-CG	6.05	118.65	112.60
2	B	100	PHE	O-C-N	-6.05	116.15	123.29
1	D	299	HIS	N-CA-C	-6.05	104.60	111.07
4	E	103	TYR	O-C-N	-6.05	114.67	122.72
2	B	292	ALA	N-CA-C	-6.05	104.76	111.71
2	B	465	ASP	CA-C-O	-6.04	111.87	120.51
1	D	65	LEU	CA-C-N	6.04	129.97	121.02
1	D	65	LEU	C-N-CA	6.04	129.97	121.02
2	B	98	GLY	O-C-N	-6.04	114.85	122.70
1	D	258	LEU	CA-C-N	6.04	130.01	120.47
1	D	258	LEU	C-N-CA	6.04	130.01	120.47
4	E	83	LEU	N-CA-C	6.04	123.66	110.80
2	B	17	PRO	CA-C-N	6.04	133.13	121.18
2	B	17	PRO	C-N-CA	6.04	133.13	121.18
2	B	292	ALA	CA-C-N	6.03	128.62	120.65
2	B	292	ALA	C-N-CA	6.03	128.62	120.65
1	D	258	LEU	N-CA-C	-6.03	103.87	111.11
1	A	188	VAL	N-CA-C	6.03	121.89	109.34
2	B	47	ASN	OD1-CG-ND2	-6.03	116.57	122.60
3	C	101	GLN	CG-CD-NE2	6.03	125.45	116.40
1	D	79	ARG	CG-CD-NE	-6.03	98.73	112.00
4	E	429	GLN	OE1-CD-NE2	-6.03	116.57	122.60
1	D	127	TYR	N-CA-C	6.03	117.27	107.32
1	A	172	GLU	OE1-CD-OE2	6.02	137.36	122.90
1	A	399	TRP	CE3-CZ3-CH2	-6.02	113.27	121.10
4	E	196	TRP	CE3-CZ3-CH2	6.02	128.93	121.10
4	E	473	GLN	N-CA-C	6.02	120.63	113.16
1	A	306	HIS	CA-C-O	-6.02	110.56	120.80
1	D	98	GLY	CA-C-N	6.02	129.66	121.05
1	D	98	GLY	C-N-CA	6.02	129.66	121.05
1	A	135	PHE	CA-C-N	-6.02	112.32	119.84
1	A	135	PHE	C-N-CA	-6.02	112.32	119.84
1	A	278	MET	CA-C-N	-6.02	109.80	120.99
1	A	278	MET	C-N-CA	-6.02	109.80	120.99
2	B	135	PHE	N-CA-C	6.02	123.11	109.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	10	ASP	N-CA-C	-6.02	104.64	111.14
1	D	208	GLN	CG-CD-NE2	6.02	125.42	116.40
4	E	421	PHE	N-CA-CB	6.02	118.96	109.82
1	D	17	LYS	CB-CA-C	6.01	118.51	109.13
1	D	301	ARG	CA-C-N	6.01	129.97	121.61
1	D	301	ARG	C-N-CA	6.01	129.97	121.61
1	A	149	TRP	N-CA-C	6.01	123.61	110.80
2	B	294	SER	O-C-N	-6.01	113.49	122.39
3	C	27	ASN	CB-CA-C	-6.01	100.73	110.77
1	D	209	ARG	NE-CZ-NH2	6.01	124.61	119.20
4	E	162	GLU	CA-C-O	-6.01	112.57	119.60
2	B	99	SER	CA-C-O	6.01	129.10	120.51
4	E	293	SER	CA-C-O	6.01	126.79	120.42
1	D	84	ASP	O-C-N	-6.01	114.60	122.59
1	D	130	ILE	CA-CB-CG1	6.00	120.61	110.40
1	A	399	TRP	CD2-CE3-CZ3	6.00	126.40	118.60
1	D	404	MET	N-CA-CB	6.00	119.50	110.19
4	E	148	GLN	CB-CG-CD	6.00	122.81	112.60
4	E	155	VAL	N-CA-CB	-6.00	100.70	111.92
1	D	86	TRP	CA-C-N	6.00	131.73	121.35
1	D	86	TRP	C-N-CA	6.00	131.73	121.35
2	B	465	ASP	N-CA-C	6.00	123.58	110.80
3	C	20	HIS	CA-C-N	6.00	130.63	123.19
3	C	20	HIS	C-N-CA	6.00	130.63	123.19
1	A	78	ILE	O-C-N	6.00	129.22	122.92
1	A	204	HIS	ND1-CE1-NE2	-6.00	102.40	108.40
2	B	64	ARG	N-CA-CB	6.00	119.87	110.46
1	A	400	LYS	N-CA-C	5.99	118.71	111.40
3	C	180	ASP	N-CA-CB	5.99	121.04	110.37
1	A	280	PHE	N-CA-CB	5.99	118.66	109.91
4	E	261	GLN	CA-C-O	-5.99	111.94	120.51
1	A	24	HIS	CG-CD2-NE2	-5.99	101.21	107.20
2	B	239	PHE	CA-CB-CG	-5.99	107.81	113.80
3	C	94	LEU	CB-CA-C	5.99	121.01	111.91
3	C	74	TYR	CA-CB-CG	5.99	124.67	113.90
3	C	153	TYR	CB-CG-CD1	-5.99	111.82	120.80
2	B	160	HIS	O-C-N	-5.98	113.94	121.78
1	A	128	CYS	CA-C-O	-5.98	114.29	120.99
1	A	407	ASP	CA-CB-CG	-5.98	106.62	112.60
4	E	45	LYS	O-C-N	5.98	128.46	122.12
4	E	204	ASP	N-CA-C	5.98	118.40	109.25
3	C	264	LEU	CA-C-O	-5.98	114.21	120.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	100	GLU	CG-CD-OE2	5.98	132.15	118.40
2	B	300	VAL	CB-CA-C	5.98	119.62	111.97
4	E	130	ALA	N-CA-C	5.97	118.51	108.23
4	E	241	PHE	CA-C-O	-5.97	113.61	120.24
4	E	464	ALA	N-CA-C	5.97	123.53	110.80
1	D	256	PHE	CA-C-N	5.97	130.83	120.68
1	D	256	PHE	C-N-CA	5.97	130.83	120.68
1	A	22	VAL	CA-CB-CG2	5.97	120.55	110.40
4	E	261	GLN	CA-C-N	-5.97	111.59	121.92
4	E	261	GLN	C-N-CA	-5.97	111.59	121.92
4	E	441	LEU	O-C-N	-5.97	112.64	121.89
2	B	106	VAL	N-CA-CB	5.97	120.41	110.86
1	D	382	ILE	O-C-N	-5.97	115.69	121.83
1	A	115	LYS	CA-C-N	-5.96	114.83	123.06
1	A	115	LYS	C-N-CA	-5.96	114.83	123.06
1	D	238	ASP	CA-C-N	5.96	132.93	121.54
1	D	238	ASP	C-N-CA	5.96	132.93	121.54
1	A	271	VAL	CA-C-N	5.96	127.56	120.23
1	A	271	VAL	C-N-CA	5.96	127.56	120.23
2	B	15	TYR	CA-CB-CG	5.96	124.63	113.90
2	B	257	LEU	O-C-N	5.96	128.97	122.11
3	C	17	TYR	CB-CG-CD1	-5.96	111.86	120.80
4	E	270	GLN	OE1-CD-NE2	5.96	128.56	122.60
1	D	196	THR	CA-C-N	5.96	127.28	119.84
1	D	196	THR	C-N-CA	5.96	127.28	119.84
1	A	376	ILE	CA-C-N	5.95	128.54	120.38
1	A	376	ILE	C-N-CA	5.95	128.54	120.38
2	B	428	TRP	CD2-CE2-CZ2	-5.95	116.45	122.40
1	D	237	THR	CA-C-N	5.95	131.56	121.14
1	D	237	THR	C-N-CA	5.95	131.56	121.14
3	C	440	ASP	O-C-N	-5.95	114.67	122.59
1	D	187	TRP	O-C-N	5.95	130.77	123.21
4	E	95	VAL	N-CA-CB	5.95	121.05	111.23
1	A	224	LEU	N-CA-C	-5.95	104.70	111.07
1	A	302	SER	CA-CB-OG	5.95	123.00	111.10
2	B	198	ARG	N-CA-C	5.95	123.48	110.80
1	A	133	THR	N-CA-C	5.95	120.23	112.92
2	B	148	SER	CA-C-N	-5.95	110.28	121.81
2	B	148	SER	C-N-CA	-5.95	110.28	121.81
2	B	448	SER	CB-CA-C	5.94	122.64	112.00
3	C	484	LYS	O-C-N	-5.94	113.49	123.00
4	E	257	VAL	N-CA-CB	5.94	121.03	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	423	VAL	N-CA-CB	5.94	121.03	111.23
2	B	160	HIS	N-CA-C	5.94	117.74	109.31
1	D	291	VAL	CA-C-O	-5.93	114.56	120.85
1	D	231	LEU	CA-C-N	-5.93	111.29	121.97
1	D	231	LEU	C-N-CA	-5.93	111.29	121.97
4	E	445	VAL	N-CA-CB	-5.93	104.39	110.62
2	B	181	THR	CA-C-O	-5.93	113.61	120.49
2	B	302	LEU	CB-CA-C	5.93	120.63	110.79
1	D	18	VAL	N-CA-CB	5.93	117.48	110.55
4	E	24	LEU	CA-C-O	-5.93	112.50	120.15
2	B	181	THR	CA-C-N	5.92	128.81	120.28
2	B	181	THR	C-N-CA	5.92	128.81	120.28
2	B	271	PRO	CA-C-N	5.92	128.81	120.28
2	B	271	PRO	C-N-CA	5.92	128.81	120.28
1	D	88	PRO	O-C-N	5.92	129.82	123.01
4	E	85	TRP	CZ3-CH2-CZ2	5.92	129.20	121.50
1	D	159	SER	O-C-N	5.92	128.10	122.06
4	E	45	LYS	N-CA-C	-5.92	104.83	111.28
1	A	277	TYR	O-C-N	-5.92	115.40	122.15
3	C	309	VAL	CA-C-O	5.92	128.18	120.78
1	D	382	ILE	N-CA-CB	5.92	119.46	110.58
4	E	458	PHE	CG-CD2-CE2	5.92	130.76	120.70
2	B	242	PRO	CA-N-CD	-5.92	103.72	112.00
2	B	243	PRO	N-CA-CB	5.92	109.46	103.25
3	C	320	HIS	ND1-CG-CD2	-5.92	100.19	106.10
2	B	225	ILE	O-C-N	-5.91	116.13	121.87
2	B	299	VAL	CA-C-N	5.91	128.01	120.56
2	B	299	VAL	C-N-CA	5.91	128.01	120.56
1	D	422	THR	CA-C-N	5.91	132.62	121.97
1	D	422	THR	C-N-CA	5.91	132.62	121.97
2	B	197	TRP	N-CA-C	5.91	117.53	110.44
1	A	429	ARG	N-CA-C	5.91	117.39	111.07
2	B	198	ARG	N-CA-CB	5.91	120.48	110.49
1	D	159	SER	CA-C-O	-5.91	113.23	119.50
1	D	289	ILE	CA-CB-CG1	-5.91	100.35	110.40
4	E	239	VAL	CA-C-N	5.91	132.63	121.81
4	E	239	VAL	C-N-CA	5.91	132.63	121.81
2	B	405	VAL	CA-C-O	-5.91	114.91	121.17
1	A	79	ARG	NE-CZ-NH1	-5.91	115.59	121.50
3	C	122	PRO	O-C-N	-5.91	114.49	121.46
3	C	308	ILE	CA-CB-CG2	5.91	120.54	110.50
3	C	143	ASN	N-CA-C	5.90	118.83	107.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	384	GLU	CA-C-O	-5.90	114.29	120.55
1	A	29	VAL	CB-CA-C	5.90	119.57	110.96
3	C	94	LEU	CA-C-O	-5.90	114.53	122.44
3	C	232	PHE	CG-CD1-CE1	5.90	130.73	120.70
4	E	18	ILE	CB-CA-C	5.90	118.23	110.91
3	C	229	VAL	CA-CB-CG1	5.90	120.42	110.40
4	E	1	ASN	N-CA-CB	-5.90	100.48	110.50
4	E	232	ILE	CB-CA-C	-5.90	104.08	112.22
1	A	422	THR	CA-C-N	5.90	132.58	121.97
1	A	422	THR	C-N-CA	5.90	132.58	121.97
4	E	64	LEU	N-CA-C	5.90	123.36	110.80
2	B	18	LYS	CA-C-O	5.89	126.71	119.05
1	D	304	SER	CA-C-N	-5.89	111.28	121.66
1	D	304	SER	C-N-CA	-5.89	111.28	121.66
2	B	255	ALA	N-CA-C	-5.89	104.55	110.97
3	C	471	PHE	O-C-N	-5.89	114.76	122.59
3	C	82	LEU	O-C-N	5.88	130.56	123.26
1	D	375	ALA	CA-C-N	5.88	127.97	120.56
1	D	375	ALA	C-N-CA	5.88	127.97	120.56
2	B	422	ASP	CA-CB-CG	5.88	118.48	112.60
1	A	117	MET	O-C-N	5.88	130.83	123.19
2	B	227	PRO	O-C-N	-5.88	115.17	122.23
3	C	464	VAL	O-C-N	5.88	127.57	121.87
1	A	215	VAL	CA-C-O	-5.87	113.44	120.78
1	D	30	ASP	O-C-N	-5.87	114.78	122.59
2	B	213	ILE	O-C-N	-5.87	116.29	122.57
3	C	312	PHE	CD1-CG-CD2	5.87	127.40	118.60
4	E	197	GLN	CA-C-N	5.87	128.95	120.38
4	E	197	GLN	C-N-CA	5.87	128.95	120.38
3	C	68	THR	CB-CA-C	-5.87	98.75	110.42
1	A	432	GLU	O-C-N	-5.87	114.42	122.46
2	B	81	PRO	O-C-N	-5.87	114.72	122.64
4	E	134	PHE	CD1-CG-CD2	-5.86	109.81	118.60
2	B	237	LEU	O-C-N	-5.86	114.80	122.59
2	B	306	HIS	CE1-NE2-CD2	5.86	114.86	109.00
1	D	297	ASN	CA-CB-CG	-5.86	106.74	112.60
1	A	212	LEU	CA-C-O	-5.85	112.14	120.51
1	D	421	GLY	O-C-N	-5.85	115.09	122.70
1	D	424	SER	CA-C-O	5.85	126.76	120.20
1	A	2	GLU	O-C-N	5.85	130.38	122.59
1	D	67	TRP	O-C-N	5.85	130.96	122.94
1	D	94	ASN	OD1-CG-ND2	-5.85	116.75	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	30	ASP	CA-C-N	5.85	129.91	122.37
1	D	30	ASP	C-N-CA	5.85	129.91	122.37
3	C	87	ILE	O-C-N	-5.84	115.27	122.57
1	A	6	ARG	CA-C-N	5.84	132.70	121.54
1	A	6	ARG	C-N-CA	5.84	132.70	121.54
1	A	214	PHE	CA-C-N	5.84	132.49	121.97
1	A	214	PHE	C-N-CA	5.84	132.49	121.97
4	E	232	ILE	CA-C-O	-5.84	114.66	120.85
2	B	437	ARG	NE-CZ-NH2	-5.84	113.94	119.20
1	A	166	ASP	CA-CB-CG	-5.84	106.76	112.60
1	D	137	PHE	CB-CG-CD1	5.84	130.62	120.70
4	E	90	VAL	CB-CA-C	-5.84	101.72	111.29
4	E	225	ILE	CA-CB-CG1	-5.83	100.48	110.40
1	D	129	GLU	O-C-N	-5.83	115.80	122.68
4	E	37	THR	CA-CB-CG2	5.83	120.42	110.50
1	A	228	LEU	CA-C-N	5.83	128.41	120.54
1	A	228	LEU	C-N-CA	5.83	128.41	120.54
4	E	195	ASN	CA-C-O	5.83	126.54	120.30
1	A	65	LEU	CA-C-O	5.83	126.47	119.59
4	E	249	GLN	OE1-CD-NE2	-5.83	116.77	122.60
2	B	291	VAL	CA-CB-CG1	5.83	120.31	110.40
4	E	119	PRO	N-CA-C	5.83	117.81	110.70
4	E	4	GLY	CA-C-N	5.83	129.16	120.31
4	E	4	GLY	C-N-CA	5.83	129.16	120.31
4	E	440	VAL	CB-CA-C	-5.83	104.24	111.70
1	A	64	ARG	CA-C-N	5.82	131.69	122.60
1	A	64	ARG	C-N-CA	5.82	131.69	122.60
4	E	419	CYS	CA-C-O	-5.82	113.27	119.97
2	B	20	ARG	NE-CZ-NH2	-5.82	113.96	119.20
3	C	6	ARG	NH1-CZ-NH2	5.82	126.87	119.30
4	E	196	TRP	CA-C-O	-5.82	112.19	120.51
1	A	206	ILE	CB-CA-C	-5.82	103.97	111.53
1	D	283	ILE	O-C-N	-5.81	116.19	121.89
1	D	391	GLU	CA-C-O	5.81	126.71	120.55
4	E	65	SER	CA-C-N	-5.81	112.39	123.32
4	E	65	SER	C-N-CA	-5.81	112.39	123.32
2	B	424	LEU	N-CA-C	-5.81	104.91	112.23
1	A	241	GLU	O-C-N	-5.81	115.12	122.27
1	D	157	SER	N-CA-C	5.81	118.94	108.48
2	B	48	GLU	N-CA-CB	5.81	120.31	110.49
4	E	133	TYR	CA-C-O	-5.81	112.20	120.51
4	E	308	LEU	N-CA-C	-5.80	98.44	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	260	THR	CA-C-O	-5.80	114.91	121.00
3	C	434	LYS	N-CA-CB	5.80	120.30	110.49
4	E	12	GLY	CA-C-N	5.80	132.62	121.54
4	E	12	GLY	C-N-CA	5.80	132.62	121.54
1	A	89	ASP	CA-C-N	5.80	129.34	120.82
1	A	89	ASP	C-N-CA	5.80	129.34	120.82
2	B	26	GLY	CA-C-N	5.80	132.61	121.54
2	B	26	GLY	C-N-CA	5.80	132.61	121.54
1	D	242	LYS	N-CA-C	5.80	118.35	110.06
1	A	170	PHE	CD1-CG-CD2	-5.79	109.91	118.60
1	D	422	THR	OG1-CB-CG2	5.79	120.88	109.30
1	A	435	GLN	N-CA-C	5.79	117.46	111.03
3	C	466	VAL	CB-CA-C	-5.79	104.45	112.04
1	D	106	THR	N-CA-C	5.79	123.13	110.80
1	A	9	ALA	CA-C-O	-5.79	114.74	120.70
3	C	253	SER	CA-CB-OG	5.79	122.67	111.10
4	E	259	LEU	N-CA-C	5.79	117.26	111.07
3	C	308	ILE	CA-C-O	-5.78	114.08	120.96
4	E	459	SER	CA-C-O	5.78	126.89	120.82
3	C	262	CYS	O-C-N	5.78	128.76	122.11
3	C	314	PHE	CD1-CG-CD2	-5.78	109.93	118.60
3	C	481	PRO	CA-C-N	5.78	127.07	119.84
3	C	481	PRO	C-N-CA	5.78	127.07	119.84
2	B	190	HIS	N-CA-C	5.78	117.03	107.73
1	D	274	ILE	CA-C-N	5.78	132.74	121.41
1	D	274	ILE	C-N-CA	5.78	132.74	121.41
1	D	277	TYR	CA-C-O	-5.78	112.25	120.51
4	E	441	LEU	N-CA-CB	-5.78	102.50	110.42
1	A	423	VAL	N-CA-CB	5.78	120.76	111.23
1	A	224	LEU	CA-C-N	5.77	130.50	120.68
1	A	224	LEU	C-N-CA	5.77	130.50	120.68
4	E	435	GLU	CA-C-O	-5.77	114.39	120.63
1	D	64	ARG	NH1-CZ-NH2	5.77	126.80	119.30
4	E	468	THR	N-CA-CB	5.77	118.70	110.16
2	B	186	TRP	CD2-CE2-CZ2	-5.77	116.63	122.40
1	D	289	ILE	CA-C-O	-5.77	114.49	121.18
1	A	219	ILE	CA-C-N	-5.77	111.46	122.13
1	A	219	ILE	C-N-CA	-5.77	111.46	122.13
2	B	137	PHE	CD1-CG-CD2	5.77	127.25	118.60
3	C	37	LEU	O-C-N	5.77	130.08	123.27
4	E	4	GLY	N-CA-C	-5.77	105.51	112.49
1	D	91	VAL	N-CA-C	5.77	121.33	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	304	SER	CA-C-O	5.76	128.75	120.51
3	C	451	GLN	CA-C-N	5.76	131.23	121.14
3	C	451	GLN	C-N-CA	5.76	131.23	121.14
1	D	173	SER	CA-C-N	5.76	132.70	121.41
1	D	173	SER	C-N-CA	5.76	132.70	121.41
3	C	424	ASP	CA-CB-CG	5.76	118.36	112.60
1	D	19	ILE	N-CA-C	5.76	117.01	109.58
4	E	156	ASN	CB-CA-C	-5.76	103.57	110.94
1	A	161	GLU	CA-C-N	5.75	132.53	121.54
1	A	161	GLU	C-N-CA	5.75	132.53	121.54
1	A	378	GLY	O-C-N	-5.75	113.49	122.18
4	E	476	GLU	CB-CG-CD	5.75	122.38	112.60
2	B	27	ASP	N-CA-CB	5.75	120.21	110.49
3	C	19	LYS	CB-CA-C	5.75	122.33	110.31
3	C	71	ALA	N-CA-C	5.75	123.05	110.80
4	E	130	ALA	CB-CA-C	5.75	120.77	111.05
4	E	229	CYS	CA-C-O	-5.75	112.32	119.28
2	B	26	GLY	O-C-N	5.75	130.17	122.70
3	C	437	ASN	CB-CG-ND2	-5.75	107.78	116.40
1	D	43	VAL	CA-CB-CG1	5.75	120.17	110.40
1	A	385	HIS	CA-CB-CG	5.74	119.54	113.80
1	A	24	HIS	O-C-N	-5.74	114.95	122.59
2	B	7	LEU	O-C-N	-5.74	114.95	122.59
2	B	288	MET	CA-CB-CG	5.74	125.58	114.10
1	D	280	PHE	O-C-N	-5.74	114.96	122.59
1	A	423	VAL	CA-C-N	5.74	127.97	120.28
1	A	423	VAL	C-N-CA	5.74	127.97	120.28
2	B	206	ASP	CA-C-N	5.74	131.13	122.98
2	B	206	ASP	C-N-CA	5.74	131.13	122.98
2	B	441	TYR	CB-CG-CD2	-5.74	112.19	120.80
3	C	482	PRO	CA-N-CD	-5.74	103.97	112.00
4	E	472	ASN	CA-C-O	-5.73	111.89	119.06
1	A	277	TYR	CB-CG-CD2	5.73	129.40	120.80
4	E	74	ILE	N-CA-C	5.73	121.27	109.34
1	D	66	ARG	NH1-CZ-NH2	5.73	126.75	119.30
2	B	300	VAL	O-C-N	-5.73	116.30	121.91
3	C	481	PRO	N-CA-CB	5.73	108.64	103.08
4	E	236	VAL	CA-C-N	5.73	130.43	120.86
4	E	236	VAL	C-N-CA	5.73	130.43	120.86
1	D	390	GLU	CB-CA-C	5.72	119.97	110.81
4	E	216	ARG	N-CA-CB	5.72	120.17	110.49
4	E	259	LEU	CB-CA-C	-5.72	101.89	110.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	91	ASP	CA-CB-CG	-5.72	106.88	112.60
4	E	93	ASN	OD1-CG-ND2	-5.72	116.88	122.60
4	E	420	ASN	O-C-N	5.72	128.18	122.12
4	E	101	VAL	CA-C-N	5.72	132.50	121.18
4	E	101	VAL	C-N-CA	5.72	132.50	121.18
2	B	272	GLU	N-CA-C	5.71	118.28	111.71
1	D	217	ASN	OD1-CG-ND2	5.71	128.31	122.60
3	C	78	SER	O-C-N	-5.71	115.00	122.59
3	C	90	PRO	N-CA-CB	5.71	109.24	103.25
1	D	143	THR	O-C-N	5.71	130.04	123.02
1	A	417	ILE	CB-CA-C	-5.71	103.02	112.26
3	C	221	ILE	O-C-N	-5.71	115.44	122.57
4	E	266	PHE	CA-CB-CG	-5.71	108.09	113.80
2	B	180	PHE	CB-CG-CD2	-5.70	111.00	120.70
3	C	314	PHE	CG-CD1-CE1	5.70	130.40	120.70
1	D	244	THR	CA-CB-OG1	-5.70	101.05	109.60
1	D	434	SER	CA-C-O	-5.70	112.80	119.24
2	B	68	ASP	O-C-N	-5.70	114.77	121.32
2	B	252	SER	CA-C-N	5.70	129.48	120.47
2	B	252	SER	C-N-CA	5.70	129.48	120.47
4	E	439	TRP	NE1-CE2-CZ2	-5.70	121.55	130.10
2	B	5	ASP	N-CA-CB	5.70	119.14	110.14
3	C	116	GLY	N-CA-C	5.70	126.69	113.18
1	A	160	PRO	CA-N-CD	-5.70	104.02	112.00
3	C	472	ILE	N-CA-CB	5.70	120.63	111.23
4	E	60	ASN	N-CA-C	5.70	118.24	109.07
1	A	96	ALA	CA-C-N	5.69	132.41	121.54
1	A	96	ALA	C-N-CA	5.69	132.41	121.54
1	D	410	LEU	CA-CB-CG	5.69	136.22	116.30
1	A	237	THR	N-CA-C	5.69	117.48	111.28
2	B	86	TRP	CZ3-CH2-CZ2	5.69	128.90	121.50
1	A	118	TRP	CB-CA-C	-5.69	103.12	111.77
1	A	152	ASP	N-CA-CB	-5.69	100.88	110.49
2	B	216	LYS	N-CA-C	5.68	119.58	108.21
2	B	426	LYS	CA-C-O	-5.68	113.68	120.10
4	E	24	LEU	CB-CA-C	-5.68	102.25	111.06
4	E	221	TYR	N-CA-C	-5.68	104.55	112.45
3	C	137	PHE	CG-CD1-CE1	-5.68	111.05	120.70
4	E	80	PRO	O-C-N	5.68	130.05	123.01
2	B	151	TYR	CB-CG-CD2	5.68	129.31	120.80
2	B	134	TYR	CA-CB-CG	5.67	124.11	113.90
3	C	456	LEU	CA-C-O	-5.67	114.57	120.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	385	HIS	CA-C-N	5.67	130.32	120.68
1	A	385	HIS	C-N-CA	5.67	130.32	120.68
1	A	148	ILE	CA-C-O	-5.67	113.69	120.78
2	B	229	ILE	N-CA-C	5.67	119.04	111.44
2	B	457	ASP	CB-CG-OD1	5.67	131.43	118.40
2	B	466	ASN	CA-C-N	-5.67	112.76	119.84
2	B	466	ASN	C-N-CA	-5.67	112.76	119.84
1	A	186	HIS	CE1-NE2-CD2	-5.66	103.34	109.00
1	D	215	VAL	O-C-N	5.66	127.66	121.83
4	E	111	ASN	O-C-N	-5.66	115.54	122.05
1	A	138	ASP	O-C-N	-5.66	115.39	122.35
3	C	188	GLY	CA-C-N	5.66	130.17	120.72
3	C	188	GLY	C-N-CA	5.66	130.17	120.72
1	D	49	ILE	CA-CB-CG1	-5.66	100.78	110.40
1	A	277	TYR	CG-CD2-CE2	5.65	129.67	121.20
4	E	206	GLN	CA-C-N	-5.65	112.38	122.32
4	E	206	GLN	C-N-CA	-5.65	112.38	122.32
2	B	238	VAL	N-CA-C	-5.65	105.66	113.00
4	E	230	VAL	CA-CB-CG2	5.65	120.00	110.40
4	E	430	ASN	N-CA-C	-5.65	105.20	111.36
1	A	116	ILE	N-CA-C	5.65	116.61	108.48
1	A	278	MET	N-CA-CB	-5.65	101.53	110.28
2	B	435	ALA	O-C-N	-5.65	115.62	122.11
3	C	473	PHE	CD1-CG-CD2	-5.64	110.13	118.60
4	E	213	ILE	O-C-N	5.64	128.83	122.68
3	C	88	TRP	CD2-CE3-CZ3	5.64	125.93	118.60
4	E	467	LEU	O-C-N	5.64	128.82	122.22
1	A	6	ARG	O-C-N	-5.64	116.14	122.12
2	B	428	TRP	CA-CB-CG	5.64	124.32	113.60
3	C	22	ARG	CB-CA-C	5.64	121.28	110.17
2	B	404	ALA	N-CA-CB	5.64	119.88	110.41
2	B	408	ILE	N-CA-CB	5.64	117.79	110.57
1	A	143	THR	CA-C-N	-5.63	114.86	122.86
1	A	143	THR	C-N-CA	-5.63	114.86	122.86
2	B	25	VAL	CA-CB-CG2	5.63	119.98	110.40
4	E	245	GLN	O-C-N	-5.63	115.10	122.59
2	B	403	GLU	N-CA-CB	5.63	120.08	110.50
3	C	143	ASN	CA-CB-CG	-5.63	106.97	112.60
1	D	95	ASN	N-CA-CB	5.63	120.01	110.49
3	C	425	SER	O-C-N	5.63	127.87	122.07
4	E	420	ASN	N-CA-C	-5.63	105.15	111.28
2	B	261	VAL	CA-C-O	-5.62	115.20	121.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	299	HIS	N-CA-C	-5.62	102.09	111.37
3	C	302	VAL	CA-C-O	-5.62	113.75	120.78
1	A	115	LYS	CB-CA-C	-5.62	101.90	109.71
2	B	89	ASP	CA-CB-CG	5.62	118.22	112.60
4	E	71	TYR	CG-CD2-CE2	-5.62	112.77	121.20
1	A	10	ASN	O-C-N	-5.62	115.12	122.59
2	B	424	LEU	CA-C-N	5.62	127.74	120.44
2	B	424	LEU	C-N-CA	5.62	127.74	120.44
3	C	231	ASN	CB-CG-ND2	-5.62	107.97	116.40
3	C	139	PHE	CA-C-N	5.62	127.80	120.28
3	C	139	PHE	C-N-CA	5.62	127.80	120.28
1	A	227	PHE	CA-CB-CG	-5.61	108.19	113.80
4	E	197	GLN	N-CA-C	5.61	118.83	109.96
3	C	223	ARG	CD-NE-CZ	5.61	132.26	124.40
1	D	218	VAL	N-CA-C	-5.61	105.05	110.72
1	D	224	LEU	N-CA-C	-5.61	105.93	112.89
4	E	262	THR	CA-CB-OG1	5.61	118.02	109.60
1	A	170	PHE	CB-CG-CD1	5.60	130.23	120.70
4	E	18	ILE	CA-CB-CG1	5.60	119.93	110.40
1	D	233	PHE	CA-CB-CG	5.60	119.40	113.80
1	D	261	VAL	CA-C-N	-5.60	112.78	120.28
1	D	261	VAL	C-N-CA	-5.60	112.78	120.28
3	C	88	TRP	N-CA-C	-5.60	101.62	109.96
1	A	72	TYR	N-CA-C	-5.60	105.09	111.14
1	D	9	ALA	CA-C-O	-5.60	114.62	120.55
1	D	204	HIS	CA-C-N	-5.59	115.22	123.05
1	D	204	HIS	C-N-CA	-5.59	115.22	123.05
3	C	319	THR	OG1-CB-CG2	-5.59	98.12	109.30
4	E	99	PHE	CA-C-O	-5.59	115.47	121.56
4	E	106	ASN	N-CA-CB	5.59	118.58	109.69
1	A	225	PHE	CD1-CG-CD2	-5.59	110.22	118.60
2	B	20	ARG	CA-C-O	-5.59	113.96	119.49
3	C	20	HIS	CA-C-O	-5.59	112.78	119.15
3	C	315	ARG	CB-CA-C	-5.59	99.94	110.67
3	C	466	VAL	CA-C-O	-5.59	114.31	120.96
1	D	74	GLY	CA-C-N	5.59	132.02	121.97
1	D	74	GLY	C-N-CA	5.59	132.02	121.97
1	D	162	SER	CA-C-N	5.59	132.21	121.54
1	D	162	SER	C-N-CA	5.59	132.21	121.54
4	E	19	LYS	CB-CG-CD	5.59	124.15	111.30
1	A	133	THR	CA-C-O	5.58	126.09	119.56
1	A	290	ILE	CA-C-O	-5.58	114.60	120.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	188	ILE	N-CA-CB	5.58	120.44	111.23
3	C	243	ALA	CA-C-O	-5.58	114.60	120.63
4	E	476	GLU	O-C-N	-5.58	114.07	123.00
3	C	158	ILE	CB-CG1-CD1	5.58	125.52	113.80
1	A	409	ILE	N-CA-C	-5.58	104.92	111.00
4	E	256	SER	O-C-N	5.58	127.89	122.09
2	B	296	ILE	CB-CA-C	-5.58	103.22	112.26
1	D	150	THR	CB-CA-C	-5.58	101.17	110.81
2	B	215	ARG	CA-CB-CG	5.57	125.24	114.10
3	C	225	PRO	CB-CA-C	-5.57	103.93	111.12
1	A	79	ARG	CB-CA-C	-5.57	101.71	110.79
3	C	320	HIS	CA-CB-CG	5.57	119.37	113.80
1	D	401	TYR	CG-CD1-CE1	5.57	129.56	121.20
1	A	66	ARG	NE-CZ-NH2	-5.57	114.19	119.20
2	B	189	GLU	CA-C-O	-5.57	115.15	121.00
3	C	122	PRO	CA-N-CD	-5.57	104.21	112.00
4	E	452	TRP	CZ3-CH2-CZ2	-5.57	114.26	121.50
1	A	270	ALA	N-CA-CB	5.57	119.09	110.80
1	D	421	GLY	N-CA-C	-5.57	99.99	113.18
1	A	111	ASP	CA-CB-CG	-5.56	107.04	112.60
1	D	134	HIS	CG-CD2-NE2	-5.56	101.64	107.20
4	E	63	ARG	CA-C-N	5.56	132.17	121.54
4	E	63	ARG	C-N-CA	5.56	132.17	121.54
4	E	263	ILE	CA-C-N	5.56	130.09	120.58
4	E	263	ILE	C-N-CA	5.56	130.09	120.58
4	E	156	ASN	OD1-CG-ND2	-5.56	117.04	122.60
4	E	305	ASN	CA-CB-CG	-5.56	107.04	112.60
1	A	155	LYS	CA-C-O	-5.56	114.60	120.55
1	D	272	PRO	CA-C-N	5.56	131.46	122.29
1	D	272	PRO	C-N-CA	5.56	131.46	122.29
1	A	421	GLY	CA-C-N	5.55	127.72	120.28
1	A	421	GLY	C-N-CA	5.55	127.72	120.28
2	B	124	TYR	CA-CB-CG	5.55	123.89	113.90
4	E	300	CYS	O-C-N	-5.55	115.45	122.17
3	C	92	ILE	CA-CB-CG2	5.55	119.93	110.50
1	D	55	ARG	CD-NE-CZ	5.55	132.17	124.40
1	D	240	GLY	CA-C-N	5.55	132.14	121.54
1	D	240	GLY	C-N-CA	5.55	132.14	121.54
4	E	303	VAL	CB-CA-C	-5.55	104.87	111.97
2	B	282	SER	CB-CA-C	-5.55	101.94	110.81
3	C	18	ASN	OD1-CG-ND2	-5.55	117.05	122.60
4	E	434	SER	O-C-N	-5.55	116.32	122.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	151	TYR	CD1-CG-CD2	-5.54	109.78	118.10
1	A	19	ILE	N-CA-C	5.54	116.85	109.37
1	A	283	ILE	N-CA-CB	5.54	120.37	111.23
4	E	172	ILE	CA-CB-CG1	5.54	119.82	110.40
2	B	1	SER	CB-CA-C	-5.54	99.58	110.10
2	B	98	GLY	CA-C-N	5.54	132.12	121.54
2	B	98	GLY	C-N-CA	5.54	132.12	121.54
3	C	431	LYS	CA-CB-CG	5.54	125.17	114.10
4	E	8	GLU	CA-C-O	5.54	126.36	120.10
4	E	86	LEU	CB-CA-C	5.54	117.52	110.16
1	A	85	VAL	CA-C-N	-5.53	115.64	122.84
1	A	85	VAL	C-N-CA	-5.53	115.64	122.84
1	A	130	ILE	CA-C-N	5.53	131.93	121.97
1	A	130	ILE	C-N-CA	5.53	131.93	121.97
1	D	37	LEU	N-CA-C	5.53	117.32	108.41
4	E	104	TYR	CA-CB-CG	5.53	123.86	113.90
4	E	159	LEU	O-C-N	5.53	130.14	122.78
3	C	89	ILE	CA-C-N	5.53	126.75	119.84
3	C	89	ILE	C-N-CA	5.53	126.75	119.84
1	D	81	PRO	O-C-N	-5.53	116.39	123.14
4	E	268	ILE	CA-C-N	5.53	128.25	120.28
4	E	268	ILE	C-N-CA	5.53	128.25	120.28
4	E	433	GLY	O-C-N	-5.53	116.88	122.19
3	C	236	CYS	CB-CA-C	5.53	121.29	110.67
3	C	480	ARG	CA-C-N	5.53	126.07	120.38
3	C	480	ARG	C-N-CA	5.53	126.07	120.38
1	A	11	LEU	CB-CA-C	-5.53	102.17	110.90
1	D	84	ASP	CA-C-O	-5.53	112.61	120.51
1	A	188	VAL	CA-CB-CG1	5.52	119.79	110.40
2	B	191	LYS	CB-CG-CD	5.52	124.00	111.30
1	A	415	MET	CA-C-O	-5.52	114.70	120.55
1	D	151	TYR	O-C-N	-5.52	116.87	123.27
1	D	436	GLU	CA-C-N	5.52	131.63	121.70
1	D	436	GLU	C-N-CA	5.52	131.63	121.70
1	A	297	ASN	CB-CG-ND2	5.52	124.67	116.40
3	C	113	ARG	NE-CZ-NH2	5.52	124.16	119.20
4	E	18	ILE	CA-C-N	5.52	128.32	120.49
4	E	18	ILE	C-N-CA	5.52	128.32	120.49
1	A	126	SER	O-C-N	5.51	130.82	122.94
1	A	247	ILE	N-CA-CB	5.51	120.33	111.23
2	B	267	ALA	N-CA-CB	-5.51	101.15	110.41
2	B	243	PRO	CA-C-O	-5.51	110.57	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	138	ASP	CB-CG-OD1	5.51	131.07	118.40
3	C	65	HIS	CA-CB-CG	-5.50	108.30	113.80
3	C	92	ILE	CA-CB-CG1	5.50	119.76	110.40
1	D	120	PRO	CA-C-O	5.50	128.54	120.56
3	C	74	TYR	N-CA-CB	-5.50	101.19	110.49
1	D	276	LYS	N-CA-CB	5.50	119.79	110.49
1	D	397	GLU	CA-C-O	-5.50	113.12	119.78
4	E	439	TRP	CE2-CD2-CE3	5.50	124.30	118.80
3	C	154	ASN	OD1-CG-ND2	-5.50	117.10	122.60
2	B	163	ASP	O-C-N	5.50	127.76	121.93
4	E	468	THR	N-CA-C	-5.50	105.37	111.36
1	A	408	HIS	CA-CB-CG	5.50	119.30	113.80
2	B	92	LEU	CA-C-O	-5.50	114.76	121.58
2	B	220	TYR	CB-CG-CD2	5.50	129.04	120.80
2	B	311	THR	CA-C-O	-5.50	115.02	120.90
3	C	422	GLY	CA-C-N	5.50	129.16	120.47
3	C	422	GLY	C-N-CA	5.50	129.16	120.47
1	D	412	CYS	N-CA-C	-5.50	102.36	111.37
3	C	213	GLN	OE1-CD-NE2	5.50	128.09	122.60
1	A	255	VAL	CA-CB-CG2	-5.49	101.06	110.40
1	D	25	HIS	CA-C-N	5.49	132.21	121.66
1	D	25	HIS	C-N-CA	5.49	132.21	121.66
1	D	385	HIS	CE1-NE2-CD2	-5.49	103.51	109.00
3	C	142	GLN	OE1-CD-NE2	-5.49	117.11	122.60
2	B	22	SER	CA-CB-OG	5.49	122.08	111.10
1	D	433	LEU	CA-C-N	5.49	131.80	122.36
1	D	433	LEU	C-N-CA	5.49	131.80	122.36
2	B	215	ARG	NE-CZ-NH1	5.49	126.99	121.50
3	C	263	VAL	N-CA-C	-5.49	105.15	110.42
4	E	132	THR	CA-CB-OG1	-5.49	101.37	109.60
4	E	155	VAL	O-C-N	-5.49	116.75	123.00
4	E	472	ASN	OD1-CG-ND2	-5.49	117.11	122.60
1	A	169	THR	CB-CA-C	-5.48	102.70	111.86
2	B	283	TYR	CB-CG-CD1	5.48	129.02	120.80
4	E	78	ARG	CA-CB-CG	5.48	125.06	114.10
2	B	188	ILE	N-CA-C	5.48	120.73	109.34
1	D	14	ASN	CA-C-N	5.48	131.79	122.37
1	D	14	ASN	C-N-CA	5.48	131.79	122.37
4	E	443	GLY	CA-C-O	-5.48	111.04	120.57
1	D	252	SER	N-CA-CB	5.47	119.74	110.49
4	E	244	ALA	CB-CA-C	5.47	119.47	110.88
3	C	433	ILE	CA-C-O	-5.47	115.05	120.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	ASN	CB-CA-C	-5.47	102.64	111.18
3	C	310	LEU	O-C-N	5.47	129.87	122.59
1	A	392	SER	O-C-N	-5.47	115.32	122.59
2	B	432	ALA	CA-C-N	5.47	128.16	120.28
2	B	432	ALA	C-N-CA	5.47	128.16	120.28
3	C	96	ASN	O-C-N	5.47	128.86	122.24
1	D	42	ASN	OD1-CG-ND2	5.47	128.07	122.60
1	D	406	ILE	CG1-CB-CG2	5.47	127.10	110.70
1	A	111	ASP	CA-C-N	-5.47	111.10	121.54
1	A	111	ASP	C-N-CA	-5.47	111.10	121.54
1	A	150	THR	O-C-N	-5.47	115.32	122.59
3	C	26	HIS	ND1-CG-CD2	5.47	111.57	106.10
1	D	417	ILE	CA-CB-CG2	-5.47	101.20	110.50
4	E	237	VAL	O-C-N	-5.46	115.83	122.06
1	D	70	ALA	CA-C-N	5.46	131.97	121.54
1	D	70	ALA	C-N-CA	5.46	131.97	121.54
1	D	225	PHE	CD1-CG-CD2	-5.46	110.41	118.60
1	D	392	SER	CA-C-N	5.46	127.86	120.65
1	D	392	SER	C-N-CA	5.46	127.86	120.65
3	C	75	SER	N-CA-CB	5.46	118.12	109.82
1	A	12	LEU	O-C-N	5.46	127.69	122.07
2	B	112	HIS	ND1-CE1-NE2	5.46	113.86	108.40
2	B	245	ALA	CA-C-O	-5.46	113.96	120.89
1	A	265	PRO	CA-CB-CG	-5.45	94.14	104.50
1	D	26	THR	CA-C-O	-5.45	115.72	121.88
1	A	270	ALA	O-C-N	5.45	128.63	122.20
2	B	29	VAL	CA-C-O	-5.45	114.77	120.27
3	C	268	ALA	N-CA-C	5.45	117.30	111.36
1	D	169	THR	CA-C-O	-5.45	115.53	121.20
2	B	156	VAL	CA-C-O	5.45	127.59	120.78
4	E	297	VAL	CA-C-O	-5.45	113.97	120.78
4	E	240	TYR	CA-C-N	5.45	129.89	120.58
4	E	240	TYR	C-N-CA	5.45	129.89	120.58
1	A	45	GLU	CB-CG-CD	-5.45	103.34	112.60
2	B	129	THR	N-CA-C	5.45	122.40	110.80
3	C	69	TRP	O-C-N	5.44	130.41	123.11
1	A	86	TRP	NE1-CE2-CD2	5.44	114.48	107.40
4	E	433	GLY	CA-C-O	5.44	127.00	120.90
3	C	62	TRP	O-C-N	5.44	129.50	123.52
1	A	250	LEU	CD1-CG-CD2	5.44	122.76	110.80
3	C	83	ARG	NH1-CZ-NH2	5.44	126.37	119.30
4	E	212	LEU	CA-C-N	-5.44	114.29	122.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	212	LEU	C-N-CA	-5.44	114.29	122.01
3	C	217	PHE	CD1-CE1-CZ	-5.44	110.22	120.00
1	D	55	ARG	NE-CZ-NH2	5.44	124.09	119.20
1	D	196	THR	N-CA-CB	-5.44	100.69	110.37
3	C	70	ASN	CA-C-O	-5.43	115.03	121.60
1	D	216	VAL	CA-C-N	-5.43	112.86	122.26
1	D	216	VAL	C-N-CA	-5.43	112.86	122.26
1	D	385	HIS	CA-C-O	-5.43	115.10	120.70
2	B	93	MET	O-C-N	5.43	129.82	122.59
1	D	261	VAL	CA-C-O	-5.43	114.76	120.57
1	D	273	LEU	N-CA-C	5.43	117.65	109.23
2	B	44	ASN	CB-CG-OD1	5.43	131.66	120.80
2	B	285	MET	CA-CB-CG	5.43	124.96	114.10
1	D	291	VAL	N-CA-C	5.43	116.20	110.72
2	B	463	PRO	CA-N-CD	-5.43	104.40	112.00
1	A	4	GLU	CA-C-N	5.42	127.49	120.44
1	A	4	GLU	C-N-CA	5.42	127.49	120.44
2	B	189	GLU	CB-CG-CD	5.42	121.82	112.60
3	C	249	LEU	CA-C-O	-5.42	112.73	120.16
4	E	70	GLU	CG-CD-OE2	5.42	130.87	118.40
1	A	281	THR	CA-C-O	5.42	126.23	120.10
1	D	65	LEU	N-CA-CB	5.42	118.52	110.49
1	A	135	PHE	N-CA-C	5.42	121.79	109.81
2	B	278	PRO	CA-C-N	5.42	131.73	121.97
2	B	278	PRO	C-N-CA	5.42	131.73	121.97
3	C	250	PRO	N-CA-CB	-5.42	98.32	103.41
1	D	27	HIS	CB-CG-ND1	-5.42	114.57	122.70
4	E	448	LYS	CA-C-O	-5.42	114.13	120.20
1	A	262	GLU	CA-C-N	5.42	127.81	120.44
1	A	262	GLU	C-N-CA	5.42	127.81	120.44
3	C	474	VAL	CG1-CB-CG2	5.42	122.71	110.80
2	B	89	ASP	N-CA-CB	5.42	119.64	110.49
4	E	66	TRP	CA-C-O	-5.42	115.05	121.60
1	D	426	PHE	CA-C-N	5.41	127.85	120.54
1	D	426	PHE	C-N-CA	5.41	127.85	120.54
4	E	74	ILE	CA-CB-CG1	5.41	119.60	110.40
2	B	433	MET	CA-C-O	5.41	126.22	120.10
1	D	412	CYS	CA-C-O	5.41	127.35	121.02
4	E	146	ARG	CA-C-O	-5.41	112.77	120.51
1	A	299	HIS	CB-CG-ND1	5.41	130.81	122.70
2	B	298	SER	CA-C-O	-5.41	114.69	120.42
3	C	270	PHE	CE1-CZ-CE2	-5.41	110.26	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	235	LEU	CB-CA-C	5.41	120.83	110.17
1	D	213	TYR	CA-C-O	-5.41	114.69	121.02
4	E	84	LEU	CA-CB-CG	5.41	135.23	116.30
4	E	215	GLN	CG-CD-OE1	-5.41	109.98	120.80
2	B	66	GLN	CB-CA-C	-5.41	102.55	110.06
2	B	154	SER	N-CA-CB	5.40	119.62	110.49
3	C	5	GLU	CA-C-O	-5.40	112.78	120.51
3	C	274	THR	CA-C-O	5.40	128.24	120.51
3	C	430	VAL	CA-CB-CG2	-5.40	101.22	110.40
1	D	17	LYS	CA-C-O	-5.40	112.39	118.55
2	B	180	PHE	CA-C-O	-5.40	115.25	121.19
2	B	229	ILE	CA-C-N	5.40	129.73	120.71
2	B	229	ILE	C-N-CA	5.40	129.73	120.71
1	D	277	TYR	O-C-N	-5.40	115.41	122.59
3	C	248	TYR	O-C-N	-5.40	116.51	122.07
4	E	291	PHE	CA-C-N	5.40	127.86	120.46
4	E	291	PHE	C-N-CA	5.40	127.86	120.46
1	A	286	ILE	CA-C-N	-5.40	112.11	120.31
1	A	286	ILE	C-N-CA	-5.40	112.11	120.31
2	B	66	GLN	CG-CD-OE1	5.40	131.60	120.80
2	B	284	LEU	CA-C-O	-5.40	112.79	120.51
1	D	80	LEU	CD1-CG-CD2	5.40	122.67	110.80
1	D	63	VAL	CA-C-O	-5.40	114.04	120.78
3	C	11	LEU	CA-C-O	-5.39	113.57	120.31
3	C	88	TRP	O-C-N	5.39	130.18	123.01
1	D	195	ASP	OD1-CG-OD2	-5.39	109.95	122.90
1	A	301	ARG	CD-NE-CZ	5.39	131.95	124.40
1	D	133	THR	O-C-N	5.39	128.67	122.25
1	A	76	LYS	O-C-N	-5.39	115.42	122.59
1	A	271	VAL	N-CA-CB	5.39	118.76	111.21
2	B	429	GLN	CG-CD-OE1	-5.39	110.02	120.80
4	E	26	HIS	ND1-CG-CD2	-5.39	100.71	106.10
2	B	14	ASN	N-CA-C	5.39	119.98	113.41
1	D	6	ARG	NE-CZ-NH1	5.39	126.89	121.50
1	A	431	ILE	O-C-N	-5.39	115.83	122.57
2	B	180	PHE	CD1-CG-CD2	5.39	126.68	118.60
2	B	306	HIS	O-C-N	-5.39	115.42	122.59
4	E	252	THR	CB-CA-C	-5.39	102.39	110.90
3	C	285	VAL	O-C-N	-5.39	114.96	121.10
1	D	397	GLU	N-CA-CB	5.39	118.66	110.42
1	A	415	MET	CB-CA-C	5.38	119.73	110.79
4	E	435	GLU	N-CA-C	-5.38	104.82	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	69	TRP	CA-C-N	5.38	133.44	123.32
3	C	69	TRP	C-N-CA	5.38	133.44	123.32
3	C	294	PHE	CB-CG-CD1	-5.38	111.55	120.70
1	D	87	LEU	N-CA-C	5.38	119.00	109.58
1	A	164	ARG	CA-C-O	-5.38	113.75	119.13
3	C	239	ILE	O-C-N	-5.38	115.85	122.57
4	E	147	SER	CA-C-O	5.38	126.73	120.49
2	B	38	THR	N-CA-C	-5.37	105.53	112.68
1	D	59	GLN	O-C-N	5.37	129.92	123.26
1	D	254	THR	O-C-N	-5.37	116.33	122.08
4	E	441	LEU	CA-C-N	5.37	129.19	122.48
4	E	441	LEU	C-N-CA	5.37	129.19	122.48
1	A	79	ARG	CA-C-O	5.37	126.20	120.46
2	B	237	LEU	CA-C-N	5.37	129.72	121.19
2	B	237	LEU	C-N-CA	5.37	129.72	121.19
1	D	232	VAL	CA-C-O	-5.37	114.07	120.78
1	A	32	THR	CA-CB-OG1	5.36	117.64	109.60
2	B	440	LEU	CA-C-O	5.36	124.95	119.05
1	D	104	HIS	CA-CB-CG	-5.36	108.44	113.80
1	D	206	ILE	O-C-N	5.36	128.88	123.20
3	C	20	HIS	CE1-NE2-CD2	-5.36	103.64	109.00
1	D	27	HIS	CG-CD2-NE2	5.36	112.56	107.20
4	E	302	ILE	O-C-N	5.36	127.31	121.90
1	D	28	PHE	CA-CB-CG	5.36	119.16	113.80
1	D	253	LEU	CA-C-O	5.36	126.96	121.07
1	A	376	ILE	CA-C-O	-5.36	115.17	120.85
1	A	427	ALA	CB-CA-C	5.36	119.68	110.79
2	B	59	ALA	O-C-N	-5.36	115.47	122.59
4	E	461	GLY	CA-C-O	5.36	129.89	120.57
1	A	223	LEU	N-CA-CB	5.35	118.08	110.16
2	B	233	ILE	N-CA-CB	5.35	116.24	110.62
3	C	141	TRP	CB-CG-CD2	-5.35	119.31	126.80
2	B	217	PRO	CA-C-O	-5.35	110.86	120.60
1	A	214	PHE	O-C-N	-5.35	115.48	122.59
1	D	392	SER	N-CA-CB	5.35	117.98	110.12
1	A	131	ILE	CA-CB-CG2	5.35	119.59	110.50
2	B	242	PRO	N-CA-C	5.35	117.22	110.70
1	A	86	TRP	O-C-N	-5.34	116.69	123.05
2	B	101	GLU	CA-C-O	-5.34	113.84	120.57
1	D	137	PHE	CA-C-N	5.34	131.20	122.65
1	D	137	PHE	C-N-CA	5.34	131.20	122.65
4	E	69	SER	CA-C-O	-5.34	112.82	119.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	288	ILE	CB-CA-C	-5.34	102.53	111.29
3	C	318	SER	CB-CA-C	5.34	119.16	110.24
1	D	17	LYS	CA-C-N	5.34	127.29	120.56
1	D	17	LYS	C-N-CA	5.34	127.29	120.56
3	C	240	SER	N-CA-CB	5.34	119.51	110.49
3	C	299	VAL	N-CA-CB	5.34	120.04	111.23
1	D	78	ILE	CB-CG1-CD1	5.34	125.02	113.80
4	E	438	ASN	CA-C-O	-5.34	112.87	120.51
4	E	449	ALA	CA-C-O	-5.34	112.81	119.38
1	A	111	ASP	O-C-N	-5.34	116.94	123.19
1	A	126	SER	N-CA-C	5.34	117.98	109.81
3	C	473	PHE	CB-CG-CD1	5.34	129.77	120.70
1	D	95	ASN	CB-CG-OD1	5.34	131.47	120.80
4	E	273	PRO	O-C-N	5.34	129.85	122.64
1	A	261	VAL	CA-C-O	-5.33	114.86	120.57
1	D	395	ALA	O-C-N	-5.33	116.12	122.20
4	E	306	VAL	O-C-N	-5.33	116.31	122.17
1	A	94	ASN	CA-C-N	5.33	131.72	121.54
1	A	94	ASN	C-N-CA	5.33	131.72	121.54
2	B	442	ILE	CA-C-N	5.33	127.73	120.54
2	B	442	ILE	C-N-CA	5.33	127.73	120.54
3	C	184	PHE	CA-CB-CG	5.33	119.13	113.80
3	C	203	GLY	O-C-N	-5.33	117.94	123.48
2	B	139	TRP	CB-CG-CD2	5.33	134.26	126.80
2	B	219	PHE	CD1-CG-CD2	-5.33	110.61	118.60
2	B	236	ILE	CB-CG1-CD1	5.33	124.98	113.80
3	C	255	GLU	N-CA-C	5.33	119.04	112.54
3	C	302	VAL	CA-CB-CG1	5.33	119.45	110.40
1	D	385	HIS	CB-CA-C	-5.33	102.48	110.90
3	C	178	ILE	CA-C-N	5.32	129.97	123.10
3	C	178	ILE	C-N-CA	5.32	129.97	123.10
1	D	217	ASN	CA-C-O	-5.32	113.08	119.15
1	A	84	ASP	O-C-N	-5.32	115.51	122.59
2	B	197	TRP	CZ3-CH2-CZ2	5.32	128.42	121.50
1	D	433	LEU	CB-CA-C	5.32	121.02	110.17
2	B	110	VAL	N-CA-CB	-5.32	104.76	111.46
2	B	113	THR	CB-CA-C	-5.32	104.68	111.22
3	C	313	HIS	ND1-CE1-NE2	-5.32	103.08	108.40
4	E	306	VAL	CA-C-O	-5.32	114.22	118.90
1	D	60	TRP	CA-C-N	5.31	131.07	122.68
1	D	60	TRP	C-N-CA	5.31	131.07	122.68
1	D	397	GLU	CA-C-N	5.31	129.71	120.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	397	GLU	C-N-CA	5.31	129.71	120.68
4	E	289	VAL	N-CA-C	5.31	115.45	110.30
2	B	190	HIS	ND1-CE1-NE2	-5.31	103.09	108.40
1	D	112	TYR	CB-CA-C	5.31	119.71	110.79
2	B	2	VAL	CA-CB-CG1	-5.31	101.38	110.40
1	D	397	GLU	N-CA-C	-5.31	106.48	113.12
3	C	456	LEU	CD1-CG-CD2	5.31	122.47	110.80
1	D	429	ARG	CA-C-O	-5.30	115.25	120.82
4	E	226	ILE	CA-C-O	-5.30	115.55	121.17
1	A	80	LEU	N-CA-C	-5.30	100.92	109.40
3	C	94	LEU	N-CA-C	-5.30	102.48	110.70
1	A	257	LEU	N-CA-CB	5.30	118.01	110.06
2	B	462	VAL	N-CA-CB	-5.30	103.79	111.21
1	A	234	TYR	CG-CD1-CE1	5.30	129.15	121.20
3	C	151	LEU	CA-C-O	5.30	127.22	121.02
4	E	418	ALA	N-CA-CB	5.29	117.87	109.82
3	C	2	ASN	CA-C-N	-5.29	114.50	122.07
3	C	2	ASN	C-N-CA	-5.29	114.50	122.07
3	C	182	GLU	CB-CG-CD	5.29	121.60	112.60
3	C	315	ARG	NE-CZ-NH2	5.29	123.96	119.20
3	C	68	THR	O-C-N	5.29	129.63	122.59
1	D	151	TYR	CB-CA-C	5.29	118.94	110.16
1	D	175	GLU	N-CA-C	-5.29	99.53	110.80
3	C	2	ASN	CB-CG-ND2	5.29	124.33	116.40
3	C	106	TYR	O-C-N	-5.29	117.03	123.27
4	E	47	GLU	CA-C-N	5.29	130.87	122.62
4	E	47	GLU	C-N-CA	5.29	130.87	122.62
1	D	15	TYR	CB-CG-CD1	-5.29	112.87	120.80
4	E	455	LEU	CA-C-O	5.29	126.16	120.55
3	C	76	ASP	CA-C-O	-5.29	112.95	120.51
4	E	128	PRO	CB-CA-C	5.29	120.28	111.56
1	D	221	PRO	N-CD-CG	-5.28	95.27	103.20
1	D	54	VAL	CA-C-N	-5.28	115.39	122.42
1	D	54	VAL	C-N-CA	-5.28	115.39	122.42
2	B	275	LEU	N-CA-CB	5.28	119.42	110.49
3	C	319	THR	CA-CB-OG1	-5.28	101.68	109.60
1	D	166	ASP	CA-C-N	-5.28	111.75	122.31
1	D	166	ASP	C-N-CA	-5.28	111.75	122.31
2	B	139	TRP	N-CA-CB	5.28	119.41	110.49
3	C	186	GLU	N-CA-CB	5.28	119.28	110.41
1	A	45	GLU	CA-CB-CG	-5.28	103.54	114.10
2	B	129	THR	O-C-N	5.28	129.61	122.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	130	ILE	CA-C-O	-5.28	114.92	120.57
3	C	93	VAL	CA-C-N	5.28	130.02	122.21
3	C	93	VAL	C-N-CA	5.28	130.02	122.21
4	E	258	LEU	O-C-N	-5.28	116.53	122.12
1	A	418	CYS	N-CA-CB	5.27	118.12	110.47
1	D	235	LEU	N-CA-C	5.27	121.47	109.81
4	E	427	LYS	CA-CB-CG	5.27	124.65	114.10
4	E	431	ASP	CA-C-O	-5.27	112.97	120.51
2	B	134	TYR	N-CA-C	-5.27	104.86	113.19
3	C	449	VAL	CG1-CB-CG2	-5.27	99.21	110.80
4	E	199	THR	CA-CB-OG1	5.27	117.50	109.60
1	A	67	TRP	CB-CG-CD1	-5.26	119.00	126.90
1	A	294	VAL	CA-C-N	5.26	127.39	120.60
1	A	294	VAL	C-N-CA	5.26	127.39	120.60
2	B	44	ASN	OD1-CG-ND2	-5.26	117.34	122.60
1	D	60	TRP	CB-CA-C	5.26	122.75	111.91
4	E	29	ASP	N-CA-C	5.26	117.20	108.20
1	A	422	THR	CB-CA-C	5.26	119.52	110.79
1	D	178	MET	CA-C-O	5.26	128.08	121.66
2	B	461	ASN	CA-C-N	5.26	131.86	122.13
2	B	461	ASN	C-N-CA	5.26	131.86	122.13
1	A	6	ARG	NH1-CZ-NH2	-5.26	112.47	119.30
1	A	264	ILE	N-CA-C	5.26	120.23	108.88
1	A	306	HIS	CA-CB-CG	5.26	119.06	113.80
2	B	289	ILE	N-CA-CB	5.26	116.34	110.51
1	D	386	MET	O-C-N	5.26	127.69	122.12
3	C	155	ALA	CA-C-N	5.25	130.46	122.37
3	C	155	ALA	C-N-CA	5.25	130.46	122.37
4	E	440	VAL	N-CA-C	5.25	115.69	110.23
1	A	268	SER	N-CA-C	-5.25	104.61	111.02
2	B	234	LEU	CA-C-O	5.25	126.04	120.10
1	D	418	CYS	O-C-N	-5.25	116.55	122.12
4	E	147	SER	O-C-N	-5.25	116.56	123.02
1	A	391	GLU	N-CA-CB	5.25	119.36	110.49
3	C	35	LEU	CA-C-N	5.25	130.40	123.00
3	C	35	LEU	C-N-CA	5.25	130.40	123.00
3	C	454	ASP	CA-CB-CG	-5.25	107.35	112.60
1	D	24	HIS	CA-C-N	5.25	131.57	121.54
1	D	24	HIS	C-N-CA	5.25	131.57	121.54
2	B	148	SER	N-CA-C	-5.25	101.60	109.79
2	B	269	LYS	CB-CA-C	-5.25	102.61	110.90
1	A	217	ASN	N-CA-CB	-5.25	101.62	110.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	72	TYR	O-C-N	5.25	128.36	122.32
1	D	302	SER	N-CA-CB	-5.25	103.35	110.23
4	E	298	THR	O-C-N	5.25	129.56	122.59
2	B	111	GLN	OE1-CD-NE2	-5.24	117.36	122.60
3	C	101	GLN	CB-CG-CD	5.24	121.51	112.60
4	E	13	ASP	N-CA-CB	5.24	119.35	110.49
2	B	139	TRP	CA-CB-CG	-5.24	103.64	113.60
2	B	184	GLY	N-CA-C	5.24	125.60	113.18
3	C	63	TYR	N-CA-CB	5.24	117.79	109.51
3	C	129	SER	O-C-N	5.24	130.64	122.67
3	C	317	PRO	CA-C-O	-5.24	111.68	119.86
3	C	424	ASP	CA-C-O	-5.24	114.87	120.42
4	E	429	GLN	CB-CG-CD	5.24	121.50	112.60
2	B	10	VAL	CA-CB-CG1	5.24	119.30	110.40
3	C	459	PHE	N-CA-C	5.24	119.38	113.15
4	E	133	TYR	CG-CD2-CE2	5.24	129.06	121.20
2	B	306	HIS	CG-CD2-NE2	-5.24	101.96	107.20
3	C	270	PHE	O-C-N	5.24	128.12	122.15
3	C	275	SER	CA-C-N	5.24	129.53	120.58
3	C	275	SER	C-N-CA	5.24	129.53	120.58
3	C	301	GLY	O-C-N	5.24	129.51	122.70
4	E	30	VAL	CA-C-N	5.23	129.94	122.72
4	E	30	VAL	C-N-CA	5.23	129.94	122.72
4	E	47	GLU	CA-CB-CG	5.23	124.56	114.10
1	A	54	VAL	N-CA-C	5.23	116.01	108.48
1	D	257	LEU	CA-C-N	5.23	127.60	120.54
1	D	257	LEU	C-N-CA	5.23	127.60	120.54
4	E	99	PHE	CD1-CG-CD2	5.23	126.45	118.60
2	B	186	TRP	O-C-N	-5.23	117.09	122.84
2	B	47	ASN	N-CA-C	-5.23	107.28	113.97
2	B	428	TRP	CE3-CZ3-CH2	-5.23	114.30	121.10
4	E	208	ILE	N-CA-CB	-5.23	105.41	112.10
2	B	286	PHE	CA-C-O	-5.22	113.62	119.79
3	C	14	VAL	N-CA-C	5.22	120.21	109.34
3	C	232	PHE	CD1-CG-CD2	-5.22	110.76	118.60
4	E	29	ASP	O-C-N	-5.22	116.83	123.05
2	B	96	ASN	CA-C-N	5.22	131.52	121.54
2	B	96	ASN	C-N-CA	5.22	131.52	121.54
3	C	226	LEU	O-C-N	-5.22	114.90	121.95
2	B	96	ASN	CB-CG-OD1	5.22	131.24	120.80
2	B	235	ALA	N-CA-CB	-5.22	101.67	110.49
1	D	17	LYS	CB-CG-CD	5.22	123.31	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	47	ASN	CA-C-O	-5.22	112.69	118.69
1	D	129	GLU	CA-C-N	-5.22	112.58	121.97
1	D	129	GLU	C-N-CA	-5.22	112.58	121.97
1	A	101	ALA	CA-C-O	-5.21	115.12	120.54
1	A	112	TYR	CD1-CG-CD2	-5.21	110.28	118.10
1	A	228	LEU	N-CA-CB	5.21	117.63	110.07
1	A	402	VAL	N-CA-CB	5.21	119.61	110.49
3	C	120	TRP	O-C-N	-5.21	117.22	123.27
3	C	482	PRO	CA-CB-CG	-5.21	94.59	104.50
4	E	311	PRO	N-CA-C	-5.21	105.34	113.78
1	A	408	HIS	CB-CG-CD2	-5.21	124.43	131.20
2	B	27	ASP	CA-CB-CG	5.21	117.81	112.60
4	E	439	TRP	CB-CG-CD1	-5.21	119.09	126.90
1	A	12	LEU	CA-C-O	-5.21	115.35	120.82
1	A	95	ASN	CB-CA-C	5.21	120.78	110.42
1	A	273	LEU	CA-C-N	-5.21	113.37	121.18
1	A	273	LEU	C-N-CA	-5.21	113.37	121.18
1	D	255	VAL	O-C-N	-5.21	116.61	121.87
4	E	145	PHE	O-C-N	-5.21	116.84	123.24
1	A	198	TYR	O-C-N	5.20	129.51	122.59
1	D	16	ASN	CA-C-N	-5.20	114.12	122.08
1	D	16	ASN	C-N-CA	-5.20	114.12	122.08
1	D	230	VAL	CB-CA-C	5.20	119.40	112.22
1	D	250	LEU	CA-C-N	5.20	127.51	120.38
1	D	250	LEU	C-N-CA	5.20	127.51	120.38
1	D	35	LEU	N-CA-CB	5.20	119.11	110.63
1	A	220	ILE	N-CA-C	5.20	120.11	108.88
1	A	193	CYS	CA-C-N	5.20	126.34	119.84
1	A	193	CYS	C-N-CA	5.20	126.34	119.84
3	C	445	ASN	CA-C-N	5.20	128.62	120.82
3	C	445	ASN	C-N-CA	5.20	128.62	120.82
1	D	118	TRP	CE2-CD2-CE3	-5.20	113.60	118.80
1	D	86	TRP	N-CA-CB	-5.20	102.80	110.49
1	A	64	ARG	NE-CZ-NH1	-5.19	116.31	121.50
1	A	429	ARG	NE-CZ-NH2	-5.19	114.53	119.20
3	C	279	PRO	N-CD-CG	-5.19	95.41	103.20
3	C	85	GLU	O-C-N	-5.19	115.38	122.33
1	D	150	THR	N-CA-CB	5.19	117.72	110.56
1	A	172	GLU	N-CA-CB	-5.18	102.02	110.42
1	A	185	LYS	O-C-N	-5.18	116.27	122.65
2	B	448	SER	CA-C-O	-5.18	115.01	120.71
3	C	196	PRO	O-C-N	-5.18	116.67	123.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	67	TRP	CH2-CZ2-CE2	5.18	124.24	117.50
4	E	87	PRO	N-CD-CG	-5.18	95.42	103.20
1	D	55	ARG	N-CA-C	-5.18	100.07	108.41
2	B	254	SER	N-CA-C	-5.18	105.81	111.82
2	B	221	ILE	O-C-N	-5.18	116.64	121.87
2	B	247	GLU	CA-C-N	5.18	128.88	120.60
2	B	247	GLU	C-N-CA	5.18	128.88	120.60
3	C	66	ARG	CA-C-O	-5.18	112.48	119.11
3	C	162	LEU	N-CA-CB	5.18	119.30	110.50
3	C	435	GLU	CA-C-N	5.18	131.43	121.54
3	C	435	GLU	C-N-CA	5.18	131.43	121.54
4	E	12	GLY	CA-C-O	-5.18	111.56	120.57
4	E	125	SER	CA-C-N	5.18	132.82	122.62
4	E	125	SER	C-N-CA	5.18	132.82	122.62
3	C	115	ASN	CA-C-N	5.17	131.55	121.41
3	C	115	ASN	C-N-CA	5.17	131.55	121.41
2	B	420	GLU	O-C-N	5.17	128.96	122.23
4	E	223	ILE	O-C-N	-5.17	115.38	122.26
2	B	302	LEU	O-C-N	5.17	127.60	122.12
1	A	120	PRO	CB-CA-C	5.17	117.22	110.92
1	A	209	ARG	CD-NE-CZ	5.17	131.63	124.40
2	B	66	GLN	CG-CD-NE2	-5.17	108.65	116.40
3	C	153	TYR	CA-CB-CG	-5.17	104.60	113.90
4	E	98	GLN	N-CA-CB	5.17	119.22	110.49
3	C	277	ARG	O-C-N	-5.17	115.33	122.46
3	C	280	GLU	N-CA-C	5.17	117.32	111.02
4	E	198	LEU	CA-CB-CG	5.17	134.38	116.30
2	B	138	ASP	OD1-CG-OD2	-5.17	110.50	122.90
3	C	480	ARG	CA-C-O	-5.17	113.08	120.16
1	A	45	GLU	CA-C-N	-5.16	112.68	121.97
1	A	45	GLU	C-N-CA	-5.16	112.68	121.97
2	B	240	TYR	CA-C-O	-5.16	112.76	118.69
3	C	62	TRP	N-CA-C	-5.16	100.67	108.46
1	D	161	GLU	CB-CA-C	5.16	117.34	109.34
1	A	105	MET	N-CA-CB	-5.16	103.50	111.65
2	B	287	ILE	O-C-N	5.16	128.81	122.05
1	D	174	GLY	O-C-N	-5.16	116.00	122.70
1	A	136	PRO	CA-N-CD	5.16	119.22	112.00
1	D	266	SER	CB-CA-C	-5.16	102.13	110.79
1	D	188	VAL	O-C-N	5.15	127.71	122.71
4	E	311	PRO	CA-N-CD	-5.15	104.78	112.00
2	B	269	LYS	CA-C-O	-5.15	115.39	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	VAL	CA-C-N	5.15	127.18	120.28
2	B	301	VAL	C-N-CA	5.15	127.18	120.28
2	B	447	CYS	CA-CB-SG	-5.15	102.55	114.40
3	C	294	PHE	CA-CB-CG	5.15	118.95	113.80
1	A	162	SER	O-C-N	-5.15	115.74	122.59
1	A	189	TYR	CD1-CG-CD2	5.15	125.82	118.10
3	C	18	ASN	N-CA-CB	-5.15	101.74	109.88
4	E	427	LYS	N-CA-CB	5.15	119.19	110.49
2	B	272	GLU	CA-C-N	5.15	130.99	121.52
2	B	272	GLU	C-N-CA	5.15	130.99	121.52
3	C	104	VAL	CA-CB-CG2	5.15	119.15	110.40
3	C	137	PHE	CD1-CE1-CZ	5.14	129.26	120.00
3	C	433	ILE	CA-C-N	5.14	131.36	121.54
3	C	433	ILE	C-N-CA	5.14	131.36	121.54
1	D	294	VAL	N-CA-C	5.14	115.29	110.30
4	E	106	ASN	N-CA-C	-5.14	102.99	110.24
3	C	9	ASN	O-C-N	-5.14	115.47	122.36
2	B	284	LEU	CB-CA-C	5.14	120.65	110.42
1	D	43	VAL	O-C-N	5.14	129.05	123.09
2	B	282	SER	O-C-N	-5.14	116.75	122.09
4	E	238	LEU	CA-C-O	-5.14	113.89	120.31
2	B	106	VAL	CA-C-O	-5.14	114.88	120.84
3	C	129	SER	N-CA-C	5.14	117.12	110.65
1	A	262	GLU	CA-C-O	5.13	125.86	120.42
1	A	436	GLU	N-CA-CB	5.13	119.17	110.49
1	A	396	ALA	O-C-N	5.13	129.42	122.59
2	B	35	LEU	N-CA-C	5.13	116.88	108.52
3	C	222	ARG	NE-CZ-NH1	5.13	126.63	121.50
4	E	284	LYS	N-CA-C	5.13	121.73	110.80
1	A	174	GLY	O-C-N	-5.13	116.60	122.91
1	A	254	THR	CA-C-O	-5.13	114.31	120.10
2	B	207	VAL	CA-C-N	5.13	129.63	121.99
2	B	207	VAL	C-N-CA	5.13	129.63	121.99
4	E	266	PHE	CA-C-O	-5.13	115.09	120.63
1	A	21	PRO	CA-C-N	5.13	130.07	123.10
1	A	21	PRO	C-N-CA	5.13	130.07	123.10
1	A	380	LYS	O-C-N	-5.13	115.56	122.43
2	B	257	LEU	CB-CA-C	-5.13	102.23	110.74
1	D	244	THR	CA-CB-CG2	-5.13	101.79	110.50
4	E	194	TYR	O-C-N	-5.13	115.97	122.43
4	E	313	THR	O-C-N	5.13	130.61	122.41
2	B	232	SER	CA-C-N	-5.12	114.06	120.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	232	SER	C-N-CA	-5.12	114.06	120.77
4	E	424	LYS	O-C-N	-5.12	115.73	122.39
4	E	239	VAL	CB-CA-C	-5.12	102.89	111.29
3	C	24	VAL	O-C-N	-5.12	116.67	122.05
3	C	81	ARG	NE-CZ-NH2	5.12	123.81	119.20
1	D	120	PRO	O-C-N	-5.12	115.42	121.46
2	B	139	TRP	CB-CG-CD1	-5.12	119.23	126.90
1	A	111	ASP	CB-CA-C	5.11	118.07	109.48
3	C	468	GLY	CA-C-O	-5.11	115.48	120.75
1	D	117	MET	CB-CG-SD	5.11	128.04	112.70
4	E	139	GLN	CA-C-N	-5.11	114.31	121.72
4	E	139	GLN	C-N-CA	-5.11	114.31	121.72
1	A	100	PHE	CA-CB-CG	5.11	118.91	113.80
1	A	390	GLU	N-CA-C	5.11	119.00	112.87
4	E	313	THR	CA-C-O	-5.11	110.73	118.91
3	C	293	MET	N-CA-CB	5.11	117.69	110.13
2	B	65	LEU	N-CA-C	5.11	120.14	112.94
2	B	149	TYR	O-C-N	-5.11	115.88	122.21
4	E	273	PRO	N-CA-C	-5.11	101.95	112.47
2	B	201	ASP	CB-CA-C	5.11	116.31	109.42
2	B	422	ASP	O-C-N	-5.11	116.71	122.12
2	B	427	ASP	CA-C-O	5.11	125.96	120.55
1	D	18	VAL	CA-CB-CG2	5.11	119.08	110.40
1	A	112	TYR	CB-CG-CD2	5.10	128.45	120.80
4	E	118	LEU	CA-C-O	-5.10	113.17	120.16
4	E	153	HIS	CB-CA-C	5.10	120.58	110.17
1	A	14	ASN	CA-C-N	5.10	131.28	121.54
1	A	14	ASN	C-N-CA	5.10	131.28	121.54
1	A	397	GLU	CB-CG-CD	-5.10	103.93	112.60
3	C	49	ASP	N-CA-C	5.10	119.19	112.92
3	C	319	THR	O-C-N	-5.10	115.49	122.33
2	B	113	THR	N-CA-C	-5.10	105.78	112.72
1	D	251	LEU	CB-CA-C	-5.10	102.01	110.68
4	E	66	TRP	CE3-CZ3-CH2	5.10	127.73	121.10
2	B	69	PRO	CA-N-CD	-5.10	104.86	112.00
3	C	84	PRO	CA-N-CD	-5.10	104.86	112.00
3	C	226	LEU	CB-CA-C	5.10	120.17	111.46
4	E	151	ASN	N-CA-CB	-5.10	102.70	110.65
1	A	299	HIS	N-CA-CB	-5.10	101.47	109.78
3	C	121	LEU	O-C-N	5.10	127.18	121.32
1	D	275	GLY	CA-C-N	5.10	131.27	121.54
1	D	275	GLY	C-N-CA	5.10	131.27	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	44	ASN	N-CA-CB	5.09	120.03	110.56
2	B	180	PHE	CG-CD1-CE1	-5.09	112.04	120.70
3	C	423	ILE	N-CA-C	5.09	117.42	111.05
3	C	435	GLU	O-C-N	5.09	127.33	122.03
1	D	299	HIS	CB-CG-ND1	-5.09	115.06	122.70
4	E	265	LEU	CB-CA-C	-5.09	100.28	110.42
4	E	239	VAL	CA-CB-CG1	5.09	119.06	110.40
1	A	95	ASN	CA-C-N	-5.09	115.81	124.31
1	A	95	ASN	C-N-CA	-5.09	115.81	124.31
3	C	449	VAL	CA-CB-CG2	5.09	119.05	110.40
4	E	90	VAL	CA-C-N	5.09	130.41	122.26
4	E	90	VAL	C-N-CA	5.09	130.41	122.26
1	A	391	GLU	O-C-N	5.09	129.35	122.59
1	D	10	ASN	CA-C-O	-5.09	115.46	120.70
2	B	69	PRO	CA-CB-CG	-5.08	94.85	104.50
4	E	201	ASP	CA-CB-CG	5.08	117.68	112.60
1	A	253	LEU	N-CA-C	5.08	119.35	112.04
2	B	264	LEU	N-CA-C	5.08	116.50	110.97
3	C	222	ARG	NE-CZ-NH2	5.08	123.77	119.20
1	D	380	LYS	CD-CE-NZ	5.08	128.14	111.90
1	A	127	TYR	CA-C-O	-5.07	113.86	120.25
1	D	87	LEU	O-C-N	-5.07	116.89	121.31
1	D	72	TYR	CA-C-N	5.07	131.35	121.41
1	D	72	TYR	C-N-CA	5.07	131.35	121.41
4	E	125	SER	O-C-N	-5.07	116.99	122.92
1	A	186	HIS	CG-CD2-NE2	5.07	112.27	107.20
3	C	430	VAL	CB-CA-C	-5.07	105.22	112.22
1	D	25	HIS	CA-C-O	-5.07	113.26	120.51
3	C	427	ASN	CB-CG-ND2	-5.07	108.80	116.40
3	C	460	ILE	CA-C-O	-5.07	116.29	120.80
1	A	165	PRO	CA-C-O	-5.07	115.02	122.31
4	E	3	GLU	N-CA-C	5.07	117.46	111.33
1	D	138	ASP	CA-CB-CG	5.06	117.66	112.60
2	B	196	ASN	CB-CG-ND2	-5.06	108.81	116.40
2	B	464	PRO	O-C-N	-5.06	115.81	122.64
3	C	97	ASN	OD1-CG-ND2	5.06	127.66	122.60
1	D	225	PHE	CB-CG-CD1	5.06	129.31	120.70
2	B	254	SER	CA-C-N	5.06	127.33	120.65
2	B	254	SER	C-N-CA	5.06	127.33	120.65
1	D	219	ILE	O-C-N	-5.06	116.64	121.90
4	E	472	ASN	O-C-N	5.06	128.32	122.25
2	B	113	THR	CA-C-O	-5.06	111.31	120.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	280	ILE	CA-C-N	5.06	131.07	121.97
2	B	280	ILE	C-N-CA	5.06	131.07	121.97
3	C	99	ASP	CA-C-N	5.06	131.32	121.41
3	C	99	ASP	C-N-CA	5.06	131.32	121.41
3	C	189	GLU	CA-C-O	-5.06	113.16	119.38
3	C	319	THR	CB-CA-C	-5.06	100.06	110.38
4	E	8	GLU	CA-C-N	5.06	131.20	121.54
4	E	8	GLU	C-N-CA	5.06	131.20	121.54
4	E	176	ASP	OD1-CG-OD2	5.06	135.04	122.90
4	E	268	ILE	N-CA-CB	5.06	119.76	110.40
1	A	434	SER	CA-C-O	-5.05	113.53	119.24
2	B	421	PHE	N-CA-CB	5.05	118.11	110.28
2	B	430	TYR	CA-C-N	5.05	128.93	120.64
2	B	430	TYR	C-N-CA	5.05	128.93	120.64
1	D	38	ILE	O-C-N	5.05	127.06	122.06
1	A	164	ARG	CA-C-N	5.05	125.77	120.11
1	A	164	ARG	C-N-CA	5.05	125.77	120.11
1	A	154	THR	CA-CB-OG1	5.05	117.18	109.60
1	A	289	ILE	CB-CG1-CD1	5.05	124.41	113.80
2	B	89	ASP	N-CA-C	5.05	121.56	110.80
2	B	190	HIS	CB-CG-ND1	-5.05	115.12	122.70
1	D	426	PHE	CA-C-O	-5.05	113.29	120.51
2	B	279	ILE	N-CA-CB	5.05	119.56	111.23
3	C	456	LEU	O-C-N	5.05	127.92	122.11
1	D	9	ALA	N-CA-C	5.05	116.78	111.28
4	E	272	VAL	N-CA-CB	5.05	118.28	111.21
1	A	160	PRO	CA-C-N	-5.04	113.49	122.42
1	A	160	PRO	C-N-CA	-5.04	113.49	122.42
3	C	288	ILE	N-CA-CB	5.04	119.55	111.23
1	D	234	TYR	CB-CG-CD1	5.04	128.37	120.80
2	B	428	TRP	CE2-CD2-CE3	5.04	123.84	118.80
1	D	170	PHE	CA-C-O	5.04	126.74	121.19
1	D	104	HIS	CG-CD2-NE2	-5.04	102.16	107.20
2	B	468	PHE	CB-CG-CD1	5.04	129.26	120.70
2	B	222	VAL	CA-C-O	-5.04	116.17	121.41
1	A	61	ILE	O-C-N	5.04	128.64	123.05
1	D	234	TYR	N-CA-CB	5.04	117.47	109.82
4	E	100	GLU	CB-CG-CD	5.04	121.16	112.60
1	D	8	VAL	O-C-N	5.03	126.97	121.94
2	B	437	ARG	N-CA-CB	-5.03	102.71	110.16
1	D	239	SER	CA-C-N	5.03	125.67	120.03
1	D	239	SER	C-N-CA	5.03	125.67	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	267	THR	CA-C-O	-5.03	115.20	120.63
3	C	280	GLU	N-CA-CB	-5.03	102.17	109.82
1	A	435	GLN	OE1-CD-NE2	5.03	127.63	122.60
2	B	75	ILE	CA-C-N	5.03	131.15	121.54
2	B	75	ILE	C-N-CA	5.03	131.15	121.54
1	D	89	ASP	O-C-N	5.03	129.01	122.38
4	E	1	ASN	CA-CB-CG	-5.03	107.57	112.60
4	E	438	ASN	CA-C-N	5.03	131.14	121.54
4	E	438	ASN	C-N-CA	5.03	131.14	121.54
2	B	218	LEU	O-C-N	5.03	128.76	122.63
4	E	205	PHE	CA-C-O	5.03	125.84	120.46
2	B	6	THR	O-C-N	-5.02	116.28	122.11
3	C	190	TRP	CA-C-N	5.02	129.83	122.39
3	C	190	TRP	C-N-CA	5.02	129.83	122.39
2	B	70	ALA	O-C-N	-5.02	115.23	122.36
2	B	144	MET	O-C-N	5.02	130.59	122.96
4	E	113	GLY	N-CA-C	-5.02	107.77	116.01
4	E	204	ASP	CB-CA-C	-5.02	102.05	110.29
4	E	291	PHE	CB-CA-C	5.02	120.63	110.38
1	A	30	ASP	N-CA-CB	5.02	117.97	109.94
2	B	133	MET	CA-CB-CG	5.02	124.14	114.10
2	B	203	SER	CA-C-N	-5.02	114.51	121.99
2	B	203	SER	C-N-CA	-5.02	114.51	121.99
2	B	277	VAL	N-CA-C	5.02	119.72	108.88
2	B	306	HIS	CA-C-O	5.02	127.69	120.51
4	E	173	ASP	CA-C-N	-5.02	113.56	119.84
4	E	173	ASP	C-N-CA	-5.02	113.56	119.84
1	A	83	ASP	CA-CB-CG	5.02	117.62	112.60
4	E	211	PHE	N-CA-C	-5.02	102.34	110.32
1	A	26	THR	O-C-N	5.01	129.26	122.59
1	A	430	LEU	N-CA-C	5.01	121.48	110.80
2	B	42	ILE	CA-C-O	5.01	127.05	120.78
2	B	125	ARG	NE-CZ-NH1	5.01	126.51	121.50
2	B	83	ASP	CA-C-O	5.01	127.68	120.51
3	C	455	ARG	O-C-N	-5.01	115.93	122.59
1	D	396	ALA	O-C-N	-5.01	115.12	122.43
4	E	226	ILE	N-CA-C	5.01	115.23	110.42
4	E	444	LYS	CB-CA-C	-5.01	101.53	110.70
1	A	11	LEU	N-CA-CB	5.01	117.33	110.07
1	A	150	THR	CA-CB-CG2	5.01	119.01	110.50
1	A	53	ASN	N-CA-C	5.01	116.80	107.99
4	E	138	TRP	NE1-CE2-CD2	5.01	113.91	107.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	27	HIS	CA-C-O	-5.00	113.70	119.61
1	A	95	ASN	OD1-CG-ND2	5.00	127.61	122.60
1	A	191	THR	N-CA-CB	5.00	119.15	110.39
1	A	409	ILE	CB-CA-C	-5.00	105.53	112.24
1	D	97	ASP	CA-C-O	-5.00	113.35	120.51
1	A	292	THR	OG1-CB-CG2	5.00	119.30	109.30
4	E	25	ASP	O-C-N	5.00	128.07	122.27

All (36) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1	SER	CA
1	A	149	TRP	CA
1	A	162	SER	CA
1	A	267	THR	CB
1	A	304	SER	CA
1	A	305	THR	CB
2	B	84	ASP	CA
2	B	89	ASP	CA
2	B	95	ASN	CA
2	B	141	ASN	CA
2	B	188	ILE	CA
2	B	198	ARG	CA
2	B	215	ARG	CA
2	B	277	VAL	CA
2	B	280	ILE	CA
2	B	307	ARG	CA
2	B	403	GLU	CA
3	C	19	LYS	CA
3	C	162	LEU	CA
3	C	180	ASP	CA
3	C	224	LYS	CA
3	C	421	SER	CA
1	D	26	THR	CA
1	D	102	ILE	CB
1	D	106	THR	CB,CA
1	D	130	ILE	CB
4	E	68	THR	CB,CA
4	E	110	TYR	CA
4	E	118	LEU	CA
4	E	126	THR	CA
4	E	148	GLN	CA

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Mol	Chain	Res	Type	Atom
4	E	173	ASP	CA
4	E	244	ALA	CA
4	E	414	SER	CA

All (608) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	102	ILE	Mainchain
1	A	104	HIS	Mainchain
1	A	110	LEU	Mainchain
1	A	111	ASP	Mainchain
1	A	112	TYR	Mainchain
1	A	113	THR	Mainchain
1	A	114	GLY	Mainchain
1	A	115	LYS	Mainchain
1	A	119	THR	Mainchain
1	A	127	TYR	Mainchain
1	A	128	CYS	Mainchain
1	A	129	GLU	Mainchain
1	A	132	VAL	Mainchain
1	A	135	PHE	Peptide
1	A	138	ASP	Mainchain
1	A	148	ILE	Mainchain
1	A	150	THR	Mainchain
1	A	151	TYR	Mainchain
1	A	152	ASP	Mainchain
1	A	154	THR	Mainchain
1	A	16	ASN	Mainchain
1	A	160	PRO	Mainchain
1	A	161	GLU	Mainchain,Peptide
1	A	162	SER	Mainchain
1	A	165	PRO	Mainchain
1	A	167	LEU	Mainchain
1	A	169	THR	Mainchain
1	A	175	GLU	Mainchain,Peptide
1	A	178	MET	Mainchain
1	A	191	THR	Mainchain
1	A	197	PRO	Mainchain
1	A	198	TYR	Mainchain
1	A	20	ARG	Mainchain
1	A	207	MET	Mainchain
1	A	208	GLN	Mainchain

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Mol	Chain	Res	Type	Group
1	A	209	ARG	Peptide
1	A	214	PHE	Peptide
1	A	216	VAL	Mainchain
1	A	217	ASN	Mainchain
1	A	219	ILE	Mainchain
1	A	22	VAL	Mainchain
1	A	221	PRO	Mainchain
1	A	222	CYS	Mainchain
1	A	226	SER	Mainchain
1	A	23	GLU	Mainchain
1	A	231	LEU	Mainchain
1	A	233	PHE	Mainchain
1	A	235	LEU	Mainchain
1	A	238	ASP	Mainchain
1	A	240	GLY	Mainchain
1	A	241	GLU	Mainchain
1	A	242	LYS	Mainchain
1	A	243	MET	Mainchain
1	A	244	THR	Mainchain
1	A	245	LEU	Mainchain
1	A	246	SER	Mainchain
1	A	248	SER	Mainchain,Peptide
1	A	252	SER	Mainchain
1	A	253	LEU	Mainchain
1	A	255	VAL	Mainchain
1	A	260	ILE	Mainchain
1	A	264	ILE	Mainchain
1	A	265	PRO	Mainchain
1	A	266	SER	Mainchain
1	A	267	THR	Mainchain
1	A	268	SER	Mainchain
1	A	269	SER	Mainchain
1	A	272	PRO	Mainchain
1	A	274	ILE	Mainchain
1	A	28	PHE	Mainchain
1	A	281	THR	Mainchain
1	A	282	MET	Mainchain
1	A	284	PHE	Mainchain
1	A	285	VAL	Mainchain
1	A	291	VAL	Mainchain
1	A	292	THR	Peptide
1	A	296	ILE	Mainchain

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Mol	Chain	Res	Type	Group
1	A	297	ASN	Mainchain
1	A	300	HIS	Peptide
1	A	301	ARG	Mainchain
1	A	303	PRO	Mainchain
1	A	304	SER	Peptide
1	A	305	THR	Mainchain
1	A	374	SER	Mainchain
1	A	378	GLY	Mainchain
1	A	38	ILE	Mainchain
1	A	386	MET	Mainchain
1	A	388	SER	Mainchain
1	A	389	ASP	Mainchain
1	A	394	ASN	Mainchain
1	A	398	GLU	Mainchain
1	A	400	LYS	Mainchain
1	A	403	ALA	Mainchain
1	A	404	MET	Mainchain
1	A	407	ASP	Mainchain
1	A	408	HIS	Mainchain
1	A	411	LEU	Mainchain
1	A	418	CYS	Mainchain
1	A	419	ILE	Mainchain
1	A	420	ILE	Mainchain
1	A	422	THR	Mainchain
1	A	427	ALA	Mainchain
1	A	431	ILE	Mainchain
1	A	434	SER	Mainchain
1	A	44	ASP	Mainchain
1	A	47	ASN	Mainchain
1	A	48	GLN	Mainchain
1	A	5	THR	Mainchain
1	A	59	GLN	Mainchain
1	A	6	ARG	Peptide
1	A	66	ARG	Mainchain
1	A	69	PRO	Mainchain
1	A	74	GLY	Mainchain
1	A	77	LYS	Mainchain
1	A	84	ASP	Mainchain
1	A	86	TRP	Mainchain
1	A	97	ASP	Mainchain,Peptide
1	A	98	GLY	Mainchain
2	B	1	SER	Mainchain

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Mol	Chain	Res	Type	Group
2	B	103	THR	Mainchain
2	B	105	HIS	Mainchain
2	B	106	VAL	Mainchain
2	B	109	LEU	Mainchain
2	B	113	THR	Mainchain
2	B	115	ALA	Mainchain
2	B	116	VAL	Mainchain
2	B	117	SER	Mainchain
2	B	119	HIS	Mainchain
2	B	12	PHE	Mainchain
2	B	130	ILE	Mainchain
2	B	131	LYS	Mainchain
2	B	133	MET	Mainchain
2	B	136	PRO	Mainchain
2	B	14	ASN	Mainchain
2	B	140	GLN	Mainchain,Peptide
2	B	142	CYS	Mainchain
2	B	148	SER	Mainchain
2	B	149	TYR	Mainchain
2	B	151	TYR	Mainchain
2	B	152	ASP	Mainchain
2	B	154	SER	Mainchain
2	B	155	GLU	Peptide
2	B	16	ASN	Mainchain
2	B	160	HIS	Mainchain
2	B	174	MET	Mainchain
2	B	176	ASN	Mainchain
2	B	177	GLN	Mainchain
2	B	178	ASP	Mainchain
2	B	184	GLY	Peptide
2	B	185	GLN	Mainchain
2	B	186	TRP	Mainchain
2	B	188	ILE	Mainchain
2	B	190	HIS	Mainchain
2	B	191	LYS	Mainchain
2	B	192	PRO	Mainchain
2	B	2	VAL	Mainchain
2	B	200	ASP	Mainchain
2	B	203	SER	Mainchain
2	B	204	TYR	Mainchain
2	B	205	GLU	Peptide
2	B	211	LEU	Mainchain

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Mol	Chain	Res	Type	Group
2	B	212	ILE	Mainchain
2	B	214	GLN	Mainchain
2	B	217	PRO	Mainchain
2	B	218	LEU	Mainchain
2	B	219	PHE	Mainchain
2	B	221	ILE	Mainchain
2	B	223	TYR	Mainchain
2	B	224	THR	Mainchain
2	B	225	ILE	Mainchain
2	B	227	PRO	Mainchain
2	B	229	ILE	Mainchain
2	B	237	LEU	Mainchain
2	B	239	PHE	Mainchain
2	B	240	TYR	Mainchain
2	B	241	LEU	Mainchain
2	B	243	PRO	Mainchain
2	B	244	ASP	Mainchain
2	B	245	ALA	Mainchain
2	B	25	VAL	Mainchain
2	B	250	SER	Mainchain
2	B	26	GLY	Peptide
2	B	260	THR	Mainchain
2	B	261	VAL	Mainchain
2	B	262	PHE	Mainchain
2	B	263	LEU	Mainchain
2	B	264	LEU	Mainchain
2	B	266	LEU	Mainchain
2	B	269	LYS	Mainchain
2	B	27	ASP	Mainchain
2	B	274	SER	Mainchain
2	B	276	SER	Peptide
2	B	278	PRO	Mainchain
2	B	279	ILE	Peptide
2	B	28	LYS	Mainchain
2	B	280	ILE	Mainchain
2	B	281	ILE	Mainchain
2	B	282	SER	Mainchain
2	B	288	MET	Mainchain
2	B	290	LEU	Mainchain
2	B	294	SER	Mainchain
2	B	299	VAL	Mainchain
2	B	300	VAL	Mainchain

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Mol	Chain	Res	Type	Group
2	B	303	ASN	Mainchain
2	B	305	HIS	Mainchain
2	B	306	HIS	Peptide
2	B	307	ARG	Mainchain
2	B	308	SER	Mainchain
2	B	38	THR	Mainchain
2	B	4	GLU	Mainchain
2	B	404	ALA	Mainchain
2	B	405	VAL	Mainchain
2	B	406	GLU	Mainchain
2	B	407	ALA	Mainchain
2	B	411	ILE	Mainchain
2	B	412	ALA	Mainchain
2	B	429	GLN	Mainchain
2	B	433	MET	Mainchain
2	B	434	VAL	Mainchain
2	B	439	PHE	Mainchain
2	B	447	CYS	Mainchain
2	B	450	GLY	Mainchain
2	B	453	SER	Mainchain
2	B	457	ASP	Mainchain
2	B	461	ASN	Mainchain
2	B	463	PRO	Mainchain
2	B	465	ASP	Mainchain
2	B	467	PRO	Mainchain
2	B	47	ASN	Mainchain
2	B	55	PHE	Mainchain
2	B	56	LEU	Mainchain
2	B	59	ALA	Mainchain
2	B	62	ASP	Mainchain
2	B	74	GLY	Mainchain
2	B	81	PRO	Mainchain
2	B	83	ASP	Mainchain
2	B	84	ASP	Mainchain
2	B	85	VAL	Peptide
2	B	88	PRO	Peptide
2	B	89	ASP	Mainchain
2	B	9	SER	Mainchain
2	B	92	LEU	Mainchain
2	B	94	ASN	Peptide
2	B	95	ASN	Mainchain
2	B	99	SER	Mainchain

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Mol	Chain	Res	Type	Group
3	C	1	VAL	Peptide
3	C	10	ASP	Mainchain
3	C	106	TYR	Mainchain
3	C	108	CYS	Mainchain
3	C	11	LEU	Mainchain
3	C	112	VAL	Mainchain
3	C	114	PRO	Mainchain
3	C	118	VAL	Mainchain
3	C	12	LEU	Mainchain
3	C	13	ILE	Mainchain
3	C	130	CYS	Mainchain
3	C	131	PRO	Mainchain
3	C	135	LEU	Mainchain
3	C	142	GLN	Mainchain
3	C	158	ILE	Mainchain
3	C	178	ILE	Mainchain
3	C	179	ILE	Peptide
3	C	180	ASP	Mainchain
3	C	181	PRO	Mainchain
3	C	183	ALA	Mainchain
3	C	187	ASN	Mainchain,Peptide
3	C	188	GLY	Mainchain
3	C	189	GLU	Mainchain
3	C	193	ILE	Mainchain
3	C	196	PRO	Mainchain
3	C	203	GLY	Mainchain
3	C	204	ASP	Mainchain
3	C	21	VAL	Mainchain
3	C	211	ASN	Mainchain
3	C	212	TYR	Mainchain
3	C	221	ILE	Mainchain
3	C	222	ARG	Mainchain
3	C	224	LYS	Mainchain
3	C	226	LEU	Mainchain
3	C	23	PRO	Mainchain
3	C	239	ILE	Mainchain
3	C	242	LEU	Mainchain
3	C	244	ALA	Mainchain
3	C	248	TYR	Mainchain
3	C	252	GLU	Mainchain
3	C	26	HIS	Mainchain
3	C	261	ILE	Mainchain

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Mol	Chain	Res	Type	Group
3	C	263	VAL	Mainchain
3	C	266	ALA	Mainchain
3	C	267	GLN	Mainchain
3	C	268	ALA	Mainchain
3	C	273	LEU	Mainchain
3	C	275	SER	Mainchain
3	C	277	ARG	Mainchain
3	C	284	ALA	Mainchain
3	C	285	VAL	Mainchain
3	C	286	PRO	Mainchain
3	C	288	ILE	Mainchain
3	C	29	GLU	Mainchain
3	C	291	TYR	Mainchain
3	C	298	LEU	Mainchain
3	C	3	GLU	Mainchain
3	C	30	VAL	Mainchain
3	C	300	THR	Mainchain,Peptide
3	C	301	GLY	Mainchain
3	C	302	VAL	Mainchain,Peptide
3	C	305	ASN	Mainchain
3	C	311	ASN	Mainchain
3	C	315	ARG	Mainchain
3	C	319	THR	Mainchain
3	C	422	GLY	Mainchain
3	C	425	SER	Mainchain
3	C	426	THR	Mainchain
3	C	435	GLU	Mainchain
3	C	437	ASN	Mainchain
3	C	439	TYR	Mainchain
3	C	440	ASP	Mainchain
3	C	443	VAL	Mainchain
3	C	445	ASN	Mainchain
3	C	447	ASN	Mainchain
3	C	450	GLY	Mainchain
3	C	451	GLN	Mainchain
3	C	452	THR	Mainchain
3	C	453	ILE	Mainchain
3	C	454	ASP	Mainchain
3	C	455	ARG	Mainchain
3	C	457	SER	Mainchain,Peptide
3	C	46	LYS	Mainchain
3	C	463	PRO	Mainchain

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Mol	Chain	Res	Type	Group
3	C	465	MET	Mainchain
3	C	466	VAL	Mainchain
3	C	467	LEU	Mainchain
3	C	47	GLU	Mainchain
3	C	474	VAL	Mainchain
3	C	475	MET	Mainchain
3	C	476	GLY	Mainchain
3	C	478	PHE	Mainchain
3	C	479	ASN	Mainchain
3	C	48	THR	Mainchain
3	C	481	PRO	Mainchain
3	C	482	PRO	Mainchain
3	C	484	LYS	Mainchain
3	C	49	ASP	Mainchain
3	C	5	GLU	Mainchain
3	C	50	GLU	Mainchain
3	C	67	LEU	Peptide
3	C	75	SER	Mainchain
3	C	78	SER	Mainchain
3	C	8	ILE	Mainchain
3	C	84	PRO	Mainchain
3	C	85	GLU	Mainchain
3	C	86	LEU	Mainchain,Peptide
3	C	87	ILE	Mainchain
3	C	89	ILE	Mainchain
3	C	9	ASN	Mainchain
3	C	90	PRO	Mainchain
3	C	94	LEU	Mainchain
3	C	95	GLN	Mainchain
3	C	97	ASN	Mainchain
3	C	98	ASN	Peptide
1	D	1	SER	Mainchain
1	D	101	ALA	Mainchain,Peptide
1	D	104	HIS	Peptide
1	D	105	MET	Mainchain
1	D	110	LEU	Mainchain
1	D	111	ASP	Mainchain
1	D	113	THR	Mainchain,Peptide
1	D	114	GLY	Mainchain
1	D	118	TRP	Mainchain
1	D	128	CYS	Mainchain
1	D	129	GLU	Mainchain

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Mol	Chain	Res	Type	Group
1	D	135	PHE	Peptide
1	D	137	PHE	Mainchain
1	D	138	ASP	Mainchain
1	D	148	ILE	Mainchain
1	D	150	THR	Mainchain
1	D	16	ASN	Mainchain
1	D	160	PRO	Mainchain
1	D	161	GLU	Peptide
1	D	162	SER	Mainchain
1	D	163	ASP	Mainchain
1	D	165	PRO	Mainchain
1	D	166	ASP	Mainchain
1	D	169	THR	Mainchain
1	D	17	LYS	Mainchain
1	D	173	SER	Peptide
1	D	188	VAL	Mainchain
1	D	194	PRO	Mainchain
1	D	195	ASP	Mainchain
1	D	197	PRO	Peptide
1	D	209	ARG	Mainchain
1	D	212	LEU	Mainchain
1	D	216	VAL	Mainchain
1	D	217	ASN	Mainchain
1	D	219	ILE	Mainchain
1	D	22	VAL	Mainchain
1	D	224	LEU	Mainchain
1	D	228	LEU	Mainchain
1	D	229	THR	Mainchain
1	D	23	GLU	Mainchain
1	D	235	LEU	Mainchain
1	D	238	ASP	Mainchain,Peptide
1	D	244	THR	Mainchain
1	D	246	SER	Mainchain
1	D	252	SER	Mainchain
1	D	255	VAL	Mainchain
1	D	258	LEU	Mainchain
1	D	26	THR	Peptide
1	D	261	VAL	Mainchain
1	D	265	PRO	Mainchain
1	D	268	SER	Mainchain
1	D	275	GLY	Mainchain
1	D	276	LYS	Mainchain

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Mol	Chain	Res	Type	Group
1	D	277	TYR	Mainchain
1	D	281	THR	Mainchain
1	D	285	VAL	Mainchain
1	D	29	VAL	Mainchain
1	D	300	HIS	Mainchain
1	D	302	SER	Mainchain
1	D	303	PRO	Mainchain
1	D	305	THR	Mainchain
1	D	32	THR	Mainchain
1	D	33	VAL	Mainchain
1	D	34	GLY	Mainchain,Peptide
1	D	35	LEU	Mainchain
1	D	374	SER	Peptide
1	D	381	TYR	Mainchain
1	D	384	GLU	Mainchain
1	D	386	MET	Mainchain
1	D	394	ASN	Mainchain
1	D	395	ALA	Mainchain
1	D	396	ALA	Mainchain
1	D	4	GLU	Mainchain
1	D	402	VAL	Mainchain
1	D	404	MET	Mainchain
1	D	410	LEU	Mainchain
1	D	413	VAL	Mainchain
1	D	414	PHE	Mainchain
1	D	416	LEU	Mainchain
1	D	423	VAL	Mainchain
1	D	428	GLY	Mainchain
1	D	432	GLU	Mainchain
1	D	434	SER	Mainchain
1	D	435	GLN	Mainchain
1	D	436	GLU	Mainchain
1	D	44	ASP	Peptide
1	D	46	VAL	Mainchain
1	D	47	ASN	Mainchain
1	D	48	GLN	Mainchain
1	D	49	ILE	Mainchain
1	D	55	ARG	Mainchain
1	D	57	ARG	Mainchain
1	D	62	ASP	Mainchain
1	D	63	VAL	Mainchain
1	D	65	LEU	Mainchain

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Mol	Chain	Res	Type	Group
1	D	72	TYR	Mainchain
1	D	73	GLY	Mainchain,Peptide
1	D	74	GLY	Mainchain
1	D	76	LYS	Mainchain
1	D	77	LYS	Mainchain
1	D	78	ILE	Mainchain
1	D	79	ARG	Mainchain
1	D	80	LEU	Mainchain
1	D	81	PRO	Mainchain
1	D	83	ASP	Mainchain
1	D	84	ASP	Mainchain
1	D	85	VAL	Mainchain
1	D	9	ALA	Mainchain
1	D	90	LEU	Mainchain
1	D	92	LEU	Mainchain
1	D	93	TYR	Mainchain
1	D	94	ASN	Mainchain
1	D	96	ALA	Peptide
1	D	97	ASP	Mainchain
1	D	98	GLY	Peptide
4	E	1	ASN	Mainchain
4	E	10	LEU	Mainchain
4	E	101	VAL	Mainchain
4	E	102	ALA	Mainchain
4	E	104	TYR	Mainchain
4	E	105	ALA	Mainchain
4	E	109	VAL	Peptide
4	E	11	LEU	Mainchain
4	E	110	TYR	Mainchain
4	E	111	ASN	Mainchain
4	E	112	ASP	Mainchain
4	E	118	LEU	Mainchain,Peptide
4	E	122	ILE	Mainchain
4	E	127	CYS	Mainchain
4	E	128	PRO	Mainchain
4	E	132	THR	Peptide
4	E	133	TYR	Mainchain,Peptide
4	E	137	ASP	Mainchain
4	E	139	GLN	Mainchain
4	E	146	ARG	Mainchain
4	E	148	GLN	Peptide
4	E	152	ALA	Mainchain

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Mol	Chain	Res	Type	Group
4	E	154	GLU	Mainchain
4	E	155	VAL	Mainchain
4	E	16	LYS	Mainchain
4	E	160	SER	Peptide
4	E	172	ILE	Mainchain,Peptide
4	E	174	PRO	Mainchain
4	E	18	ILE	Mainchain
4	E	180	ASN	Mainchain,Peptide
4	E	181	GLY	Mainchain,Peptide
4	E	182	GLU	Mainchain
4	E	187	HIS	Mainchain
4	E	189	PRO	Mainchain
4	E	190	ALA	Mainchain
4	E	196	TRP	Mainchain
4	E	201	ASP	Mainchain
4	E	205	PHE	Mainchain
4	E	206	GLN	Mainchain
4	E	217	LYS	Mainchain
4	E	22	LYS	Mainchain
4	E	221	TYR	Mainchain
4	E	226	ILE	Mainchain
4	E	229	CYS	Mainchain
4	E	23	THR	Mainchain
4	E	236	VAL	Mainchain
4	E	237	VAL	Mainchain
4	E	238	LEU	Mainchain
4	E	24	LEU	Mainchain
4	E	245	GLN	Mainchain
4	E	250	LYS	Peptide
4	E	252	THR	Mainchain,Peptide
4	E	26	HIS	Mainchain,Peptide
4	E	260	ALA	Mainchain
4	E	267	LEU	Mainchain
4	E	270	GLN	Mainchain
4	E	271	LYS	Mainchain
4	E	276	SER	Mainchain
4	E	277	LEU	Mainchain
4	E	278	ASN	Mainchain
4	E	279	VAL	Mainchain
4	E	280	PRO	Mainchain
4	E	281	LEU	Mainchain
4	E	287	ILE	Mainchain

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Mol	Chain	Res	Type	Group
4	E	297	VAL	Mainchain
4	E	303	VAL	Mainchain
4	E	305	ASN	Mainchain
4	E	306	VAL	Mainchain
4	E	307	SER	Mainchain
4	E	308	LEU	Mainchain
4	E	310	THR	Mainchain
4	E	39	LEU	Mainchain
4	E	416	VAL	Mainchain
4	E	417	GLU	Mainchain
4	E	425	SER	Mainchain
4	E	428	GLU	Mainchain
4	E	43	ASN	Mainchain
4	E	434	SER	Mainchain
4	E	453	ILE	Mainchain
4	E	455	LEU	Mainchain
4	E	456	LEU	Mainchain
4	E	460	LEU	Mainchain
4	E	463	LEU	Mainchain
4	E	47	GLU	Mainchain
4	E	473	GLN	Mainchain
4	E	476	GLU	Mainchain
4	E	5	ARG	Mainchain
4	E	59	TRP	Mainchain
4	E	61	ASP	Mainchain
4	E	65	SER	Mainchain
4	E	67	ASN	Mainchain,Peptide
4	E	69	SER	Mainchain
4	E	70	GLU	Mainchain
4	E	72	GLU	Mainchain
4	E	73	GLY	Mainchain
4	E	75	ASP	Mainchain
4	E	78	ARG	Mainchain
4	E	79	ILE	Mainchain,Peptide
4	E	81	SER	Mainchain
4	E	82	GLU	Mainchain
4	E	84	LEU	Mainchain
4	E	85	TRP	Mainchain
4	E	92	GLU	Mainchain
4	E	93	ASN	Mainchain
4	E	95	VAL	Mainchain
4	E	96	ASP	Mainchain

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Mol	Chain	Res	Type	Group
4	E	97	GLY	Mainchain
4	E	98	GLN	Mainchain
4	E	99	PHE	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2991	0	3006	925	0
1	D	2991	0	3006	920	0
2	B	2972	0	2953	815	0
3	C	2983	0	2987	908	0
4	E	2987	0	2994	915	0
All	All	14924	0	14946	4319	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 145.

All (4319) 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:D:86:TRP:CD2	1:D:86:TRP:O	1.68	1.44
4:E:217:LYS:O	4:E:217:LYS:CE	1.74	1.36
4:E:284:LYS:N	4:E:284:LYS:HE3	1.42	1.29
3:C:278:LEU:C	3:C:278:LEU:HD12	1.58	1.28
2:B:130:ILE:HB	2:B:134:TYR:CD2	1.67	1.27
1:D:86:TRP:O	1:D:86:TRP:CG	1.83	1.26
4:E:217:LYS:O	4:E:217:LYS:HE3	1.11	1.25
3:C:67:LEU:CB	3:C:116:GLY:HA2	1.66	1.25
4:E:26:HIS:CG	4:E:26:HIS:O	1.92	1.20
3:C:148:PHE:HB2	3:C:215:VAL:CG2	1.72	1.20
1:D:72:TYR:CD1	1:D:72:TYR:C	2.09	1.19
2:B:160:HIS:CE1	2:B:207:VAL:HG11	1.76	1.19
1:D:152:ASP:CB	1:D:197:PRO:HA	1.72	1.19
2:B:176:ASN:HB2	2:B:191:LYS:HB3	1.25	1.18
2:B:297:LEU:CD1	2:B:445:THR:HG21	1.72	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:56:GLU:HB2	4:E:118:LEU:HD22	1.21	1.18
1:A:250:LEU:CD2	1:A:292:THR:HG22	1.72	1.18
3:C:12:LEU:HB2	3:C:16:LYS:HG2	1.18	1.18
1:D:245:LEU:HD21	4:E:255:ILE:HG13	1.24	1.17
4:E:79:ILE:HG12	4:E:80:PRO:HD2	1.22	1.17
2:B:104:LEU:HD12	2:B:118:TRP:CH2	1.80	1.17
3:C:67:LEU:HB3	3:C:116:GLY:CA	1.72	1.17
1:D:189:TYR:HA	1:D:197:PRO:HD2	1.21	1.17
4:E:183:TRP:CB	4:E:216:ARG:HG2	1.75	1.17
3:C:247:PHE:CE1	3:C:309:VAL:HG22	1.80	1.16
1:D:87:LEU:HD12	1:D:88:PRO:HD2	1.19	1.16
2:B:263:LEU:HD22	2:B:291:VAL:HG22	1.27	1.16
1:D:160:PRO:HD3	1:D:185:LYS:HB3	1.23	1.16
1:A:256:PHE:CZ	2:B:261:VAL:HG23	1.80	1.16
4:E:45:LYS:HD2	4:E:46:GLU:HG2	1.26	1.16
4:E:235:LEU:HD12	4:E:235:LEU:O	1.45	1.16
1:A:137:PHE:CE1	1:A:210:ILE:HD12	1.80	1.16
1:A:175:GLU:HB3	1:A:211:PRO:CG	1.75	1.15
1:D:36:GLN:CG	1:D:55:ARG:HG3	1.76	1.15
2:B:248:LYS:CD	2:B:252:SER:HB3	1.74	1.15
1:D:131:ILE:HG13	1:D:133:THR:H	1.09	1.15
1:A:57:ARG:HA	1:A:119:THR:CG2	1.75	1.15
1:D:136:PRO:HG3	1:D:274:ILE:HD11	1.29	1.15
1:D:35:LEU:HD11	1:D:54:VAL:HG11	1.22	1.15
4:E:240:TYR:CD2	4:E:453:ILE:HD13	1.82	1.15
2:B:269:LYS:HE3	2:B:270:VAL:CG2	1.74	1.15
1:D:145:LYS:C	1:D:146:LEU:HD12	1.72	1.15
4:E:129:ILE:HG22	4:E:133:TYR:CD2	1.82	1.15
1:A:57:ARG:CA	1:A:119:THR:HG22	1.78	1.14
1:D:198:TYR:HD1	1:D:198:TYR:N	1.40	1.14
1:A:380:LYS:HB3	2:B:408:ILE:HD13	1.20	1.14
2:B:248:LYS:HD3	2:B:252:SER:CB	1.76	1.14
3:C:285:VAL:O	3:C:285:VAL:CG2	1.81	1.13
1:D:166:ASP:HB2	1:D:181:TYR:CB	1.77	1.13
4:E:138:TRP:CZ2	4:E:215:GLN:HB2	1.84	1.13
4:E:62:TYR:O	4:E:62:TYR:HD1	1.30	1.13
3:C:242:LEU:HD22	3:C:267:GLN:HB3	1.17	1.12
2:B:28:LYS:HB2	2:B:156:VAL:HA	1.29	1.12
4:E:79:ILE:HG12	4:E:80:PRO:CD	1.78	1.12
1:A:133:THR:HA	1:A:274:ILE:HG22	1.13	1.12
2:B:28:LYS:HG2	2:B:155:GLU:HA	1.27	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:175:GLU:HB3	1:D:211:PRO:HD3	1.14	1.12
2:B:133:MET:HG2	2:B:140:GLN:HG3	1.12	1.12
3:C:445:ASN:HA	3:C:448:LEU:HG	1.23	1.12
1:D:145:LYS:CG	1:D:202:THR:HG23	1.78	1.12
2:B:269:LYS:HE3	2:B:270:VAL:HG22	1.17	1.11
3:C:122:PRO:HB2	3:C:123:PRO:HD2	1.14	1.11
3:C:142:GLN:HG3	3:C:143:ASN:H	1.07	1.11
1:A:160:PRO:HG3	1:A:185:LYS:CB	1.80	1.11
1:A:131:ILE:HD11	1:A:140:GLN:CD	1.74	1.11
2:B:176:ASN:HD22	2:B:188:ILE:HG21	1.10	1.10
1:A:380:LYS:CB	2:B:408:ILE:HD13	1.79	1.10
1:D:129:GLU:OE1	1:D:129:GLU:HA	1.37	1.10
4:E:44:GLU:HB3	4:E:280:PRO:CD	1.81	1.10
4:E:90:VAL:HG22	4:E:95:VAL:HG11	1.33	1.10
1:D:175:GLU:HB3	1:D:211:PRO:CD	1.79	1.10
4:E:44:GLU:CG	4:E:280:PRO:HB3	1.79	1.10
4:E:236:VAL:HA	4:E:239:VAL:HG23	1.31	1.10
2:B:87:GLN:HB3	2:B:104:LEU:HD11	1.32	1.10
2:B:91:VAL:HA	2:B:96:ASN:ND2	1.66	1.10
1:A:94:ASN:O	1:A:94:ASN:ND2	1.83	1.10
1:A:130:ILE:HD13	1:A:131:ILE:H	1.07	1.10
1:A:257:LEU:HD13	1:A:285:VAL:HG23	1.31	1.10
3:C:138:PRO:HB3	3:C:290:LYS:HE3	1.27	1.10
1:A:274:ILE:HG12	1:A:277:TYR:HD1	1.15	1.09
3:C:296:MET:HA	3:C:296:MET:HE2	1.32	1.09
1:D:152:ASP:HB3	1:D:197:PRO:HA	1.13	1.09
4:E:44:GLU:HB3	4:E:280:PRO:HD3	1.30	1.09
4:E:44:GLU:CB	4:E:280:PRO:HB3	1.82	1.09
1:D:46:VAL:HA	1:D:272:PRO:CD	1.81	1.09
2:B:153:THR:HB	2:B:204:TYR:HB2	1.18	1.09
2:B:185:GLN:HB3	2:B:219:PHE:HE2	1.11	1.09
3:C:78:SER:C	3:C:114:PRO:HB3	1.78	1.09
1:A:145:LYS:HG3	1:A:202:THR:HG22	1.22	1.09
1:A:175:GLU:HB3	1:A:211:PRO:HG3	1.21	1.09
2:B:236:ILE:HB	2:B:446:MET:HE1	1.12	1.09
3:C:113:ARG:HD2	3:C:117:TYR:HB3	1.18	1.09
1:D:379:VAL:HA	1:D:382:ILE:CG1	1.81	1.09
1:A:236:PRO:HB3	1:A:299:HIS:CE1	1.88	1.09
1:D:145:LYS:HG3	1:D:202:THR:CG2	1.82	1.09
2:B:46:LYS:HE2	2:B:278:PRO:HG3	1.23	1.08
4:E:56:GLU:CB	4:E:118:LEU:HD22	1.83	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:211:PHE:C	4:E:212:LEU:HD12	1.78	1.08
1:A:380:LYS:HB3	2:B:408:ILE:CD1	1.81	1.08
1:D:72:TYR:HB2	1:D:112:TYR:HB2	1.16	1.08
1:D:167:LEU:HG	1:D:178:MET:HB2	1.33	1.08
2:B:224:THR:C	2:B:227:PRO:HD2	1.79	1.08
2:B:243:PRO:HB3	2:B:435:ALA:HB1	1.28	1.08
3:C:94:LEU:HB2	3:C:98:ASN:HB2	1.33	1.08
1:D:113:THR:HG22	1:D:114:GLY:HA3	1.13	1.08
1:D:20:ARG:HG2	1:D:20:ARG:HH11	1.10	1.08
1:A:406:ILE:HG23	1:A:409:ILE:HD11	1.30	1.07
2:B:191:LYS:HG3	2:B:191:LYS:O	1.30	1.07
4:E:56:GLU:HA	4:E:118:LEU:HB2	1.31	1.07
3:C:434:LYS:HD3	3:C:435:GLU:HG3	1.30	1.07
4:E:37:THR:HA	4:E:176:ASP:HB3	1.30	1.07
4:E:189:PRO:HD2	4:E:211:PHE:CB	1.83	1.07
1:A:155:LYS:CE	4:E:76:LEU:HD13	1.85	1.07
1:A:72:TYR:HB2	1:A:112:TYR:HB3	1.11	1.07
3:C:50:GLU:HA	3:C:132:ILE:HD13	1.37	1.07
4:E:54:TRP:HB3	4:E:118:LEU:HD11	1.28	1.07
1:A:38:ILE:HD11	1:A:55:ARG:HG3	1.07	1.06
2:B:75:ILE:CD1	2:B:78:LEU:HD13	1.85	1.06
1:D:91:VAL:HG22	1:D:96:ALA:HB2	1.32	1.06
1:A:113:THR:O	1:A:113:THR:HG22	1.53	1.06
1:A:251:LEU:HD22	4:E:260:ALA:CB	1.84	1.06
2:B:308:SER:HB2	2:B:311:THR:HG22	1.09	1.06
1:A:160:PRO:HG3	1:A:185:LYS:HB3	1.12	1.06
1:D:46:VAL:HA	1:D:272:PRO:HD3	1.14	1.06
1:D:398:GLU:HA	1:D:401:TYR:CZ	1.90	1.06
2:B:75:ILE:O	2:B:75:ILE:HG13	1.55	1.06
1:A:250:LEU:HD22	1:A:292:THR:HG22	1.31	1.06
2:B:129:THR:HG23	2:B:129:THR:O	1.56	1.06
4:E:91:LEU:HD13	4:E:145:PHE:HB3	1.10	1.06
1:A:257:LEU:HD13	1:A:285:VAL:CG2	1.86	1.05
2:B:189:GLU:HG3	2:B:468:PHE:HB3	1.35	1.05
3:C:69:TRP:HZ2	3:C:112:VAL:HG12	1.16	1.05
1:D:169:THR:O	1:D:169:THR:HG22	1.49	1.05
1:A:279:LEU:HA	1:A:282:MET:HB2	1.37	1.05
1:D:238:ASP:HB3	4:E:308:LEU:HD23	1.38	1.05
4:E:44:GLU:HG2	4:E:280:PRO:HB3	1.36	1.05
4:E:47:GLU:HA	4:E:129:ILE:HD11	1.34	1.05
4:E:246:ALA:HB1	4:E:250:LYS:HG3	1.36	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:LEU:HD22	1:A:87:LEU:H	1.21	1.05
1:A:250:LEU:HD11	1:A:296:ILE:HG21	1.38	1.05
3:C:69:TRP:CZ2	3:C:112:VAL:HG12	1.91	1.05
3:C:279:PRO:HA	3:C:282:ALA:HB3	1.35	1.05
1:D:166:ASP:HB2	1:D:181:TYR:HB2	1.39	1.05
4:E:183:TRP:HB3	4:E:216:ARG:HG2	1.38	1.05
1:A:113:THR:O	1:A:113:THR:CG2	2.05	1.05
1:D:160:PRO:CD	1:D:185:LYS:HB3	1.87	1.05
4:E:80:PRO:HB2	4:E:83:LEU:HD23	1.37	1.05
2:B:37:LEU:CA	2:B:54:VAL:HG12	1.85	1.04
3:C:31:VAL:O	3:C:31:VAL:HG13	1.54	1.04
1:A:133:THR:HA	1:A:274:ILE:CG2	1.88	1.04
3:C:48:THR:HA	3:C:286:PRO:HD3	1.33	1.04
1:D:189:TYR:HA	1:D:197:PRO:CD	1.87	1.04
1:D:152:ASP:HB3	1:D:197:PRO:CA	1.86	1.04
3:C:316:THR:CG2	3:C:317:PRO:HD2	1.86	1.03
1:D:32:THR:HB	1:D:59:GLN:HB3	1.39	1.03
2:B:131:LYS:HD3	2:B:132:VAL:H	0.90	1.03
3:C:278:LEU:C	3:C:278:LEU:CD1	2.28	1.03
3:C:426:THR:HG22	3:C:426:THR:O	1.54	1.03
1:D:35:LEU:HD12	1:D:36:GLN:H	1.22	1.03
1:A:46:VAL:HG23	1:A:271:VAL:N	1.74	1.03
2:B:48:GLU:HA	2:B:130:ILE:HD11	1.38	1.03
2:B:92:LEU:H	2:B:96:ASN:HB2	1.14	1.03
2:B:134:TYR:CE1	2:B:213:ILE:HG13	1.94	1.03
4:E:44:GLU:HB3	4:E:280:PRO:CB	1.88	1.03
1:A:2:GLU:O	1:A:2:GLU:HG2	1.57	1.03
3:C:288:ILE:CD1	3:C:290:LYS:HE2	1.89	1.03
1:D:379:VAL:HA	1:D:382:ILE:HG13	1.36	1.03
1:A:166:ASP:HB2	1:A:181:TYR:CG	1.94	1.02
2:B:75:ILE:HD11	2:B:78:LEU:HD13	1.39	1.02
2:B:297:LEU:HD11	2:B:445:THR:HG21	1.34	1.02
2:B:308:SER:CB	2:B:311:THR:HG22	1.88	1.02
3:C:115:ASN:O	3:C:115:ASN:ND2	1.91	1.02
3:C:285:VAL:O	3:C:285:VAL:HG22	1.52	1.02
4:E:189:PRO:CD	4:E:211:PHE:HB2	1.89	1.02
1:A:207:MET:O	1:A:207:MET:HG2	1.56	1.02
2:B:131:LYS:HD3	2:B:132:VAL:N	1.74	1.02
3:C:319:THR:O	3:C:319:THR:HG23	1.56	1.02
1:A:251:LEU:HD22	4:E:260:ALA:HB3	1.40	1.02
1:A:419:ILE:HG23	1:A:420:ILE:H	1.17	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:104:LEU:HA	2:B:118:TRP:CH2	1.94	1.02
1:A:250:LEU:CD1	1:A:296:ILE:HG21	1.88	1.02
1:A:256:PHE:CE1	2:B:261:VAL:HG23	1.93	1.02
2:B:142:CYS:HB3	2:B:211:LEU:HG	1.38	1.02
1:D:36:GLN:HG3	1:D:55:ARG:HG3	1.04	1.02
1:D:46:VAL:CA	1:D:272:PRO:HD3	1.87	1.02
3:C:115:ASN:O	3:C:115:ASN:CG	2.01	1.02
3:C:145:SER:C	3:C:146:LEU:HD12	1.83	1.02
3:C:316:THR:HG22	3:C:317:PRO:HD2	1.36	1.02
1:D:78:ILE:HD12	1:D:78:ILE:O	1.59	1.01
1:D:236:PRO:HB3	1:D:299:HIS:NE2	1.75	1.01
4:E:34:LEU:HD12	4:E:210:PHE:CE2	1.95	1.01
4:E:62:TYR:O	4:E:62:TYR:CD1	2.12	1.01
1:A:77:LYS:HG3	1:A:77:LYS:O	1.56	1.01
1:A:239:SER:HB2	2:B:312:HIS:HB3	1.43	1.01
1:D:35:LEU:HD11	1:D:54:VAL:CG1	1.89	1.01
1:D:75:ILE:HG13	1:D:78:ILE:HG23	1.42	1.01
4:E:26:HIS:O	4:E:26:HIS:CD2	2.13	1.01
4:E:223:ILE:HA	4:E:226:ILE:HB	1.40	1.01
1:A:155:LYS:HE3	4:E:76:LEU:CD1	1.89	1.01
2:B:10:VAL:HG13	2:B:11:LEU:HD22	1.40	1.01
3:C:17:TYR:CE2	3:C:19:LYS:HB2	1.96	1.01
3:C:288:ILE:HD11	3:C:290:LYS:HE2	1.02	1.01
2:B:37:LEU:HA	2:B:54:VAL:CG1	1.90	1.01
3:C:434:LYS:HG3	1:D:386:MET:HE2	1.40	1.01
4:E:91:LEU:CD1	4:E:145:PHE:HB3	1.90	1.01
4:E:189:PRO:HD2	4:E:211:PHE:HB2	1.04	1.01
1:A:189:TYR:HA	1:A:197:PRO:HD2	1.43	1.01
3:C:155:ALA:HB2	3:C:211:ASN:HA	1.40	1.01
1:D:43:VAL:HG22	1:D:50:VAL:HA	1.39	1.01
1:D:136:PRO:HG3	1:D:274:ILE:CD1	1.89	1.01
4:E:184:THR:CG2	4:E:215:GLN:HG2	1.90	1.01
4:E:134:PHE:HB3	4:E:282:ILE:HG21	1.39	1.00
1:A:76:LYS:HG2	1:A:77:LYS:H	1.24	1.00
4:E:279:VAL:HB	4:E:280:PRO:HD2	1.43	1.00
1:A:20:ARG:HG2	1:A:20:ARG:HH11	1.26	1.00
1:A:38:ILE:CD1	1:A:55:ARG:HG3	1.90	1.00
3:C:273:LEU:HA	3:C:276:GLN:HG2	1.41	1.00
3:C:113:ARG:HE	3:C:119:THR:HG23	1.25	1.00
1:D:7:LEU:CD2	1:D:70:ALA:HB1	1.92	1.00
1:A:16:ASN:HB2	1:A:19:ILE:HD12	1.43	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:296:MET:HA	3:C:296:MET:CE	1.90	1.00
1:A:38:ILE:HD11	1:A:55:ARG:CG	1.92	0.99
1:A:46:VAL:HG21	1:A:270:ALA:HA	1.44	0.99
3:C:159:SER:HA	3:C:213:GLN:HG3	1.39	0.99
3:C:60:HIS:HB3	3:C:62:TRP:HZ3	1.27	0.99
2:B:186:TRP:HB3	2:B:215:ARG:CG	1.92	0.99
1:D:160:PRO:HD3	1:D:185:LYS:CB	1.91	0.99
2:B:37:LEU:HA	2:B:54:VAL:HG12	1.00	0.99
4:E:69:SER:O	4:E:69:SER:OG	1.59	0.99
3:C:78:SER:CA	3:C:114:PRO:HB3	1.92	0.99
1:A:20:ARG:HG3	1:A:22:VAL:HG22	1.44	0.99
2:B:9:SER:HA	2:B:12:PHE:CD1	1.98	0.99
3:C:190:TRP:CD1	3:C:221:ILE:HD12	1.98	0.99
1:D:175:GLU:CB	1:D:211:PRO:HD3	1.93	0.99
4:E:94:ASN:HB3	4:E:125:SER:HB3	1.43	0.99
1:A:274:ILE:HG12	1:A:277:TYR:CD1	1.96	0.98
3:C:180:ASP:OD1	3:C:192:ILE:HG21	1.63	0.98
4:E:44:GLU:CD	4:E:129:ILE:HB	1.87	0.98
3:C:50:GLU:CA	3:C:132:ILE:HD13	1.92	0.98
1:A:148:ILE:HG22	1:A:198:TYR:HD2	1.28	0.98
2:B:425:LYS:HA	2:B:428:TRP:CD1	1.97	0.98
1:D:40:LEU:HD13	1:D:52:THR:HB	1.44	0.98
2:B:131:LYS:CD	2:B:132:VAL:H	1.77	0.98
4:E:66:TRP:HE1	4:E:111:ASN:HA	1.27	0.98
4:E:91:LEU:HD13	4:E:145:PHE:CB	1.94	0.98
4:E:94:ASN:HD22	4:E:125:SER:HB2	1.25	0.98
4:E:183:TRP:HB2	4:E:216:ARG:HG2	1.46	0.98
3:C:285:VAL:O	3:C:285:VAL:HG23	1.63	0.98
4:E:94:ASN:ND2	4:E:143:LEU:HD23	1.78	0.98
3:C:247:PHE:HE1	3:C:309:VAL:HG22	1.17	0.98
1:A:135:PHE:O	1:A:135:PHE:CD1	2.17	0.97
2:B:186:TRP:HB3	2:B:215:ARG:HG3	1.44	0.97
2:B:220:TYR:HD2	2:B:223:TYR:HH	1.07	0.97
4:E:66:TRP:NE1	4:E:111:ASN:HA	1.78	0.97
3:C:159:SER:HA	3:C:213:GLN:CG	1.93	0.97
3:C:195:LYS:HE3	3:C:217:PHE:HB3	1.45	0.97
4:E:6:LEU:CD1	4:E:69:SER:HB3	1.93	0.97
4:E:6:LEU:HD12	4:E:69:SER:HB3	1.45	0.97
2:B:132:VAL:HG13	2:B:279:ILE:HA	1.43	0.97
3:C:452:THR:O	3:C:452:THR:HG23	1.60	0.97
2:B:91:VAL:HG11	2:B:149:TYR:CD1	1.99	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:187:TRP:HB2	1:D:199:LEU:HD23	1.44	0.97
4:E:14:TYR:HE2	4:E:16:LYS:HE3	1.30	0.97
4:E:44:GLU:HB3	4:E:280:PRO:CG	1.94	0.97
3:C:48:THR:HB	3:C:284:ALA:C	1.89	0.97
1:A:130:ILE:HD13	1:A:131:ILE:N	1.78	0.97
2:B:189:GLU:HG3	2:B:468:PHE:CB	1.95	0.97
3:C:242:LEU:HD22	3:C:267:GLN:CB	1.93	0.97
1:D:239:SER:HB2	1:D:242:LYS:HE2	1.44	0.97
4:E:138:TRP:HB2	4:E:213:ILE:HG12	1.46	0.96
1:A:209:ARG:HG3	1:A:210:ILE:H	1.30	0.96
1:A:420:ILE:HG13	1:A:421:GLY:N	1.79	0.96
3:C:138:PRO:HB3	3:C:290:LYS:CE	1.96	0.96
4:E:173:ASP:CG	4:E:185:ILE:HD13	1.90	0.96
4:E:45:LYS:HE2	4:E:278:ASN:C	1.90	0.96
1:D:167:LEU:CG	1:D:178:MET:HB2	1.95	0.96
4:E:284:LYS:N	4:E:284:LYS:CE	2.28	0.96
3:C:288:ILE:HD11	3:C:290:LYS:CE	1.95	0.96
4:E:80:PRO:HB2	4:E:83:LEU:CD2	1.95	0.96
3:C:42:LEU:HD22	3:C:190:TRP:CH2	2.00	0.96
3:C:1:VAL:HA	3:C:4:GLU:HG2	1.48	0.96
3:C:278:LEU:HD12	3:C:278:LEU:O	1.63	0.96
3:C:319:THR:HB	3:C:447:ASN:HB3	1.48	0.96
2:B:142:CYS:HB3	2:B:211:LEU:CG	1.95	0.96
3:C:83:ARG:O	3:C:87:ILE:HG13	1.65	0.96
4:E:129:ILE:HG22	4:E:133:TYR:HD2	1.23	0.96
4:E:184:THR:HG21	4:E:215:GLN:HG2	1.48	0.96
4:E:188:ARG:HG3	4:E:188:ARG:O	1.65	0.96
4:E:146:ARG:NH1	4:E:205:PHE:HB3	1.81	0.95
4:E:197:GLN:HG2	4:E:198:LEU:H	1.29	0.95
4:E:456:LEU:O	4:E:456:LEU:HD22	1.66	0.95
3:C:138:PRO:HG3	3:C:288:ILE:CD1	1.96	0.95
1:A:160:PRO:HG2	1:A:185:LYS:NZ	1.80	0.95
3:C:138:PRO:HG3	3:C:288:ILE:HD11	1.45	0.95
4:E:89:VAL:HG23	4:E:99:PHE:CZ	2.00	0.95
1:A:160:PRO:HG2	1:A:185:LYS:CE	1.96	0.95
1:D:170:PHE:HE2	1:D:176:TRP:CD1	1.83	0.95
1:D:187:TRP:CZ2	1:D:189:TYR:HB3	2.02	0.95
1:A:64:ARG:HA	1:A:66:ARG:NH1	1.80	0.95
2:B:176:ASN:ND2	2:B:188:ILE:HG21	1.80	0.95
2:B:185:GLN:HB3	2:B:219:PHE:CE2	2.01	0.95
3:C:247:PHE:HE1	3:C:309:VAL:CG2	1.78	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:44:GLU:HB3	4:E:280:PRO:HB3	1.42	0.95
1:D:26:THR:HG22	1:D:27:HIS:H	1.29	0.95
4:E:235:LEU:HD12	4:E:235:LEU:C	1.91	0.95
3:C:249:LEU:HB3	3:C:256:LYS:NZ	1.80	0.95
1:D:152:ASP:CA	1:D:197:PRO:HA	1.95	0.95
3:C:149:THR:HG21	3:C:214:ASP:HB3	1.48	0.95
1:A:416:LEU:O	1:A:419:ILE:HG22	1.65	0.95
1:A:152:ASP:HA	1:A:198:TYR:H	1.30	0.94
4:E:236:VAL:HA	4:E:239:VAL:CG2	1.96	0.94
1:A:406:ILE:CG2	1:A:409:ILE:HD11	1.96	0.94
3:C:42:LEU:HG	3:C:54:THR:HG23	1.49	0.94
3:C:149:THR:CG2	3:C:214:ASP:HB3	1.98	0.94
1:D:57:ARG:CZ	1:D:117:MET:HE1	1.97	0.94
1:D:217:ASN:HA	1:D:220:ILE:HD11	1.47	0.94
4:E:183:TRP:HB3	4:E:216:ARG:CG	1.97	0.94
1:A:245:LEU:HD22	2:B:250:SER:HA	1.49	0.94
2:B:68:ASP:HB3	2:B:69:PRO:CD	1.97	0.94
2:B:311:THR:HB	2:B:430:TYR:HD2	1.31	0.94
4:E:305:ASN:HA	4:E:308:LEU:HD12	1.49	0.94
1:D:28:PHE:HD2	1:D:157:SER:HB3	1.28	0.94
1:D:78:ILE:CD1	1:D:110:LEU:HB3	1.98	0.94
1:A:152:ASP:HB3	1:A:197:PRO:HA	1.49	0.94
2:B:191:LYS:O	2:B:191:LYS:CG	2.16	0.94
4:E:249:GLN:HE22	4:E:250:LYS:HE3	1.30	0.94
2:B:311:THR:HB	2:B:430:TYR:CD2	2.02	0.94
1:D:49:ILE:HG21	1:D:125:LYS:NZ	1.83	0.94
1:D:187:TRP:HB2	1:D:199:LEU:CD2	1.97	0.94
1:D:203:TYR:N	1:D:203:TYR:HD1	1.66	0.94
4:E:262:THR:HG23	4:E:265:LEU:HD12	1.50	0.94
4:E:313:THR:HB	4:E:440:VAL:HG12	1.47	0.94
3:C:443:VAL:HA	3:C:446:TRP:CD1	2.01	0.94
1:D:77:LYS:HA	1:D:111:ASP:HA	1.48	0.94
1:A:148:ILE:HD11	1:A:156:VAL:HG13	1.50	0.94
2:B:91:VAL:HG23	2:B:96:ASN:CG	1.92	0.94
1:D:72:TYR:C	1:D:72:TYR:HD1	1.73	0.94
4:E:44:GLU:HA	4:E:129:ILE:CD1	1.98	0.94
4:E:90:VAL:HG13	4:E:95:VAL:HB	1.48	0.94
4:E:449:ALA:HA	4:E:452:TRP:CD1	2.02	0.94
1:A:72:TYR:HB2	1:A:112:TYR:CB	1.95	0.93
1:A:102:ILE:O	1:A:102:ILE:HG22	1.67	0.93
2:B:132:VAL:CG1	2:B:279:ILE:HA	1.98	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:282:MET:HG3	1:D:286:ILE:HD11	1.49	0.93
3:C:4:GLU:HG3	3:C:5:GLU:H	1.33	0.93
1:D:166:ASP:HB2	1:D:181:TYR:HB3	1.47	0.93
4:E:436:ASN:HA	4:E:439:TRP:HE1	1.33	0.93
1:D:130:ILE:HG12	1:D:131:ILE:N	1.83	0.93
2:B:226:VAL:HG22	2:B:227:PRO:HD3	1.50	0.93
3:C:309:VAL:O	3:C:313:HIS:HB3	1.68	0.93
4:E:134:PHE:HB3	4:E:282:ILE:CG2	1.97	0.93
1:A:171:MET:HE3	1:A:176:TRP:CZ2	2.04	0.93
3:C:115:ASN:N	3:C:115:ASN:HD22	1.65	0.93
4:E:271:LYS:C	4:E:273:PRO:HD2	1.93	0.93
3:C:52:LEU:HD21	3:C:130:CYS:HB2	1.51	0.93
1:A:245:LEU:CD2	2:B:250:SER:HA	1.98	0.93
2:B:279:ILE:CG2	2:B:280:ILE:HD13	1.99	0.93
3:C:122:PRO:HB2	3:C:123:PRO:CD	1.96	0.93
1:D:189:TYR:CA	1:D:197:PRO:HD2	1.98	0.93
4:E:172:ILE:HD11	4:E:187:HIS:C	1.94	0.93
2:B:34:GLY:C	2:B:35:LEU:HD23	1.94	0.93
1:A:145:LYS:HG3	1:A:202:THR:CG2	1.99	0.92
3:C:434:LYS:HG3	1:D:386:MET:CE	1.98	0.92
2:B:9:SER:HA	2:B:12:PHE:CE1	2.04	0.92
2:B:247:GLU:C	2:B:249:MET:HG3	1.92	0.92
1:D:261:VAL:HA	1:D:264:ILE:HD12	1.50	0.92
1:D:302:SER:HB3	1:D:400:LYS:HG2	1.50	0.92
1:A:142:CYS:HB2	1:A:205:PHE:HB2	1.51	0.92
4:E:31:THR:O	4:E:32:LEU:HD23	1.69	0.92
4:E:67:ASN:HD22	4:E:67:ASN:N	1.64	0.92
4:E:284:LYS:HE3	4:E:284:LYS:H	1.30	0.92
1:A:41:ILE:HD11	1:A:51:GLU:CD	1.93	0.92
1:D:38:ILE:C	1:D:169:THR:HG21	1.94	0.92
3:C:69:TRP:HE3	3:C:73:GLU:HB3	1.33	0.92
3:C:113:ARG:HD2	3:C:117:TYR:CB	2.00	0.92
1:D:217:ASN:HA	1:D:220:ILE:CD1	1.99	0.92
1:D:104:HIS:HB2	1:D:105:MET:SD	2.10	0.92
4:E:282:ILE:HG23	4:E:282:ILE:O	1.69	0.92
1:A:267:THR:HG23	1:A:271:VAL:HG22	1.50	0.92
3:C:56:VAL:HG13	3:C:126:PHE:HE2	1.35	0.92
3:C:247:PHE:CD2	3:C:460:ILE:HG12	2.05	0.92
1:D:56:LEU:N	1:D:56:LEU:HD23	1.85	0.92
4:E:56:GLU:HA	4:E:118:LEU:CB	1.99	0.92
1:A:397:GLU:HA	1:A:400:LYS:HD2	1.52	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:253:LEU:HD23	1:D:254:THR:N	1.84	0.91
4:E:129:ILE:HG22	4:E:133:TYR:CE2	2.04	0.91
4:E:219:LEU:HB3	4:E:222:ILE:HB	1.50	0.91
1:A:133:THR:CA	1:A:274:ILE:HG22	1.98	0.91
2:B:130:ILE:HB	2:B:134:TYR:CE2	2.06	0.91
2:B:421:PHE:HA	2:B:424:LEU:HB2	1.49	0.91
3:C:253:SER:HB2	1:D:306:HIS:HB3	1.52	0.91
1:D:45:GLU:HB3	1:D:271:VAL:CG2	1.99	0.91
1:A:133:THR:O	1:A:133:THR:HG22	1.70	0.91
1:A:176:TRP:CB	1:A:209:ARG:HD2	2.00	0.91
3:C:42:LEU:HG	3:C:54:THR:CG2	2.01	0.91
1:D:302:SER:HB2	1:D:305:THR:HG23	1.52	0.91
3:C:319:THR:O	3:C:319:THR:CG2	2.15	0.91
4:E:39:LEU:HD23	4:E:183:TRP:HZ2	1.35	0.91
4:E:44:GLU:HG2	4:E:280:PRO:CB	2.01	0.91
1:A:41:ILE:HD11	1:A:51:GLU:HB3	1.53	0.91
1:A:160:PRO:CG	1:A:185:LYS:HB3	2.00	0.91
3:C:7:LEU:HD23	3:C:10:ASP:HB2	1.50	0.91
4:E:36:LEU:CD2	4:E:51:THR:HG21	2.01	0.91
4:E:247:GLY:H	4:E:250:LYS:HZ2	1.16	0.91
1:D:238:ASP:HB3	4:E:308:LEU:CD2	2.01	0.91
4:E:140:ASN:C	4:E:140:ASN:HD22	1.79	0.91
3:C:144:CYS:SG	3:C:146:LEU:HD11	2.11	0.91
4:E:172:ILE:HD12	4:E:188:ARG:HB3	1.50	0.91
2:B:160:HIS:NE2	2:B:207:VAL:HG11	1.84	0.91
2:B:287:ILE:HA	2:B:290:LEU:HD12	1.52	0.91
4:E:138:TRP:HB2	4:E:213:ILE:CG1	2.01	0.91
1:D:113:THR:HG22	1:D:114:GLY:CA	2.00	0.90
4:E:32:LEU:O	4:E:33:LYS:HG3	1.70	0.90
1:A:47:ASN:O	1:A:49:ILE:HG13	1.71	0.90
2:B:131:LYS:HZ2	2:B:132:VAL:HB	1.34	0.90
2:B:406:GLU:HA	2:B:409:LYS:HD2	1.52	0.90
1:D:252:SER:HB2	4:E:259:LEU:HD13	1.53	0.90
1:D:405:VAL:O	1:D:409:ILE:HG23	1.71	0.90
1:D:35:LEU:HD23	1:D:164:ARG:NH1	1.87	0.90
1:A:64:ARG:HA	1:A:66:ARG:HH11	1.36	0.90
4:E:27:VAL:HG12	4:E:154:GLU:HA	1.53	0.90
4:E:62:TYR:HD1	4:E:62:TYR:C	1.78	0.90
4:E:76:LEU:HD23	4:E:77:VAL:H	1.35	0.90
1:A:155:LYS:HE3	4:E:76:LEU:HD13	0.93	0.90
1:D:28:PHE:CD2	1:D:157:SER:HB3	2.07	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:LYS:C	1:A:146:LEU:HD12	1.96	0.90
1:D:78:ILE:O	1:D:78:ILE:CD1	2.19	0.90
3:C:30:VAL:HG22	3:C:157:GLU:C	1.96	0.90
3:C:110:VAL:HG13	3:C:120:TRP:HB2	1.54	0.90
4:E:141:CYS:HB3	4:E:212:LEU:HB2	1.53	0.90
1:A:33:VAL:CG2	1:A:158:ILE:HG12	2.00	0.90
4:E:6:LEU:HD12	4:E:69:SER:CB	2.00	0.90
2:B:133:MET:CG	2:B:140:GLN:HG3	2.02	0.90
1:D:135:PHE:C	1:D:135:PHE:CD1	2.48	0.90
2:B:104:LEU:HD12	2:B:118:TRP:CZ3	2.06	0.89
2:B:409:LYS:HZ3	3:C:423:ILE:HG23	1.37	0.89
1:D:118:TRP:HE1	1:D:120:PRO:HB3	1.35	0.89
1:D:305:THR:CG2	1:D:400:LYS:HB3	2.01	0.89
4:E:67:ASN:HD22	4:E:67:ASN:H	0.90	0.89
4:E:136:PHE:CZ	4:E:217:LYS:HD2	2.07	0.89
1:A:106:THR:HG22	1:A:107:LYS:H	1.36	0.89
1:A:152:ASP:HA	1:A:198:TYR:N	1.87	0.89
1:D:37:LEU:HD12	1:D:53:ASN:O	1.72	0.89
4:E:31:THR:HB	4:E:58:GLN:HB2	1.54	0.89
1:A:166:ASP:HB3	1:A:178:MET:CE	2.02	0.89
3:C:148:PHE:HB2	3:C:215:VAL:HG22	1.54	0.89
1:D:48:GLN:HB3	1:D:130:ILE:CD1	2.02	0.89
1:D:91:VAL:HG22	1:D:96:ALA:CB	2.01	0.89
3:C:269:VAL:HG13	3:C:270:PHE:CD1	2.07	0.89
1:D:301:ARG:HH12	1:D:406:ILE:HD11	1.36	0.89
4:E:37:THR:HA	4:E:176:ASP:CB	2.00	0.89
4:E:37:THR:CA	4:E:176:ASP:HB3	2.02	0.89
1:A:235:LEU:HD21	1:A:242:LYS:HE3	1.54	0.89
1:D:29:VAL:HG12	1:D:60:TRP:CD1	2.06	0.89
4:E:44:GLU:CB	4:E:280:PRO:HD3	2.02	0.89
4:E:66:TRP:HB2	4:E:71:TYR:H	1.36	0.89
4:E:66:TRP:CD1	4:E:111:ASN:HA	2.08	0.89
2:B:129:THR:CG2	2:B:142:CYS:HA	2.02	0.89
3:C:80:LEU:HD11	1:D:20:ARG:HH22	1.38	0.89
1:D:137:PHE:HD2	1:D:431:ILE:HG21	1.36	0.89
4:E:279:VAL:CB	4:E:280:PRO:HD2	2.03	0.89
4:E:284:LYS:CE	4:E:284:LYS:H	1.86	0.89
2:B:306:HIS:C	2:B:306:HIS:HD1	1.81	0.89
1:D:36:GLN:HG3	1:D:55:ARG:CG	1.99	0.89
1:D:132:VAL:C	1:D:274:ILE:HG23	1.97	0.89
1:D:305:THR:HG1	1:D:401:TYR:HD2	0.94	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:20:ARG:HH11	1:D:20:ARG:CG	1.85	0.89
1:D:75:ILE:HG13	1:D:78:ILE:CG2	2.03	0.89
1:A:380:LYS:CA	2:B:408:ILE:HD13	2.03	0.88
2:B:263:LEU:HD22	2:B:291:VAL:CG2	2.02	0.88
2:B:306:HIS:C	2:B:306:HIS:ND1	2.32	0.88
3:C:453:ILE:HG23	3:C:454:ASP:H	1.37	0.88
1:A:79:ARG:HD2	1:A:107:LYS:HD2	1.55	0.88
2:B:269:LYS:CE	2:B:270:VAL:HG22	2.02	0.88
2:B:407:ALA:O	2:B:411:ILE:HG13	1.72	0.88
3:C:65:HIS:CD2	3:C:65:HIS:H	1.91	0.88
4:E:44:GLU:CG	4:E:129:ILE:HB	2.03	0.88
4:E:62:TYR:CD1	4:E:62:TYR:C	2.50	0.88
4:E:149:THR:HG23	4:E:150:TYR:H	1.38	0.88
2:B:2:VAL:HG12	2:B:69:PRO:HG3	1.55	0.88
2:B:129:THR:HG22	2:B:142:CYS:HA	1.55	0.88
4:E:172:ILE:HD11	4:E:187:HIS:CA	2.03	0.88
1:A:63:VAL:O	1:A:66:ARG:HD2	1.73	0.88
1:A:141:ASN:HA	1:A:205:PHE:O	1.74	0.88
1:A:175:GLU:CB	1:A:211:PRO:HG3	2.04	0.88
1:D:412:CYS:O	1:D:416:LEU:HD23	1.74	0.88
4:E:244:ALA:HB2	4:E:446:ILE:CG2	2.03	0.88
3:C:434:LYS:CE	3:C:435:GLU:HG2	2.04	0.88
1:A:251:LEU:CD2	4:E:260:ALA:HB3	2.03	0.88
2:B:175:ILE:HG12	2:B:176:ASN:H	1.38	0.88
2:B:186:TRP:HB3	2:B:215:ARG:CD	2.04	0.88
3:C:45:LEU:HD12	3:C:190:TRP:CE3	2.09	0.88
3:C:279:PRO:HA	3:C:282:ALA:CB	2.03	0.88
3:C:434:LYS:HD3	3:C:435:GLU:CG	2.03	0.88
4:E:66:TRP:CD1	4:E:111:ASN:HB2	2.09	0.88
1:D:203:TYR:N	1:D:203:TYR:CD1	2.34	0.88
4:E:249:GLN:NE2	4:E:250:LYS:HE3	1.88	0.88
1:A:247:ILE:O	1:A:247:ILE:HD13	1.74	0.88
1:D:31:ILE:HG22	1:D:158:ILE:HG23	1.56	0.88
1:D:72:TYR:HB2	1:D:112:TYR:CB	2.04	0.88
4:E:44:GLU:HG3	4:E:129:ILE:CG1	2.05	0.88
4:E:292:VAL:O	4:E:296:ILE:HG23	1.74	0.88
1:A:29:VAL:HG21	1:A:86:TRP:CZ3	2.09	0.87
1:A:148:ILE:CG2	1:A:198:TYR:HD2	1.87	0.87
2:B:45:GLU:OE1	2:B:277:VAL:HB	1.73	0.87
3:C:247:PHE:CE2	3:C:460:ILE:HD11	2.09	0.87
4:E:262:THR:CG2	4:E:265:LEU:HD12	2.03	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:113:ARG:CD	3:C:117:TYR:HB3	2.03	0.87
4:E:36:LEU:HD23	4:E:51:THR:HG21	1.56	0.87
4:E:44:GLU:HA	4:E:129:ILE:HD12	1.55	0.87
4:E:159:LEU:HD12	4:E:191:LYS:C	2.00	0.87
2:B:97:ASP:HB3	2:B:125:ARG:HG3	1.56	0.87
4:E:67:ASN:H	4:E:67:ASN:ND2	1.72	0.87
2:B:28:LYS:CB	2:B:156:VAL:HA	2.03	0.87
1:D:112:TYR:HD1	1:D:113:THR:H	1.14	0.87
1:D:167:LEU:N	1:D:167:LEU:HD12	1.90	0.87
1:A:79:ARG:CD	1:A:107:LYS:HD2	2.03	0.87
1:A:107:LYS:C	1:A:108:LEU:HD23	2.00	0.87
4:E:152:ALA:H	4:E:205:PHE:HD1	1.22	0.87
1:A:238:ASP:HB3	2:B:306:HIS:CE1	2.10	0.87
1:D:274:ILE:HB	1:D:276:LYS:HD3	1.56	0.87
1:D:7:LEU:HD22	1:D:70:ALA:HB1	1.57	0.87
4:E:185:ILE:HG12	4:E:214:ILE:CG2	2.05	0.87
2:B:236:ILE:CB	2:B:446:MET:HE1	2.04	0.87
4:E:33:LYS:HE3	4:E:160:SER:CB	2.05	0.87
1:A:46:VAL:HG21	1:A:270:ALA:CA	2.05	0.86
1:A:101:ALA:HB3	1:A:123:ILE:O	1.74	0.86
3:C:18:ASN:CB	3:C:21:VAL:HB	2.04	0.86
3:C:438:ALA:HA	3:C:441:GLU:CD	2.00	0.86
1:D:48:GLN:OE1	1:D:130:ILE:HD13	1.75	0.86
1:D:60:TRP:CZ2	1:D:86:TRP:CZ3	2.63	0.86
1:D:187:TRP:CZ3	1:D:189:TYR:CD1	2.63	0.86
2:B:56:LEU:CD1	2:B:103:THR:HG23	2.04	0.86
2:B:160:HIS:H	2:B:195:LYS:HZ1	1.21	0.86
1:A:176:TRP:HB3	1:A:209:ARG:HD2	1.56	0.86
2:B:232:SER:O	2:B:236:ILE:HG22	1.75	0.86
4:E:267:LEU:O	4:E:270:GLN:HG3	1.75	0.86
2:B:23:GLN:HE21	2:B:23:GLN:N	1.73	0.86
3:C:18:ASN:HB3	3:C:21:VAL:HB	1.56	0.86
3:C:299:VAL:O	3:C:303:VAL:HG23	1.75	0.86
2:B:436:ASP:O	2:B:440:LEU:HD12	1.75	0.86
3:C:16:LYS:HA	3:C:16:LYS:HE3	1.55	0.86
3:C:204:ASP:OD1	3:C:205:LYS:HD3	1.76	0.86
4:E:159:LEU:HD21	4:E:208:ILE:HG23	1.57	0.86
4:E:173:ASP:CB	4:E:185:ILE:HD13	2.06	0.86
3:C:154:ASN:HA	3:C:211:ASN:HB2	1.56	0.86
3:C:216:THR:C	3:C:217:PHE:HD1	1.83	0.86
2:B:31:VAL:HG21	2:B:86:TRP:HZ3	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:190:TRP:CB	3:C:223:ARG:HB2	2.04	0.86
3:C:249:LEU:HB3	3:C:256:LYS:HZ2	1.36	0.86
1:D:107:LYS:HD3	1:D:107:LYS:N	1.88	0.86
1:D:239:SER:O	1:D:242:LYS:HG2	1.75	0.86
4:E:446:ILE:HG22	4:E:447:ASP:N	1.89	0.86
1:A:2:GLU:CD	1:A:74:GLY:HA2	2.00	0.86
3:C:122:PRO:CB	3:C:123:PRO:HD2	2.04	0.86
3:C:212:TYR:CD1	3:C:212:TYR:O	2.29	0.86
1:A:2:GLU:OE2	1:A:74:GLY:HA2	1.74	0.86
1:A:245:LEU:HD11	2:B:250:SER:O	1.76	0.86
1:D:41:ILE:HD12	1:D:51:GLU:O	1.76	0.86
1:D:46:VAL:HB	1:D:271:VAL:HA	1.57	0.86
1:D:72:TYR:CB	1:D:112:TYR:HB2	2.05	0.86
1:D:414:PHE:O	1:D:414:PHE:CD1	2.29	0.86
4:E:250:LYS:HA	4:E:253:LEU:HB3	1.58	0.86
4:E:267:LEU:HD12	4:E:270:GLN:CD	2.01	0.86
2:B:46:LYS:HB2	2:B:276:SER:C	2.01	0.86
2:B:176:ASN:CB	2:B:191:LYS:HB3	2.03	0.86
2:B:297:LEU:HD12	2:B:445:THR:HG21	1.58	0.85
3:C:8:ILE:HG23	3:C:8:ILE:O	1.74	0.85
3:C:478:PHE:CD1	3:C:478:PHE:C	2.53	0.85
4:E:217:LYS:O	4:E:217:LYS:HE2	1.75	0.85
4:E:271:LYS:HZ3	4:E:271:LYS:HB2	1.40	0.85
3:C:478:PHE:C	3:C:478:PHE:HD1	1.84	0.85
1:D:419:ILE:HD12	1:D:420:ILE:N	1.91	0.85
4:E:54:TRP:CB	4:E:118:LEU:HD11	2.06	0.85
3:C:56:VAL:HG13	3:C:126:PHE:CE2	2.11	0.85
3:C:449:VAL:HG12	3:C:452:THR:HB	1.57	0.85
1:D:213:TYR:O	1:D:216:VAL:HG23	1.76	0.85
4:E:109:VAL:HG12	4:E:110:TYR:O	1.76	0.85
3:C:155:ALA:CB	3:C:211:ASN:HA	2.06	0.85
3:C:282:ALA:HB2	3:C:287:LEU:HD11	1.58	0.85
4:E:236:VAL:CA	4:E:239:VAL:HG23	2.06	0.85
1:A:47:ASN:O	1:A:48:GLN:HG2	1.75	0.85
3:C:48:THR:HA	3:C:286:PRO:CD	2.06	0.85
3:C:307:GLY:HA2	3:C:310:LEU:HD23	1.58	0.85
4:E:94:ASN:CG	4:E:143:LEU:HD23	2.01	0.85
2:B:104:LEU:HA	2:B:118:TRP:HH2	1.34	0.85
2:B:243:PRO:HB3	2:B:435:ALA:CB	2.05	0.85
1:A:216:VAL:HG13	1:A:220:ILE:HD11	1.56	0.85
1:A:277:TYR:HA	1:A:280:PHE:CZ	2.12	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:SER:HA	1:A:400:LYS:HD3	1.59	0.85
1:D:257:LEU:C	1:D:257:LEU:HD12	2.01	0.85
1:A:76:LYS:HG3	1:A:112:TYR:CE2	2.12	0.85
2:B:46:LYS:HG3	2:B:278:PRO:HD2	1.58	0.85
3:C:42:LEU:HA	3:C:54:THR:HG22	1.57	0.85
3:C:154:ASN:HB3	3:C:211:ASN:HB3	1.59	0.85
3:C:194:HIS:CG	3:C:195:LYS:H	1.95	0.85
1:D:379:VAL:HA	1:D:382:ILE:HG12	1.57	0.85
3:C:35:LEU:HD22	3:C:215:VAL:HG11	1.59	0.85
3:C:227:PHE:O	3:C:230:ILE:HG12	1.76	0.85
1:D:257:LEU:HD12	1:D:258:LEU:N	1.90	0.85
4:E:45:LYS:NZ	4:E:278:ASN:HA	1.91	0.85
1:A:302:SER:HB2	1:A:306:HIS:C	2.02	0.85
1:D:291:VAL:O	1:D:295:VAL:HG13	1.76	0.85
4:E:268:ILE:HG13	4:E:269:ALA:N	1.90	0.84
4:E:284:LYS:O	4:E:287:ILE:HG23	1.77	0.84
4:E:449:ALA:O	4:E:452:TRP:HB2	1.77	0.84
1:A:94:ASN:HD22	1:A:94:ASN:C	1.83	0.84
1:A:148:ILE:HG22	1:A:198:TYR:CD2	2.11	0.84
3:C:220:ILE:HG13	3:C:220:ILE:O	1.77	0.84
1:D:48:GLN:HB3	1:D:130:ILE:HD12	1.59	0.84
1:D:135:PHE:C	1:D:135:PHE:HD1	1.84	0.84
2:B:176:ASN:HD22	2:B:188:ILE:CG2	1.89	0.84
2:B:7:LEU:O	2:B:11:LEU:HD23	1.77	0.84
1:D:107:LYS:NZ	4:E:149:THR:HA	1.93	0.84
3:C:67:LEU:HD12	3:C:116:GLY:C	2.01	0.84
3:C:159:SER:CA	3:C:213:GLN:HG3	2.07	0.84
3:C:179:ILE:HG13	3:C:181:PRO:HD3	1.57	0.84
1:D:20:ARG:HG2	1:D:20:ARG:NH1	1.78	0.84
1:D:49:ILE:HD12	1:D:125:LYS:HE3	1.57	0.84
4:E:28:ILE:HD11	4:E:60:ASN:O	1.77	0.84
1:A:102:ILE:O	1:A:102:ILE:CG2	2.26	0.84
2:B:259:LEU:HD23	2:B:259:LEU:O	1.78	0.84
3:C:78:SER:HA	3:C:114:PRO:HB3	1.56	0.84
1:A:77:LYS:O	1:A:77:LYS:CG	2.25	0.84
3:C:479:ASN:ND2	3:C:479:ASN:C	2.36	0.84
1:D:203:TYR:HD1	1:D:203:TYR:H	1.20	0.84
1:A:160:PRO:HG2	1:A:185:LYS:HZ3	1.42	0.84
2:B:46:LYS:HG3	2:B:278:PRO:CD	2.08	0.84
1:D:229:THR:O	1:D:232:VAL:HB	1.77	0.84
4:E:142:SER:OG	4:E:209:ILE:HD11	1.78	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:SER:CB	2:B:312:HIS:HB3	2.07	0.84
3:C:59:ASP:OD1	3:C:121:LEU:HB2	1.78	0.84
1:D:77:LYS:HG3	1:D:77:LYS:O	1.75	0.84
1:D:415:MET:O	1:D:419:ILE:HG23	1.78	0.84
1:A:35:LEU:HD21	1:A:37:LEU:HD23	1.60	0.83
3:C:106:TYR:C	3:C:107:PHE:HD1	1.85	0.83
3:C:471:PHE:HD1	3:C:471:PHE:C	1.86	0.83
1:D:253:LEU:HD23	1:D:254:THR:H	1.42	0.83
4:E:28:ILE:HG21	4:E:85:TRP:CZ3	2.13	0.83
1:A:265:PRO:HA	1:A:268:SER:HB3	1.60	0.83
1:A:419:ILE:HG23	1:A:420:ILE:N	1.93	0.83
2:B:81:PRO:HD3	3:C:22:ARG:HH22	1.41	0.83
2:B:435:ALA:O	2:B:439:PHE:HB3	1.79	0.83
3:C:253:SER:HB2	1:D:306:HIS:CB	2.07	0.83
1:D:65:LEU:HD23	1:D:110:LEU:CD1	2.08	0.83
4:E:182:GLU:O	4:E:218:PRO:HD2	1.77	0.83
3:C:241:PHE:HA	3:C:244:ALA:HB3	1.60	0.83
1:D:7:LEU:HD21	1:D:70:ALA:HB1	1.57	0.83
1:D:245:LEU:HD21	4:E:255:ILE:CG1	2.06	0.83
2:B:104:LEU:HD12	2:B:118:TRP:HH2	1.40	0.83
1:D:228:LEU:O	1:D:232:VAL:HG23	1.78	0.83
1:A:175:GLU:HB3	1:A:211:PRO:CD	2.09	0.83
1:D:92:LEU:HD13	1:D:146:LEU:HG	1.61	0.83
1:D:151:TYR:O	1:D:198:TYR:HB3	1.79	0.83
1:D:166:ASP:OD1	1:D:178:MET:HE2	1.78	0.83
1:D:414:PHE:O	1:D:414:PHE:HD1	1.61	0.83
4:E:222:ILE:O	4:E:226:ILE:HG13	1.78	0.83
1:A:108:LEU:HD13	1:A:118:TRP:HB2	1.61	0.83
2:B:405:VAL:O	2:B:408:ILE:HG22	1.78	0.83
1:D:64:ARG:HA	1:D:66:ARG:NH1	1.93	0.83
1:D:144:MET:HE3	1:D:205:PHE:CE1	2.14	0.83
1:D:232:VAL:HG22	1:D:250:LEU:HD11	1.59	0.83
4:E:229:CYS:HA	4:E:232:ILE:HB	1.58	0.83
1:A:37:LEU:CD2	1:A:54:VAL:HG12	2.08	0.83
3:C:110:VAL:CG1	3:C:120:TRP:HB2	2.08	0.83
4:E:144:VAL:HA	4:E:208:ILE:O	1.79	0.83
1:A:43:VAL:HG22	1:A:50:VAL:HG13	1.61	0.82
2:B:90:ILE:HG23	2:B:147:LYS:H	1.41	0.82
3:C:138:PRO:CB	3:C:290:LYS:HE3	2.09	0.82
4:E:173:ASP:HB3	4:E:185:ILE:HD13	1.61	0.82
2:B:185:GLN:CB	2:B:217:PRO:HB3	2.09	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:408:ILE:HG23	2:B:409:LYS:N	1.92	0.82
1:D:101:ALA:C	1:D:102:ILE:HD13	2.04	0.82
1:D:176:TRP:HB3	1:D:209:ARG:HD2	1.59	0.82
1:A:43:VAL:HG13	1:A:50:VAL:HG22	1.61	0.82
3:C:31:VAL:O	3:C:31:VAL:CG1	2.23	0.82
3:C:319:THR:HB	3:C:447:ASN:CB	2.08	0.82
3:C:426:THR:O	3:C:426:THR:CG2	2.25	0.82
1:D:141:ASN:HA	1:D:205:PHE:O	1.78	0.82
1:D:198:TYR:N	1:D:198:TYR:CD1	2.13	0.82
2:B:129:THR:HG22	2:B:142:CYS:SG	2.20	0.82
3:C:58:MET:SD	3:C:92:ILE:HD11	2.20	0.82
3:C:316:THR:HG22	3:C:317:PRO:CD	2.09	0.82
1:D:276:LYS:H	1:D:276:LYS:HD2	1.44	0.82
4:E:89:VAL:CG2	4:E:99:PHE:CE2	2.63	0.82
4:E:265:LEU:O	4:E:268:ILE:HG23	1.79	0.82
1:A:136:PRO:HA	1:A:277:TYR:OH	1.79	0.82
3:C:319:THR:HG22	3:C:320:HIS:N	1.94	0.82
4:E:162:GLU:HA	4:E:190:ALA:H	1.45	0.82
1:A:155:LYS:CG	4:E:78:ARG:HH21	1.93	0.82
2:B:216:LYS:HD2	2:B:216:LYS:O	1.79	0.82
3:C:38:THR:CG2	3:C:57:TRP:CE3	2.63	0.82
1:D:376:ILE:HG22	1:D:380:LYS:NZ	1.94	0.82
4:E:76:LEU:HD23	4:E:77:VAL:N	1.95	0.82
1:A:136:PRO:HD3	1:A:274:ILE:HG23	1.59	0.82
1:A:242:LYS:HB2	1:A:245:LEU:HB2	1.60	0.82
1:A:419:ILE:CG2	1:A:420:ILE:H	1.93	0.82
1:D:201:ILE:HG22	1:D:203:TYR:CE1	2.14	0.82
1:D:229:THR:HA	1:D:232:VAL:CG2	2.10	0.82
4:E:35:THR:HG23	4:E:175:GLU:OE1	1.78	0.82
2:B:52:THR:HG22	2:B:53:SER:H	1.44	0.82
2:B:65:LEU:HD23	2:B:110:VAL:CG1	2.09	0.82
1:D:60:TRP:CE2	1:D:86:TRP:CH2	2.68	0.82
4:E:151:ASN:HA	4:E:205:PHE:CD1	2.15	0.82
1:A:251:LEU:HD13	4:E:260:ALA:HB2	1.60	0.82
4:E:74:ILE:HG12	4:E:76:LEU:O	1.79	0.81
2:B:185:GLN:CB	2:B:219:PHE:HE2	1.92	0.81
2:B:241:LEU:HG	2:B:248:LYS:HE2	1.62	0.81
3:C:276:GLN:O	3:C:279:PRO:HD2	1.79	0.81
1:D:10:ASN:OD1	1:D:11:LEU:HD23	1.80	0.81
2:B:230:LEU:HA	2:B:233:ILE:HG13	1.61	0.81
3:C:94:LEU:CB	3:C:98:ASN:HB2	2.09	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:245:LEU:O	3:C:249:LEU:HD13	1.81	0.81
3:C:463:PRO:HA	3:C:466:VAL:HG23	1.61	0.81
3:C:471:PHE:C	3:C:471:PHE:CD1	2.56	0.81
1:D:175:GLU:HB3	1:D:211:PRO:CG	2.09	0.81
1:D:379:VAL:O	1:D:379:VAL:HG12	1.77	0.81
4:E:33:LYS:HG2	4:E:160:SER:HB3	1.61	0.81
1:D:187:TRP:CZ2	1:D:196:THR:HG23	2.16	0.81
4:E:44:GLU:CA	4:E:129:ILE:HD12	2.10	0.81
1:A:106:THR:HG22	1:A:107:LYS:N	1.95	0.81
1:D:102:ILE:HD12	4:E:98:GLN:NE2	1.95	0.81
1:D:395:ALA:O	1:D:398:GLU:HG2	1.79	0.81
2:B:2:VAL:CG1	2:B:69:PRO:HG3	2.09	0.81
2:B:31:VAL:HG21	2:B:86:TRP:CZ3	2.15	0.81
2:B:405:VAL:HG12	2:B:409:LYS:NZ	1.95	0.81
1:D:250:LEU:HD22	1:D:292:THR:CB	2.10	0.81
3:C:137:PHE:CD1	3:C:288:ILE:HB	2.15	0.81
3:C:192:ILE:HD12	3:C:219:LEU:HD11	1.63	0.81
4:E:146:ARG:CZ	4:E:205:PHE:HB3	2.11	0.81
4:E:183:TRP:HB3	4:E:216:ARG:CD	2.10	0.81
4:E:436:ASN:HA	4:E:439:TRP:NE1	1.95	0.81
2:B:306:HIS:ND1	2:B:306:HIS:O	2.14	0.81
3:C:67:LEU:C	3:C:116:GLY:H	1.89	0.81
3:C:137:PHE:CD1	3:C:137:PHE:C	2.59	0.81
1:D:113:THR:CG2	1:D:114:GLY:HA3	2.06	0.81
1:D:215:VAL:O	1:D:219:ILE:HG23	1.81	0.81
1:D:243:MET:H	1:D:243:MET:HE2	1.46	0.81
1:A:152:ASP:CB	1:A:197:PRO:HA	2.10	0.81
3:C:106:TYR:O	3:C:106:TYR:HD1	1.63	0.81
1:D:239:SER:CB	1:D:242:LYS:HE2	2.11	0.81
1:D:408:HIS:O	1:D:412:CYS:HB2	1.81	0.81
2:B:1:SER:O	2:B:1:SER:OG	1.98	0.81
4:E:135:PRO:HG2	4:E:137:ASP:O	1.79	0.81
1:A:94:ASN:ND2	1:A:94:ASN:C	2.35	0.80
1:A:133:THR:O	1:A:136:PRO:HG2	1.81	0.80
1:A:148:ILE:HG21	1:A:198:TYR:HB2	1.63	0.80
2:B:92:LEU:N	2:B:96:ASN:HB2	1.95	0.80
3:C:30:VAL:HG22	3:C:157:GLU:CA	2.12	0.80
3:C:47:GLU:HG2	3:C:286:PRO:HD2	1.62	0.80
1:D:30:ASP:OD1	1:D:30:ASP:N	2.11	0.80
1:D:106:THR:HG23	1:D:107:LYS:CE	2.11	0.80
1:D:305:THR:HG22	1:D:400:LYS:HB3	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:409:LYS:NZ	3:C:423:ILE:HG23	1.96	0.80
2:B:24:THR:HG22	2:B:25:VAL:H	1.47	0.80
4:E:122:ILE:H	4:E:122:ILE:HD13	1.46	0.80
4:E:185:ILE:HG12	4:E:214:ILE:HG22	1.61	0.80
1:A:382:ILE:O	1:A:386:MET:HG2	1.81	0.80
3:C:11:LEU:O	3:C:16:LYS:HB2	1.80	0.80
1:D:233:PHE:CZ	1:D:291:VAL:HG11	2.15	0.80
4:E:39:LEU:HD23	4:E:183:TRP:CZ2	2.15	0.80
4:E:197:GLN:HG2	4:E:198:LEU:N	1.93	0.80
2:B:191:LYS:HA	2:B:210:TYR:O	1.81	0.80
3:C:47:GLU:HB3	3:C:285:VAL:HB	1.64	0.80
3:C:180:ASP:HB3	3:C:181:PRO:HD3	1.61	0.80
3:C:190:TRP:HB3	3:C:223:ARG:HB2	1.64	0.80
3:C:199:LYS:HZ2	3:C:199:LYS:C	1.88	0.80
1:D:136:PRO:HA	1:D:277:TYR:OH	1.82	0.80
4:E:63:ARG:HB2	4:E:63:ARG:HH11	1.46	0.80
4:E:94:ASN:ND2	4:E:125:SER:HB2	1.96	0.80
2:B:70:ALA:O	2:B:74:GLY:HA3	1.81	0.80
2:B:147:LYS:HG3	2:B:148:SER:N	1.96	0.80
2:B:301:VAL:O	2:B:304:LEU:HB3	1.80	0.80
3:C:137:PHE:HZ	3:C:291:TYR:CD2	1.99	0.80
4:E:463:LEU:HD12	4:E:463:LEU:O	1.81	0.80
2:B:31:VAL:HG12	2:B:158:LEU:HD21	1.64	0.80
3:C:121:LEU:HD12	3:C:121:LEU:O	1.80	0.80
3:C:275:SER:O	3:C:279:PRO:HD3	1.81	0.80
1:A:209:ARG:C	1:A:210:ILE:HG13	2.05	0.80
1:A:257:LEU:CD1	1:A:285:VAL:CG2	2.60	0.80
1:A:267:THR:HG23	1:A:271:VAL:CG2	2.11	0.80
2:B:160:HIS:HE1	2:B:207:VAL:HG11	1.41	0.80
1:D:55:ARG:HA	1:D:120:PRO:O	1.82	0.80
1:A:56:LEU:O	1:A:119:THR:HA	1.81	0.80
1:A:141:ASN:HB3	1:A:206:ILE:HG13	1.64	0.80
3:C:472:ILE:HB	3:C:475:MET:SD	2.21	0.80
1:D:60:TRP:CH2	1:D:86:TRP:CZ3	2.69	0.80
1:D:432:GLU:HG2	1:D:435:GLN:NE2	1.95	0.80
2:B:175:ILE:HG12	2:B:176:ASN:N	1.97	0.80
2:B:304:LEU:HD23	2:B:304:LEU:C	2.07	0.80
3:C:29:GLU:O	3:C:30:VAL:HG23	1.81	0.80
3:C:142:GLN:HG3	3:C:143:ASN:N	1.92	0.80
3:C:316:THR:CG2	3:C:317:PRO:CD	2.60	0.80
1:A:255:VAL:O	1:A:259:VAL:HG23	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:243:PRO:CB	2:B:435:ALA:HB1	2.09	0.79
3:C:148:PHE:HB2	3:C:215:VAL:HG21	1.60	0.79
1:D:85:VAL:HG13	1:D:86:TRP:CE3	2.17	0.79
1:D:88:PRO:HG2	1:D:88:PRO:O	1.81	0.79
4:E:100:GLU:HB2	4:E:122:ILE:CD1	2.12	0.79
1:A:155:LYS:HG3	4:E:78:ARG:HH21	1.46	0.79
1:A:207:MET:O	1:A:207:MET:CG	2.30	0.79
2:B:56:LEU:HB2	2:B:120:PRO:HG2	1.62	0.79
2:B:132:VAL:HG13	2:B:279:ILE:CA	2.13	0.79
3:C:69:TRP:HB2	3:C:74:TYR:HB2	1.64	0.79
3:C:248:TYR:C	3:C:250:PRO:HD2	2.08	0.79
3:C:288:ILE:HG12	3:C:289:GLY:H	1.47	0.79
1:D:187:TRP:HZ2	1:D:196:THR:HA	1.47	0.79
4:E:127:CYS:SG	4:E:128:PRO:HD2	2.22	0.79
4:E:138:TRP:CE2	4:E:215:GLN:HB2	2.16	0.79
4:E:262:THR:CB	4:E:265:LEU:HD12	2.12	0.79
3:C:275:SER:O	3:C:278:LEU:HB3	1.81	0.79
1:D:45:GLU:HB3	1:D:271:VAL:HG23	1.64	0.79
4:E:159:LEU:HB2	4:E:192:LYS:HB2	1.62	0.79
4:E:191:LYS:O	4:E:209:ILE:HG22	1.82	0.79
1:A:209:ARG:CG	1:A:210:ILE:H	1.95	0.79
3:C:69:TRP:CZ2	3:C:112:VAL:CG1	2.65	0.79
4:E:138:TRP:HB3	4:E:214:ILE:O	1.82	0.79
2:B:90:ILE:HG23	2:B:147:LYS:N	1.98	0.79
2:B:266:LEU:O	2:B:269:LYS:HG3	1.81	0.79
2:B:287:ILE:C	2:B:287:ILE:HD12	2.06	0.79
3:C:42:LEU:HD22	3:C:190:TRP:CZ2	2.18	0.79
4:E:313:THR:O	4:E:313:THR:OG1	2.00	0.79
1:A:56:LEU:HD23	1:A:57:ARG:N	1.98	0.79
3:C:37:LEU:HD12	3:C:217:PHE:CD2	2.17	0.79
3:C:201:ILE:HG13	3:C:211:ASN:O	1.81	0.79
1:D:35:LEU:HD12	1:D:36:GLN:N	1.96	0.79
4:E:433:GLY:O	4:E:436:ASN:HB2	1.82	0.79
1:A:17:LYS:HE3	1:A:84:ASP:HA	1.65	0.79
2:B:40:LEU:HD23	2:B:52:THR:OG1	1.82	0.79
4:E:140:ASN:HD21	4:E:211:PHE:HA	1.47	0.79
4:E:184:THR:HG23	4:E:215:GLN:HG2	1.63	0.79
1:A:41:ILE:HD11	1:A:51:GLU:CB	2.13	0.79
1:A:304:SER:HB2	1:A:400:LYS:NZ	1.98	0.79
2:B:68:ASP:O	2:B:72:TYR:HB3	1.82	0.79
3:C:7:LEU:HD23	3:C:10:ASP:CB	2.12	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:175:GLU:OE1	1:D:211:PRO:HB3	1.82	0.79
1:A:242:LYS:HB2	1:A:245:LEU:CB	2.12	0.79
3:C:190:TRP:HD1	3:C:221:ILE:HD12	1.48	0.79
1:D:87:LEU:HD12	1:D:88:PRO:CD	2.09	0.79
1:D:135:PHE:HZ	1:D:273:LEU:HD12	1.47	0.79
1:D:232:VAL:CG2	1:D:250:LEU:HD11	2.13	0.79
4:E:33:LYS:HE3	4:E:160:SER:HB2	1.65	0.79
4:E:172:ILE:HD11	4:E:187:HIS:HA	1.65	0.79
2:B:242:PRO:HD3	2:B:248:LYS:HE3	1.64	0.79
3:C:279:PRO:CA	3:C:282:ALA:HB3	2.11	0.79
4:E:162:GLU:O	4:E:189:PRO:HA	1.83	0.79
1:A:420:ILE:HG13	1:A:421:GLY:H	1.46	0.78
2:B:55:PHE:HA	2:B:120:PRO:O	1.83	0.78
2:B:197:TRP:CD1	2:B:204:TYR:HB3	2.18	0.78
2:B:112:HIS:CD2	2:B:113:THR:HG23	2.18	0.78
1:D:187:TRP:CZ3	1:D:189:TYR:HD1	2.01	0.78
4:E:35:THR:HG23	4:E:175:GLU:CD	2.08	0.78
4:E:45:LYS:HE2	4:E:278:ASN:O	1.82	0.78
4:E:59:TRP:C	4:E:60:ASN:HD22	1.91	0.78
4:E:89:VAL:HG23	4:E:99:PHE:CE2	2.19	0.78
3:C:3:GLU:OE1	3:C:7:LEU:HD12	1.83	0.78
3:C:273:LEU:HD23	3:C:276:GLN:CG	2.13	0.78
3:C:210:THR:HG22	3:C:211:ASN:H	1.47	0.78
1:D:244:THR:HG23	1:D:245:LEU:N	1.98	0.78
4:E:262:THR:HG23	4:E:265:LEU:CD1	2.14	0.78
1:A:59:GLN:HE22	1:A:117:MET:CG	1.97	0.78
1:A:76:LYS:HG2	1:A:77:LYS:N	1.99	0.78
1:A:189:TYR:HA	1:A:197:PRO:CD	2.13	0.78
1:A:251:LEU:HD22	4:E:260:ALA:HB1	1.66	0.78
2:B:279:ILE:HG22	2:B:280:ILE:HD13	1.66	0.78
1:D:401:TYR:O	1:D:401:TYR:HD1	1.67	0.78
2:B:31:VAL:HG12	2:B:158:LEU:CD2	2.14	0.78
2:B:46:LYS:HE2	2:B:278:PRO:CG	2.10	0.78
2:B:131:LYS:NZ	2:B:132:VAL:HB	1.97	0.78
2:B:311:THR:CB	2:B:430:TYR:CD2	2.66	0.78
2:B:415:LEU:HD13	2:B:415:LEU:C	2.08	0.78
4:E:470:HIS:CE1	4:E:474:VAL:HG23	2.18	0.78
1:A:245:LEU:HD13	2:B:250:SER:HB2	1.65	0.78
3:C:50:GLU:HA	3:C:132:ILE:CD1	2.13	0.78
1:D:60:TRP:CZ2	1:D:86:TRP:CH2	2.71	0.78
4:E:209:ILE:HG12	4:E:211:PHE:HE1	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:283:GLY:O	4:E:287:ILE:HG22	1.84	0.78
1:A:305:THR:HB	1:A:400:LYS:HB2	1.64	0.78
1:A:422:THR:O	1:A:425:VAL:HG12	1.83	0.78
3:C:38:THR:CG2	3:C:57:TRP:HE3	1.96	0.78
1:D:46:VAL:HB	1:D:271:VAL:CA	2.14	0.78
1:A:41:ILE:HD11	1:A:51:GLU:OE1	1.83	0.78
1:A:257:LEU:CD1	1:A:285:VAL:HG23	2.13	0.78
2:B:442:ILE:O	2:B:446:MET:HG2	1.84	0.78
4:E:237:VAL:CG2	4:E:457:LEU:HD21	2.14	0.78
1:A:35:LEU:HD21	1:A:37:LEU:CD2	2.14	0.78
1:A:151:TYR:O	1:A:198:TYR:HB3	1.84	0.78
3:C:232:PHE:C	3:C:235:PRO:HD2	2.09	0.78
1:D:92:LEU:CD2	1:D:92:LEU:H	1.96	0.78
1:D:187:TRP:CH2	1:D:189:TYR:HB3	2.18	0.78
4:E:132:THR:O	4:E:135:PRO:HD3	1.84	0.78
4:E:187:HIS:CE1	4:E:189:PRO:HG3	2.19	0.78
4:E:270:GLN:C	4:E:273:PRO:HD2	2.09	0.78
4:E:435:GLU:HB3	4:E:439:TRP:CZ2	2.19	0.78
1:A:135:PHE:HB3	1:A:273:LEU:HA	1.66	0.77
4:E:215:GLN:HG3	4:E:216:ARG:N	1.98	0.77
2:B:81:PRO:HD3	3:C:22:ARG:NH2	1.99	0.77
3:C:12:LEU:HB2	3:C:16:LYS:CG	2.09	0.77
3:C:12:LEU:CB	3:C:16:LYS:HG2	2.08	0.77
3:C:160:MET:H	3:C:213:GLN:HB2	1.49	0.77
3:C:242:LEU:HD21	3:C:263:VAL:HG12	1.65	0.77
1:D:72:TYR:HD1	1:D:72:TYR:O	1.65	0.77
1:D:131:ILE:HG13	1:D:133:THR:N	1.95	0.77
1:D:137:PHE:HD2	1:D:431:ILE:CG2	1.97	0.77
4:E:141:CYS:SG	4:E:143:LEU:HD11	2.25	0.77
4:E:273:PRO:HG2	4:E:274:GLU:H	1.49	0.77
1:D:302:SER:CB	1:D:305:THR:HG23	2.15	0.77
1:A:137:PHE:HB3	1:A:435:GLN:HG3	1.65	0.77
2:B:251:LEU:C	2:B:251:LEU:HD12	2.08	0.77
4:E:79:ILE:O	4:E:79:ILE:CG2	2.33	0.77
1:A:2:GLU:O	1:A:7:LEU:HD21	1.83	0.77
1:A:43:VAL:CG1	1:A:50:VAL:HG22	2.15	0.77
1:A:95:ASN:HA	1:A:127:TYR:HB3	1.66	0.77
3:C:143:ASN:OD1	3:C:220:ILE:HB	1.83	0.77
3:C:466:VAL:O	3:C:470:ILE:HG12	1.85	0.77
4:E:233:SER:O	4:E:237:VAL:HG23	1.84	0.77
1:A:41:ILE:CD1	1:A:51:GLU:HB3	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:241:LEU:HD21	2:B:251:LEU:HD11	1.66	0.77
2:B:449:ILE:HA	2:B:452:PHE:CD2	2.20	0.77
3:C:58:MET:HE1	3:C:105:ALA:O	1.84	0.77
3:C:155:ALA:N	3:C:211:ASN:HA	1.99	0.77
4:E:20:PRO:HG3	4:E:61:ASP:HA	1.66	0.77
4:E:310:THR:HB	4:E:313:THR:HG22	1.67	0.77
2:B:9:SER:HA	2:B:12:PHE:HD1	1.48	0.77
2:B:10:VAL:CG1	2:B:11:LEU:HD22	2.13	0.77
2:B:68:ASP:HB3	2:B:69:PRO:HD3	1.65	0.77
2:B:186:TRP:HB3	2:B:215:ARG:HD2	1.67	0.77
1:D:3:HIS:HB3	1:D:7:LEU:HG	1.64	0.77
4:E:27:VAL:HG12	4:E:153:HIS:C	2.10	0.77
4:E:279:VAL:HB	4:E:280:PRO:CD	2.15	0.77
2:B:20:ARG:HD3	2:B:20:ARG:H	1.48	0.77
2:B:278:PRO:O	2:B:278:PRO:HG2	1.85	0.77
3:C:195:LYS:HG3	3:C:195:LYS:O	1.83	0.77
1:A:57:ARG:HD3	1:A:161:GLU:OE1	1.85	0.77
1:A:179:LYS:HE2	1:A:208:GLN:CD	2.09	0.77
2:B:35:LEU:O	2:B:174:MET:HE1	1.85	0.77
2:B:38:THR:HG22	2:B:55:PHE:HE1	1.50	0.77
3:C:148:PHE:CB	3:C:215:VAL:CG2	2.61	0.77
1:D:58:GLN:NE2	1:D:88:PRO:HG3	2.00	0.77
1:D:153:GLY:HA3	1:D:196:THR:HG22	1.66	0.77
1:A:43:VAL:CG2	1:A:50:VAL:HG22	2.15	0.76
3:C:22:ARG:O	3:C:24:VAL:HG23	1.85	0.76
3:C:113:ARG:NE	3:C:119:THR:HG23	1.99	0.76
3:C:162:LEU:C	3:C:162:LEU:HD22	2.09	0.76
4:E:152:ALA:HB3	4:E:204:ASP:O	1.84	0.76
4:E:250:LYS:HB3	4:E:253:LEU:HD23	1.67	0.76
2:B:185:GLN:HB3	2:B:217:PRO:HB3	1.66	0.76
1:D:40:LEU:CD1	1:D:52:THR:HB	2.14	0.76
1:D:72:TYR:CD1	1:D:72:TYR:O	2.38	0.76
4:E:14:TYR:CE2	4:E:16:LYS:HE3	2.19	0.76
4:E:262:THR:OG1	4:E:265:LEU:HD12	1.85	0.76
1:A:60:TRP:HE1	1:A:116:ILE:HD12	1.51	0.76
1:A:66:ARG:HD3	1:A:66:ARG:N	2.00	0.76
1:A:380:LYS:HD3	2:B:408:ILE:HB	1.67	0.76
2:B:47:ASN:HB2	2:B:49:GLU:OE1	1.84	0.76
3:C:4:GLU:HG3	3:C:5:GLU:N	2.00	0.76
3:C:453:ILE:CG2	3:C:454:ASP:H	1.97	0.76
4:E:44:GLU:HG3	4:E:129:ILE:CB	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:LEU:CD1	1:A:100:PHE:HE2	1.99	0.76
1:A:174:GLY:HA2	1:A:176:TRP:CZ3	2.21	0.76
3:C:318:SER:HB2	3:C:447:ASN:HD22	1.49	0.76
4:E:39:LEU:HD12	4:E:49:LEU:HD13	1.66	0.76
1:A:2:GLU:O	1:A:2:GLU:CG	2.34	0.76
2:B:47:ASN:O	2:B:48:GLU:HG2	1.85	0.76
3:C:316:THR:HG21	3:C:447:ASN:HB3	1.67	0.76
1:A:3:HIS:HB2	1:A:7:LEU:CD2	2.16	0.76
1:A:46:VAL:CG2	1:A:270:ALA:CA	2.63	0.76
1:A:306:HIS:O	1:A:306:HIS:CD2	2.38	0.76
2:B:27:ASP:C	2:B:28:LYS:HG3	2.08	0.76
2:B:65:LEU:HD23	2:B:110:VAL:HG11	1.66	0.76
2:B:212:ILE:HG22	2:B:212:ILE:O	1.86	0.76
3:C:84:PRO:HG3	3:C:107:PHE:O	1.86	0.76
3:C:135:LEU:O	3:C:138:PRO:HD2	1.86	0.76
3:C:161:ASP:HA	3:C:199:LYS:HG2	1.68	0.76
1:A:46:VAL:CG2	1:A:270:ALA:C	2.58	0.76
1:A:155:LYS:HG3	4:E:78:ARG:HE	1.50	0.76
2:B:56:LEU:HD11	2:B:103:THR:HG23	1.66	0.76
2:B:439:PHE:HA	2:B:442:ILE:HB	1.67	0.76
3:C:36:SER:HB3	3:C:59:ASP:CB	2.16	0.76
1:D:86:TRP:O	1:D:86:TRP:CE2	2.37	0.76
1:D:233:PHE:HZ	1:D:291:VAL:HG11	1.49	0.76
2:B:91:VAL:C	2:B:92:LEU:HD23	2.11	0.76
3:C:58:MET:SD	3:C:92:ILE:CD1	2.74	0.76
1:D:49:ILE:HG22	1:D:49:ILE:O	1.84	0.76
1:D:401:TYR:O	1:D:401:TYR:CD1	2.39	0.76
1:D:412:CYS:HB3	1:D:413:VAL:HG23	1.67	0.76
1:A:46:VAL:HG23	1:A:270:ALA:C	2.10	0.76
1:A:139:GLN:HG3	1:A:207:MET:N	2.00	0.76
1:A:291:VAL:O	1:A:295:VAL:HG23	1.86	0.76
3:C:445:ASN:CA	3:C:448:LEU:HG	2.12	0.76
1:D:231:LEU:O	1:D:235:LEU:HG	1.86	0.76
4:E:66:TRP:CD1	4:E:111:ASN:CA	2.69	0.76
4:E:173:ASP:HB3	4:E:185:ILE:HG21	1.67	0.76
4:E:211:PHE:O	4:E:212:LEU:HD12	1.83	0.76
1:A:43:VAL:HG22	1:A:50:VAL:HG22	1.66	0.75
3:C:273:LEU:HD23	3:C:276:GLN:CB	2.16	0.75
1:D:166:ASP:CB	1:D:181:TYR:HB2	2.16	0.75
1:D:271:VAL:O	1:D:271:VAL:CG1	2.34	0.75
4:E:91:LEU:HB2	4:E:95:VAL:H	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:214:ILE:C	4:E:214:ILE:HD12	2.10	0.75
1:A:107:LYS:HE2	2:B:150:THR:HB	1.66	0.75
1:A:107:LYS:CE	2:B:150:THR:HB	2.16	0.75
1:A:293:VAL:HG22	4:E:238:LEU:HD21	1.66	0.75
2:B:265:LEU:HA	2:B:268:ASP:OD2	1.87	0.75
3:C:316:THR:HG21	3:C:447:ASN:CB	2.16	0.75
1:D:260:ILE:HG22	1:D:264:ILE:HD11	1.66	0.75
4:E:82:GLU:C	4:E:83:LEU:HD22	2.11	0.75
4:E:132:THR:C	4:E:135:PRO:HD3	2.11	0.75
1:A:282:MET:O	1:A:286:ILE:HG13	1.85	0.75
2:B:181:THR:CG2	2:B:184:GLY:H	1.99	0.75
2:B:263:LEU:CD2	2:B:291:VAL:HG22	2.13	0.75
1:D:118:TRP:NE1	1:D:120:PRO:HB3	2.02	0.75
1:D:384:GLU:HG2	4:E:422:ILE:HD12	1.69	0.75
4:E:90:VAL:CG2	4:E:95:VAL:HG11	2.14	0.75
1:A:256:PHE:CE1	2:B:261:VAL:CG2	2.70	0.75
1:D:176:TRP:CB	1:D:209:ARG:HD2	2.16	0.75
1:A:406:ILE:HG23	1:A:409:ILE:CD1	2.15	0.75
2:B:112:HIS:NE2	2:B:113:THR:HG23	2.00	0.75
3:C:77:ILE:CD1	3:C:80:LEU:HD13	2.15	0.75
3:C:431:LYS:NZ	1:D:379:VAL:HG22	2.01	0.75
1:D:49:ILE:HG21	1:D:125:LYS:HZ1	1.50	0.75
4:E:101:VAL:CG2	4:E:101:VAL:O	2.35	0.75
1:A:72:TYR:CD1	1:A:72:TYR:C	2.63	0.75
3:C:132:ILE:O	3:C:136:TYR:HB2	1.87	0.75
3:C:241:PHE:CD1	3:C:245:LEU:HD22	2.20	0.75
3:C:280:GLU:HG3	3:C:281:THR:N	2.00	0.75
3:C:443:VAL:O	3:C:443:VAL:HG12	1.86	0.75
1:D:11:LEU:O	1:D:15:TYR:HB2	1.86	0.75
1:D:101:ALA:O	1:D:102:ILE:HD13	1.86	0.75
4:E:159:LEU:HD12	4:E:192:LYS:CA	2.16	0.75
1:A:135:PHE:N	1:A:136:PRO:HD2	2.02	0.75
3:C:33:ILE:O	3:C:160:MET:HA	1.87	0.75
3:C:78:SER:O	3:C:114:PRO:HB3	1.87	0.75
3:C:431:LYS:CE	1:D:379:VAL:HG22	2.16	0.75
1:D:63:VAL:O	1:D:63:VAL:HG22	1.86	0.75
1:D:109:LEU:O	1:D:116:ILE:HG22	1.86	0.75
1:D:167:LEU:N	1:D:167:LEU:CD1	2.48	0.75
1:A:276:LYS:HD2	1:A:276:LYS:H	1.52	0.75
1:D:216:VAL:O	1:D:220:ILE:HG13	1.86	0.75
2:B:223:TYR:O	2:B:226:VAL:HG22	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:242:LEU:HD22	3:C:267:GLN:CG	2.17	0.75
3:C:282:ALA:HB2	3:C:287:LEU:CD1	2.16	0.75
1:D:222:CYS:SG	1:D:225:PHE:CZ	2.79	0.75
4:E:44:GLU:CB	4:E:129:ILE:HD12	2.17	0.75
4:E:100:GLU:HB2	4:E:122:ILE:HD11	1.69	0.75
1:A:131:ILE:HD11	1:A:140:GLN:CG	2.16	0.74
1:A:433:LEU:O	1:A:433:LEU:HD12	1.87	0.74
3:C:78:SER:HA	3:C:114:PRO:CB	2.17	0.74
1:D:255:VAL:O	1:D:259:VAL:HG23	1.87	0.74
4:E:55:ILE:HG13	4:E:57:ILE:HG13	1.67	0.74
4:E:66:TRP:CD1	4:E:111:ASN:CB	2.69	0.74
4:E:188:ARG:O	4:E:188:ARG:CG	2.35	0.74
1:A:52:THR:O	1:A:123:ILE:HG13	1.87	0.74
2:B:67:TRP:HB2	2:B:72:TYR:HB2	1.67	0.74
2:B:289:ILE:HG22	2:B:293:PHE:CZ	2.22	0.74
3:C:48:THR:N	3:C:285:VAL:HA	2.01	0.74
1:D:109:LEU:HD12	1:D:117:MET:HB3	1.69	0.74
4:E:183:TRP:HA	4:E:216:ARG:HA	1.69	0.74
1:A:251:LEU:CD2	4:E:260:ALA:CB	2.63	0.74
1:D:229:THR:HA	1:D:232:VAL:HG23	1.68	0.74
4:E:45:LYS:N	4:E:280:PRO:HA	2.03	0.74
4:E:448:LYS:N	4:E:448:LYS:HD2	1.99	0.74
1:A:137:PHE:CD1	1:A:210:ILE:HD12	2.22	0.74
3:C:30:VAL:CG2	3:C:157:GLU:CA	2.66	0.74
3:C:81:ARG:NH1	3:C:111:LEU:HB2	2.03	0.74
3:C:93:VAL:HG11	3:C:151:LEU:HD13	1.68	0.74
1:D:86:TRP:CD2	1:D:86:TRP:C	2.63	0.74
1:A:148:ILE:HD11	1:A:156:VAL:CG1	2.16	0.74
1:A:148:ILE:CG2	1:A:198:TYR:CD2	2.69	0.74
2:B:155:GLU:O	2:B:156:VAL:HG13	1.87	0.74
3:C:138:PRO:CA	3:C:288:ILE:HD12	2.17	0.74
1:D:92:LEU:HD22	1:D:92:LEU:N	2.02	0.74
4:E:55:ILE:C	4:E:118:LEU:HD13	2.13	0.74
1:A:379:VAL:HA	1:A:382:ILE:HD11	1.69	0.74
3:C:269:VAL:HG13	3:C:270:PHE:HD1	1.51	0.74
1:D:63:VAL:O	1:D:63:VAL:CG2	2.35	0.74
1:D:227:PHE:O	1:D:230:VAL:HG12	1.87	0.74
1:A:380:LYS:HD3	2:B:408:ILE:CB	2.16	0.74
3:C:25:LYS:HG3	3:C:25:LYS:O	1.87	0.74
3:C:179:ILE:CG2	3:C:181:PRO:HD2	2.17	0.74
1:A:156:VAL:HG22	1:A:157:SER:N	2.02	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:VAL:HG13	1:A:219:ILE:N	2.02	0.74
1:A:423:VAL:O	1:A:426:PHE:HB3	1.87	0.74
3:C:30:VAL:CG2	3:C:157:GLU:C	2.60	0.74
3:C:241:PHE:CD1	3:C:241:PHE:C	2.65	0.74
3:C:316:THR:HG23	3:C:317:PRO:HD2	1.70	0.74
1:D:237:THR:OG1	1:D:406:ILE:HG23	1.88	0.74
4:E:19:LYS:NZ	4:E:154:GLU:HB3	2.03	0.74
2:B:33:VAL:HG21	2:B:158:LEU:HD13	1.69	0.74
3:C:13:ILE:O	3:C:17:TYR:HB3	1.87	0.74
3:C:470:ILE:O	3:C:474:VAL:HG23	1.88	0.74
1:D:64:ARG:HH11	1:D:64:ARG:HG3	1.52	0.74
1:D:132:VAL:O	1:D:274:ILE:HG12	1.87	0.74
1:D:166:ASP:OD2	1:D:181:TYR:HB2	1.88	0.74
4:E:144:VAL:HG12	4:E:209:ILE:HA	1.68	0.74
1:A:3:HIS:HB2	1:A:7:LEU:HD21	1.70	0.73
1:A:54:VAL:CG2	1:A:122:ALA:HB3	2.18	0.73
1:A:207:MET:H	1:A:207:MET:HE2	1.53	0.73
1:A:281:THR:O	1:A:285:VAL:HG12	1.88	0.73
1:A:87:LEU:H	1:A:87:LEU:CD2	1.98	0.73
1:A:236:PRO:HB3	1:A:299:HIS:NE2	2.03	0.73
1:A:250:LEU:HD11	1:A:296:ILE:CG2	2.16	0.73
3:C:257:MET:HE1	3:C:314:PHE:CB	2.18	0.73
3:C:279:PRO:C	3:C:282:ALA:HB3	2.13	0.73
3:C:434:LYS:HE2	3:C:435:GLU:HG2	1.69	0.73
1:D:398:GLU:HA	1:D:401:TYR:CE1	2.22	0.73
1:D:409:ILE:HA	1:D:412:CYS:HB2	1.71	0.73
4:E:80:PRO:CB	4:E:83:LEU:HD23	2.18	0.73
1:A:41:ILE:CG1	1:A:51:GLU:HB3	2.17	0.73
1:A:139:GLN:NE2	1:A:206:ILE:HG23	2.03	0.73
1:A:259:VAL:HG13	1:A:262:GLU:OE1	1.88	0.73
3:C:138:PRO:HB2	3:C:140:ASP:OD1	1.88	0.73
4:E:44:GLU:HG3	4:E:129:ILE:HB	1.69	0.73
4:E:138:TRP:CE3	4:E:215:GLN:HA	2.22	0.73
4:E:463:LEU:HG	4:E:464:ALA:N	2.03	0.73
1:A:145:LYS:HZ2	1:A:202:THR:HG23	1.54	0.73
3:C:102:TYR:CE1	3:C:106:TYR:HB3	2.24	0.73
3:C:453:ILE:HG23	3:C:454:ASP:N	1.98	0.73
1:D:142:CYS:SG	1:D:144:MET:HG3	2.28	0.73
1:D:301:ARG:HH22	1:D:406:ILE:CD1	2.01	0.73
4:E:14:TYR:HE2	4:E:16:LYS:CE	2.01	0.73
4:E:444:LYS:O	4:E:448:LYS:HG2	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:28:LYS:HB3	2:B:155:GLU:C	2.12	0.73
3:C:252:GLU:HG3	1:D:300:HIS:C	2.14	0.73
4:E:416:VAL:HG22	4:E:417:GLU:N	2.04	0.73
1:A:406:ILE:CG2	1:A:409:ILE:CD1	2.67	0.73
1:D:53:ASN:HB2	1:D:123:ILE:HG12	1.70	0.73
1:D:56:LEU:HD21	1:D:122:ALA:HB3	1.70	0.73
3:C:196:PRO:HD2	3:C:218:TYR:O	1.87	0.73
1:D:252:SER:HB2	4:E:259:LEU:CD1	2.18	0.73
4:E:262:THR:HG23	4:E:265:LEU:HB2	1.69	0.73
1:A:41:ILE:HG13	1:A:42:ASN:N	2.04	0.73
2:B:48:GLU:HB2	2:B:130:ILE:HG12	1.71	0.73
3:C:223:ARG:O	3:C:224:LYS:HG3	1.88	0.73
1:D:65:LEU:HD23	1:D:110:LEU:HD13	1.67	0.73
1:D:86:TRP:O	1:D:86:TRP:CE3	2.38	0.73
4:E:44:GLU:CG	4:E:129:ILE:HD12	2.17	0.73
1:A:148:ILE:HG21	1:A:198:TYR:CB	2.18	0.73
2:B:23:GLN:N	2:B:23:GLN:NE2	2.36	0.73
2:B:129:THR:O	2:B:129:THR:CG2	2.25	0.73
1:D:38:ILE:HG22	1:D:38:ILE:O	1.89	0.73
1:D:92:LEU:CB	1:D:95:ASN:HB2	2.19	0.73
4:E:42:LEU:HD22	4:E:183:TRP:CZ2	2.24	0.73
4:E:79:ILE:HG12	4:E:80:PRO:HD3	1.70	0.73
1:A:148:ILE:CG2	1:A:198:TYR:HB2	2.19	0.73
2:B:297:LEU:O	2:B:297:LEU:HD23	1.89	0.73
3:C:155:ALA:HB2	3:C:211:ASN:CA	2.18	0.73
1:D:43:VAL:HG22	1:D:50:VAL:CA	2.18	0.73
4:E:267:LEU:HD12	4:E:270:GLN:OE1	1.87	0.73
1:A:41:ILE:CD1	1:A:51:GLU:CD	2.62	0.72
3:C:252:GLU:HG3	1:D:300:HIS:CB	2.19	0.72
1:D:78:ILE:HD12	1:D:110:LEU:HB3	1.70	0.72
1:D:236:PRO:HB3	1:D:299:HIS:HE2	1.53	0.72
4:E:219:LEU:HB3	4:E:222:ILE:CB	2.19	0.72
3:C:65:HIS:CD2	3:C:65:HIS:N	2.54	0.72
3:C:69:TRP:CE3	3:C:73:GLU:HB3	2.21	0.72
1:D:91:VAL:CG2	1:D:96:ALA:CB	2.67	0.72
3:C:51:THR:HA	3:C:128:SER:O	1.89	0.72
3:C:276:GLN:C	3:C:279:PRO:HD2	2.14	0.72
3:C:455:ARG:O	3:C:459:PHE:HD1	1.73	0.72
4:E:20:PRO:HB3	4:E:61:ASP:OD1	1.88	0.72
2:B:248:LYS:HD3	2:B:252:SER:HB3	0.82	0.72
1:D:157:SER:HA	1:D:199:LEU:HD12	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:109:LEU:HB2	2:B:119:HIS:NE2	2.05	0.72
2:B:218:LEU:HD13	2:B:221:ILE:CG1	2.19	0.72
3:C:278:LEU:CD1	3:C:278:LEU:O	2.35	0.72
1:D:176:TRP:CE3	1:D:209:ARG:NE	2.57	0.72
4:E:66:TRP:HD1	4:E:111:ASN:HB2	1.53	0.72
4:E:216:ARG:O	4:E:217:LYS:HG3	1.90	0.72
1:A:7:LEU:HD22	1:A:70:ALA:C	2.14	0.72
1:A:233:PHE:O	1:A:236:PRO:HG2	1.89	0.72
3:C:46:LYS:HG3	3:C:49:ASP:OD1	1.90	0.72
1:D:136:PRO:CG	1:D:274:ILE:HD11	2.15	0.72
1:D:167:LEU:CD1	1:D:178:MET:HB2	2.19	0.72
1:A:124:PHE:CD1	1:A:124:PHE:C	2.67	0.72
1:A:250:LEU:HD22	1:A:292:THR:CG2	2.13	0.72
2:B:181:THR:HG23	2:B:184:GLY:H	1.55	0.72
3:C:469:THR:O	3:C:473:PHE:HB2	1.90	0.72
1:D:15:TYR:CE2	1:D:84:ASP:HB3	2.25	0.72
1:D:169:THR:O	1:D:169:THR:CG2	2.27	0.72
4:E:35:THR:HB	4:E:54:TRP:HE3	1.54	0.72
1:A:406:ILE:HA	1:A:409:ILE:HD11	1.70	0.72
3:C:43:ILE:H	3:C:43:ILE:HD12	1.52	0.72
3:C:141:TRP:CZ3	3:C:223:ARG:HB3	2.24	0.72
1:D:201:ILE:O	1:D:203:TYR:HE1	1.73	0.72
1:D:241:GLU:O	1:D:243:MET:HE1	1.90	0.72
1:D:379:VAL:CA	1:D:382:ILE:HG13	2.17	0.72
4:E:469:GLY:O	4:E:473:GLN:HB2	1.90	0.72
1:A:155:LYS:HG3	4:E:78:ARG:NH2	2.05	0.72
2:B:176:ASN:ND2	2:B:188:ILE:HD12	2.05	0.72
3:C:67:LEU:HD21	3:C:112:VAL:HG13	1.71	0.72
1:D:166:ASP:CG	1:D:178:MET:HE2	2.14	0.72
1:A:171:MET:HE3	1:A:176:TRP:CH2	2.24	0.72
1:D:398:GLU:HA	1:D:401:TYR:CE2	2.25	0.72
4:E:284:LYS:HE3	4:E:284:LYS:CA	2.19	0.72
2:B:28:LYS:CG	2:B:155:GLU:HA	2.13	0.71
2:B:91:VAL:HA	2:B:96:ASN:HD22	1.52	0.71
2:B:425:LYS:HA	2:B:428:TRP:HD1	1.52	0.71
3:C:7:LEU:HA	3:C:10:ASP:OD2	1.90	0.71
3:C:137:PHE:CD1	3:C:137:PHE:O	2.43	0.71
1:D:191:THR:O	1:D:191:THR:HG22	1.88	0.71
4:E:55:ILE:CG2	4:E:119:PRO:HG2	2.20	0.71
4:E:162:GLU:HA	4:E:190:ALA:N	2.04	0.71
4:E:431:ASP:O	4:E:435:GLU:HG3	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:142:CYS:O	2:B:210:TYR:HA	1.91	0.71
2:B:277:VAL:H	2:B:278:PRO:HD3	1.55	0.71
1:D:287:SER:HA	1:D:290:ILE:CD1	2.20	0.71
1:A:57:ARG:HA	1:A:119:THR:HG22	0.84	0.71
1:A:237:THR:OG1	1:A:406:ILE:HB	1.91	0.71
1:A:413:VAL:O	1:A:416:LEU:HB3	1.89	0.71
2:B:269:LYS:C	2:B:271:PRO:HD2	2.14	0.71
3:C:60:HIS:CD2	3:C:92:ILE:HD13	2.24	0.71
3:C:247:PHE:CE1	3:C:309:VAL:CG2	2.61	0.71
3:C:296:MET:CE	3:C:296:MET:CA	2.68	0.71
1:D:133:THR:HG23	1:D:274:ILE:HD13	1.70	0.71
1:D:141:ASN:HB3	1:D:206:ILE:CD1	2.20	0.71
1:D:152:ASP:HA	1:D:197:PRO:HA	1.71	0.71
4:E:91:LEU:HB3	4:E:94:ASN:H	1.55	0.71
4:E:138:TRP:CZ2	4:E:215:GLN:CB	2.70	0.71
2:B:23:GLN:NE2	2:B:23:GLN:H	1.88	0.71
2:B:130:ILE:HB	2:B:134:TYR:HD2	1.52	0.71
3:C:272:LEU:O	3:C:276:GLN:HG2	1.90	0.71
1:D:289:ILE:HG22	1:D:290:ILE:N	2.04	0.71
2:B:132:VAL:CG1	2:B:279:ILE:CA	2.68	0.71
2:B:281:ILE:HG22	2:B:285:MET:N	2.05	0.71
3:C:457:SER:O	3:C:461:ILE:HG13	1.91	0.71
1:D:395:ALA:HB1	1:D:399:TRP:CZ2	2.25	0.71
4:E:79:ILE:CG1	4:E:80:PRO:CD	2.63	0.71
4:E:236:VAL:O	4:E:239:VAL:HG23	1.88	0.71
4:E:283:GLY:C	4:E:284:LYS:HE3	2.13	0.71
1:A:278:MET:O	1:A:281:THR:HG22	1.90	0.71
3:C:30:VAL:HG21	3:C:158:ILE:N	2.04	0.71
3:C:247:PHE:C	3:C:250:PRO:HD3	2.15	0.71
3:C:42:LEU:HD22	3:C:190:TRP:HH2	1.49	0.71
3:C:319:THR:H	3:C:447:ASN:CB	2.03	0.71
1:D:170:PHE:CE2	1:D:176:TRP:CD1	2.75	0.71
4:E:81:SER:O	4:E:86:LEU:HD11	1.91	0.71
4:E:174:PRO:HA	4:E:177:PHE:HB2	1.72	0.71
1:A:56:LEU:HD22	1:A:58:GLN:HG3	1.72	0.71
1:A:250:LEU:CD2	1:A:292:THR:CG2	2.61	0.71
1:A:380:LYS:HB3	2:B:408:ILE:CG1	2.21	0.71
1:A:35:LEU:HD23	1:A:35:LEU:C	2.15	0.71
1:A:239:SER:HB2	2:B:312:HIS:CB	2.19	0.71
2:B:266:LEU:O	2:B:270:VAL:HG23	1.91	0.71
2:B:438:LEU:HA	2:B:441:TYR:HB3	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:52:LEU:HD23	3:C:128:SER:OG	1.90	0.71
3:C:90:PRO:HD2	3:C:120:TRP:HZ3	1.55	0.71
3:C:318:SER:HB2	3:C:447:ASN:ND2	2.05	0.71
1:D:7:LEU:O	1:D:11:LEU:HG	1.91	0.71
1:A:52:THR:O	1:A:123:ILE:HA	1.90	0.71
1:A:52:THR:C	1:A:123:ILE:HG13	2.15	0.71
2:B:109:LEU:HB3	2:B:117:SER:HB2	1.71	0.71
3:C:79:ILE:HG23	3:C:111:LEU:HD11	1.70	0.71
1:D:37:LEU:HD11	1:D:52:THR:OG1	1.90	0.71
1:D:391:GLU:HA	1:D:394:ASN:OD1	1.90	0.71
4:E:240:TYR:CG	4:E:453:ILE:HD13	2.26	0.71
2:B:141:ASN:ND2	2:B:212:ILE:HG12	2.06	0.70
3:C:36:SER:HB3	3:C:59:ASP:HB3	1.71	0.70
3:C:463:PRO:O	3:C:467:LEU:HD23	1.91	0.70
2:B:11:LEU:H	2:B:11:LEU:CD2	2.04	0.70
2:B:287:ILE:HA	2:B:290:LEU:CD1	2.21	0.70
3:C:443:VAL:HA	3:C:446:TRP:HD1	1.50	0.70
1:D:160:PRO:CG	1:D:185:LYS:HB3	2.21	0.70
4:E:28:ILE:HG21	4:E:85:TRP:HZ3	1.56	0.70
2:B:47:ASN:HB2	2:B:49:GLU:CD	2.16	0.70
3:C:60:HIS:HB3	3:C:62:TRP:CZ3	2.18	0.70
3:C:138:PRO:CG	3:C:288:ILE:CD1	2.70	0.70
3:C:452:THR:HA	3:C:455:ARG:HD3	1.72	0.70
1:D:80:LEU:O	1:D:108:LEU:HB3	1.91	0.70
1:D:129:GLU:OE1	1:D:129:GLU:CA	2.25	0.70
1:A:139:GLN:HB2	1:A:207:MET:C	2.16	0.70
1:A:167:LEU:HD12	1:A:178:MET:HB2	1.72	0.70
2:B:224:THR:O	2:B:227:PRO:HD2	1.90	0.70
3:C:137:PHE:CZ	3:C:291:TYR:CD2	2.79	0.70
3:C:269:VAL:HG13	3:C:270:PHE:CE1	2.27	0.70
1:D:67:TRP:CD1	1:D:71:ASP:CG	2.69	0.70
1:D:146:LEU:HD13	1:D:203:TYR:CE1	2.27	0.70
1:A:245:LEU:HD13	2:B:250:SER:CB	2.21	0.70
2:B:287:ILE:CA	2:B:290:LEU:HD12	2.22	0.70
3:C:38:THR:HG22	3:C:57:TRP:CE3	2.25	0.70
3:C:431:LYS:HZ1	1:D:379:VAL:HG22	1.54	0.70
4:E:6:LEU:HD11	4:E:69:SER:HB3	1.73	0.70
2:B:220:TYR:HB3	2:B:223:TYR:CE2	2.26	0.70
2:B:265:LEU:O	2:B:268:ASP:HB2	1.92	0.70
3:C:80:LEU:CD1	1:D:20:ARG:HH22	2.04	0.70
3:C:431:LYS:HE2	1:D:379:VAL:HG13	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:290:ILE:O	1:D:293:VAL:HB	1.90	0.70
4:E:128:PRO:C	4:E:129:ILE:HG23	2.17	0.70
4:E:172:ILE:CD1	4:E:187:HIS:HA	2.22	0.70
1:A:201:ILE:HG21	1:A:203:TYR:HE1	1.55	0.70
2:B:55:PHE:N	2:B:55:PHE:CD1	2.60	0.70
2:B:176:ASN:HB2	2:B:191:LYS:CB	2.14	0.70
3:C:273:LEU:HD23	3:C:276:GLN:HG3	1.73	0.70
1:D:58:GLN:HE21	1:D:88:PRO:HG3	1.55	0.70
1:D:67:TRP:CD1	1:D:71:ASP:CB	2.75	0.70
1:D:178:MET:SD	1:D:207:MET:HB3	2.32	0.70
1:D:278:MET:O	1:D:278:MET:HE3	1.90	0.70
1:D:296:ILE:HA	1:D:299:HIS:CB	2.21	0.70
4:E:152:ALA:HA	4:E:155:VAL:O	1.91	0.70
1:A:36:GLN:C	1:A:36:GLN:OE1	2.33	0.70
1:A:41:ILE:HD11	1:A:51:GLU:CG	2.22	0.70
3:C:229:VAL:O	3:C:233:ILE:HG12	1.92	0.70
1:A:256:PHE:CZ	2:B:261:VAL:CG2	2.70	0.70
1:A:426:PHE:HD1	1:A:427:ALA:N	1.90	0.70
3:C:42:LEU:HD13	3:C:190:TRP:HZ2	1.56	0.70
3:C:223:ARG:HG2	3:C:224:LYS:N	2.05	0.70
1:D:76:LYS:HG2	1:D:112:TYR:CE2	2.27	0.70
1:D:145:LYS:HG3	1:D:202:THR:HG23	0.85	0.70
4:E:30:VAL:O	4:E:158:GLN:HG3	1.92	0.70
4:E:138:TRP:CZ3	4:E:215:GLN:HA	2.27	0.70
1:A:131:ILE:HD11	1:A:140:GLN:NE2	2.05	0.70
2:B:226:VAL:O	2:B:230:LEU:HG	1.91	0.70
3:C:33:ILE:HG12	3:C:62:TRP:HB3	1.72	0.70
3:C:153:TYR:HB2	3:C:158:ILE:HG13	1.74	0.70
4:E:22:LYS:HG3	4:E:23:THR:N	2.05	0.70
4:E:52:ASN:HD21	4:E:120:PRO:HB2	1.57	0.70
2:B:56:LEU:HG	2:B:103:THR:HG23	1.74	0.69
3:C:38:THR:HG21	3:C:57:TRP:CE3	2.27	0.69
3:C:230:ILE:HG13	3:C:231:ASN:N	2.07	0.69
1:D:20:ARG:CG	1:D:20:ARG:NH1	2.49	0.69
1:D:398:GLU:CA	1:D:401:TYR:CZ	2.72	0.69
3:C:319:THR:H	3:C:447:ASN:HB3	1.56	0.69
4:E:103:TYR:C	4:E:104:TYR:CD1	2.70	0.69
1:A:75:ILE:HG13	1:A:78:ILE:CG2	2.21	0.69
1:A:128:CYS:SG	1:A:144:MET:HE2	2.33	0.69
3:C:38:THR:OG1	3:C:178:ILE:HG21	1.92	0.69
3:C:437:ASN:O	3:C:441:GLU:HG3	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:107:LYS:CE	4:E:149:THR:HA	2.22	0.69
1:A:87:LEU:O	1:A:87:LEU:HD23	1.92	0.69
1:A:175:GLU:OE1	1:A:175:GLU:HA	1.92	0.69
1:A:229:THR:O	1:A:232:VAL:HB	1.93	0.69
1:A:261:VAL:O	1:A:261:VAL:CG1	2.40	0.69
1:D:132:VAL:HB	1:D:274:ILE:HA	1.73	0.69
2:B:56:LEU:CG	2:B:103:THR:HG23	2.22	0.69
2:B:92:LEU:H	2:B:96:ASN:CB	1.98	0.69
2:B:108:VAL:HG13	2:B:118:TRP:HB2	1.74	0.69
2:B:140:GLN:O	2:B:213:ILE:HD13	1.93	0.69
3:C:87:ILE:HG22	3:C:88:TRP:O	1.93	0.69
3:C:195:LYS:CE	3:C:217:PHE:HB3	2.22	0.69
3:C:234:THR:O	3:C:238:LEU:HD13	1.93	0.69
1:D:26:THR:CG2	1:D:27:HIS:H	2.05	0.69
4:E:129:ILE:CG2	4:E:133:TYR:HD2	2.02	0.69
1:A:414:PHE:HA	1:A:417:ILE:HD12	1.74	0.69
2:B:236:ILE:HB	2:B:446:MET:CE	2.07	0.69
3:C:135:LEU:C	3:C:138:PRO:HD2	2.17	0.69
3:C:162:LEU:HG	3:C:217:PHE:HZ	1.57	0.69
3:C:25:LYS:HB3	3:C:28:ASN:HD21	1.57	0.69
1:A:43:VAL:HG13	1:A:50:VAL:CG2	2.23	0.69
1:A:286:ILE:O	1:A:289:ILE:HB	1.93	0.69
2:B:46:LYS:HA	2:B:278:PRO:HD2	1.73	0.69
2:B:142:CYS:CB	2:B:211:LEU:HD12	2.23	0.69
2:B:186:TRP:CE3	2:B:215:ARG:CZ	2.75	0.69
2:B:269:LYS:HE3	2:B:270:VAL:HG23	1.69	0.69
3:C:247:PHE:HA	3:C:250:PRO:HG3	1.73	0.69
3:C:435:GLU:O	3:C:438:ALA:HB3	1.92	0.69
1:D:46:VAL:HB	1:D:270:ALA:C	2.17	0.69
1:D:92:LEU:HD13	1:D:146:LEU:CG	2.23	0.69
1:D:129:GLU:C	1:D:130:ILE:HG23	2.17	0.69
1:D:238:ASP:CB	4:E:308:LEU:CD2	2.71	0.69
4:E:237:VAL:HG22	4:E:457:LEU:CD2	2.22	0.69
1:A:130:ILE:O	1:A:134:HIS:HB2	1.92	0.69
1:A:271:VAL:HG23	1:A:271:VAL:O	1.92	0.69
3:C:130:CYS:SG	3:C:146:LEU:HD11	2.33	0.69
3:C:279:PRO:O	3:C:282:ALA:HB3	1.92	0.69
2:B:59:ALA:HA	2:B:116:VAL:O	1.93	0.69
2:B:251:LEU:HD12	2:B:251:LEU:O	1.93	0.69
3:C:77:ILE:O	3:C:77:ILE:HG13	1.91	0.69
1:D:107:LYS:HZ1	4:E:149:THR:HA	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:228:PRO:O	4:E:231:LEU:HD23	1.92	0.69
1:A:247:ILE:O	1:A:247:ILE:CD1	2.41	0.68
3:C:201:ILE:HB	3:C:213:GLN:OE1	1.92	0.68
3:C:233:ILE:HD13	3:C:233:ILE:N	2.07	0.68
3:C:247:PHE:C	3:C:250:PRO:CD	2.66	0.68
1:A:46:VAL:HG23	1:A:271:VAL:H	1.58	0.68
1:A:292:THR:O	1:A:296:ILE:HG12	1.93	0.68
2:B:40:LEU:HD13	2:B:40:LEU:C	2.18	0.68
2:B:152:ASP:HB3	2:B:203:SER:HB2	1.75	0.68
1:D:48:GLN:HB3	1:D:130:ILE:HD13	1.73	0.68
4:E:42:LEU:HD22	4:E:183:TRP:CE2	2.28	0.68
4:E:138:TRP:HH2	4:E:215:GLN:NE2	1.92	0.68
4:E:284:LYS:H	4:E:284:LYS:CD	2.05	0.68
2:B:46:LYS:HB2	2:B:277:VAL:N	2.07	0.68
2:B:195:LYS:HA	2:B:207:VAL:HG13	1.76	0.68
2:B:440:LEU:O	2:B:443:PHE:HB3	1.94	0.68
3:C:59:ASP:HA	3:C:121:LEU:CB	2.23	0.68
3:C:106:TYR:C	3:C:107:PHE:CD1	2.70	0.68
3:C:138:PRO:N	3:C:288:ILE:HD12	2.08	0.68
3:C:461:ILE:O	3:C:464:VAL:HG12	1.93	0.68
1:D:420:ILE:O	1:D:420:ILE:HG13	1.91	0.68
1:A:39:GLN:O	1:A:53:ASN:HB2	1.94	0.68
1:A:382:ILE:O	1:A:386:MET:HE2	1.92	0.68
2:B:284:LEU:HD23	2:B:287:ILE:HD11	1.75	0.68
1:D:35:LEU:CD1	1:D:54:VAL:CG1	2.70	0.68
1:D:376:ILE:C	1:D:380:LYS:HE2	2.18	0.68
1:A:67:TRP:CD1	1:A:71:ASP:CG	2.71	0.68
1:A:104:HIS:C	1:A:105:MET:SD	2.77	0.68
2:B:111:GLN:CD	2:B:115:ALA:HB3	2.19	0.68
2:B:186:TRP:CB	2:B:215:ARG:HG3	2.21	0.68
2:B:236:ILE:O	2:B:240:TYR:HB2	1.94	0.68
1:D:171:MET:HG2	1:D:174:GLY:H	1.56	0.68
1:D:376:ILE:O	1:D:380:LYS:HG3	1.93	0.68
1:A:251:LEU:HD13	4:E:260:ALA:CB	2.24	0.68
1:A:270:ALA:O	1:A:271:VAL:HG13	1.92	0.68
1:A:292:THR:HA	1:A:296:ILE:HD11	1.73	0.68
3:C:2:ASN:O	3:C:3:GLU:HB3	1.92	0.68
3:C:81:ARG:CZ	3:C:111:LEU:HD13	2.24	0.68
3:C:248:TYR:C	3:C:250:PRO:CD	2.66	0.68
1:D:282:MET:HG3	1:D:286:ILE:CD1	2.23	0.68
1:D:381:TYR:CE1	4:E:419:CYS:SG	2.80	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:390:GLU:O	1:D:393:SER:HB2	1.94	0.68
4:E:45:LYS:CA	4:E:280:PRO:HA	2.23	0.68
4:E:138:TRP:CH2	4:E:215:GLN:NE2	2.62	0.68
4:E:289:VAL:O	4:E:293:SER:HB3	1.94	0.68
2:B:40:LEU:HA	2:B:52:THR:HG23	1.74	0.68
3:C:299:VAL:O	3:C:302:VAL:HG23	1.93	0.68
1:D:130:ILE:O	1:D:134:HIS:HB2	1.94	0.68
1:D:233:PHE:CE2	1:D:295:VAL:HG11	2.29	0.68
1:D:287:SER:HA	1:D:290:ILE:HG12	1.75	0.68
4:E:172:ILE:CD1	4:E:188:ARG:HB3	2.24	0.68
1:A:37:LEU:HA	1:A:53:ASN:O	1.94	0.68
2:B:222:VAL:O	2:B:225:ILE:HB	1.94	0.68
1:D:60:TRP:CH2	1:D:86:TRP:HZ3	2.12	0.68
1:A:7:LEU:HD22	1:A:70:ALA:O	1.93	0.68
1:A:34:GLY:HA3	1:A:57:ARG:CD	2.24	0.68
2:B:129:THR:HG22	2:B:142:CYS:CA	2.22	0.68
2:B:147:LYS:HG3	2:B:148:SER:H	1.59	0.68
3:C:18:ASN:HB2	3:C:21:VAL:HB	1.76	0.68
3:C:460:ILE:O	3:C:463:PRO:HG2	1.94	0.68
1:D:271:VAL:O	1:D:271:VAL:HG13	1.93	0.68
4:E:34:LEU:HD12	4:E:210:PHE:HE2	1.56	0.68
4:E:44:GLU:HA	4:E:129:ILE:HD11	1.75	0.68
4:E:81:SER:HA	4:E:107:VAL:HG23	1.76	0.68
1:A:132:VAL:O	1:A:274:ILE:HG22	1.94	0.68
1:A:384:GLU:HA	1:A:387:LYS:CG	2.24	0.68
2:B:58:LEU:HD11	2:B:118:TRP:HE3	1.59	0.68
2:B:272:GLU:O	2:B:275:LEU:HB2	1.93	0.68
3:C:137:PHE:H	3:C:138:PRO:CD	2.06	0.68
1:D:181:TYR:HE1	1:D:203:TYR:HB3	1.59	0.68
4:E:173:ASP:OD1	4:E:173:ASP:O	2.11	0.68
1:A:54:VAL:HG23	1:A:122:ALA:HB3	1.74	0.67
1:A:75:ILE:HG13	1:A:78:ILE:HG21	1.75	0.67
2:B:143:THR:HG23	2:B:208:THR:HG23	1.75	0.67
2:B:218:LEU:HD11	2:B:222:VAL:HG22	1.75	0.67
2:B:226:VAL:CG2	2:B:227:PRO:HD3	2.22	0.67
3:C:30:VAL:HG22	3:C:157:GLU:HA	1.75	0.67
3:C:93:VAL:HG11	3:C:151:LEU:HB2	1.74	0.67
1:D:75:ILE:CG1	1:D:78:ILE:CG2	2.72	0.67
1:D:130:ILE:O	1:D:131:ILE:HG12	1.94	0.67
1:D:178:MET:HA	1:D:207:MET:CB	2.24	0.67
4:E:56:GLU:CA	4:E:118:LEU:HB2	2.17	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:ASP:HB2	1:A:181:TYR:CB	2.23	0.67
2:B:198:ARG:HH11	2:B:198:ARG:HG3	1.59	0.67
3:C:19:LYS:O	3:C:19:LYS:HD2	1.93	0.67
3:C:216:THR:O	3:C:217:PHE:HD1	1.78	0.67
3:C:318:SER:CB	3:C:447:ASN:ND2	2.57	0.67
1:D:214:PHE:O	1:D:218:VAL:HG23	1.93	0.67
1:A:34:GLY:HA3	1:A:57:ARG:HD3	1.76	0.67
2:B:10:VAL:CG1	2:B:11:LEU:CD2	2.72	0.67
2:B:223:TYR:O	2:B:223:TYR:CD1	2.47	0.67
2:B:308:SER:HB2	2:B:311:THR:CG2	2.05	0.67
3:C:14:VAL:HG13	3:C:86:LEU:HD23	1.76	0.67
1:D:145:LYS:O	1:D:146:LEU:HD12	1.93	0.67
1:D:283:ILE:HA	1:D:286:ILE:HD12	1.75	0.67
1:D:287:SER:O	1:D:291:VAL:HG23	1.94	0.67
4:E:134:PHE:CB	4:E:282:ILE:CG2	2.72	0.67
1:A:255:VAL:HA	1:A:258:LEU:HD12	1.76	0.67
2:B:55:PHE:N	2:B:55:PHE:HD1	1.91	0.67
1:A:34:GLY:CA	1:A:57:ARG:HG2	2.25	0.67
2:B:28:LYS:HG2	2:B:155:GLU:CA	2.16	0.67
2:B:142:CYS:HB3	2:B:211:LEU:CD1	2.23	0.67
1:D:75:ILE:CD1	1:D:78:ILE:CG2	2.72	0.67
4:E:191:LYS:H	4:E:209:ILE:HG23	1.59	0.67
1:A:235:LEU:HB3	1:A:236:PRO:CD	2.25	0.67
1:A:405:VAL:HG23	1:A:405:VAL:O	1.95	0.67
2:B:262:PHE:CZ	3:C:269:VAL:HB	2.29	0.67
3:C:19:LYS:O	3:C:19:LYS:CD	2.43	0.67
3:C:35:LEU:HD22	3:C:215:VAL:HG21	1.77	0.67
3:C:220:ILE:O	3:C:220:ILE:CG1	2.42	0.67
1:D:252:SER:O	1:D:255:VAL:HG12	1.95	0.67
1:D:393:SER:O	1:D:396:ALA:HB3	1.94	0.67
4:E:131:VAL:HA	4:E:281:LEU:O	1.95	0.67
1:A:66:ARG:O	1:A:66:ARG:CD	2.43	0.67
1:A:133:THR:C	1:A:136:PRO:HG2	2.20	0.67
2:B:263:LEU:CD2	2:B:291:VAL:CG2	2.70	0.67
3:C:67:LEU:HB3	3:C:116:GLY:HA2	0.78	0.67
4:E:238:LEU:C	4:E:242:LEU:HD23	2.19	0.67
1:A:224:LEU:HG	1:A:225:PHE:N	2.10	0.67
1:A:306:HIS:C	1:A:306:HIS:CD2	2.73	0.67
2:B:37:LEU:HD23	2:B:179:ALA:HB3	1.76	0.67
4:E:149:THR:HG23	4:E:150:TYR:N	2.08	0.67
1:A:37:LEU:HD23	1:A:54:VAL:HG12	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:ILE:HG12	1:A:51:GLU:O	1.94	0.67
1:A:104:HIS:HB2	1:A:105:MET:SD	2.35	0.67
1:A:166:ASP:HB3	1:A:178:MET:HE2	1.76	0.67
1:A:380:LYS:O	1:A:384:GLU:HB2	1.94	0.67
2:B:139:TRP:HE3	2:B:468:PHE:CE1	2.11	0.67
2:B:223:TYR:O	2:B:223:TYR:HD1	1.77	0.67
3:C:69:TRP:NE1	3:C:114:PRO:HA	2.09	0.67
3:C:257:MET:HE1	3:C:314:PHE:HA	1.77	0.67
4:E:195:ASN:HB3	4:E:205:PHE:H	1.60	0.67
2:B:104:LEU:HA	2:B:118:TRP:CZ2	2.29	0.67
3:C:293:MET:O	3:C:297:SER:HB3	1.95	0.67
3:C:434:LYS:HE3	1:D:386:MET:HE1	1.77	0.67
1:A:257:LEU:CD1	1:A:285:VAL:HG22	2.25	0.66
3:C:137:PHE:CZ	3:C:291:TYR:CE2	2.83	0.66
1:D:95:ASN:HD22	1:D:127:TYR:H	1.42	0.66
1:D:130:ILE:HG12	1:D:131:ILE:H	1.59	0.66
4:E:437:GLU:O	4:E:441:LEU:HG	1.95	0.66
2:B:216:LYS:HE3	2:B:216:LYS:H	1.59	0.66
3:C:138:PRO:HG3	3:C:290:LYS:HE2	1.77	0.66
3:C:270:PHE:HD1	3:C:270:PHE:N	1.93	0.66
1:A:221:PRO:HA	1:A:224:LEU:HB3	1.77	0.66
2:B:92:LEU:HA	2:B:145:VAL:O	1.95	0.66
3:C:273:LEU:HA	3:C:276:GLN:CG	2.20	0.66
1:D:77:LYS:HB2	1:D:111:ASP:OD1	1.95	0.66
1:D:92:LEU:CD2	1:D:92:LEU:N	2.57	0.66
1:D:102:ILE:HD12	4:E:98:GLN:HE22	1.60	0.66
1:D:130:ILE:HG22	1:D:134:HIS:CD2	2.31	0.66
1:D:137:PHE:CD2	1:D:431:ILE:HG21	2.26	0.66
4:E:59:TRP:CZ2	4:E:115:MET:HB3	2.30	0.66
1:A:380:LYS:HD3	2:B:408:ILE:CG2	2.25	0.66
3:C:30:VAL:CG2	3:C:157:GLU:N	2.59	0.66
1:D:250:LEU:HD22	1:D:292:THR:HB	1.75	0.66
1:A:166:ASP:HB3	1:A:178:MET:HE1	1.77	0.66
1:A:187:TRP:CH2	1:A:189:TYR:HB3	2.31	0.66
1:A:216:VAL:HG13	1:A:220:ILE:CD1	2.26	0.66
1:A:243:MET:HG2	1:A:244:THR:H	1.59	0.66
1:A:380:LYS:CD	2:B:408:ILE:HB	2.26	0.66
2:B:118:TRP:CD1	2:B:120:PRO:HD3	2.30	0.66
3:C:115:ASN:ND2	3:C:115:ASN:C	2.45	0.66
3:C:266:ALA:HB1	3:C:270:PHE:CZ	2.30	0.66
3:C:270:PHE:CD1	3:C:270:PHE:N	2.62	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:55:ILE:HG23	4:E:119:PRO:CD	2.25	0.66
4:E:282:ILE:CG2	4:E:282:ILE:O	2.43	0.66
1:A:145:LYS:NZ	1:A:202:THR:CG2	2.58	0.66
1:A:175:GLU:HB3	1:A:211:PRO:HD3	1.77	0.66
1:A:376:ILE:HG23	1:A:380:LYS:NZ	2.10	0.66
2:B:285:MET:O	2:B:289:ILE:HG12	1.96	0.66
3:C:35:LEU:HD12	3:C:60:HIS:NE2	2.10	0.66
4:E:134:PHE:HB3	4:E:282:ILE:CB	2.26	0.66
3:C:60:HIS:NE2	3:C:92:ILE:HG21	2.10	0.66
3:C:259:THR:O	3:C:263:VAL:HG23	1.94	0.66
3:C:316:THR:CG2	3:C:447:ASN:HB3	2.25	0.66
4:E:146:ARG:HD2	4:E:206:GLN:O	1.95	0.66
1:A:227:PHE:HA	1:A:230:VAL:HB	1.78	0.66
1:A:238:ASP:CB	2:B:306:HIS:CE1	2.78	0.66
2:B:40:LEU:HD13	2:B:41:LEU:N	2.10	0.66
2:B:40:LEU:HD22	2:B:51:THR:O	1.96	0.66
2:B:136:PRO:HD3	2:B:280:ILE:CD1	2.26	0.66
2:B:185:GLN:HB2	2:B:217:PRO:HB3	1.76	0.66
1:D:29:VAL:HG12	1:D:60:TRP:NE1	2.10	0.66
1:D:106:THR:HG23	1:D:107:LYS:HD3	1.78	0.66
1:D:220:ILE:HG21	4:E:294:LEU:CD1	2.26	0.66
1:D:292:THR:HA	1:D:295:VAL:HG22	1.77	0.66
1:D:410:LEU:O	1:D:414:PHE:HB2	1.95	0.66
1:A:107:LYS:O	1:A:108:LEU:HD23	1.96	0.66
1:A:171:MET:HG2	1:A:174:GLY:H	1.59	0.66
1:A:235:LEU:HB3	1:A:236:PRO:HD3	1.77	0.66
2:B:4:GLU:OE1	2:B:8:LEU:HG	1.96	0.66
2:B:27:ASP:C	2:B:28:LYS:CG	2.69	0.66
2:B:128:CYS:SG	2:B:144:MET:HG2	2.36	0.66
3:C:26:HIS:CE1	3:C:66:ARG:HH22	2.13	0.66
3:C:35:LEU:HD21	3:C:37:LEU:CD2	2.26	0.66
3:C:90:PRO:HD2	3:C:120:TRP:CZ3	2.30	0.66
4:E:237:VAL:HG21	4:E:457:LEU:HD21	1.77	0.66
1:A:216:VAL:CG1	1:A:220:ILE:CD1	2.74	0.66
2:B:403:GLU:OE1	2:B:403:GLU:HA	1.95	0.66
3:C:434:LYS:CD	3:C:435:GLU:HG3	2.19	0.66
1:D:92:LEU:HB2	1:D:95:ASN:HB2	1.78	0.66
1:D:106:THR:CG2	1:D:107:LYS:H	2.09	0.66
1:D:296:ILE:HA	1:D:299:HIS:HB2	1.78	0.66
4:E:303:VAL:HG12	4:E:304:LEU:N	2.10	0.66
1:A:66:ARG:HA	1:A:113:THR:C	2.21	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:ILE:O	1:A:199:LEU:HB2	1.94	0.65
2:B:65:LEU:CD2	2:B:110:VAL:HG11	2.25	0.65
2:B:144:MET:HE2	2:B:211:LEU:HD21	1.78	0.65
3:C:68:THR:HA	3:C:115:ASN:HA	1.78	0.65
3:C:191:GLU:CG	3:C:222:ARG:HB3	2.26	0.65
1:D:302:SER:CB	1:D:305:THR:CG2	2.75	0.65
4:E:267:LEU:HA	4:E:270:GLN:CG	2.26	0.65
1:A:34:GLY:HA3	1:A:57:ARG:HG2	1.78	0.65
1:A:107:LYS:HG2	2:B:150:THR:HG21	1.77	0.65
1:A:243:MET:HG2	1:A:244:THR:N	2.11	0.65
2:B:264:LEU:O	2:B:267:ALA:HB3	1.97	0.65
2:B:408:ILE:CG2	2:B:409:LYS:N	2.58	0.65
3:C:67:LEU:CG	3:C:116:GLY:HA2	2.25	0.65
3:C:93:VAL:CG1	3:C:151:LEU:HB2	2.26	0.65
3:C:179:ILE:HG23	3:C:181:PRO:CD	2.26	0.65
3:C:432:GLN:O	3:C:436:LYS:HB2	1.97	0.65
1:D:146:LEU:HD22	1:D:203:TYR:CZ	2.31	0.65
4:E:32:LEU:HD12	4:E:208:ILE:HD11	1.78	0.65
2:B:130:ILE:HD12	2:B:134:TYR:HE2	1.59	0.65
3:C:282:ALA:CB	3:C:287:LEU:CD1	2.74	0.65
1:D:284:PHE:O	1:D:287:SER:HB3	1.96	0.65
1:A:156:VAL:CG2	1:A:157:SER:N	2.58	0.65
1:A:378:GLY:O	1:A:382:ILE:HG12	1.97	0.65
2:B:132:VAL:O	2:B:279:ILE:HG23	1.96	0.65
3:C:210:THR:HG22	3:C:211:ASN:N	2.11	0.65
3:C:256:LYS:HB2	3:C:259:THR:HG22	1.79	0.65
1:D:106:THR:HG23	1:D:107:LYS:CD	2.27	0.65
1:D:259:VAL:HA	1:D:262:GLU:CD	2.22	0.65
4:E:35:THR:CG2	4:E:175:GLU:CD	2.70	0.65
4:E:184:THR:HG23	4:E:215:GLN:CG	2.25	0.65
1:A:146:LEU:HD12	1:A:146:LEU:N	2.11	0.65
1:A:155:LYS:HG3	4:E:78:ARG:NE	2.11	0.65
2:B:35:LEU:HD13	2:B:56:LEU:HD22	1.78	0.65
2:B:153:THR:O	2:B:204:TYR:HD2	1.79	0.65
3:C:102:TYR:HD1	3:C:102:TYR:O	1.78	0.65
3:C:107:PHE:O	3:C:107:PHE:CG	2.50	0.65
1:D:36:GLN:HE21	1:D:38:ILE:HG13	1.62	0.65
1:D:76:LYS:HG2	1:D:112:TYR:CD2	2.31	0.65
1:D:149:TRP:CE2	1:D:150:THR:HB	2.31	0.65
1:A:46:VAL:CG2	1:A:270:ALA:HA	2.23	0.65
2:B:46:LYS:CG	2:B:278:PRO:HD2	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:145:VAL:CG1	2:B:206:ASP:HB2	2.25	0.65
1:D:187:TRP:CH2	1:D:189:TYR:CD1	2.84	0.65
4:E:32:LEU:HD12	4:E:157:LEU:HD13	1.77	0.65
4:E:146:ARG:HD2	4:E:205:PHE:CD2	2.31	0.65
1:A:108:LEU:CD1	1:A:118:TRP:HB2	2.26	0.65
1:A:235:LEU:N	1:A:236:PRO:HD2	2.11	0.65
3:C:252:GLU:OE2	1:D:301:ARG:HA	1.96	0.65
1:D:187:TRP:CE2	1:D:196:THR:HG23	2.32	0.65
4:E:26:HIS:C	4:E:27:VAL:HG13	2.21	0.65
4:E:55:ILE:N	4:E:118:LEU:HD13	2.12	0.65
4:E:132:THR:O	4:E:282:ILE:HD12	1.97	0.65
1:A:45:GLU:HB3	1:A:271:VAL:HA	1.77	0.65
1:A:117:MET:HE3	1:A:119:THR:OG1	1.96	0.65
1:A:160:PRO:CG	1:A:185:LYS:CE	2.74	0.65
1:A:156:VAL:CG2	1:A:157:SER:H	2.10	0.65
1:A:166:ASP:CB	1:A:181:TYR:HB3	2.27	0.65
4:E:49:LEU:O	4:E:124:ARG:HD2	1.97	0.65
1:A:3:HIS:CB	1:A:7:LEU:HD23	2.26	0.65
1:A:417:ILE:HA	1:A:420:ILE:HG12	1.79	0.65
2:B:15:TYR:O	2:B:15:TYR:CD1	2.50	0.65
2:B:130:ILE:CB	2:B:134:TYR:CE2	2.79	0.65
3:C:48:THR:HB	3:C:285:VAL:N	2.12	0.65
3:C:462:THR:HB	3:C:463:PRO:CD	2.26	0.65
1:D:36:GLN:CB	1:D:55:ARG:HG3	2.26	0.65
4:E:159:LEU:CD2	4:E:208:ILE:HG23	2.27	0.65
1:A:170:PHE:HE1	1:A:176:TRP:NE1	1.95	0.64
2:B:15:TYR:O	2:B:15:TYR:HD1	1.80	0.64
1:D:87:LEU:HD22	1:D:118:TRP:CH2	2.33	0.64
1:D:132:VAL:O	1:D:274:ILE:HG23	1.97	0.64
4:E:178:THR:HG22	4:E:180:ASN:H	1.62	0.64
1:A:29:VAL:HB	1:A:31:ILE:HD12	1.80	0.64
2:B:223:TYR:O	2:B:227:PRO:HD3	1.97	0.64
3:C:110:VAL:HG13	3:C:120:TRP:CB	2.26	0.64
1:D:112:TYR:N	1:D:112:TYR:CD1	2.65	0.64
1:D:412:CYS:O	1:D:415:MET:HE2	1.97	0.64
4:E:134:PHE:CB	4:E:282:ILE:HG21	2.21	0.64
4:E:159:LEU:HD12	4:E:192:LYS:HA	1.79	0.64
4:E:213:ILE:HG23	4:E:213:ILE:O	1.98	0.64
4:E:240:TYR:C	4:E:243:PRO:HD2	2.22	0.64
1:A:31:ILE:CG1	1:A:60:TRP:HB3	2.27	0.64
2:B:91:VAL:HG23	2:B:96:ASN:CB	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:287:ILE:HA	2:B:290:LEU:HB2	1.79	0.64
3:C:59:ASP:OD1	3:C:121:LEU:HD13	1.97	0.64
3:C:80:LEU:CD1	1:D:20:ARG:NH2	2.60	0.64
1:D:274:ILE:HG22	1:D:276:LYS:NZ	2.12	0.64
4:E:237:VAL:HG22	4:E:457:LEU:HD21	1.78	0.64
4:E:444:LYS:CE	4:E:444:LYS:HA	2.27	0.64
1:A:48:GLN:HB2	1:A:128:CYS:O	1.96	0.64
1:A:209:ARG:HG3	1:A:210:ILE:N	2.08	0.64
2:B:11:LEU:HD22	2:B:11:LEU:H	1.62	0.64
2:B:218:LEU:HD13	2:B:221:ILE:HG13	1.77	0.64
2:B:277:VAL:H	2:B:278:PRO:CD	2.10	0.64
3:C:42:LEU:CD2	3:C:190:TRP:CH2	2.77	0.64
3:C:242:LEU:CD2	3:C:267:GLN:HG2	2.27	0.64
3:C:315:ARG:H	3:C:315:ARG:CD	2.11	0.64
4:E:33:LYS:CG	4:E:160:SER:HB3	2.26	0.64
4:E:39:LEU:CD1	4:E:49:LEU:HD13	2.26	0.64
2:B:133:MET:HG2	2:B:140:GLN:CG	2.08	0.64
2:B:186:TRP:CB	2:B:215:ARG:CG	2.74	0.64
3:C:63:TYR:CE1	3:C:116:GLY:HA3	2.33	0.64
3:C:142:GLN:CG	3:C:143:ASN:H	1.87	0.64
1:D:36:GLN:NE2	1:D:38:ILE:HG13	2.12	0.64
1:A:36:GLN:HA	1:A:164:ARG:NH2	2.12	0.64
1:A:67:TRP:CG	1:A:71:ASP:HB3	2.32	0.64
2:B:307:ARG:O	2:B:307:ARG:HG2	1.97	0.64
1:D:3:HIS:HB3	1:D:7:LEU:CG	2.27	0.64
1:D:37:LEU:CB	1:D:54:VAL:HG13	2.27	0.64
1:D:187:TRP:CZ2	1:D:196:THR:HA	2.30	0.64
1:D:243:MET:HE2	1:D:243:MET:N	2.13	0.64
4:E:56:GLU:CA	4:E:118:LEU:HD22	2.28	0.64
4:E:240:TYR:HB3	4:E:453:ILE:CD1	2.28	0.64
1:D:135:PHE:HE1	1:D:277:TYR:CE2	2.16	0.64
1:D:141:ASN:HB3	1:D:206:ILE:HG12	1.79	0.64
1:D:233:PHE:CE2	1:D:413:VAL:HG11	2.32	0.64
4:E:38:ASN:O	4:E:51:THR:HA	1.97	0.64
4:E:212:LEU:HD12	4:E:212:LEU:N	2.13	0.64
1:A:134:HIS:C	1:A:136:PRO:HD2	2.23	0.64
2:B:153:THR:HG23	2:B:156:VAL:O	1.97	0.64
2:B:405:VAL:HG12	2:B:409:LYS:HZ3	1.62	0.64
3:C:206:PHE:C	3:C:206:PHE:CD1	2.75	0.64
1:D:233:PHE:HE2	1:D:295:VAL:HG11	1.63	0.64
1:D:244:THR:HG23	1:D:245:LEU:H	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:254:THR:HG23	1:D:255:VAL:N	2.12	0.64
1:D:302:SER:HB3	1:D:305:THR:CG2	2.28	0.64
2:B:11:LEU:HD22	2:B:11:LEU:N	2.12	0.64
2:B:283:TYR:HD1	2:B:283:TYR:H	1.46	0.64
3:C:241:PHE:HD1	3:C:245:LEU:HD22	1.63	0.64
3:C:252:GLU:HG3	1:D:300:HIS:HB3	1.78	0.64
1:D:72:TYR:CD1	1:D:73:GLY:N	2.66	0.64
4:E:159:LEU:HD12	4:E:192:LYS:N	2.12	0.64
4:E:184:THR:O	4:E:214:ILE:HB	1.98	0.64
1:A:166:ASP:CB	1:A:178:MET:CE	2.75	0.64
2:B:35:LEU:HD23	2:B:35:LEU:N	2.10	0.64
3:C:137:PHE:CD1	3:C:288:ILE:CG2	2.81	0.64
3:C:199:LYS:HD2	3:C:200:ASN:N	2.13	0.64
3:C:257:MET:O	3:C:261:ILE:HG12	1.98	0.64
1:D:30:ASP:O	1:D:60:TRP:HB2	1.97	0.64
1:D:178:MET:SD	1:D:207:MET:CB	2.86	0.64
4:E:32:LEU:CD1	4:E:157:LEU:HD13	2.26	0.64
4:E:94:ASN:HB3	4:E:125:SER:CB	2.22	0.64
1:A:139:GLN:OE1	1:A:179:LYS:HG3	1.98	0.63
2:B:69:PRO:O	2:B:73:GLU:HB2	1.98	0.63
2:B:101:GLU:C	2:B:102:ILE:HG13	2.23	0.63
2:B:134:TYR:HE1	2:B:213:ILE:HG13	1.56	0.63
3:C:1:VAL:O	3:C:1:VAL:HG12	1.96	0.63
3:C:17:TYR:HE2	3:C:19:LYS:HB2	1.58	0.63
3:C:475:MET:HG2	3:C:476:GLY:N	2.12	0.63
4:E:2:GLU:HA	4:E:5:ARG:HG3	1.78	0.63
4:E:44:GLU:CD	4:E:129:ILE:CB	2.66	0.63
4:E:242:LEU:C	4:E:242:LEU:HD12	2.23	0.63
4:E:313:THR:OG1	4:E:441:LEU:HB3	1.98	0.63
1:A:90:LEU:HD13	1:A:100:PHE:HE2	1.62	0.63
2:B:218:LEU:HA	2:B:221:ILE:HD11	1.80	0.63
2:B:224:THR:C	2:B:227:PRO:CD	2.66	0.63
3:C:160:MET:H	3:C:213:GLN:CB	2.10	0.63
1:D:135:PHE:CZ	1:D:273:LEU:HB2	2.33	0.63
1:D:236:PRO:HB3	1:D:299:HIS:CE1	2.33	0.63
1:D:247:ILE:HG22	1:D:248:SER:N	2.13	0.63
1:D:384:GLU:OE1	1:D:384:GLU:HA	1.98	0.63
1:A:176:TRP:HB2	1:A:209:ARG:HD2	1.77	0.63
2:B:147:LYS:CG	2:B:148:SER:N	2.61	0.63
2:B:286:PHE:CE1	2:B:287:ILE:HG23	2.32	0.63
4:E:209:ILE:HG12	4:E:211:PHE:CE1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:GLU:O	1:A:211:PRO:HB3	1.98	0.63
1:A:279:LEU:CA	1:A:282:MET:HB2	2.21	0.63
2:B:429:GLN:HA	2:B:429:GLN:HE21	1.63	0.63
2:B:434:VAL:CG1	2:B:438:LEU:HD12	2.28	0.63
3:C:262:CYS:SG	1:D:251:LEU:HD11	2.39	0.63
3:C:282:ALA:CB	3:C:287:LEU:HD12	2.29	0.63
3:C:295:ILE:O	3:C:299:VAL:HG23	1.99	0.63
1:D:377:GLU:HB2	4:E:415:CYS:SG	2.39	0.63
4:E:89:VAL:O	4:E:90:VAL:HG23	1.98	0.63
4:E:219:LEU:HB3	4:E:222:ILE:CG2	2.28	0.63
4:E:250:LYS:HD2	4:E:253:LEU:HD22	1.78	0.63
1:A:93:TYR:N	1:A:93:TYR:CD1	2.63	0.63
1:A:165:PRO:C	1:A:181:TYR:HD1	2.07	0.63
2:B:48:GLU:HA	2:B:130:ILE:CD1	2.22	0.63
3:C:247:PHE:CD2	3:C:460:ILE:CG1	2.81	0.63
3:C:282:ALA:HB1	3:C:287:LEU:HD12	1.80	0.63
1:D:107:LYS:HE3	4:E:149:THR:HA	1.80	0.63
1:D:382:ILE:O	1:D:386:MET:HG2	1.98	0.63
4:E:44:GLU:HG3	4:E:129:ILE:HG13	1.81	0.63
4:E:270:GLN:C	4:E:273:PRO:CD	2.71	0.63
1:A:97:ASP:HB2	1:A:127:TYR:HB2	1.78	0.63
3:C:65:HIS:H	3:C:65:HIS:HD2	1.44	0.63
3:C:102:TYR:HE1	3:C:106:TYR:HB3	1.64	0.63
1:D:170:PHE:CD2	1:D:178:MET:HG2	2.32	0.63
4:E:88:ASP:O	4:E:147:SER:HA	1.99	0.63
4:E:303:VAL:CG1	4:E:304:LEU:N	2.61	0.63
4:E:305:ASN:HA	4:E:308:LEU:CD1	2.27	0.63
1:A:35:LEU:HD23	1:A:36:GLN:N	2.12	0.63
1:A:157:SER:HB2	1:A:199:LEU:CD1	2.28	0.63
3:C:37:LEU:HD12	3:C:217:PHE:CE2	2.33	0.63
1:D:92:LEU:HB3	1:D:95:ASN:HB2	1.80	0.63
4:E:6:LEU:HD12	4:E:69:SER:OG	1.98	0.63
4:E:31:THR:CB	4:E:58:GLN:HB2	2.28	0.63
4:E:33:LYS:CE	4:E:160:SER:CB	2.77	0.63
4:E:50:THR:HA	4:E:123:TYR:O	1.97	0.63
4:E:276:SER:HB3	4:E:281:LEU:HD13	1.81	0.63
1:A:34:GLY:HA3	1:A:57:ARG:CG	2.29	0.63
1:A:111:ASP:OD1	1:A:111:ASP:N	2.32	0.63
1:A:129:GLU:OE2	1:A:140:GLN:HG3	1.98	0.63
1:A:171:MET:HG2	1:A:174:GLY:N	2.13	0.63
2:B:147:LYS:CG	2:B:148:SER:H	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:220:TYR:HE2	3:C:279:PRO:HB2	1.63	0.63
3:C:162:LEU:HG	3:C:217:PHE:CZ	2.34	0.63
3:C:242:LEU:HD21	3:C:263:VAL:CG1	2.27	0.63
3:C:306:CYS:O	3:C:309:VAL:HB	1.98	0.63
3:C:429:ILE:HG13	3:C:430:VAL:N	2.13	0.63
4:E:31:THR:HA	4:E:158:GLN:HG3	1.81	0.63
4:E:140:ASN:OD1	4:E:211:PHE:HB3	1.99	0.63
1:A:92:LEU:CB	1:A:95:ASN:HB2	2.29	0.63
2:B:58:LEU:CD1	2:B:118:TRP:HB3	2.28	0.63
3:C:180:ASP:CG	3:C:192:ILE:HG21	2.24	0.63
1:D:92:LEU:HD21	1:D:124:PHE:CZ	2.34	0.63
4:E:240:TYR:HB3	4:E:453:ILE:HD11	1.81	0.63
4:E:291:PHE:O	4:E:295:VAL:HG23	1.99	0.63
1:A:35:LEU:HD13	1:A:203:TYR:OH	1.99	0.62
1:A:108:LEU:HB3	1:A:117:MET:O	1.99	0.62
1:A:132:VAL:C	1:A:274:ILE:HG22	2.24	0.62
1:A:388:SER:HA	1:A:391:GLU:HB3	1.81	0.62
2:B:136:PRO:HD3	2:B:280:ILE:HD11	1.80	0.62
2:B:175:ILE:CG1	2:B:176:ASN:H	2.10	0.62
3:C:58:MET:O	3:C:58:MET:HG2	1.99	0.62
1:D:77:LYS:O	1:D:77:LYS:CG	2.45	0.62
4:E:195:ASN:HB3	4:E:205:PHE:N	2.13	0.62
1:A:133:THR:O	1:A:133:THR:CG2	2.47	0.62
1:D:242:LYS:HD2	1:D:245:LEU:HD13	1.79	0.62
1:D:260:ILE:HA	1:D:263:LEU:HD12	1.80	0.62
1:D:395:ALA:HB1	1:D:399:TRP:CE2	2.34	0.62
4:E:140:ASN:HD21	4:E:211:PHE:CA	2.12	0.62
4:E:187:HIS:ND1	4:E:189:PRO:HG3	2.13	0.62
4:E:200:LYS:O	4:E:200:LYS:HG3	2.00	0.62
1:A:43:VAL:HG22	1:A:50:VAL:CG1	2.29	0.62
1:A:401:TYR:CD1	1:A:401:TYR:O	2.52	0.62
1:A:419:ILE:CG2	1:A:420:ILE:N	2.58	0.62
3:C:257:MET:CE	3:C:314:PHE:CB	2.78	0.62
3:C:291:TYR:N	3:C:291:TYR:HD1	1.96	0.62
1:D:37:LEU:CD1	1:D:54:VAL:HG13	2.28	0.62
1:D:229:THR:HG22	1:D:253:LEU:CD1	2.29	0.62
1:D:305:THR:HG22	1:D:400:LYS:HG2	1.81	0.62
4:E:66:TRP:HB2	4:E:71:TYR:N	2.10	0.62
4:E:189:PRO:HB2	4:E:211:PHE:CD2	2.35	0.62
2:B:201:ASP:OD1	2:B:202:PRO:HD2	1.99	0.62
1:D:7:LEU:HA	1:D:10:ASN:ND2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:187:TRP:HB2	1:D:199:LEU:HD21	1.81	0.62
1:D:187:TRP:CB	1:D:199:LEU:HD23	2.23	0.62
1:D:377:GLU:HG3	4:E:415:CYS:HB2	1.80	0.62
4:E:34:LEU:HB2	4:E:210:PHE:HZ	1.65	0.62
4:E:45:LYS:HZ3	4:E:278:ASN:HA	1.62	0.62
4:E:146:ARG:NH1	4:E:205:PHE:CB	2.61	0.62
1:A:265:PRO:CA	1:A:268:SER:HB3	2.28	0.62
2:B:58:LEU:HD11	2:B:118:TRP:HB3	1.82	0.62
2:B:130:ILE:CB	2:B:134:TYR:CD2	2.63	0.62
3:C:16:LYS:HA	3:C:16:LYS:CE	2.30	0.62
3:C:160:MET:H	3:C:213:GLN:CG	2.10	0.62
3:C:221:ILE:HG13	3:C:222:ARG:N	2.13	0.62
3:C:431:LYS:CE	1:D:379:VAL:CG2	2.77	0.62
1:D:167:LEU:CD1	1:D:167:LEU:H	2.10	0.62
1:D:301:ARG:HH22	1:D:406:ILE:HD13	1.65	0.62
1:A:90:LEU:HD12	1:A:100:PHE:HE2	1.65	0.62
1:A:236:PRO:CB	1:A:299:HIS:CE1	2.77	0.62
2:B:251:LEU:HD13	3:C:261:ILE:HG21	1.81	0.62
3:C:455:ARG:H	3:C:455:ARG:HD2	1.63	0.62
1:D:177:VAL:O	1:D:207:MET:HB2	2.00	0.62
4:E:1:ASN:O	4:E:69:SER:HB2	1.98	0.62
4:E:76:LEU:CD2	4:E:77:VAL:N	2.63	0.62
1:A:218:VAL:O	1:A:221:PRO:HD2	1.99	0.62
2:B:129:THR:HG22	2:B:142:CYS:CB	2.30	0.62
2:B:430:TYR:O	2:B:430:TYR:HD1	1.82	0.62
3:C:56:VAL:CG2	3:C:124:ALA:HB3	2.29	0.62
3:C:146:LEU:HD12	3:C:146:LEU:N	2.14	0.62
3:C:147:LYS:HE2	3:C:216:THR:HG23	1.82	0.62
1:D:67:TRP:CD1	1:D:71:ASP:HB3	2.34	0.62
1:D:167:LEU:CD1	1:D:178:MET:CB	2.77	0.62
4:E:27:VAL:HG12	4:E:154:GLU:CA	2.27	0.62
4:E:54:TRP:C	4:E:118:LEU:HD13	2.25	0.62
4:E:313:THR:HB	4:E:440:VAL:CG1	2.24	0.62
3:C:30:VAL:HG23	3:C:156:ASN:C	2.25	0.62
3:C:42:LEU:HA	3:C:54:THR:CG2	2.29	0.62
3:C:67:LEU:HD12	3:C:116:GLY:O	2.00	0.62
3:C:138:PRO:CB	3:C:290:LYS:CE	2.71	0.62
1:D:86:TRP:O	1:D:86:TRP:CD1	2.49	0.62
4:E:66:TRP:CE3	4:E:70:GLU:HB3	2.34	0.62
4:E:138:TRP:CH2	4:E:215:GLN:CD	2.77	0.62
4:E:244:ALA:HB2	4:E:446:ILE:HG22	1.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:ARG:HH11	1:A:107:LYS:NZ	1.96	0.62
1:A:110:LEU:HD12	1:A:111:ASP:N	2.14	0.62
3:C:155:ALA:H	3:C:211:ASN:HB3	1.65	0.62
1:D:63:VAL:HG13	1:D:64:ARG:N	2.14	0.62
1:D:249:VAL:O	1:D:253:LEU:HB3	1.99	0.62
4:E:191:LYS:NZ	4:E:211:PHE:CZ	2.66	0.62
1:A:249:VAL:HG13	1:A:253:LEU:HD23	1.81	0.62
2:B:152:ASP:CB	2:B:203:SER:HB2	2.29	0.62
2:B:263:LEU:O	2:B:266:LEU:HB2	2.00	0.62
3:C:273:LEU:O	3:C:276:GLN:HB2	1.99	0.62
3:C:434:LYS:CD	3:C:435:GLU:CG	2.78	0.62
1:D:48:GLN:CD	1:D:130:ILE:HD13	2.25	0.62
1:D:106:THR:HG22	1:D:107:LYS:H	1.64	0.62
1:D:176:TRP:HB3	1:D:209:ARG:CD	2.30	0.62
1:D:235:LEU:HD23	1:D:235:LEU:N	2.14	0.62
4:E:14:TYR:CE2	4:E:16:LYS:CE	2.81	0.62
4:E:131:VAL:HA	4:E:281:LEU:C	2.24	0.62
3:C:141:TRP:CH2	3:C:223:ARG:HD3	2.34	0.61
3:C:190:TRP:HB2	3:C:223:ARG:HB2	1.81	0.61
3:C:438:ALA:HA	3:C:441:GLU:OE1	1.99	0.61
1:D:46:VAL:O	1:D:272:PRO:HG3	2.00	0.61
1:D:60:TRP:CZ3	1:D:116:ILE:HG13	2.35	0.61
4:E:14:TYR:OH	4:E:83:LEU:HB3	2.00	0.61
4:E:303:VAL:O	4:E:303:VAL:HG13	2.00	0.61
1:A:38:ILE:H	1:A:38:ILE:HD12	1.65	0.61
1:A:414:PHE:CD1	1:A:417:ILE:HD12	2.35	0.61
2:B:72:TYR:O	2:B:76:LYS:HG2	2.00	0.61
3:C:137:PHE:CE1	3:C:288:ILE:HG22	2.35	0.61
4:E:138:TRP:CZ2	4:E:215:GLN:CD	2.78	0.61
4:E:235:LEU:C	4:E:235:LEU:CD1	2.62	0.61
1:A:148:ILE:CG2	1:A:198:TYR:CB	2.76	0.61
1:A:220:ILE:N	1:A:221:PRO:HD2	2.16	0.61
1:A:304:SER:HB2	1:A:400:LYS:HZ2	1.65	0.61
3:C:150:ALA:H	3:C:160:MET:HE2	1.65	0.61
3:C:225:PRO:HG2	3:C:228:TYR:CD1	2.35	0.61
3:C:429:ILE:O	3:C:433:ILE:HG13	2.00	0.61
4:E:94:ASN:ND2	4:E:143:LEU:CD2	2.60	0.61
1:A:62:ASP:HB3	1:A:65:LEU:CD1	2.30	0.61
1:A:117:MET:SD	1:A:119:THR:HG21	2.40	0.61
3:C:33:ILE:HG22	3:C:160:MET:SD	2.40	0.61
3:C:55:ASN:HA	3:C:124:ALA:O	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:69:TRP:HB2	3:C:74:TYR:N	2.16	0.61
1:D:209:ARG:CG	1:D:210:ILE:H	2.12	0.61
1:D:263:LEU:O	1:D:267:THR:HG22	2.00	0.61
1:D:286:ILE:O	1:D:290:ILE:HG23	1.99	0.61
4:E:67:ASN:N	4:E:67:ASN:ND2	2.37	0.61
4:E:271:LYS:HB2	4:E:271:LYS:NZ	2.14	0.61
3:C:462:THR:HB	3:C:463:PRO:HD3	1.83	0.61
1:D:46:VAL:CB	1:D:271:VAL:HA	2.30	0.61
1:A:178:MET:HA	1:A:207:MET:CB	2.31	0.61
2:B:75:ILE:HD11	2:B:78:LEU:CD1	2.24	0.61
2:B:81:PRO:HA	2:B:107:ASN:HA	1.83	0.61
2:B:141:ASN:HD21	2:B:212:ILE:HG12	1.65	0.61
3:C:66:ARG:HG2	3:C:66:ARG:HH11	1.63	0.61
1:D:49:ILE:CD1	1:D:125:LYS:HE3	2.27	0.61
1:D:209:ARG:C	1:D:210:ILE:HG13	2.24	0.61
1:A:216:VAL:CG1	1:A:220:ILE:HD11	2.27	0.61
2:B:38:THR:HG22	2:B:55:PHE:CE1	2.34	0.61
2:B:58:LEU:HD11	2:B:118:TRP:CE3	2.35	0.61
3:C:137:PHE:CD1	3:C:288:ILE:CB	2.83	0.61
2:B:421:PHE:CA	2:B:424:LEU:HB2	2.27	0.61
3:C:35:LEU:O	3:C:162:LEU:HD23	2.01	0.61
3:C:49:ASP:O	3:C:50:GLU:HG3	2.01	0.61
3:C:60:HIS:CE1	3:C:160:MET:HE1	2.36	0.61
3:C:443:VAL:O	3:C:443:VAL:CG1	2.48	0.61
1:D:47:ASN:C	1:D:48:GLN:HG2	2.26	0.61
1:D:249:VAL:HA	1:D:252:SER:HB3	1.80	0.61
1:D:409:ILE:HG13	1:D:410:LEU:N	2.16	0.61
4:E:34:LEU:HD23	4:E:55:ILE:HA	1.82	0.61
4:E:52:ASN:HA	4:E:121:ALA:O	2.01	0.61
4:E:252:THR:O	4:E:252:THR:OG1	2.06	0.61
2:B:145:VAL:HA	2:B:207:VAL:O	1.99	0.61
2:B:189:GLU:HB3	2:B:212:ILE:HG22	1.83	0.61
2:B:304:LEU:O	2:B:307:ARG:HB3	2.00	0.61
3:C:50:GLU:O	3:C:129:SER:HA	2.00	0.61
3:C:291:TYR:N	3:C:291:TYR:CD1	2.68	0.61
4:E:17:ARG:HH11	4:E:18:ILE:HG22	1.66	0.61
4:E:101:VAL:O	4:E:101:VAL:HG22	2.00	0.61
1:A:50:VAL:HG12	1:A:51:GLU:N	2.16	0.61
1:A:131:ILE:HD11	1:A:140:GLN:HG2	1.82	0.61
1:A:394:ASN:O	1:A:398:GLU:HG3	2.00	0.61
2:B:92:LEU:HD22	2:B:146:PHE:CD1	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:80:LEU:O	3:C:112:VAL:HB	2.00	0.61
1:D:49:ILE:HG21	1:D:125:LYS:HZ2	1.63	0.61
1:D:56:LEU:HD23	1:D:56:LEU:H	1.64	0.61
1:D:133:THR:HG22	1:D:136:PRO:HG2	1.83	0.61
1:D:178:MET:HA	1:D:207:MET:HB2	1.83	0.61
4:E:140:ASN:HD22	4:E:141:CYS:N	1.99	0.61
4:E:242:LEU:HD12	4:E:242:LEU:O	2.00	0.61
2:B:268:ASP:C	2:B:271:PRO:HD2	2.26	0.60
3:C:153:TYR:HB2	3:C:158:ILE:HB	1.83	0.60
3:C:179:ILE:HG23	3:C:181:PRO:HD2	1.81	0.60
3:C:228:TYR:CD1	3:C:229:VAL:N	2.69	0.60
3:C:247:PHE:CE2	3:C:460:ILE:CD1	2.82	0.60
3:C:318:SER:HB2	3:C:444:GLY:HA2	1.83	0.60
1:D:145:LYS:C	1:D:146:LEU:CD1	2.64	0.60
4:E:93:ASN:CG	4:E:93:ASN:O	2.43	0.60
4:E:105:ALA:HB3	4:E:117:TRP:HE1	1.65	0.60
4:E:183:TRP:HB3	4:E:216:ARG:NE	2.15	0.60
4:E:219:LEU:CB	4:E:222:ILE:HB	2.28	0.60
1:A:46:VAL:HG12	1:A:47:ASN:ND2	2.16	0.60
2:B:181:THR:O	2:B:181:THR:HG22	2.01	0.60
1:D:245:LEU:HD23	1:D:245:LEU:C	2.26	0.60
4:E:217:LYS:N	4:E:218:PRO:HD2	2.16	0.60
1:A:124:PHE:C	1:A:124:PHE:HD1	2.08	0.60
1:A:187:TRP:HD1	1:A:199:LEU:HD23	1.66	0.60
1:A:201:ILE:CG2	1:A:203:TYR:HE1	2.14	0.60
1:A:305:THR:HG21	1:A:397:GLU:O	2.01	0.60
2:B:29:VAL:H	2:B:156:VAL:HG12	1.65	0.60
3:C:20:HIS:O	3:C:20:HIS:CG	2.54	0.60
3:C:249:LEU:N	3:C:250:PRO:CD	2.63	0.60
4:E:116:TYR:CD1	4:E:116:TYR:C	2.80	0.60
4:E:246:ALA:CB	4:E:250:LYS:HG3	2.21	0.60
4:E:416:VAL:CG2	4:E:417:GLU:N	2.63	0.60
1:A:20:ARG:HH11	1:A:20:ARG:CG	2.10	0.60
1:A:145:LYS:HZ2	1:A:202:THR:CG2	2.13	0.60
1:A:385:HIS:HD1	1:A:385:HIS:C	2.10	0.60
2:B:108:VAL:HG22	2:B:118:TRP:CG	2.36	0.60
2:B:112:HIS:CG	2:B:113:THR:N	2.68	0.60
2:B:261:VAL:O	2:B:265:LEU:HG	2.02	0.60
3:C:263:VAL:O	3:C:267:GLN:HG2	2.01	0.60
1:D:36:GLN:C	1:D:54:VAL:HG12	2.27	0.60
1:D:167:LEU:HD11	1:D:178:MET:CB	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:33:LYS:CE	4:E:160:SER:HB2	2.31	0.60
4:E:83:LEU:HD22	4:E:83:LEU:N	2.16	0.60
4:E:108:LEU:O	4:E:115:MET:HA	2.01	0.60
4:E:310:THR:HB	4:E:313:THR:CG2	2.32	0.60
4:E:444:LYS:HA	4:E:444:LYS:HE3	1.81	0.60
1:A:3:HIS:CB	1:A:7:LEU:CD2	2.79	0.60
1:A:136:PRO:CD	1:A:274:ILE:HG23	2.31	0.60
1:A:147:GLY:HA2	1:A:158:ILE:HD13	1.84	0.60
2:B:65:LEU:HD23	2:B:110:VAL:HG13	1.83	0.60
2:B:452:PHE:O	2:B:456:LEU:HD23	2.02	0.60
1:D:242:LYS:HD2	1:D:245:LEU:CD1	2.32	0.60
4:E:100:GLU:HB2	4:E:122:ILE:CG1	2.31	0.60
2:B:142:CYS:HB2	2:B:211:LEU:HD12	1.83	0.60
2:B:227:PRO:O	2:B:231:ILE:HG12	2.01	0.60
2:B:267:ALA:O	2:B:271:PRO:HD3	2.02	0.60
3:C:153:TYR:O	3:C:212:TYR:HB3	2.02	0.60
3:C:258:SER:O	3:C:261:ILE:HB	2.01	0.60
4:E:32:LEU:HA	4:E:56:GLU:O	2.02	0.60
4:E:34:LEU:CD2	4:E:55:ILE:HA	2.32	0.60
4:E:90:VAL:HG22	4:E:95:VAL:CG1	2.22	0.60
4:E:173:ASP:OD1	4:E:173:ASP:C	2.43	0.60
1:A:90:LEU:O	1:A:91:VAL:HG23	2.02	0.60
1:A:261:VAL:O	1:A:265:PRO:HD3	2.01	0.60
2:B:142:CYS:O	2:B:210:TYR:HD1	1.85	0.60
2:B:152:ASP:HB3	2:B:203:SER:CB	2.30	0.60
2:B:408:ILE:HG23	2:B:409:LYS:H	1.66	0.60
2:B:444:ILE:HG23	2:B:445:THR:N	2.16	0.60
3:C:25:LYS:O	3:C:25:LYS:CG	2.46	0.60
4:E:9:LYS:O	4:E:9:LYS:HD2	2.02	0.60
4:E:133:TYR:C	4:E:135:PRO:HD2	2.27	0.60
1:A:135:PHE:N	1:A:136:PRO:CD	2.65	0.60
1:A:209:ARG:CG	1:A:210:ILE:N	2.65	0.60
2:B:9:SER:CA	2:B:12:PHE:CE1	2.80	0.60
2:B:82:SER:C	2:B:84:ASP:H	2.09	0.60
2:B:189:GLU:HG3	2:B:468:PHE:HB2	1.81	0.60
3:C:36:SER:HB3	3:C:59:ASP:HB2	1.83	0.60
1:D:191:THR:O	1:D:191:THR:CG2	2.50	0.60
1:D:407:ASP:OD1	1:D:408:HIS:HD2	1.85	0.60
1:D:420:ILE:HA	1:D:423:VAL:CG2	2.31	0.60
4:E:138:TRP:HH2	4:E:215:GLN:HE21	1.48	0.60
1:A:29:VAL:HG21	1:A:86:TRP:HZ3	1.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:THR:HG22	1:A:305:THR:O	2.02	0.60
2:B:19:VAL:HG22	2:B:20:ARG:HD3	1.82	0.60
3:C:33:ILE:HG12	3:C:62:TRP:CB	2.32	0.60
3:C:42:LEU:CD2	3:C:190:TRP:CZ2	2.85	0.60
1:D:135:PHE:CZ	1:D:273:LEU:HD12	2.35	0.60
1:D:435:GLN:C	1:D:437:GLY:H	2.09	0.60
4:E:34:LEU:HD12	4:E:210:PHE:CZ	2.37	0.60
4:E:95:VAL:O	4:E:95:VAL:HG12	2.01	0.60
4:E:149:THR:CG2	4:E:150:TYR:H	2.14	0.60
1:A:214:PHE:CD1	1:A:214:PHE:C	2.79	0.60
3:C:216:THR:C	3:C:217:PHE:CD1	2.73	0.60
1:D:35:LEU:CD2	1:D:164:ARG:NH1	2.64	0.60
1:A:218:VAL:CG1	1:A:219:ILE:N	2.65	0.59
1:A:413:VAL:O	1:A:417:ILE:HG13	2.02	0.59
2:B:33:VAL:HG22	2:B:158:LEU:HD22	1.83	0.59
3:C:59:ASP:HA	3:C:121:LEU:HB3	1.84	0.59
3:C:257:MET:HE1	3:C:314:PHE:CA	2.31	0.59
1:D:232:VAL:HG22	1:D:250:LEU:CD1	2.32	0.59
4:E:66:TRP:CE3	4:E:70:GLU:CG	2.85	0.59
4:E:86:LEU:HD12	4:E:103:TYR:OH	2.02	0.59
4:E:473:GLN:OE1	4:E:473:GLN:O	2.20	0.59
1:A:85:VAL:CG1	1:A:86:TRP:N	2.65	0.59
1:A:406:ILE:HA	1:A:409:ILE:CD1	2.32	0.59
2:B:35:LEU:CD2	2:B:56:LEU:HA	2.32	0.59
3:C:155:ALA:CA	3:C:211:ASN:HA	2.31	0.59
1:D:28:PHE:HB3	1:D:156:VAL:C	2.27	0.59
1:D:250:LEU:HD22	1:D:292:THR:OG1	2.01	0.59
1:D:398:GLU:HG3	1:D:399:TRP:CE3	2.37	0.59
4:E:79:ILE:O	4:E:79:ILE:HG23	2.00	0.59
1:A:79:ARG:HD3	1:A:107:LYS:HD2	1.83	0.59
2:B:108:VAL:CG1	2:B:118:TRP:HB2	2.32	0.59
2:B:139:TRP:HE3	2:B:468:PHE:CZ	2.20	0.59
3:C:67:LEU:HD21	3:C:112:VAL:CG1	2.33	0.59
3:C:247:PHE:CG	3:C:460:ILE:HG12	2.37	0.59
3:C:429:ILE:HG13	3:C:430:VAL:H	1.67	0.59
3:C:434:LYS:CE	3:C:435:GLU:CG	2.79	0.59
1:D:38:ILE:O	1:D:39:GLN:HG3	2.02	0.59
1:D:107:LYS:HE3	4:E:149:THR:O	2.02	0.59
1:D:264:ILE:HA	1:D:267:THR:CG2	2.32	0.59
4:E:103:TYR:C	4:E:104:TYR:HD1	2.07	0.59
4:E:470:HIS:NE2	4:E:474:VAL:HG23	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:GLN:O	1:A:38:ILE:HD12	2.02	0.59
1:A:117:MET:CG	1:A:119:THR:HG23	2.32	0.59
2:B:186:TRP:CB	2:B:215:ARG:HD2	2.31	0.59
3:C:239:ILE:HG22	3:C:240:SER:N	2.17	0.59
3:C:241:PHE:C	3:C:241:PHE:HD1	2.07	0.59
3:C:252:GLU:CG	1:D:300:HIS:C	2.75	0.59
1:D:231:LEU:HD22	1:D:235:LEU:HD21	1.84	0.59
4:E:27:VAL:CG1	4:E:154:GLU:HA	2.30	0.59
4:E:100:GLU:HB2	4:E:122:ILE:HG12	1.84	0.59
4:E:261:GLN:HE21	4:E:265:LEU:HD11	1.68	0.59
1:A:284:PHE:CD1	1:A:284:PHE:N	2.70	0.59
2:B:240:TYR:O	2:B:240:TYR:HD1	1.84	0.59
2:B:283:TYR:HA	2:B:286:PHE:CZ	2.37	0.59
3:C:319:THR:HB	3:C:447:ASN:C	2.28	0.59
1:D:29:VAL:CG1	1:D:60:TRP:HE1	2.15	0.59
1:D:160:PRO:HG3	1:D:185:LYS:HB3	1.84	0.59
1:D:166:ASP:CB	1:D:181:TYR:CB	2.68	0.59
1:D:170:PHE:CE2	1:D:176:TRP:NE1	2.71	0.59
1:D:243:MET:H	1:D:243:MET:CE	2.13	0.59
1:D:301:ARG:HH12	1:D:406:ILE:CD1	2.13	0.59
4:E:247:GLY:N	4:E:250:LYS:HZ2	1.92	0.59
2:B:46:LYS:HD2	2:B:275:LEU:O	2.02	0.59
2:B:111:GLN:HB2	2:B:115:ALA:HB3	1.83	0.59
3:C:110:VAL:HG12	3:C:111:LEU:N	2.17	0.59
3:C:479:ASN:C	3:C:479:ASN:HD22	2.10	0.59
1:D:46:VAL:HA	1:D:272:PRO:HD2	1.81	0.59
1:D:79:ARG:NH1	4:E:154:GLU:CD	2.60	0.59
4:E:28:ILE:HD13	4:E:85:TRP:HZ3	1.68	0.59
4:E:144:VAL:HG12	4:E:209:ILE:CA	2.32	0.59
4:E:158:GLN:O	4:E:159:LEU:HD23	2.02	0.59
4:E:215:GLN:HG3	4:E:216:ARG:H	1.64	0.59
4:E:244:ALA:HB2	4:E:446:ILE:HG21	1.84	0.59
4:E:454:ALA:O	4:E:457:LEU:HB3	2.01	0.59
1:A:59:GLN:NE2	1:A:117:MET:SD	2.75	0.59
1:A:171:MET:CE	1:A:176:TRP:CH2	2.86	0.59
1:A:207:MET:O	1:A:207:MET:CE	2.50	0.59
1:A:305:THR:HB	1:A:400:LYS:CB	2.33	0.59
3:C:48:THR:HG21	3:C:283:LEU:O	2.03	0.59
3:C:154:ASN:CA	3:C:211:ASN:HB2	2.31	0.59
1:D:152:ASP:HA	1:D:198:TYR:N	2.18	0.59
1:D:305:THR:HG22	1:D:400:LYS:CB	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:173:ASP:CB	4:E:185:ILE:HG21	2.31	0.59
2:B:9:SER:HA	2:B:12:PHE:HE1	1.61	0.59
3:C:201:ILE:HD12	3:C:213:GLN:OE1	2.03	0.59
1:D:129:GLU:O	1:D:130:ILE:HG23	2.02	0.59
1:D:176:TRP:CE3	1:D:209:ARG:CZ	2.85	0.59
1:D:260:ILE:O	1:D:264:ILE:HG13	2.03	0.59
4:E:161:ALA:O	4:E:190:ALA:HB3	2.02	0.59
1:A:29:VAL:HB	1:A:31:ILE:CD1	2.32	0.59
1:A:66:ARG:HD3	1:A:66:ARG:O	2.03	0.59
1:A:165:PRO:C	1:A:181:TYR:CD1	2.81	0.59
1:A:298:THR:HG23	1:A:301:ARG:HD3	1.85	0.59
2:B:409:LYS:NZ	3:C:423:ILE:CG2	2.65	0.59
3:C:111:LEU:HB3	3:C:119:THR:OG1	2.03	0.59
3:C:137:PHE:H	3:C:138:PRO:HD2	1.66	0.59
1:D:28:PHE:HA	1:D:155:LYS:O	2.02	0.59
1:D:201:ILE:O	1:D:203:TYR:CE1	2.56	0.59
4:E:103:TYR:CG	4:E:104:TYR:N	2.67	0.59
1:A:254:THR:O	1:A:258:LEU:HG	2.02	0.59
1:A:261:VAL:O	1:A:261:VAL:HG12	2.03	0.59
3:C:153:TYR:CB	3:C:158:ILE:HG13	2.33	0.59
1:A:139:GLN:NE2	1:A:206:ILE:CG2	2.66	0.58
1:A:216:VAL:HG12	1:A:220:ILE:HD12	1.84	0.58
2:B:268:ASP:O	2:B:271:PRO:HD2	2.03	0.58
2:B:304:LEU:C	2:B:304:LEU:CD2	2.76	0.58
1:D:175:GLU:HB3	1:D:211:PRO:HG3	1.81	0.58
4:E:41:SER:O	4:E:49:LEU:HA	2.03	0.58
4:E:162:GLU:CA	4:E:190:ALA:H	2.13	0.58
1:A:106:THR:CG2	1:A:107:LYS:H	2.13	0.58
2:B:175:ILE:CG1	2:B:176:ASN:N	2.66	0.58
2:B:439:PHE:O	2:B:442:ILE:HG22	2.04	0.58
1:D:134:HIS:NE2	1:D:207:MET:HE3	2.18	0.58
1:D:220:ILE:N	1:D:221:PRO:HD2	2.18	0.58
4:E:225:ILE:C	4:E:228:PRO:HD2	2.28	0.58
4:E:463:LEU:O	4:E:463:LEU:CD1	2.51	0.58
1:A:92:LEU:HB2	1:A:96:ALA:N	2.18	0.58
1:A:170:PHE:HE1	1:A:176:TRP:CD1	2.22	0.58
2:B:160:HIS:NE2	2:B:207:VAL:CG1	2.64	0.58
2:B:230:LEU:CA	2:B:233:ILE:HG13	2.33	0.58
3:C:30:VAL:CG2	3:C:158:ILE:N	2.66	0.58
3:C:69:TRP:CH2	3:C:112:VAL:CG1	2.85	0.58
3:C:138:PRO:CG	3:C:288:ILE:HD12	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:65:LEU:HD23	1:D:110:LEU:HD11	1.86	0.58
1:D:226:SER:O	1:D:230:VAL:HB	2.03	0.58
1:D:376:ILE:HG22	1:D:380:LYS:HZ1	1.68	0.58
4:E:19:LYS:NZ	4:E:154:GLU:CB	2.66	0.58
4:E:54:TRP:C	4:E:118:LEU:CD1	2.77	0.58
1:A:113:THR:O	1:A:113:THR:HG23	2.01	0.58
2:B:48:GLU:HG3	2:B:48:GLU:O	2.04	0.58
2:B:232:SER:HA	2:B:235:ALA:HB3	1.84	0.58
3:C:14:VAL:HG13	3:C:86:LEU:CD2	2.33	0.58
3:C:50:GLU:CB	3:C:132:ILE:HD13	2.33	0.58
3:C:137:PHE:CE1	3:C:288:ILE:CG2	2.86	0.58
1:D:106:THR:HG23	1:D:107:LYS:HE2	1.85	0.58
1:D:242:LYS:O	1:D:245:LEU:HB3	2.04	0.58
1:D:419:ILE:HD12	1:D:419:ILE:C	2.28	0.58
1:D:429:ARG:N	1:D:429:ARG:HE	2.01	0.58
4:E:474:VAL:HG12	4:E:475:PRO:HD3	1.85	0.58
1:A:31:ILE:HG13	1:A:60:TRP:HB3	1.85	0.58
1:A:37:LEU:HD22	1:A:54:VAL:HG12	1.83	0.58
1:A:46:VAL:HG21	1:A:270:ALA:N	2.18	0.58
2:B:160:HIS:H	2:B:195:LYS:NZ	1.99	0.58
2:B:304:LEU:HD23	2:B:304:LEU:O	2.04	0.58
2:B:408:ILE:CG2	2:B:409:LYS:H	2.15	0.58
3:C:35:LEU:HD22	3:C:215:VAL:CG1	2.32	0.58
3:C:242:LEU:CD2	3:C:263:VAL:HG12	2.33	0.58
3:C:447:ASN:O	3:C:449:VAL:HG23	2.04	0.58
1:D:256:PHE:CZ	4:E:263:ILE:CG1	2.87	0.58
4:E:45:LYS:CE	4:E:278:ASN:HA	2.32	0.58
4:E:162:GLU:HG2	4:E:190:ALA:O	2.03	0.58
1:A:15:TYR:OH	1:A:84:ASP:HB3	2.04	0.58
1:A:133:THR:C	1:A:136:PRO:HD2	2.28	0.58
3:C:472:ILE:HA	3:C:475:MET:HB3	1.85	0.58
4:E:184:THR:HG23	4:E:215:GLN:C	2.28	0.58
1:A:9:ALA:O	1:A:13:GLU:HG3	2.03	0.58
1:A:12:LEU:HG	1:A:13:GLU:N	2.18	0.58
1:A:32:THR:HG23	1:A:159:SER:O	2.04	0.58
1:A:58:GLN:NE2	1:A:90:LEU:HD11	2.19	0.58
1:A:155:LYS:HG3	4:E:78:ARG:CZ	2.33	0.58
1:A:178:MET:HA	1:A:207:MET:HB2	1.85	0.58
2:B:35:LEU:CD1	2:B:56:LEU:HD22	2.34	0.58
2:B:130:ILE:O	2:B:134:TYR:HB2	2.04	0.58
2:B:189:GLU:CG	2:B:468:PHE:CB	2.77	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:60:HIS:CD2	3:C:92:ILE:CD1	2.87	0.58
3:C:159:SER:HA	3:C:213:GLN:HG2	1.83	0.58
3:C:179:ILE:HG21	3:C:181:PRO:HD2	1.85	0.58
3:C:434:LYS:NZ	3:C:435:GLU:HG2	2.18	0.58
1:D:45:GLU:HB3	1:D:271:VAL:HG22	1.81	0.58
1:D:129:GLU:O	1:D:142:CYS:HB2	2.04	0.58
1:D:409:ILE:CA	1:D:412:CYS:HB2	2.33	0.58
4:E:77:VAL:CG1	4:E:78:ARG:N	2.67	0.58
4:E:248:GLY:C	4:E:250:LYS:H	2.12	0.58
1:A:66:ARG:HD3	1:A:66:ARG:H	1.69	0.58
1:A:129:GLU:CD	1:A:140:GLN:HG3	2.28	0.58
1:A:265:PRO:HG2	1:A:266:SER:N	2.18	0.58
3:C:51:THR:C	3:C:52:LEU:HD13	2.28	0.58
3:C:147:LYS:HE2	3:C:216:THR:CG2	2.33	0.58
3:C:199:LYS:O	3:C:199:LYS:NZ	2.33	0.58
1:D:53:ASN:HD21	1:D:121:PRO:C	2.11	0.58
1:D:280:PHE:N	1:D:280:PHE:CD1	2.68	0.58
1:D:286:ILE:HG22	1:D:290:ILE:HG23	1.85	0.58
4:E:91:LEU:H	4:E:95:VAL:CG2	2.17	0.58
4:E:172:ILE:HG23	4:E:174:PRO:CD	2.34	0.58
4:E:441:LEU:C	4:E:441:LEU:HD12	2.29	0.58
2:B:136:PRO:CD	2:B:280:ILE:HD11	2.33	0.58
2:B:189:GLU:O	2:B:190:HIS:CD2	2.57	0.58
3:C:42:LEU:CD1	3:C:190:TRP:HZ2	2.16	0.58
3:C:141:TRP:CH2	3:C:223:ARG:HB3	2.38	0.58
3:C:215:VAL:HG23	3:C:215:VAL:O	2.04	0.58
1:D:68:ASN:HB2	1:D:69:PRO:CD	2.33	0.58
4:E:226:ILE:O	4:E:230:VAL:HG23	2.04	0.58
4:E:453:ILE:C	4:E:453:ILE:HD12	2.29	0.58
1:A:166:ASP:CB	1:A:178:MET:HE2	2.33	0.58
1:A:386:MET:HG3	4:E:427:LYS:HD3	1.86	0.58
1:A:389:ASP:O	1:A:392:SER:HB3	2.04	0.58
2:B:247:GLU:HA	2:B:249:MET:CG	2.34	0.58
3:C:60:HIS:NE2	3:C:92:ILE:HD13	2.19	0.58
3:C:141:TRP:HB2	3:C:222:ARG:HA	1.85	0.58
1:D:38:ILE:O	1:D:169:THR:HG21	2.04	0.58
1:A:43:VAL:HG22	1:A:50:VAL:CG2	2.34	0.57
1:A:135:PHE:O	1:A:135:PHE:CG	2.57	0.57
1:A:145:LYS:NZ	1:A:202:THR:HG23	2.19	0.57
2:B:218:LEU:C	2:B:219:PHE:CD1	2.82	0.57
2:B:278:PRO:CG	2:B:278:PRO:O	2.49	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:3:GLU:OE1	3:C:3:GLU:O	2.22	0.57
3:C:30:VAL:CG1	3:C:31:VAL:N	2.67	0.57
3:C:137:PHE:HD1	3:C:288:ILE:HB	1.68	0.57
3:C:471:PHE:HD1	3:C:471:PHE:O	1.87	0.57
1:D:298:THR:O	1:D:301:ARG:HD3	2.04	0.57
4:E:159:LEU:HD21	4:E:208:ILE:CG2	2.33	0.57
1:A:25:HIS:O	1:A:25:HIS:CG	2.57	0.57
1:A:166:ASP:OD1	1:A:166:ASP:O	2.21	0.57
1:A:190:TYR:HB2	1:A:192:CYS:SG	2.43	0.57
1:A:271:VAL:CG2	1:A:271:VAL:O	2.52	0.57
3:C:60:HIS:HE1	3:C:160:MET:HE1	1.69	0.57
1:D:296:ILE:HA	1:D:299:HIS:HB3	1.84	0.57
4:E:49:LEU:HD12	4:E:50:THR:N	2.18	0.57
1:A:108:LEU:HD13	1:A:118:TRP:CB	2.32	0.57
1:A:147:GLY:HA2	1:A:158:ILE:HG21	1.87	0.57
2:B:28:LYS:HB2	2:B:156:VAL:CA	2.20	0.57
3:C:67:LEU:CD1	3:C:116:GLY:CA	2.82	0.57
3:C:153:TYR:HB2	3:C:158:ILE:CG1	2.34	0.57
4:E:34:LEU:HB2	4:E:210:PHE:CZ	2.39	0.57
2:B:31:VAL:CG2	2:B:86:TRP:HZ3	2.15	0.57
2:B:68:ASP:CB	2:B:69:PRO:CD	2.78	0.57
2:B:69:PRO:HG2	2:B:70:ALA:H	1.68	0.57
1:D:1:SER:N	1:D:4:GLU:HB2	2.19	0.57
1:D:29:VAL:CG1	1:D:60:TRP:NE1	2.67	0.57
1:D:189:TYR:HA	1:D:197:PRO:HD3	1.82	0.57
1:D:223:LEU:HD23	1:D:223:LEU:C	2.29	0.57
1:D:291:VAL:O	1:D:295:VAL:HG22	2.04	0.57
1:A:166:ASP:HB2	1:A:181:TYR:HB3	1.86	0.57
2:B:288:MET:O	2:B:291:VAL:HG12	2.04	0.57
3:C:52:LEU:HD22	3:C:52:LEU:N	2.18	0.57
3:C:92:ILE:HA	3:C:149:THR:O	2.04	0.57
3:C:316:THR:HG23	3:C:317:PRO:CD	2.31	0.57
1:D:91:VAL:CG2	1:D:96:ALA:HB1	2.33	0.57
4:E:146:ARG:HB3	4:E:207:GLU:HA	1.86	0.57
1:A:62:ASP:HB3	1:A:65:LEU:HD12	1.86	0.57
1:A:305:THR:OG1	1:A:400:LYS:HB3	2.05	0.57
3:C:219:LEU:HD11	3:C:221:ILE:HG22	1.86	0.57
1:D:38:ILE:O	1:D:38:ILE:CG2	2.53	0.57
4:E:59:TRP:HH2	4:E:107:VAL:CG1	2.17	0.57
4:E:116:TYR:C	4:E:116:TYR:HD1	2.13	0.57
1:A:163:ASP:C	1:A:164:ARG:HG3	2.30	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:49:ASP:C	3:C:50:GLU:HG3	2.30	0.57
3:C:191:GLU:HG2	3:C:222:ARG:C	2.30	0.57
3:C:318:SER:CA	3:C:447:ASN:ND2	2.68	0.57
1:D:233:PHE:CZ	1:D:291:VAL:CG1	2.88	0.57
1:D:233:PHE:O	1:D:236:PRO:HG2	2.04	0.57
1:D:287:SER:HA	1:D:290:ILE:CG1	2.34	0.57
4:E:61:ASP:OD2	4:E:84:LEU:HD21	2.05	0.57
1:A:38:ILE:HD12	1:A:38:ILE:N	2.19	0.57
1:A:105:MET:O	1:A:105:MET:HG2	2.03	0.57
1:A:136:PRO:HG3	1:A:274:ILE:CG2	2.34	0.57
1:A:225:PHE:CD1	1:A:225:PHE:C	2.81	0.57
1:A:244:THR:O	1:A:247:ILE:HG22	2.03	0.57
3:C:106:TYR:CD1	3:C:107:PHE:CD1	2.93	0.57
3:C:234:THR:N	3:C:235:PRO:HD2	2.20	0.57
3:C:482:PRO:HG2	3:C:483:ALA:N	2.19	0.57
1:D:75:ILE:CG1	1:D:78:ILE:HG23	2.27	0.57
4:E:453:ILE:O	4:E:457:LEU:HB2	2.04	0.57
1:A:134:HIS:N	1:A:136:PRO:HD2	2.20	0.57
1:A:175:GLU:CB	1:A:211:PRO:HD3	2.34	0.57
1:A:262:GLU:C	1:A:265:PRO:HD2	2.30	0.57
2:B:33:VAL:HG11	2:B:158:LEU:HD11	1.87	0.57
2:B:252:SER:O	2:B:255:ALA:HB3	2.05	0.57
1:D:102:ILE:O	1:D:102:ILE:HG22	2.05	0.57
4:E:62:TYR:C	4:E:64:LEU:H	2.12	0.57
4:E:232:ILE:HG22	4:E:233:SER:N	2.20	0.57
1:A:43:VAL:CB	1:A:50:VAL:HG22	2.34	0.57
2:B:95:ASN:HB3	2:B:127:SER:H	1.69	0.57
3:C:12:LEU:HB3	3:C:15:ASN:HB3	1.87	0.57
4:E:45:LYS:HE2	4:E:278:ASN:CA	2.35	0.57
4:E:144:VAL:HG23	4:E:144:VAL:O	2.05	0.57
4:E:195:ASN:HB2	4:E:205:PHE:O	2.04	0.57
4:E:227:ALA:N	4:E:228:PRO:CD	2.68	0.57
1:A:249:VAL:HG12	1:A:250:LEU:N	2.19	0.56
2:B:415:LEU:C	2:B:415:LEU:CD1	2.78	0.56
3:C:249:LEU:N	3:C:250:PRO:HD3	2.20	0.56
1:D:43:VAL:CG2	1:D:50:VAL:HG13	2.34	0.56
1:D:167:LEU:HD11	1:D:178:MET:HB3	1.87	0.56
4:E:44:GLU:OE2	4:E:129:ILE:HB	2.02	0.56
4:E:133:TYR:CD1	4:E:139:GLN:CB	2.88	0.56
1:A:3:HIS:C	1:A:7:LEU:HG	2.30	0.56
1:A:130:ILE:CD1	1:A:130:ILE:H	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:92:LEU:HD13	2:B:146:PHE:CE1	2.39	0.56
2:B:192:PRO:HD2	2:B:210:TYR:HB2	1.86	0.56
1:D:32:THR:CB	1:D:59:GLN:HB3	2.23	0.56
1:D:170:PHE:HE2	1:D:176:TRP:NE1	2.03	0.56
1:D:241:GLU:C	1:D:243:MET:HE1	2.30	0.56
4:E:76:LEU:C	4:E:77:VAL:HG23	2.29	0.56
4:E:79:ILE:O	4:E:79:ILE:HG22	2.05	0.56
1:A:33:VAL:HG23	1:A:158:ILE:HG12	1.82	0.56
1:A:41:ILE:HG12	1:A:51:GLU:HB3	1.86	0.56
1:A:60:TRP:NE1	1:A:116:ILE:HD12	2.19	0.56
1:A:67:TRP:CD1	1:A:71:ASP:HB3	2.40	0.56
1:A:67:TRP:NE1	1:A:71:ASP:CG	2.63	0.56
1:A:106:THR:CG2	1:A:107:LYS:N	2.67	0.56
1:A:135:PHE:CD1	1:A:135:PHE:C	2.82	0.56
1:A:148:ILE:CD1	1:A:156:VAL:HG13	2.30	0.56
1:A:417:ILE:O	1:A:417:ILE:HG22	2.04	0.56
2:B:185:GLN:HB3	2:B:217:PRO:CB	2.34	0.56
3:C:69:TRP:CH2	3:C:112:VAL:HG11	2.39	0.56
3:C:158:ILE:HG22	3:C:212:TYR:HA	1.86	0.56
3:C:274:THR:HG22	3:C:275:SER:N	2.21	0.56
1:D:56:LEU:N	1:D:56:LEU:CD2	2.58	0.56
1:D:256:PHE:CE2	4:E:263:ILE:HA	2.41	0.56
1:D:427:ALA:O	1:D:431:ILE:HG13	2.06	0.56
4:E:261:GLN:HE22	4:E:296:ILE:HD11	1.71	0.56
1:A:27:HIS:C	1:A:28:PHE:CG	2.83	0.56
1:A:160:PRO:HG3	1:A:185:LYS:HB2	1.81	0.56
3:C:234:THR:HB	3:C:235:PRO:HD3	1.87	0.56
3:C:288:ILE:CD1	3:C:290:LYS:CE	2.69	0.56
3:C:431:LYS:HE2	1:D:379:VAL:CG1	2.36	0.56
1:D:35:LEU:CD1	1:D:36:GLN:H	2.07	0.56
1:D:37:LEU:CA	1:D:54:VAL:HG13	2.36	0.56
1:D:146:LEU:HD12	1:D:146:LEU:N	2.18	0.56
1:D:176:TRP:CE3	1:D:209:ARG:HD2	2.40	0.56
4:E:22:LYS:HG3	4:E:23:THR:HB	1.87	0.56
4:E:80:PRO:HB2	4:E:83:LEU:HD21	1.85	0.56
4:E:273:PRO:HG2	4:E:274:GLU:N	2.19	0.56
1:A:144:MET:HB2	1:A:203:TYR:HB2	1.86	0.56
2:B:75:ILE:O	2:B:75:ILE:CG1	2.40	0.56
2:B:269:LYS:HD2	2:B:270:VAL:N	2.19	0.56
3:C:35:LEU:CD2	3:C:215:VAL:HG11	2.33	0.56
3:C:222:ARG:NH2	3:C:223:ARG:C	2.64	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:45:LYS:HA	4:E:280:PRO:HA	1.86	0.56
4:E:246:ALA:HA	4:E:250:LYS:NZ	2.21	0.56
4:E:261:GLN:HG3	4:E:262:THR:N	2.18	0.56
4:E:425:SER:O	4:E:429:GLN:HB3	2.06	0.56
1:A:149:TRP:HH2	4:E:119:PRO:HA	1.71	0.56
1:A:416:LEU:O	1:A:420:ILE:HG23	2.05	0.56
2:B:46:LYS:CG	2:B:278:PRO:CD	2.80	0.56
2:B:132:VAL:HG12	2:B:279:ILE:C	2.30	0.56
2:B:187:SER:C	2:B:188:ILE:HG12	2.30	0.56
3:C:35:LEU:HD21	3:C:37:LEU:HD21	1.88	0.56
3:C:69:TRP:HH2	3:C:112:VAL:HG11	1.69	0.56
3:C:257:MET:CE	3:C:314:PHE:HB2	2.35	0.56
1:D:171:MET:SD	1:D:176:TRP:CH2	2.98	0.56
1:D:257:LEU:C	1:D:257:LEU:CD1	2.76	0.56
1:D:305:THR:HG21	1:D:400:LYS:HB3	1.86	0.56
4:E:55:ILE:HG23	4:E:119:PRO:HD2	1.87	0.56
4:E:59:TRP:CD2	4:E:115:MET:HB2	2.41	0.56
4:E:61:ASP:OD1	4:E:63:ARG:HB3	2.06	0.56
4:E:173:ASP:HB3	4:E:185:ILE:CD1	2.34	0.56
1:A:4:GLU:HA	1:A:7:LEU:CD1	2.35	0.56
1:A:276:LYS:HD2	1:A:276:LYS:N	2.19	0.56
2:B:269:LYS:O	2:B:273:THR:HG23	2.06	0.56
3:C:228:TYR:HD1	3:C:229:VAL:H	1.53	0.56
1:D:1:SER:H3	1:D:4:GLU:HB2	1.70	0.56
1:D:416:LEU:C	1:D:419:ILE:HG13	2.30	0.56
4:E:287:ILE:HG13	4:E:291:PHE:CE2	2.41	0.56
1:A:56:LEU:HD23	1:A:57:ARG:H	1.71	0.56
1:A:148:ILE:O	1:A:198:TYR:CD2	2.59	0.56
1:A:187:TRP:CZ2	1:A:189:TYR:HB3	2.41	0.56
2:B:197:TRP:CB	2:B:204:TYR:HD1	2.19	0.56
3:C:77:ILE:HD12	3:C:80:LEU:HD13	1.88	0.56
3:C:106:TYR:C	3:C:106:TYR:HD1	2.14	0.56
1:D:167:LEU:HD21	1:D:178:MET:C	2.31	0.56
4:E:45:LYS:N	4:E:280:PRO:CA	2.69	0.56
4:E:58:GLN:C	4:E:59:TRP:HE3	2.13	0.56
4:E:138:TRP:O	4:E:213:ILE:HG13	2.06	0.56
1:A:265:PRO:C	1:A:268:SER:HB3	2.31	0.56
1:A:379:VAL:HA	1:A:382:ILE:CD1	2.36	0.56
2:B:9:SER:CA	2:B:12:PHE:HE1	2.17	0.56
2:B:186:TRP:HB2	2:B:215:ARG:HB2	1.88	0.56
3:C:106:TYR:O	3:C:107:PHE:HD1	1.89	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:35:LEU:HD23	1:D:164:ARG:HH11	1.67	0.56
1:D:37:LEU:HB2	1:D:54:VAL:HG13	1.87	0.56
1:D:130:ILE:HG22	1:D:134:HIS:HD2	1.70	0.56
1:D:137:PHE:CD2	1:D:431:ILE:CG2	2.85	0.56
1:D:152:ASP:HA	1:D:197:PRO:C	2.31	0.56
1:D:420:ILE:HA	1:D:423:VAL:HG23	1.88	0.56
4:E:45:LYS:HG2	4:E:278:ASN:C	2.31	0.56
4:E:133:TYR:CG	4:E:139:GLN:HB3	2.41	0.56
4:E:140:ASN:C	4:E:140:ASN:ND2	2.54	0.56
2:B:142:CYS:CB	2:B:211:LEU:CD1	2.82	0.56
3:C:29:GLU:O	3:C:156:ASN:HA	2.06	0.56
3:C:319:THR:N	3:C:447:ASN:CB	2.69	0.56
3:C:471:PHE:C	3:C:473:PHE:H	2.13	0.56
1:D:88:PRO:O	1:D:88:PRO:CG	2.50	0.56
1:D:261:VAL:O	1:D:261:VAL:CG1	2.53	0.56
4:E:92:GLU:HB3	4:E:144:VAL:HG23	1.87	0.56
4:E:255:ILE:HD11	4:E:304:LEU:HD22	1.87	0.56
4:E:271:LYS:NZ	4:E:271:LYS:CB	2.68	0.56
1:A:17:LYS:HE3	1:A:84:ASP:CA	2.36	0.55
1:A:117:MET:SD	1:A:119:THR:CG2	2.94	0.55
2:B:181:THR:CG2	2:B:181:THR:O	2.50	0.55
2:B:212:ILE:O	2:B:212:ILE:CG2	2.53	0.55
2:B:240:TYR:O	2:B:244:ASP:HB2	2.06	0.55
2:B:299:VAL:HG12	2:B:299:VAL:O	2.06	0.55
1:D:46:VAL:C	1:D:272:PRO:HD3	2.31	0.55
1:D:54:VAL:O	1:D:56:LEU:HD23	2.06	0.55
1:D:264:ILE:HB	1:D:265:PRO:HD2	1.87	0.55
4:E:83:LEU:O	4:E:84:LEU:HB2	2.05	0.55
1:A:139:GLN:CB	1:A:207:MET:C	2.79	0.55
1:A:200:ASP:OD1	1:A:200:ASP:N	2.39	0.55
3:C:113:ARG:HB2	3:C:117:TYR:O	2.06	0.55
3:C:150:ALA:HB3	3:C:158:ILE:CD1	2.36	0.55
1:D:220:ILE:HG21	4:E:294:LEU:HD11	1.88	0.55
1:D:240:GLY:C	1:D:242:LYS:H	2.14	0.55
4:E:102:ALA:HB2	4:E:121:ALA:HB2	1.88	0.55
4:E:117:TRP:CD1	4:E:119:PRO:HD3	2.42	0.55
1:A:45:GLU:CD	1:A:271:VAL:HB	2.31	0.55
1:A:107:LYS:NZ	2:B:151:TYR:CD1	2.69	0.55
1:A:296:ILE:HD13	1:A:296:ILE:N	2.21	0.55
1:A:385:HIS:C	1:A:385:HIS:ND1	2.64	0.55
3:C:115:ASN:ND2	3:C:115:ASN:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:193:ILE:HD11	3:C:222:ARG:HB2	1.88	0.55
4:E:79:ILE:CG1	4:E:80:PRO:HD3	2.35	0.55
1:A:46:VAL:HB	1:A:270:ALA:C	2.32	0.55
1:A:108:LEU:HD22	1:A:118:TRP:HA	1.89	0.55
1:A:262:GLU:C	1:A:265:PRO:CD	2.80	0.55
3:C:42:LEU:CA	3:C:54:THR:HG22	2.32	0.55
3:C:141:TRP:CB	3:C:222:ARG:HA	2.37	0.55
1:D:36:GLN:HB3	1:D:55:ARG:CG	2.36	0.55
1:D:132:VAL:HB	1:D:274:ILE:HG23	1.88	0.55
1:D:144:MET:O	1:D:203:TYR:CD1	2.59	0.55
1:D:280:PHE:HB3	1:D:284:PHE:CZ	2.41	0.55
4:E:59:TRP:N	4:E:59:TRP:CE3	2.75	0.55
4:E:135:PRO:HB2	4:E:137:ASP:OD1	2.07	0.55
1:A:54:VAL:HG22	1:A:122:ALA:HB3	1.89	0.55
1:A:56:LEU:CD2	1:A:57:ARG:N	2.67	0.55
1:A:178:MET:SD	1:A:207:MET:HB3	2.46	0.55
1:A:222:CYS:HA	1:A:225:PHE:HD2	1.71	0.55
2:B:56:LEU:HD11	2:B:103:THR:CG2	2.35	0.55
2:B:185:GLN:O	2:B:217:PRO:HB3	2.06	0.55
2:B:287:ILE:HD12	2:B:288:MET:N	2.21	0.55
2:B:439:PHE:CA	2:B:442:ILE:HB	2.36	0.55
3:C:138:PRO:HA	3:C:288:ILE:HD12	1.89	0.55
3:C:219:LEU:HG	3:C:221:ILE:HG23	1.89	0.55
1:D:153:GLY:H	1:D:197:PRO:C	2.14	0.55
1:D:295:VAL:O	1:D:299:HIS:HB2	2.06	0.55
4:E:40:ILE:HB	4:E:50:THR:HB	1.88	0.55
4:E:470:HIS:NE2	4:E:474:VAL:CG2	2.69	0.55
1:A:69:PRO:HA	1:A:73:GLY:HA3	1.87	0.55
1:A:426:PHE:CD1	1:A:426:PHE:C	2.83	0.55
2:B:11:LEU:O	2:B:15:TYR:HB3	2.06	0.55
3:C:56:VAL:HG22	3:C:124:ALA:HB3	1.89	0.55
3:C:132:ILE:HG22	3:C:133:ASN:N	2.22	0.55
3:C:138:PRO:CD	3:C:288:ILE:HD12	2.36	0.55
1:D:130:ILE:C	1:D:134:HIS:HB2	2.30	0.55
4:E:45:LYS:HB3	4:E:279:VAL:O	2.06	0.55
4:E:66:TRP:CE3	4:E:70:GLU:CB	2.90	0.55
2:B:56:LEU:HB2	2:B:120:PRO:CG	2.32	0.55
2:B:85:VAL:HG12	2:B:86:TRP:N	2.21	0.55
2:B:85:VAL:O	2:B:87:GLN:HG3	2.06	0.55
3:C:425:SER:O	3:C:429:ILE:HG23	2.07	0.55
1:D:176:TRP:CZ3	1:D:209:ARG:CZ	2.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:416:LEU:HA	1:D:419:ILE:CG1	2.37	0.55
4:E:143:LEU:O	4:E:210:PHE:HB2	2.06	0.55
4:E:145:PHE:O	4:E:208:ILE:HD12	2.06	0.55
1:A:69:PRO:O	1:A:73:GLY:HA3	2.07	0.55
1:A:72:TYR:C	1:A:72:TYR:HD1	2.14	0.55
1:A:304:SER:CA	1:A:400:LYS:HD3	2.34	0.55
1:A:380:LYS:HB3	2:B:408:ILE:CB	2.37	0.55
1:A:380:LYS:HA	2:B:408:ILE:HD13	1.86	0.55
3:C:38:THR:HG21	3:C:57:TRP:CZ3	2.42	0.55
1:D:167:LEU:HD21	1:D:178:MET:O	2.07	0.55
1:D:222:CYS:O	1:D:225:PHE:CD1	2.60	0.55
4:E:128:PRO:C	4:E:129:ILE:HG12	2.31	0.55
4:E:143:LEU:H	4:E:143:LEU:HD12	1.72	0.55
4:E:200:LYS:O	4:E:200:LYS:CG	2.54	0.55
4:E:246:ALA:HB1	4:E:250:LYS:CG	2.25	0.55
4:E:436:ASN:CA	4:E:439:TRP:NE1	2.70	0.55
1:A:128:CYS:HB3	1:A:144:MET:HE2	1.88	0.55
2:B:4:GLU:HG2	2:B:70:ALA:HB3	1.89	0.55
3:C:162:LEU:C	3:C:162:LEU:CD2	2.79	0.55
3:C:288:ILE:HG12	3:C:289:GLY:N	2.21	0.55
1:D:35:LEU:HB3	1:D:164:ARG:CZ	2.37	0.55
1:D:419:ILE:O	1:D:423:VAL:HG23	2.06	0.55
4:E:133:TYR:C	4:E:135:PRO:CD	2.80	0.55
4:E:136:PHE:CZ	4:E:217:LYS:CD	2.87	0.55
4:E:138:TRP:HE1	4:E:186:ARG:HD2	1.70	0.55
1:A:108:LEU:HD21	1:A:118:TRP:CD1	2.43	0.55
1:A:223:LEU:HA	1:A:226:SER:OG	2.07	0.55
2:B:112:HIS:CG	2:B:113:THR:H	2.25	0.55
2:B:263:LEU:HA	2:B:266:LEU:HD12	1.88	0.55
1:D:58:GLN:NE2	1:D:88:PRO:CG	2.70	0.55
1:D:76:LYS:HA	1:D:112:TYR:CD2	2.42	0.55
1:D:242:LYS:HA	1:D:243:MET:HE2	1.89	0.55
4:E:33:LYS:HG2	4:E:160:SER:CB	2.33	0.55
4:E:146:ARG:HH11	4:E:205:PHE:C	2.15	0.55
1:A:33:VAL:HG22	1:A:158:ILE:HG12	1.85	0.54
1:A:131:ILE:CD1	1:A:140:GLN:NE2	2.70	0.54
1:A:133:THR:C	1:A:136:PRO:CG	2.80	0.54
2:B:28:LYS:HD3	2:B:156:VAL:N	2.22	0.54
2:B:130:ILE:HD12	2:B:134:TYR:CE2	2.42	0.54
2:B:187:SER:O	2:B:188:ILE:HG12	2.07	0.54
3:C:33:ILE:CG2	3:C:160:MET:SD	2.94	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:305:ASN:O	3:C:309:VAL:HG23	2.08	0.54
1:D:51:GLU:HA	1:D:124:PHE:O	2.07	0.54
1:D:85:VAL:HG13	1:D:86:TRP:HE3	1.71	0.54
1:D:419:ILE:O	1:D:422:THR:HG22	2.07	0.54
4:E:88:ASP:O	4:E:88:ASP:CG	2.50	0.54
4:E:143:LEU:HD12	4:E:143:LEU:N	2.22	0.54
4:E:293:SER:O	4:E:296:ILE:HG12	2.08	0.54
1:A:250:LEU:CD1	1:A:296:ILE:CG2	2.77	0.54
2:B:218:LEU:CD1	2:B:221:ILE:CG1	2.84	0.54
2:B:276:SER:C	2:B:277:VAL:CG1	2.80	0.54
3:C:68:THR:HG22	3:C:69:TRP:N	2.20	0.54
3:C:242:LEU:CD2	3:C:267:GLN:CG	2.83	0.54
3:C:278:LEU:N	3:C:279:PRO:CD	2.70	0.54
1:D:244:THR:CG2	1:D:245:LEU:N	2.68	0.54
4:E:134:PHE:HB3	4:E:282:ILE:HB	1.88	0.54
4:E:273:PRO:CG	4:E:274:GLU:H	2.18	0.54
1:A:3:HIS:HB3	1:A:7:LEU:HD23	1.89	0.54
1:A:137:PHE:CE1	1:A:210:ILE:CD1	2.73	0.54
2:B:3:MET:O	2:B:7:LEU:HG	2.07	0.54
2:B:46:LYS:HG3	2:B:278:PRO:CG	2.37	0.54
2:B:108:VAL:HG13	2:B:117:SER:C	2.32	0.54
2:B:139:TRP:CE3	2:B:468:PHE:CZ	2.95	0.54
2:B:239:PHE:N	2:B:239:PHE:CD1	2.72	0.54
3:C:67:LEU:CD1	3:C:116:GLY:C	2.78	0.54
3:C:160:MET:N	3:C:213:GLN:HB2	2.19	0.54
1:D:188:VAL:O	1:D:197:PRO:HB2	2.07	0.54
4:E:48:ALA:HA	4:E:125:SER:O	2.06	0.54
4:E:216:ARG:C	4:E:218:PRO:HD2	2.32	0.54
2:B:40:LEU:CA	2:B:52:THR:HG23	2.36	0.54
2:B:145:VAL:HG12	2:B:206:ASP:HB2	1.88	0.54
2:B:274:SER:O	2:B:278:PRO:HD3	2.08	0.54
1:D:90:LEU:O	1:D:91:VAL:HB	2.06	0.54
1:D:239:SER:CB	1:D:242:LYS:CE	2.84	0.54
4:E:44:GLU:HG3	4:E:129:ILE:CD1	2.37	0.54
4:E:452:TRP:CE3	4:E:452:TRP:HA	2.43	0.54
1:A:165:PRO:O	1:A:181:TYR:CE1	2.61	0.54
2:B:135:PHE:N	2:B:136:PRO:CD	2.70	0.54
2:B:441:TYR:O	2:B:444:ILE:HG22	2.06	0.54
2:B:463:PRO:HB2	2:B:464:PRO:HD3	1.89	0.54
3:C:228:TYR:CD1	3:C:229:VAL:HG22	2.43	0.54
4:E:91:LEU:HD13	4:E:145:PHE:CA	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:449:ALA:HA	4:E:452:TRP:CG	2.42	0.54
1:A:217:ASN:O	1:A:221:PRO:HD3	2.07	0.54
1:A:380:LYS:HB3	2:B:408:ILE:HB	1.88	0.54
1:A:384:GLU:HA	1:A:387:LYS:HG3	1.87	0.54
1:A:431:ILE:HG22	1:A:431:ILE:O	2.07	0.54
2:B:46:LYS:CB	2:B:278:PRO:HD2	2.38	0.54
2:B:244:ASP:CG	3:C:314:PHE:HE1	2.16	0.54
3:C:155:ALA:N	3:C:211:ASN:CA	2.70	0.54
3:C:193:ILE:CD1	3:C:222:ARG:HB2	2.38	0.54
3:C:266:ALA:O	3:C:270:PHE:CD1	2.61	0.54
3:C:429:ILE:CG1	3:C:430:VAL:N	2.71	0.54
3:C:431:LYS:HZ1	1:D:382:ILE:CD1	2.20	0.54
1:D:37:LEU:HD13	1:D:54:VAL:HG13	1.89	0.54
1:D:253:LEU:HD23	1:D:254:THR:CA	2.38	0.54
1:A:207:MET:H	1:A:207:MET:CE	2.19	0.54
1:A:306:HIS:C	1:A:306:HIS:HD2	2.15	0.54
2:B:32:ARG:HH21	2:B:60:TRP:C	2.16	0.54
2:B:289:ILE:HG22	2:B:293:PHE:CE2	2.43	0.54
3:C:102:TYR:O	3:C:102:TYR:CD1	2.61	0.54
3:C:150:ALA:CB	3:C:158:ILE:HD12	2.38	0.54
4:E:56:GLU:HB2	4:E:118:LEU:CD2	2.15	0.54
4:E:266:PHE:CD1	4:E:266:PHE:O	2.61	0.54
1:A:58:GLN:HB3	1:A:60:TRP:CZ3	2.42	0.54
1:A:190:TYR:HD1	1:A:197:PRO:HG2	1.73	0.54
1:A:306:HIS:O	1:A:306:HIS:CG	2.60	0.54
2:B:280:ILE:C	2:B:282:SER:H	2.15	0.54
2:B:453:SER:HA	2:B:456:LEU:HB2	1.90	0.54
3:C:161:ASP:OD1	3:C:199:LYS:HD3	2.07	0.54
3:C:179:ILE:HG13	3:C:181:PRO:CD	2.34	0.54
3:C:231:ASN:O	3:C:235:PRO:HD3	2.07	0.54
3:C:474:VAL:O	3:C:478:PHE:CD2	2.60	0.54
1:D:78:ILE:HD11	1:D:110:LEU:HD23	1.90	0.54
1:D:289:ILE:O	1:D:292:THR:HG22	2.07	0.54
1:D:305:THR:OG1	1:D:305:THR:O	2.24	0.54
4:E:74:ILE:C	4:E:76:LEU:H	2.14	0.54
4:E:88:ASP:CG	4:E:149:THR:HB	2.33	0.54
4:E:183:TRP:HB2	4:E:215:GLN:O	2.07	0.54
1:A:304:SER:HB2	1:A:400:LYS:HZ3	1.73	0.54
1:A:379:VAL:HA	1:A:382:ILE:CG1	2.38	0.54
2:B:9:SER:O	2:B:13:GLU:HG3	2.07	0.54
2:B:132:VAL:C	2:B:279:ILE:HG23	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:155:ALA:H	3:C:211:ASN:CB	2.21	0.54
3:C:264:LEU:HD22	3:C:310:LEU:HD21	1.89	0.54
3:C:438:ALA:O	3:C:442:GLU:HB2	2.08	0.54
1:D:16:ASN:C	1:D:17:LYS:HG3	2.32	0.54
1:D:40:LEU:HD22	1:D:52:THR:OG1	2.07	0.54
1:D:49:ILE:CG2	1:D:125:LYS:HE3	2.38	0.54
1:D:223:LEU:HD23	1:D:223:LEU:O	2.08	0.54
1:A:238:ASP:HB3	2:B:306:HIS:NE2	2.23	0.54
2:B:91:VAL:CG2	2:B:96:ASN:CB	2.86	0.54
3:C:106:TYR:C	3:C:106:TYR:CD1	2.86	0.54
3:C:154:ASN:CB	3:C:211:ASN:HB3	2.34	0.54
1:D:38:ILE:CA	1:D:169:THR:HG21	2.38	0.54
1:D:102:ILE:O	1:D:102:ILE:CG2	2.56	0.54
1:D:120:PRO:O	1:D:120:PRO:HG2	2.08	0.54
1:D:242:LYS:CA	1:D:243:MET:HE2	2.38	0.54
1:D:305:THR:CG2	1:D:400:LYS:CB	2.82	0.54
1:A:409:ILE:HA	1:A:412:CYS:HB2	1.89	0.53
2:B:54:VAL:C	2:B:55:PHE:HD1	2.16	0.53
2:B:75:ILE:CD1	2:B:78:LEU:CD1	2.74	0.53
2:B:152:ASP:OD1	2:B:203:SER:HB2	2.09	0.53
2:B:241:LEU:HB3	2:B:242:PRO:CD	2.37	0.53
3:C:252:GLU:HG3	1:D:300:HIS:O	2.08	0.53
3:C:482:PRO:HG2	3:C:483:ALA:H	1.72	0.53
1:D:135:PHE:CE1	1:D:273:LEU:HB2	2.42	0.53
1:A:45:GLU:OE1	1:A:271:VAL:HB	2.08	0.53
1:A:274:ILE:O	1:A:277:TYR:HB2	2.09	0.53
3:C:63:TYR:HD1	3:C:64:ASP:N	2.04	0.53
3:C:305:ASN:O	3:C:308:ILE:HG22	2.09	0.53
1:D:49:ILE:CG2	1:D:125:LYS:NZ	2.66	0.53
1:D:379:VAL:O	1:D:379:VAL:CG1	2.47	0.53
4:E:112:ASP:OD1	4:E:112:ASP:N	2.41	0.53
1:A:131:ILE:CD1	1:A:140:GLN:HG2	2.37	0.53
1:A:160:PRO:CG	1:A:185:LYS:HE2	2.38	0.53
1:A:252:SER:O	1:A:256:PHE:CD1	2.62	0.53
1:A:252:SER:OG	2:B:257:LEU:HD22	2.08	0.53
2:B:28:LYS:CB	2:B:156:VAL:CA	2.84	0.53
2:B:226:VAL:C	2:B:230:LEU:HG	2.33	0.53
3:C:80:LEU:O	3:C:112:VAL:HG23	2.09	0.53
1:D:46:VAL:CG2	1:D:270:ALA:C	2.82	0.53
1:D:282:MET:C	1:D:286:ILE:HD12	2.34	0.53
4:E:195:ASN:H	4:E:204:ASP:HB3	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:207:GLU:C	4:E:208:ILE:HG13	2.29	0.53
4:E:265:LEU:HD21	4:E:296:ILE:HD11	1.89	0.53
1:A:56:LEU:CD2	1:A:56:LEU:C	2.81	0.53
1:A:66:ARG:HA	1:A:113:THR:CA	2.37	0.53
1:A:107:LYS:HE3	2:B:150:THR:HB	1.90	0.53
1:A:135:PHE:CD1	1:A:273:LEU:HB2	2.43	0.53
1:A:201:ILE:CG2	1:A:203:TYR:CE1	2.91	0.53
1:A:242:LYS:HB2	1:A:245:LEU:HB3	1.89	0.53
1:A:406:ILE:HG22	1:A:409:ILE:CD1	2.38	0.53
2:B:56:LEU:CD1	2:B:103:THR:CG2	2.83	0.53
2:B:104:LEU:CD1	2:B:118:TRP:CZ3	2.87	0.53
1:D:112:TYR:HD1	1:D:113:THR:N	1.96	0.53
1:D:256:PHE:CZ	4:E:263:ILE:HG13	2.43	0.53
4:E:436:ASN:CA	4:E:439:TRP:HE1	2.15	0.53
1:A:20:ARG:HG2	1:A:20:ARG:NH1	2.01	0.53
1:A:92:LEU:HB3	1:A:95:ASN:ND2	2.23	0.53
1:A:186:HIS:CE1	1:A:187:TRP:O	2.61	0.53
1:A:382:ILE:O	1:A:386:MET:CE	2.56	0.53
1:A:416:LEU:C	1:A:419:ILE:HG22	2.32	0.53
1:D:32:THR:HB	1:D:59:GLN:CB	2.26	0.53
1:D:170:PHE:CE1	1:D:171:MET:O	2.61	0.53
1:D:301:ARG:NH2	1:D:406:ILE:CD1	2.71	0.53
4:E:88:ASP:O	4:E:88:ASP:OD1	2.26	0.53
1:A:31:ILE:HG12	1:A:60:TRP:HB3	1.90	0.53
1:A:66:ARG:HA	1:A:113:THR:HA	1.89	0.53
1:A:216:VAL:CG1	1:A:220:ILE:HD12	2.38	0.53
1:A:230:VAL:HG22	1:A:414:PHE:HZ	1.74	0.53
2:B:150:THR:O	2:B:150:THR:HG22	2.08	0.53
2:B:160:HIS:NE2	2:B:209:PHE:HE1	2.07	0.53
3:C:80:LEU:HD12	1:D:20:ARG:NH2	2.23	0.53
3:C:148:PHE:CB	3:C:215:VAL:HG22	2.34	0.53
3:C:192:ILE:HD13	3:C:221:ILE:CG2	2.38	0.53
3:C:215:VAL:HB	3:C:217:PHE:CE1	2.43	0.53
1:D:404:MET:HG3	1:D:405:VAL:HG23	1.91	0.53
4:E:222:ILE:HG23	4:E:223:ILE:H	1.73	0.53
1:A:260:ILE:O	1:A:264:ILE:HG23	2.08	0.53
2:B:28:LYS:CB	2:B:155:GLU:C	2.82	0.53
2:B:247:GLU:HA	2:B:249:MET:HG3	1.91	0.53
2:B:420:GLU:O	2:B:424:LEU:HG	2.09	0.53
2:B:439:PHE:O	2:B:439:PHE:CD1	2.62	0.53
3:C:194:HIS:ND1	3:C:195:LYS:N	2.54	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:253:LEU:CD2	1:D:254:THR:N	2.65	0.53
1:D:254:THR:CG2	1:D:255:VAL:N	2.71	0.53
1:D:282:MET:HE2	1:D:286:ILE:HD11	1.91	0.53
1:D:387:LYS:O	1:D:391:GLU:HG3	2.09	0.53
4:E:20:PRO:HG3	4:E:61:ASP:CB	2.39	0.53
4:E:143:LEU:HD12	4:E:210:PHE:O	2.08	0.53
4:E:447:ASP:O	4:E:450:CYS:HB2	2.08	0.53
1:A:265:PRO:CD	1:A:266:SER:H	2.21	0.53
1:A:396:ALA:O	1:A:399:TRP:HB2	2.09	0.53
2:B:242:PRO:HB2	2:B:243:PRO:HD3	1.91	0.53
2:B:297:LEU:CD1	2:B:445:THR:CG2	2.67	0.53
2:B:406:GLU:HG2	2:B:409:LYS:HD2	1.91	0.53
1:D:130:ILE:CA	1:D:134:HIS:HB2	2.38	0.53
4:E:27:VAL:HG12	4:E:153:HIS:O	2.08	0.53
4:E:418:ALA:HA	4:E:421:PHE:CD2	2.43	0.53
1:A:6:ARG:CB	1:A:6:ARG:HH11	2.22	0.53
2:B:46:LYS:CA	2:B:278:PRO:HD2	2.37	0.53
2:B:133:MET:SD	2:B:140:GLN:HB2	2.49	0.53
2:B:223:TYR:CD1	2:B:223:TYR:C	2.86	0.53
3:C:25:LYS:HA	3:C:25:LYS:NZ	2.23	0.53
3:C:155:ALA:N	3:C:211:ASN:CB	2.72	0.53
1:D:21:PRO:HB3	1:D:62:ASP:CG	2.34	0.53
1:D:35:LEU:CD1	1:D:54:VAL:HG12	2.39	0.53
1:D:289:ILE:CG2	1:D:290:ILE:N	2.72	0.53
4:E:116:TYR:HD1	4:E:117:TRP:N	2.07	0.53
4:E:253:LEU:HG	4:E:254:SER:N	2.23	0.53
4:E:471:LEU:O	4:E:471:LEU:HD12	2.09	0.53
1:A:46:VAL:HG21	1:A:269:SER:O	2.09	0.53
1:A:221:PRO:O	1:A:225:PHE:HB3	2.09	0.53
1:A:376:ILE:HG23	1:A:380:LYS:HZ3	1.73	0.53
1:A:388:SER:O	1:A:391:GLU:HB3	2.09	0.53
2:B:450:GLY:O	2:B:454:ILE:HG13	2.09	0.53
1:D:141:ASN:HB3	1:D:206:ILE:CG1	2.38	0.53
1:D:176:TRP:HE3	1:D:209:ARG:NE	2.06	0.53
1:A:72:TYR:CB	1:A:112:TYR:HB3	2.07	0.52
3:C:135:LEU:C	3:C:137:PHE:H	2.16	0.52
3:C:212:TYR:CD1	3:C:212:TYR:C	2.87	0.52
4:E:2:GLU:CA	4:E:5:ARG:HG3	2.38	0.52
4:E:131:VAL:HG22	4:E:281:LEU:HB3	1.90	0.52
1:A:3:HIS:HB2	1:A:7:LEU:HD23	1.88	0.52
1:A:35:LEU:C	1:A:35:LEU:CD2	2.81	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:ASP:C	1:A:168:SER:H	2.17	0.52
2:B:189:GLU:O	2:B:190:HIS:CG	2.62	0.52
1:D:305:THR:HG22	1:D:400:LYS:CG	2.40	0.52
4:E:59:TRP:CH2	4:E:115:MET:HB3	2.43	0.52
1:A:66:ARG:O	1:A:66:ARG:CG	2.57	0.52
1:A:87:LEU:CD2	1:A:87:LEU:N	2.66	0.52
1:A:140:GLN:O	1:A:207:MET:HE1	2.09	0.52
1:A:187:TRP:HD1	1:A:199:LEU:CD2	2.23	0.52
2:B:189:GLU:CG	2:B:468:PHE:HB2	2.38	0.52
2:B:308:SER:CB	2:B:311:THR:CG2	2.76	0.52
3:C:319:THR:CB	3:C:447:ASN:C	2.83	0.52
1:D:384:GLU:HG2	4:E:422:ILE:CD1	2.38	0.52
4:E:14:TYR:HE1	4:E:84:LEU:HD12	1.74	0.52
4:E:20:PRO:HG3	4:E:61:ASP:CG	2.34	0.52
4:E:462:THR:O	4:E:466:PHE:HB3	2.10	0.52
1:A:50:VAL:HG12	1:A:52:THR:HG23	1.89	0.52
1:A:176:TRP:CD2	1:A:209:ARG:NH1	2.77	0.52
2:B:112:HIS:C	2:B:114:GLY:H	2.16	0.52
2:B:241:LEU:HD12	2:B:241:LEU:O	2.09	0.52
2:B:279:ILE:HG22	2:B:280:ILE:N	2.24	0.52
3:C:113:ARG:HB3	3:C:114:PRO:HD2	1.92	0.52
1:D:72:TYR:HA	1:D:112:TYR:HB3	1.91	0.52
1:D:76:LYS:HD2	1:D:112:TYR:HE2	1.74	0.52
1:D:135:PHE:CZ	1:D:273:LEU:CB	2.92	0.52
4:E:75:ASP:HA	4:E:111:ASN:HD22	1.75	0.52
4:E:126:THR:O	4:E:126:THR:HG22	2.10	0.52
4:E:262:THR:HG23	4:E:265:LEU:CB	2.38	0.52
4:E:414:SER:HA	4:E:416:VAL:HG13	1.91	0.52
4:E:473:GLN:HA	4:E:476:GLU:HB2	1.91	0.52
1:A:46:VAL:HA	1:A:272:PRO:HD2	1.91	0.52
1:A:64:ARG:CA	1:A:66:ARG:HH11	2.16	0.52
1:A:166:ASP:CB	1:A:178:MET:HE1	2.40	0.52
3:C:86:LEU:C	3:C:87:ILE:HG12	2.34	0.52
3:C:160:MET:N	3:C:213:GLN:HG3	2.25	0.52
3:C:434:LYS:HG3	1:D:386:MET:HE1	1.86	0.52
1:D:3:HIS:HB3	1:D:7:LEU:CD2	2.39	0.52
1:D:75:ILE:CD1	1:D:78:ILE:HG22	2.39	0.52
1:D:166:ASP:CG	1:D:181:TYR:HB2	2.34	0.52
1:D:187:TRP:CD1	1:D:197:PRO:O	2.63	0.52
4:E:1:ASN:C	4:E:3:GLU:N	2.67	0.52
4:E:103:TYR:CD2	4:E:104:TYR:CD1	2.97	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:303:VAL:O	4:E:306:VAL:HB	2.09	0.52
1:A:77:LYS:HA	1:A:110:LEU:O	2.10	0.52
1:A:196:THR:HG22	1:A:196:THR:O	2.09	0.52
1:A:241:GLU:O	1:A:243:MET:HE1	2.08	0.52
1:A:278:MET:HE1	1:A:282:MET:HE1	1.90	0.52
1:A:306:HIS:NE2	1:A:401:TYR:HB2	2.25	0.52
2:B:233:ILE:O	2:B:237:LEU:HB2	2.09	0.52
2:B:276:SER:C	2:B:277:VAL:HG13	2.34	0.52
3:C:42:LEU:CG	3:C:54:THR:CG2	2.82	0.52
3:C:143:ASN:OD1	3:C:220:ILE:CB	2.56	0.52
3:C:222:ARG:NH2	3:C:224:LYS:CA	2.73	0.52
1:D:141:ASN:HB3	1:D:206:ILE:HD11	1.90	0.52
4:E:279:VAL:CG1	4:E:280:PRO:HD2	2.39	0.52
1:A:7:LEU:CD2	1:A:70:ALA:HA	2.39	0.52
2:B:37:LEU:CB	2:B:54:VAL:HG12	2.38	0.52
2:B:220:TYR:CB	2:B:223:TYR:CE2	2.93	0.52
3:C:137:PHE:O	3:C:137:PHE:CG	2.61	0.52
3:C:233:ILE:N	3:C:233:ILE:CD1	2.73	0.52
3:C:315:ARG:CD	3:C:315:ARG:N	2.72	0.52
3:C:431:LYS:NZ	1:D:382:ILE:HD12	2.25	0.52
3:C:431:LYS:HA	3:C:434:LYS:HB3	1.91	0.52
3:C:436:LYS:O	3:C:439:TYR:HB2	2.10	0.52
1:D:47:ASN:C	1:D:48:GLN:CG	2.83	0.52
1:D:381:TYR:CD1	4:E:419:CYS:SG	3.03	0.52
1:D:398:GLU:CA	1:D:401:TYR:CE1	2.92	0.52
4:E:279:VAL:CB	4:E:280:PRO:CD	2.76	0.52
4:E:310:THR:OG1	4:E:313:THR:HG23	2.09	0.52
1:A:40:LEU:HB2	1:A:171:MET:HB2	1.90	0.52
1:A:265:PRO:CG	1:A:266:SER:N	2.72	0.52
1:A:277:TYR:HA	1:A:280:PHE:CE1	2.43	0.52
2:B:10:VAL:O	2:B:13:GLU:HB2	2.09	0.52
3:C:150:ALA:CB	3:C:158:ILE:CD1	2.88	0.52
1:D:140:GLN:HG3	1:D:141:ASN:H	1.75	0.52
1:D:383:ALA:HA	1:D:386:MET:HG2	1.92	0.52
4:E:83:LEU:CD2	4:E:83:LEU:N	2.73	0.52
4:E:134:PHE:CB	4:E:282:ILE:HB	2.40	0.52
4:E:174:PRO:HA	4:E:177:PHE:CB	2.38	0.52
4:E:262:THR:HA	4:E:265:LEU:HB2	1.90	0.52
1:A:72:TYR:CD1	1:A:73:GLY:N	2.78	0.52
1:A:166:ASP:CG	1:A:178:MET:CE	2.83	0.52
1:A:186:HIS:CE1	1:A:188:VAL:HG22	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:LEU:HD13	1:A:296:ILE:HG21	1.86	0.52
2:B:109:LEU:HB3	2:B:117:SER:CB	2.40	0.52
2:B:261:VAL:HG12	2:B:262:PHE:HD1	1.74	0.52
3:C:94:LEU:N	3:C:94:LEU:HD23	2.25	0.52
3:C:155:ALA:H	3:C:211:ASN:HA	1.72	0.52
3:C:192:ILE:CD1	3:C:221:ILE:CG2	2.88	0.52
3:C:318:SER:CB	3:C:447:ASN:HD22	2.16	0.52
1:D:176:TRP:CG	1:D:209:ARG:HD2	2.45	0.52
1:D:416:LEU:HA	1:D:419:ILE:HG13	1.92	0.52
4:E:103:TYR:CD2	4:E:104:TYR:HD1	2.27	0.52
1:A:65:LEU:HB2	1:A:114:GLY:HA2	1.92	0.52
1:A:90:LEU:HD12	1:A:100:PHE:CE2	2.45	0.52
1:A:92:LEU:HB2	1:A:95:ASN:HB2	1.92	0.52
1:A:431:ILE:N	1:A:431:ILE:CD1	2.73	0.52
2:B:82:SER:O	2:B:83:ASP:HB3	2.08	0.52
4:E:182:GLU:C	4:E:218:PRO:HD2	2.34	0.52
4:E:261:GLN:HE21	4:E:265:LEU:CD1	2.23	0.52
1:A:175:GLU:C	1:A:211:PRO:HD3	2.35	0.51
2:B:108:VAL:HG22	2:B:118:TRP:HB2	1.92	0.51
2:B:248:LYS:HA	2:B:251:LEU:HD23	1.91	0.51
2:B:310:ASN:HD22	2:B:429:GLN:HG2	1.75	0.51
3:C:57:TRP:HA	3:C:122:PRO:O	2.10	0.51
3:C:121:LEU:O	3:C:121:LEU:CD1	2.53	0.51
3:C:296:MET:HA	3:C:296:MET:HE3	1.83	0.51
1:D:227:PHE:C	1:D:227:PHE:HD1	2.18	0.51
1:D:253:LEU:CD2	1:D:254:THR:H	2.19	0.51
4:E:237:VAL:HG22	4:E:457:LEU:HD22	1.92	0.51
1:A:35:LEU:CD1	1:A:203:TYR:OH	2.58	0.51
1:A:257:LEU:HD13	1:A:285:VAL:HG22	1.78	0.51
2:B:211:LEU:N	2:B:211:LEU:HD23	2.26	0.51
2:B:258:ALA:HB2	3:C:265:LEU:HD13	1.91	0.51
2:B:281:ILE:H	2:B:281:ILE:HD12	1.74	0.51
3:C:38:THR:CG2	3:C:57:TRP:CZ3	2.93	0.51
3:C:253:SER:CB	1:D:306:HIS:CB	2.86	0.51
1:D:287:SER:O	1:D:290:ILE:HG12	2.10	0.51
4:E:26:HIS:O	4:E:27:VAL:HG22	2.09	0.51
4:E:34:LEU:HA	4:E:54:TRP:O	2.09	0.51
1:A:50:VAL:CG1	1:A:51:GLU:N	2.74	0.51
1:A:165:PRO:O	1:A:181:TYR:CD1	2.63	0.51
1:A:255:VAL:CG1	1:A:256:PHE:N	2.73	0.51
2:B:48:GLU:CA	2:B:130:ILE:HD11	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:238:VAL:CG2	2:B:255:ALA:HB1	2.41	0.51
2:B:287:ILE:C	2:B:287:ILE:CD1	2.76	0.51
3:C:106:TYR:CE1	3:C:107:PHE:HE1	2.27	0.51
3:C:191:GLU:HG3	3:C:222:ARG:HB3	1.92	0.51
1:D:63:VAL:HG13	1:D:64:ARG:H	1.76	0.51
1:D:241:GLU:C	1:D:243:MET:CE	2.83	0.51
4:E:91:LEU:H	4:E:95:VAL:HG23	1.75	0.51
1:A:107:LYS:HE3	2:B:150:THR:CG2	2.40	0.51
1:A:166:ASP:N	1:A:181:TYR:CD1	2.78	0.51
1:A:171:MET:HE3	1:A:176:TRP:HZ2	1.70	0.51
2:B:91:VAL:HG12	2:B:147:LYS:O	2.11	0.51
2:B:103:THR:OG1	2:B:122:ALA:CB	2.58	0.51
2:B:162:LEU:C	2:B:174:MET:N	2.68	0.51
3:C:43:ILE:HD12	3:C:43:ILE:N	2.21	0.51
3:C:50:GLU:HB3	3:C:132:ILE:HD13	1.93	0.51
1:D:46:VAL:HA	1:D:271:VAL:HA	1.93	0.51
1:D:106:THR:CG2	1:D:107:LYS:N	2.74	0.51
1:D:152:ASP:HA	1:D:197:PRO:CA	2.39	0.51
4:E:9:LYS:HD2	4:E:9:LYS:C	2.35	0.51
4:E:123:TYR:N	4:E:123:TYR:CD1	2.76	0.51
1:A:4:GLU:HA	1:A:7:LEU:HD12	1.91	0.51
1:A:39:GLN:C	1:A:40:LEU:HD23	2.35	0.51
1:A:187:TRP:CD1	1:A:199:LEU:HD23	2.45	0.51
2:B:271:PRO:O	2:B:275:LEU:HD13	2.10	0.51
3:C:241:PHE:CA	3:C:244:ALA:HB3	2.38	0.51
1:D:33:VAL:HA	1:D:57:ARG:O	2.10	0.51
1:D:392:SER:O	1:D:395:ALA:HB3	2.11	0.51
4:E:172:ILE:CD1	4:E:187:HIS:C	2.79	0.51
1:A:36:GLN:OE1	1:A:36:GLN:O	2.27	0.51
1:A:175:GLU:HB3	1:A:211:PRO:CB	2.37	0.51
1:A:231:LEU:C	1:A:233:PHE:N	2.69	0.51
2:B:92:LEU:HD22	2:B:146:PHE:HA	1.93	0.51
2:B:221:ILE:C	2:B:224:THR:HB	2.35	0.51
3:C:110:VAL:HG13	3:C:120:TRP:CA	2.41	0.51
1:D:36:GLN:NE2	1:D:38:ILE:CG1	2.74	0.51
1:D:38:ILE:HA	1:D:169:THR:HG21	1.92	0.51
1:D:140:GLN:HG3	1:D:141:ASN:N	2.26	0.51
1:D:419:ILE:CD1	1:D:420:ILE:HG23	2.41	0.51
4:E:191:LYS:H	4:E:209:ILE:CG2	2.24	0.51
2:B:94:ASN:HB3	2:B:95:ASN:OD1	2.11	0.51
2:B:108:VAL:HG13	2:B:117:SER:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:190:TRP:HB2	3:C:222:ARG:O	2.11	0.51
1:D:37:LEU:HD13	1:D:54:VAL:HG22	1.91	0.51
1:D:46:VAL:HG21	1:D:270:ALA:C	2.36	0.51
1:D:57:ARG:NH2	1:D:117:MET:HE1	2.26	0.51
1:D:176:TRP:CD2	1:D:209:ARG:HD2	2.45	0.51
1:D:398:GLU:OE2	1:D:399:TRP:CZ3	2.63	0.51
4:E:14:TYR:CE1	4:E:84:LEU:HD12	2.46	0.51
4:E:33:LYS:CE	4:E:160:SER:HB3	2.41	0.51
4:E:38:ASN:O	4:E:51:THR:HG23	2.11	0.51
4:E:240:TYR:HD2	4:E:453:ILE:HD13	1.59	0.51
1:A:77:LYS:HB2	1:A:110:LEU:O	2.11	0.51
1:A:111:ASP:C	1:A:113:THR:N	2.68	0.51
1:A:176:TRP:CE3	1:A:209:ARG:NH1	2.79	0.51
2:B:2:VAL:CG1	2:B:69:PRO:CG	2.86	0.51
2:B:91:VAL:CG2	2:B:96:ASN:HB3	2.41	0.51
2:B:438:LEU:O	2:B:442:ILE:CD1	2.58	0.51
3:C:30:VAL:HG13	3:C:31:VAL:N	2.26	0.51
3:C:47:GLU:OE1	3:C:285:VAL:CG2	2.58	0.51
3:C:63:TYR:CD1	3:C:116:GLY:HA3	2.45	0.51
3:C:300:THR:HG22	3:C:300:THR:O	2.10	0.51
1:D:66:ARG:O	1:D:67:TRP:CE3	2.64	0.51
1:D:220:ILE:HG21	4:E:294:LEU:HD13	1.92	0.51
1:D:407:ASP:OD1	1:D:408:HIS:CD2	2.63	0.51
4:E:123:TYR:N	4:E:123:TYR:HD1	2.09	0.51
4:E:133:TYR:CE1	4:E:139:GLN:N	2.79	0.51
4:E:185:ILE:HG12	4:E:214:ILE:HG21	1.88	0.51
4:E:269:ALA:O	4:E:273:PRO:HD3	2.11	0.51
1:A:67:TRP:CD1	1:A:71:ASP:OD1	2.64	0.51
1:A:92:LEU:HB3	1:A:95:ASN:HD22	1.76	0.51
1:A:107:LYS:O	1:A:108:LEU:CD2	2.59	0.51
1:A:108:LEU:CD2	1:A:118:TRP:CD1	2.94	0.51
1:A:117:MET:HG3	1:A:119:THR:HG23	1.93	0.51
1:A:229:THR:HA	1:A:232:VAL:HB	1.91	0.51
1:A:280:PHE:HB3	1:A:284:PHE:CE2	2.46	0.51
1:A:381:TYR:O	1:A:385:HIS:HB2	2.11	0.51
1:A:431:ILE:N	1:A:431:ILE:HD12	2.26	0.51
2:B:274:SER:HB2	2:B:278:PRO:HB3	1.93	0.51
3:C:150:ALA:HB3	3:C:158:ILE:HD12	1.93	0.51
3:C:190:TRP:CD1	3:C:221:ILE:CD1	2.84	0.51
3:C:219:LEU:HG	3:C:221:ILE:CG2	2.41	0.51
4:E:270:GLN:O	4:E:273:PRO:CG	2.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:289:VAL:HG12	4:E:290:MET:N	2.25	0.51
1:A:129:GLU:CD	1:A:140:GLN:CG	2.84	0.51
1:A:243:MET:HE2	1:A:244:THR:HG22	1.93	0.51
2:B:91:VAL:CG1	2:B:149:TYR:CD1	2.85	0.51
3:C:48:THR:CA	3:C:285:VAL:HA	2.40	0.51
3:C:114:PRO:O	3:C:115:ASN:HB3	2.10	0.51
3:C:271:LEU:HD11	3:C:303:VAL:HG22	1.93	0.51
4:E:71:TYR:HA	4:E:111:ASN:HB2	1.92	0.51
1:A:47:ASN:C	1:A:48:GLN:HG2	2.34	0.50
1:A:51:GLU:HA	1:A:124:PHE:O	2.11	0.50
1:A:93:TYR:N	1:A:93:TYR:HD1	2.08	0.50
1:A:305:THR:O	1:A:306:HIS:CB	2.59	0.50
2:B:137:PHE:H	2:B:137:PHE:HD1	1.57	0.50
2:B:144:MET:CE	2:B:211:LEU:HD21	2.41	0.50
2:B:153:THR:HB	2:B:204:TYR:CB	2.13	0.50
3:C:307:GLY:O	3:C:310:LEU:HB2	2.11	0.50
1:D:137:PHE:HB2	1:D:431:ILE:CG2	2.41	0.50
1:D:420:ILE:HA	1:D:423:VAL:HB	1.93	0.50
4:E:250:LYS:CA	4:E:253:LEU:HB3	2.35	0.50
4:E:313:THR:O	4:E:314:HIS:CG	2.64	0.50
1:A:239:SER:CB	2:B:312:HIS:CB	2.82	0.50
2:B:92:LEU:N	2:B:92:LEU:HD23	2.19	0.50
2:B:137:PHE:CD1	2:B:137:PHE:N	2.75	0.50
2:B:283:TYR:CD1	2:B:283:TYR:N	2.79	0.50
2:B:424:LEU:HB3	2:B:428:TRP:CZ2	2.47	0.50
2:B:424:LEU:O	2:B:427:ASP:HB3	2.11	0.50
3:C:16:LYS:CE	3:C:16:LYS:CA	2.89	0.50
3:C:56:VAL:HG23	3:C:124:ALA:HB3	1.93	0.50
1:D:241:GLU:O	1:D:243:MET:CE	2.59	0.50
1:D:409:ILE:HA	1:D:412:CYS:CB	2.38	0.50
4:E:35:THR:HB	4:E:54:TRP:CE3	2.42	0.50
4:E:55:ILE:O	4:E:118:LEU:HB2	2.09	0.50
4:E:138:TRP:CH2	4:E:215:GLN:CB	2.95	0.50
4:E:474:VAL:HG12	4:E:475:PRO:CD	2.40	0.50
1:A:149:TRP:CH2	4:E:119:PRO:HA	2.46	0.50
1:A:250:LEU:HD23	1:A:292:THR:HG22	1.85	0.50
2:B:69:PRO:HG2	2:B:70:ALA:N	2.27	0.50
2:B:185:GLN:O	2:B:217:PRO:CB	2.59	0.50
2:B:230:LEU:HA	2:B:233:ILE:CG1	2.38	0.50
3:C:68:THR:HA	3:C:115:ASN:CA	2.42	0.50
3:C:89:ILE:CD1	3:C:107:PHE:HB3	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:200:ASN:ND2	3:C:201:ILE:H	2.10	0.50
3:C:271:LEU:C	3:C:271:LEU:CD2	2.84	0.50
1:D:175:GLU:OE1	1:D:211:PRO:CB	2.57	0.50
4:E:70:GLU:OE1	4:E:70:GLU:HA	2.12	0.50
1:A:110:LEU:HD11	1:A:114:GLY:HA2	1.92	0.50
1:A:130:ILE:HD13	1:A:130:ILE:H	1.76	0.50
2:B:3:MET:O	2:B:6:THR:HB	2.12	0.50
2:B:50:MET:HB3	2:B:126:SER:OG	2.11	0.50
2:B:101:GLU:CD	2:B:123:ILE:HG22	2.36	0.50
2:B:132:VAL:HG12	2:B:279:ILE:HA	1.88	0.50
2:B:297:LEU:HD11	2:B:445:THR:CG2	2.25	0.50
3:C:37:LEU:HD21	3:C:148:PHE:CD2	2.47	0.50
3:C:201:ILE:HG12	3:C:202:TYR:N	2.25	0.50
3:C:205:LYS:HD3	3:C:205:LYS:H	1.76	0.50
3:C:462:THR:O	3:C:466:VAL:HG23	2.12	0.50
1:D:281:THR:O	1:D:285:VAL:HB	2.11	0.50
4:E:91:LEU:CB	4:E:95:VAL:H	2.21	0.50
4:E:435:GLU:HB3	4:E:439:TRP:CH2	2.46	0.50
1:A:38:ILE:O	1:A:169:THR:HB	2.12	0.50
1:A:229:THR:O	1:A:233:PHE:CD1	2.64	0.50
2:B:160:HIS:CE1	2:B:207:VAL:CG1	2.71	0.50
3:C:283:LEU:C	3:C:285:VAL:H	2.20	0.50
3:C:296:MET:HE2	3:C:296:MET:CA	2.17	0.50
1:D:242:LYS:HB2	1:D:245:LEU:HD12	1.94	0.50
4:E:304:LEU:C	4:E:306:VAL:H	2.19	0.50
1:A:26:THR:O	1:A:28:PHE:CD1	2.65	0.50
1:A:107:LYS:HE3	2:B:150:THR:CB	2.42	0.50
2:B:249:MET:HE2	2:B:250:SER:N	2.26	0.50
3:C:68:THR:N	3:C:116:GLY:H	2.10	0.50
3:C:115:ASN:HD22	3:C:115:ASN:H	1.54	0.50
1:D:130:ILE:C	1:D:131:ILE:HG12	2.36	0.50
1:D:174:GLY:C	1:D:176:TRP:N	2.67	0.50
1:D:257:LEU:HA	1:D:260:ILE:HB	1.93	0.50
1:A:107:LYS:NZ	2:B:151:TYR:CG	2.80	0.50
1:A:110:LEU:HD13	1:A:114:GLY:O	2.11	0.50
2:B:175:ILE:HG23	2:B:178:ASP:H	1.77	0.50
1:D:137:PHE:HB2	1:D:431:ILE:HG22	1.92	0.50
1:D:174:GLY:C	1:D:176:TRP:H	2.20	0.50
1:D:242:LYS:HB2	1:D:245:LEU:CB	2.41	0.50
4:E:91:LEU:HA	4:E:145:PHE:HA	1.93	0.50
1:A:50:VAL:HG12	1:A:52:THR:CG2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:LEU:HD21	1:A:296:ILE:CD1	2.42	0.50
2:B:242:PRO:HD3	2:B:248:LYS:CE	2.38	0.50
1:D:85:VAL:HG13	1:D:86:TRP:N	2.26	0.50
1:D:85:VAL:CG1	1:D:86:TRP:N	2.73	0.50
1:D:135:PHE:CE1	1:D:277:TYR:CE2	2.98	0.50
1:A:397:GLU:HA	1:A:400:LYS:CD	2.35	0.50
2:B:135:PHE:N	2:B:136:PRO:HD2	2.26	0.50
3:C:110:VAL:HG12	3:C:111:LEU:H	1.77	0.50
3:C:241:PHE:CE1	3:C:245:LEU:HD22	2.47	0.50
1:D:61:ILE:HA	1:D:116:ILE:HD11	1.93	0.50
1:D:76:LYS:HA	1:D:112:TYR:HD2	1.77	0.50
1:D:91:VAL:CG2	1:D:96:ALA:HB2	2.19	0.50
1:D:186:HIS:CG	1:D:187:TRP:N	2.79	0.50
1:D:198:TYR:HD1	1:D:198:TYR:H	0.65	0.50
1:D:212:LEU:O	1:D:215:VAL:HB	2.12	0.50
1:D:253:LEU:HD23	1:D:254:THR:HB	1.94	0.50
1:D:376:ILE:HG22	1:D:380:LYS:HZ3	1.75	0.50
1:A:24:HIS:CD2	1:A:24:HIS:N	2.78	0.49
1:A:267:THR:O	1:A:271:VAL:HG22	2.12	0.49
3:C:222:ARG:HH21	3:C:223:ARG:C	2.20	0.49
3:C:300:THR:O	3:C:300:THR:CG2	2.60	0.49
3:C:308:ILE:CG2	3:C:309:VAL:N	2.75	0.49
3:C:315:ARG:N	3:C:315:ARG:HD3	2.27	0.49
3:C:465:MET:HE2	3:C:466:VAL:HA	1.94	0.49
1:D:60:TRP:CE2	1:D:86:TRP:HH2	2.28	0.49
1:D:242:LYS:HB2	1:D:245:LEU:CD1	2.42	0.49
4:E:146:ARG:CD	4:E:205:PHE:CD2	2.95	0.49
2:B:152:ASP:OD1	2:B:203:SER:CB	2.61	0.49
2:B:197:TRP:HB3	2:B:204:TYR:HD1	1.75	0.49
2:B:218:LEU:HD13	2:B:221:ILE:HD11	1.93	0.49
2:B:438:LEU:HD23	2:B:441:TYR:CB	2.42	0.49
3:C:93:VAL:HG21	3:C:151:LEU:HD22	1.95	0.49
3:C:210:THR:CG2	3:C:211:ASN:H	2.19	0.49
3:C:262:CYS:SG	1:D:251:LEU:CD1	3.00	0.49
1:D:46:VAL:HB	1:D:271:VAL:N	2.26	0.49
1:D:53:ASN:HD22	1:D:123:ILE:CG1	2.25	0.49
4:E:44:GLU:CG	4:E:129:ILE:CD1	2.90	0.49
4:E:452:TRP:HA	4:E:452:TRP:HE3	1.76	0.49
4:E:455:LEU:HD12	4:E:455:LEU:O	2.12	0.49
1:A:170:PHE:CE1	1:A:176:TRP:CD1	3.00	0.49
1:A:410:LEU:HD13	1:A:410:LEU:C	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:96:ASN:C	2:B:98:GLY:H	2.20	0.49
3:C:35:LEU:HD12	3:C:92:ILE:HG21	1.93	0.49
3:C:77:ILE:C	3:C:79:ILE:H	2.20	0.49
3:C:226:LEU:H	3:C:227:PHE:HD1	1.60	0.49
1:D:236:PRO:HA	1:D:240:GLY:HA2	1.94	0.49
4:E:71:TYR:HA	4:E:111:ASN:CB	2.42	0.49
4:E:133:TYR:CD1	4:E:139:GLN:HB3	2.47	0.49
4:E:310:THR:CB	4:E:313:THR:CG2	2.90	0.49
1:A:92:LEU:HB3	1:A:95:ASN:HB2	1.93	0.49
1:A:287:SER:HA	1:A:290:ILE:HG13	1.93	0.49
2:B:52:THR:HG22	2:B:53:SER:N	2.20	0.49
2:B:54:VAL:O	2:B:121:SER:HA	2.11	0.49
3:C:316:THR:CG2	3:C:447:ASN:CG	2.86	0.49
1:D:134:HIS:C	1:D:134:HIS:ND1	2.71	0.49
4:E:212:LEU:O	4:E:214:ILE:HG23	2.12	0.49
4:E:270:GLN:C	4:E:273:PRO:CG	2.86	0.49
1:A:130:ILE:CD1	1:A:131:ILE:N	2.65	0.49
1:A:376:ILE:O	1:A:380:LYS:HE2	2.13	0.49
1:A:395:ALA:O	1:A:399:TRP:CG	2.65	0.49
2:B:29:VAL:O	2:B:156:VAL:HG12	2.11	0.49
2:B:90:ILE:HA	2:B:148:SER:HA	1.94	0.49
2:B:446:MET:HA	2:B:449:ILE:HG12	1.95	0.49
3:C:6:ARG:O	3:C:9:ASN:HB3	2.11	0.49
3:C:56:VAL:CG1	3:C:126:PHE:CE2	2.93	0.49
3:C:84:PRO:HB2	3:C:107:PHE:HB2	1.94	0.49
3:C:116:GLY:O	3:C:118:VAL:HG23	2.12	0.49
3:C:180:ASP:HB3	3:C:181:PRO:CD	2.37	0.49
3:C:266:ALA:CB	1:D:251:LEU:HD13	2.42	0.49
3:C:278:LEU:N	3:C:279:PRO:HD2	2.28	0.49
3:C:316:THR:CG2	3:C:447:ASN:CB	2.87	0.49
1:D:246:SER:O	1:D:250:LEU:HD12	2.12	0.49
1:D:435:GLN:C	1:D:437:GLY:N	2.70	0.49
4:E:66:TRP:HD1	4:E:111:ASN:CB	2.18	0.49
4:E:227:ALA:N	4:E:228:PRO:HD2	2.27	0.49
4:E:456:LEU:C	4:E:456:LEU:HD13	2.38	0.49
1:A:2:GLU:CG	1:A:74:GLY:HA2	2.42	0.49
2:B:20:ARG:HG3	2:B:155:GLU:OE1	2.12	0.49
2:B:37:LEU:HD12	2:B:54:VAL:HG11	1.95	0.49
2:B:438:LEU:HD22	2:B:441:TYR:CD2	2.47	0.49
3:C:77:ILE:HD11	3:C:80:LEU:HD13	1.94	0.49
3:C:223:ARG:HG2	3:C:224:LYS:H	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:LEU:CD2	1:A:242:LYS:HE3	2.35	0.49
1:A:431:ILE:O	1:A:431:ILE:CG2	2.60	0.49
2:B:32:ARG:NH2	2:B:60:TRP:C	2.71	0.49
2:B:46:LYS:HD2	2:B:275:LEU:C	2.38	0.49
3:C:106:TYR:CD1	3:C:107:PHE:HD1	2.31	0.49
3:C:223:ARG:CG	3:C:224:LYS:N	2.73	0.49
3:C:241:PHE:O	3:C:245:LEU:HB2	2.13	0.49
1:D:211:PRO:HB2	1:D:213:TYR:CD2	2.46	0.49
1:D:212:LEU:O	1:D:216:VAL:HG22	2.12	0.49
1:D:256:PHE:CZ	4:E:263:ILE:HG12	2.47	0.49
1:D:282:MET:HA	1:D:282:MET:HE3	1.94	0.49
1:D:377:GLU:N	1:D:380:LYS:HE2	2.26	0.49
4:E:55:ILE:HG23	4:E:119:PRO:HG2	1.95	0.49
4:E:173:ASP:CG	4:E:185:ILE:CD1	2.76	0.49
1:A:15:TYR:HE2	1:A:84:ASP:OD2	1.95	0.49
1:A:87:LEU:HD22	1:A:87:LEU:N	2.02	0.49
1:A:174:GLY:HA2	1:A:176:TRP:CE3	2.48	0.49
1:A:290:ILE:O	1:A:293:VAL:HG12	2.13	0.49
2:B:35:LEU:C	2:B:174:MET:HE1	2.37	0.49
2:B:139:TRP:O	2:B:140:GLN:HG2	2.12	0.49
3:C:77:ILE:O	3:C:77:ILE:CG1	2.59	0.49
3:C:234:THR:N	3:C:235:PRO:CD	2.75	0.49
3:C:464:VAL:HG13	3:C:465:MET:N	2.26	0.49
1:D:201:ILE:CG2	1:D:203:TYR:CE1	2.92	0.49
1:D:233:PHE:CE2	1:D:291:VAL:CG1	2.94	0.49
4:E:146:ARG:NE	4:E:205:PHE:HD2	2.10	0.49
4:E:191:LYS:CE	4:E:211:PHE:CZ	2.95	0.49
1:A:132:VAL:O	1:A:274:ILE:CA	2.61	0.49
1:A:207:MET:O	1:A:207:MET:HE2	2.13	0.49
1:A:385:HIS:ND1	1:A:385:HIS:O	2.46	0.49
1:A:393:SER:O	1:A:396:ALA:HB3	2.13	0.49
2:B:10:VAL:HG12	2:B:11:LEU:CD2	2.42	0.49
2:B:97:ASP:OD2	2:B:127:SER:HB2	2.13	0.49
2:B:218:LEU:HD13	2:B:221:ILE:CD1	2.42	0.49
1:D:175:GLU:OE1	1:D:175:GLU:HA	2.12	0.49
1:D:175:GLU:O	1:D:209:ARG:HG3	2.13	0.49
1:A:7:LEU:O	1:A:11:LEU:HG	2.12	0.49
1:A:166:ASP:CG	1:A:178:MET:HE2	2.38	0.49
1:A:295:VAL:O	1:A:299:HIS:HB2	2.12	0.49
2:B:132:VAL:HG12	2:B:279:ILE:CA	2.41	0.49
3:C:1:VAL:O	3:C:1:VAL:CG1	2.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:7:LEU:O	3:C:10:ASP:HB2	2.13	0.49
3:C:191:GLU:HG3	3:C:191:GLU:O	2.11	0.49
1:D:301:ARG:NH1	1:D:406:ILE:HD11	2.17	0.49
4:E:269:ALA:O	4:E:273:PRO:HG3	2.13	0.49
1:A:52:THR:O	1:A:123:ILE:CG1	2.60	0.48
1:A:186:HIS:ND1	1:A:187:TRP:N	2.60	0.48
1:A:265:PRO:O	1:A:268:SER:HB3	2.13	0.48
2:B:247:GLU:CA	2:B:249:MET:HG3	2.43	0.48
2:B:255:ALA:O	2:B:258:ALA:HB3	2.13	0.48
3:C:82:LEU:HG	3:C:86:LEU:HB2	1.94	0.48
3:C:109:ASN:OD1	3:C:109:ASN:C	2.56	0.48
3:C:179:ILE:CD1	3:C:195:LYS:HB3	2.42	0.48
3:C:266:ALA:HB2	1:D:251:LEU:HD13	1.95	0.48
3:C:429:ILE:HG13	3:C:430:VAL:HG22	1.95	0.48
3:C:464:VAL:CG1	3:C:465:MET:N	2.75	0.48
1:D:46:VAL:CA	1:D:271:VAL:HA	2.42	0.48
1:D:49:ILE:HG23	1:D:125:LYS:HE3	1.95	0.48
4:E:30:VAL:O	4:E:158:GLN:CG	2.60	0.48
4:E:59:TRP:HH2	4:E:107:VAL:HG12	1.76	0.48
4:E:138:TRP:CH2	4:E:215:GLN:HB2	2.45	0.48
4:E:172:ILE:HG23	4:E:174:PRO:HD2	1.94	0.48
4:E:236:VAL:C	4:E:239:VAL:HG23	2.37	0.48
1:A:6:ARG:NH1	1:A:6:ARG:HB2	2.28	0.48
1:A:100:PHE:HB3	1:A:103:VAL:CG2	2.43	0.48
1:A:148:ILE:O	1:A:198:TYR:HD2	1.96	0.48
1:A:285:VAL:O	1:A:288:SER:HB3	2.13	0.48
1:A:295:VAL:HB	1:A:296:ILE:HD13	1.94	0.48
2:B:274:SER:O	2:B:278:PRO:HB3	2.12	0.48
2:B:299:VAL:O	2:B:299:VAL:CG1	2.60	0.48
3:C:3:GLU:O	3:C:3:GLU:CG	2.60	0.48
3:C:63:TYR:HB2	3:C:117:TYR:CE1	2.48	0.48
3:C:68:THR:CG2	3:C:69:TRP:N	2.75	0.48
3:C:233:ILE:C	3:C:235:PRO:HD2	2.38	0.48
3:C:431:LYS:HE2	1:D:382:ILE:HG13	1.95	0.48
3:C:452:THR:CA	3:C:455:ARG:HD3	2.41	0.48
1:D:157:SER:CA	1:D:199:LEU:HD12	2.40	0.48
1:D:233:PHE:CZ	1:D:417:ILE:HD11	2.47	0.48
1:D:237:THR:HG1	1:D:406:ILE:HG23	1.78	0.48
4:E:19:LYS:HZ1	4:E:154:GLU:HB3	1.76	0.48
4:E:217:LYS:N	4:E:218:PRO:CD	2.76	0.48
1:A:242:LYS:HD2	1:A:245:LEU:HD23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:HIS:O	1:A:306:HIS:HD2	1.90	0.48
2:B:409:LYS:CE	3:C:423:ILE:HG23	2.42	0.48
3:C:38:THR:OG1	3:C:178:ILE:HD13	2.13	0.48
3:C:139:PHE:O	3:C:222:ARG:HG2	2.12	0.48
4:E:29:ASP:N	4:E:29:ASP:OD1	2.45	0.48
4:E:138:TRP:HB2	4:E:213:ILE:HG13	1.90	0.48
4:E:161:ALA:HA	4:E:163:GLU:OE2	2.13	0.48
1:A:72:TYR:HD1	1:A:72:TYR:O	1.96	0.48
1:A:179:LYS:HE2	1:A:208:GLN:OE1	2.12	0.48
1:A:235:LEU:HD21	1:A:242:LYS:CE	2.34	0.48
1:A:305:THR:CB	1:A:400:LYS:HB2	2.40	0.48
2:B:184:GLY:C	2:B:186:TRP:H	2.21	0.48
2:B:218:LEU:C	2:B:219:PHE:CG	2.91	0.48
2:B:220:TYR:CD2	2:B:223:TYR:HE2	2.31	0.48
3:C:67:LEU:CD1	3:C:116:GLY:HA2	2.42	0.48
3:C:81:ARG:HA	3:C:112:VAL:HG23	1.94	0.48
1:D:274:ILE:HG22	1:D:276:LYS:HZ3	1.77	0.48
4:E:27:VAL:CG1	4:E:153:HIS:C	2.84	0.48
4:E:85:TRP:O	4:E:86:LEU:HD23	2.14	0.48
4:E:288:PHE:O	4:E:292:VAL:HG23	2.14	0.48
4:E:313:THR:C	4:E:314:HIS:CG	2.91	0.48
1:A:59:GLN:HE22	1:A:117:MET:HG3	1.76	0.48
1:A:156:VAL:HG22	1:A:157:SER:H	1.71	0.48
1:A:167:LEU:CD1	1:A:178:MET:HB2	2.41	0.48
1:A:230:VAL:HG22	1:A:414:PHE:CZ	2.48	0.48
2:B:279:ILE:CG2	2:B:280:ILE:N	2.76	0.48
3:C:67:LEU:C	3:C:116:GLY:N	2.67	0.48
3:C:319:THR:N	3:C:447:ASN:HB2	2.27	0.48
1:D:76:LYS:HD2	1:D:112:TYR:CE2	2.48	0.48
1:D:106:THR:CG2	1:D:107:LYS:HE2	2.43	0.48
1:D:132:VAL:HB	1:D:274:ILE:CG2	2.43	0.48
1:D:225:PHE:HD1	1:D:226:SER:N	2.11	0.48
1:D:276:LYS:HD2	1:D:276:LYS:N	2.20	0.48
1:D:419:ILE:HD12	1:D:420:ILE:HG23	1.96	0.48
4:E:33:LYS:CD	4:E:160:SER:HB3	2.43	0.48
4:E:214:ILE:C	4:E:214:ILE:CD1	2.77	0.48
1:A:250:LEU:HD21	1:A:296:ILE:HD12	1.95	0.48
1:A:380:LYS:HD3	2:B:408:ILE:HG21	1.95	0.48
3:C:106:TYR:O	3:C:106:TYR:CD1	2.54	0.48
3:C:281:THR:O	3:C:284:ALA:HB3	2.14	0.48
3:C:445:ASN:HA	3:C:448:LEU:CG	2.16	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:110:LEU:HA	1:D:116:ILE:HG22	1.95	0.48
1:D:166:ASP:OD2	1:D:181:TYR:CB	2.61	0.48
1:D:176:TRP:CE3	1:D:209:ARG:CD	2.96	0.48
1:D:225:PHE:HD1	1:D:225:PHE:C	2.21	0.48
4:E:216:ARG:C	4:E:218:PRO:CD	2.86	0.48
4:E:223:ILE:HG12	4:E:226:ILE:HD12	1.96	0.48
1:A:3:HIS:O	1:A:7:LEU:HG	2.13	0.48
1:A:218:VAL:CG1	1:A:219:ILE:H	2.26	0.48
1:A:301:ARG:HH11	1:A:301:ARG:HG2	1.77	0.48
2:B:92:LEU:HB2	2:B:95:ASN:HB2	1.95	0.48
3:C:26:HIS:HE1	3:C:66:ARG:HH22	1.58	0.48
3:C:148:PHE:CD1	3:C:148:PHE:N	2.82	0.48
3:C:315:ARG:H	3:C:315:ARG:HD2	1.79	0.48
1:D:64:ARG:HH11	1:D:64:ARG:CG	2.22	0.48
1:D:419:ILE:HD12	1:D:420:ILE:CG2	2.43	0.48
4:E:182:GLU:HA	4:E:218:PRO:HG2	1.96	0.48
1:A:1:SER:HA	1:A:4:GLU:HB2	1.94	0.48
1:A:120:PRO:HA	1:A:121:PRO:HD3	1.65	0.48
1:A:171:MET:HG2	1:A:173:SER:H	1.79	0.48
1:A:264:ILE:N	1:A:265:PRO:CD	2.77	0.48
2:B:269:LYS:CG	2:B:270:VAL:N	2.77	0.48
2:B:431:VAL:O	2:B:432:ALA:HB3	2.13	0.48
2:B:438:LEU:O	2:B:442:ILE:HB	2.14	0.48
3:C:39:LEU:HD12	3:C:39:LEU:N	2.28	0.48
3:C:53:THR:HA	3:C:126:PHE:O	2.13	0.48
3:C:216:THR:O	3:C:217:PHE:CD1	2.64	0.48
3:C:474:VAL:HA	3:C:477:ASN:OD1	2.14	0.48
1:D:105:MET:HG2	1:D:105:MET:O	2.14	0.48
4:E:272:VAL:O	4:E:272:VAL:HG22	2.13	0.48
4:E:302:ILE:O	4:E:305:ASN:HB3	2.14	0.48
4:E:450:CYS:O	4:E:453:ILE:HG13	2.13	0.48
1:A:160:PRO:HG2	1:A:185:LYS:HE2	1.84	0.48
1:A:255:VAL:HG23	1:A:258:LEU:HD12	1.96	0.48
2:B:9:SER:O	2:B:12:PHE:CD1	2.67	0.48
2:B:284:LEU:O	2:B:287:ILE:HG13	2.14	0.48
2:B:451:THR:HA	2:B:454:ILE:HD12	1.95	0.48
3:C:69:TRP:CD1	3:C:114:PRO:C	2.92	0.48
3:C:83:ARG:HD3	3:C:83:ARG:HA	1.73	0.48
3:C:120:TRP:CD1	3:C:122:PRO:HD3	2.48	0.48
3:C:434:LYS:CG	3:C:435:GLU:N	2.76	0.48
3:C:437:ASN:O	3:C:441:GLU:CG	2.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:292:THR:HA	1:D:295:VAL:CG2	2.44	0.48
1:D:305:THR:OG1	1:D:401:TYR:HD2	1.76	0.48
1:D:429:ARG:NE	1:D:429:ARG:HA	2.29	0.48
1:A:56:LEU:HD12	1:A:90:LEU:HD13	1.95	0.48
1:A:67:TRP:CD1	1:A:71:ASP:CB	2.97	0.48
1:A:75:ILE:O	1:A:78:ILE:HG23	2.14	0.48
1:A:166:ASP:HB3	1:A:181:TYR:HB3	1.95	0.48
1:A:380:LYS:CB	2:B:408:ILE:HB	2.43	0.48
2:B:175:ILE:HG23	2:B:178:ASP:N	2.29	0.48
2:B:258:ALA:O	2:B:262:PHE:CD1	2.66	0.48
2:B:259:LEU:HD23	2:B:259:LEU:C	2.38	0.48
3:C:194:HIS:CG	3:C:195:LYS:N	2.64	0.48
3:C:217:PHE:CD1	3:C:217:PHE:N	2.82	0.48
3:C:247:PHE:CZ	3:C:460:ILE:HD11	2.48	0.48
1:D:376:ILE:O	1:D:380:LYS:HE2	2.14	0.48
4:E:30:VAL:HG22	4:E:59:TRP:HB3	1.96	0.48
4:E:241:PHE:C	4:E:243:PRO:HD2	2.39	0.48
4:E:293:SER:O	4:E:297:VAL:HG23	2.14	0.48
1:A:20:ARG:CG	1:A:20:ARG:NH1	2.73	0.47
1:A:132:VAL:O	1:A:274:ILE:CG2	2.61	0.47
1:A:244:THR:HA	1:A:247:ILE:HB	1.95	0.47
3:C:25:LYS:HA	3:C:25:LYS:HZ2	1.79	0.47
3:C:106:TYR:CD1	3:C:107:PHE:CE1	3.02	0.47
3:C:429:ILE:C	3:C:429:ILE:HD12	2.38	0.47
1:D:45:GLU:CD	1:D:271:VAL:CG2	2.87	0.47
1:D:289:ILE:O	1:D:293:VAL:HG23	2.14	0.47
4:E:45:LYS:HG2	4:E:279:VAL:C	2.39	0.47
4:E:219:LEU:HD13	4:E:222:ILE:HB	1.96	0.47
4:E:310:THR:OG1	4:E:313:THR:CG2	2.62	0.47
1:A:6:ARG:CB	1:A:6:ARG:NH1	2.77	0.47
2:B:21:PRO:HB2	2:B:29:VAL:HG21	1.95	0.47
2:B:101:GLU:CD	2:B:123:ILE:CG2	2.87	0.47
2:B:220:TYR:CG	2:B:223:TYR:HE2	2.32	0.47
3:C:42:LEU:CD2	3:C:190:TRP:HH2	2.20	0.47
3:C:147:LYS:HA	3:C:215:VAL:O	2.14	0.47
3:C:149:THR:HG22	3:C:214:ASP:HB3	1.90	0.47
3:C:247:PHE:O	3:C:250:PRO:CD	2.62	0.47
1:D:41:ILE:HG21	4:E:96:ASP:OD2	2.13	0.47
1:D:43:VAL:CG1	1:D:50:VAL:HG22	2.44	0.47
1:D:49:ILE:CG1	1:D:125:LYS:HE3	2.44	0.47
4:E:58:GLN:CA	4:E:59:TRP:HE3	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:140:ASN:CG	4:E:211:PHE:HB3	2.39	0.47
4:E:159:LEU:CB	4:E:192:LYS:HB2	2.41	0.47
4:E:177:PHE:CE1	4:E:178:THR:O	2.67	0.47
4:E:264:PHE:N	4:E:264:PHE:CD1	2.82	0.47
4:E:416:VAL:HG22	4:E:417:GLU:H	1.73	0.47
4:E:435:GLU:CB	4:E:439:TRP:CZ2	2.95	0.47
1:A:220:ILE:N	1:A:221:PRO:CD	2.77	0.47
1:A:259:VAL:O	1:A:263:LEU:HG	2.13	0.47
2:B:59:ALA:CB	2:B:116:VAL:O	2.62	0.47
2:B:91:VAL:HG11	2:B:149:TYR:CE1	2.49	0.47
2:B:144:MET:HE2	2:B:211:LEU:CD2	2.44	0.47
2:B:155:GLU:C	2:B:156:VAL:HG22	2.35	0.47
2:B:247:GLU:HA	2:B:249:MET:HG2	1.95	0.47
2:B:261:VAL:HG12	2:B:262:PHE:CD1	2.49	0.47
3:C:122:PRO:CB	3:C:123:PRO:CD	2.73	0.47
3:C:449:VAL:O	3:C:452:THR:HG22	2.14	0.47
1:D:225:PHE:CD1	1:D:225:PHE:C	2.92	0.47
1:D:229:THR:HG22	1:D:253:LEU:HD11	1.94	0.47
1:D:229:THR:HG21	1:D:288:SER:OG	2.15	0.47
1:A:246:SER:O	1:A:250:LEU:HD12	2.14	0.47
1:A:296:ILE:HA	1:A:299:HIS:HB2	1.95	0.47
2:B:174:MET:HG3	2:B:191:LYS:HE2	1.96	0.47
2:B:197:TRP:HB3	2:B:204:TYR:CD1	2.49	0.47
2:B:242:PRO:CD	2:B:248:LYS:HE3	2.38	0.47
2:B:449:ILE:HA	2:B:452:PHE:HD2	1.75	0.47
3:C:118:VAL:HG12	3:C:119:THR:N	2.29	0.47
3:C:148:PHE:C	3:C:149:THR:HG22	2.38	0.47
3:C:230:ILE:CG1	3:C:231:ASN:N	2.76	0.47
3:C:478:PHE:O	3:C:482:PRO:HD3	2.15	0.47
1:D:49:ILE:CG2	1:D:125:LYS:CE	2.92	0.47
1:D:413:VAL:HA	1:D:416:LEU:HB2	1.95	0.47
4:E:44:GLU:HG3	4:E:129:ILE:HD12	1.92	0.47
4:E:240:TYR:O	4:E:243:PRO:CG	2.62	0.47
1:A:31:ILE:HG23	1:A:60:TRP:HE3	1.79	0.47
1:A:133:THR:N	1:A:274:ILE:HG22	2.30	0.47
1:A:294:VAL:HG13	1:A:295:VAL:N	2.30	0.47
2:B:269:LYS:HG3	2:B:270:VAL:H	1.78	0.47
3:C:154:ASN:HA	3:C:211:ASN:CB	2.37	0.47
1:D:28:PHE:HB3	1:D:156:VAL:CA	2.44	0.47
1:D:56:LEU:HG	1:D:120:PRO:HG2	1.96	0.47
1:D:233:PHE:CE2	1:D:291:VAL:HG11	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:LYS:HG3	1:A:112:TYR:CD2	2.49	0.47
1:A:133:THR:C	1:A:136:PRO:CD	2.87	0.47
1:A:279:LEU:HD13	1:A:282:MET:CB	2.44	0.47
2:B:32:ARG:HE	2:B:59:ALA:C	2.22	0.47
2:B:176:ASN:HD21	2:B:188:ILE:HD12	1.78	0.47
2:B:286:PHE:CD1	2:B:287:ILE:N	2.82	0.47
3:C:63:TYR:CD1	3:C:64:ASP:N	2.83	0.47
3:C:104:VAL:HA	3:C:106:TYR:CE1	2.50	0.47
1:D:43:VAL:HG21	1:D:50:VAL:HG13	1.95	0.47
4:E:9:LYS:HG3	4:E:10:LEU:N	2.28	0.47
4:E:33:LYS:HE3	4:E:160:SER:HB3	1.90	0.47
1:A:46:VAL:CG2	1:A:269:SER:O	2.63	0.47
1:A:58:GLN:HE21	1:A:90:LEU:HD21	1.80	0.47
1:A:69:PRO:HA	1:A:73:GLY:CA	2.45	0.47
1:A:80:LEU:HD23	1:A:110:LEU:HB2	1.95	0.47
1:A:199:LEU:C	1:A:200:ASP:OD1	2.57	0.47
1:A:255:VAL:O	1:A:258:LEU:HB2	2.15	0.47
1:A:293:VAL:CG2	4:E:238:LEU:HD21	2.41	0.47
1:A:294:VAL:CG1	1:A:295:VAL:N	2.77	0.47
2:B:9:SER:CB	2:B:12:PHE:HE1	2.28	0.47
2:B:35:LEU:HD22	2:B:55:PHE:O	2.14	0.47
2:B:58:LEU:HD21	2:B:118:TRP:CE3	2.50	0.47
2:B:59:ALA:CA	2:B:116:VAL:O	2.62	0.47
2:B:108:VAL:CG2	2:B:118:TRP:HB2	2.45	0.47
2:B:245:ALA:O	2:B:248:LYS:HB3	2.14	0.47
3:C:56:VAL:CG1	3:C:126:PHE:HE2	2.16	0.47
3:C:81:ARG:NH1	3:C:111:LEU:HD13	2.29	0.47
3:C:221:ILE:HG13	3:C:222:ARG:H	1.78	0.47
3:C:264:LEU:HA	3:C:267:GLN:HG3	1.97	0.47
3:C:271:LEU:C	3:C:271:LEU:HD23	2.40	0.47
3:C:306:CYS:O	3:C:310:LEU:HD22	2.15	0.47
3:C:482:PRO:CG	3:C:483:ALA:H	2.28	0.47
1:D:76:LYS:CD	1:D:112:TYR:CE2	2.98	0.47
1:D:157:SER:HB2	1:D:199:LEU:CD1	2.44	0.47
1:D:170:PHE:CD1	1:D:170:PHE:C	2.93	0.47
1:D:178:MET:CE	1:D:207:MET:HB3	2.44	0.47
1:D:224:LEU:HD21	4:E:297:VAL:HG11	1.97	0.47
4:E:157:LEU:CD1	4:E:208:ILE:HD11	2.44	0.47
4:E:159:LEU:HD11	4:E:208:ILE:HG23	1.96	0.47
1:A:6:ARG:HH11	1:A:6:ARG:HB3	1.78	0.47
1:A:265:PRO:HD2	1:A:266:SER:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:ILE:HG22	1:A:409:ILE:HD12	1.96	0.47
2:B:241:LEU:HG	2:B:248:LYS:CE	2.40	0.47
3:C:251:ALA:C	3:C:253:SER:H	2.21	0.47
1:D:63:VAL:C	1:D:65:LEU:H	2.22	0.47
1:D:120:PRO:O	1:D:120:PRO:CG	2.63	0.47
1:D:394:ASN:C	1:D:396:ALA:N	2.67	0.47
1:D:431:ILE:HG22	1:D:431:ILE:O	2.15	0.47
4:E:128:PRO:C	4:E:129:ILE:CG2	2.88	0.47
4:E:271:LYS:C	4:E:273:PRO:CD	2.78	0.47
4:E:272:VAL:HA	4:E:275:THR:OG1	2.15	0.47
1:A:93:TYR:OH	1:A:198:TYR:CE2	2.58	0.47
1:A:110:LEU:HD12	1:A:111:ASP:H	1.76	0.47
1:A:251:LEU:CD1	4:E:260:ALA:CB	2.93	0.47
2:B:134:TYR:CD1	2:B:213:ILE:HG13	2.48	0.47
3:C:61:ALA:HB1	3:C:113:ARG:NH2	2.30	0.47
3:C:69:TRP:HB2	3:C:74:TYR:CB	2.39	0.47
3:C:247:PHE:O	3:C:250:PRO:CG	2.63	0.47
3:C:288:ILE:HG23	3:C:290:LYS:N	2.30	0.47
1:D:48:GLN:CB	1:D:130:ILE:HD13	2.41	0.47
1:D:54:VAL:O	1:D:56:LEU:CD2	2.63	0.47
1:D:186:HIS:CE1	1:D:187:TRP:O	2.68	0.47
1:D:232:VAL:CG1	1:D:250:LEU:HD11	2.45	0.47
1:D:282:MET:CE	1:D:286:ILE:HD11	2.44	0.47
4:E:30:VAL:HG12	4:E:157:LEU:HD22	1.97	0.47
4:E:104:TYR:CD1	4:E:104:TYR:N	2.83	0.47
4:E:232:ILE:O	4:E:236:VAL:HG22	2.15	0.47
1:A:41:ILE:O	1:A:42:ASN:CG	2.57	0.47
2:B:68:ASP:HB3	2:B:69:PRO:HD2	1.92	0.47
2:B:95:ASN:HB3	2:B:126:SER:HB2	1.96	0.47
3:C:230:ILE:HG13	3:C:231:ASN:H	1.76	0.47
1:D:250:LEU:HA	1:D:253:LEU:HD22	1.96	0.47
1:D:274:ILE:HG13	1:D:277:TYR:CD2	2.50	0.47
1:D:376:ILE:HG22	1:D:380:LYS:CE	2.44	0.47
4:E:60:ASN:HD22	4:E:60:ASN:N	2.11	0.47
4:E:174:PRO:HD3	4:E:185:ILE:HB	1.95	0.47
1:A:92:LEU:C	1:A:95:ASN:HD22	2.23	0.46
1:A:218:VAL:C	1:A:221:PRO:HD2	2.40	0.46
1:A:282:MET:O	1:A:285:VAL:HG12	2.15	0.46
2:B:233:ILE:HG22	2:B:237:LEU:HD22	1.97	0.46
2:B:444:ILE:CG2	2:B:445:THR:N	2.77	0.46
3:C:63:TYR:HE1	3:C:116:GLY:HA3	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:89:ILE:HD11	3:C:107:PHE:HB3	1.97	0.46
1:D:76:LYS:CG	1:D:112:TYR:CE2	2.96	0.46
1:D:256:PHE:HZ	4:E:263:ILE:HG13	1.80	0.46
1:D:377:GLU:HB2	4:E:415:CYS:HB2	1.97	0.46
4:E:55:ILE:HG13	4:E:57:ILE:CG1	2.40	0.46
4:E:66:TRP:CD2	4:E:70:GLU:HB3	2.49	0.46
4:E:138:TRP:CH2	4:E:215:GLN:CG	2.98	0.46
4:E:145:PHE:CZ	4:E:208:ILE:HD13	2.50	0.46
4:E:159:LEU:CD1	4:E:191:LYS:C	2.79	0.46
4:E:456:LEU:O	4:E:456:LEU:CD2	2.53	0.46
1:A:224:LEU:C	1:A:224:LEU:HD12	2.39	0.46
2:B:34:GLY:O	2:B:35:LEU:HD23	2.12	0.46
3:C:281:THR:O	3:C:285:VAL:HG13	2.15	0.46
3:C:316:THR:HB	3:C:320:HIS:H	1.80	0.46
3:C:467:LEU:O	3:C:468:GLY:C	2.57	0.46
1:D:75:ILE:HD12	1:D:78:ILE:HG22	1.95	0.46
1:D:245:LEU:C	1:D:245:LEU:CD2	2.88	0.46
4:E:19:LYS:HZ3	4:E:154:GLU:CB	2.27	0.46
4:E:222:ILE:O	4:E:225:ILE:HB	2.15	0.46
4:E:302:ILE:O	4:E:306:VAL:HG23	2.15	0.46
1:A:46:VAL:HG21	1:A:269:SER:C	2.40	0.46
1:A:171:MET:CG	1:A:173:SER:H	2.27	0.46
1:A:176:TRP:CE3	1:A:209:ARG:CZ	2.99	0.46
1:A:258:LEU:O	1:A:261:VAL:HB	2.15	0.46
2:B:226:VAL:HB	2:B:230:LEU:HD11	1.98	0.46
2:B:233:ILE:O	2:B:236:ILE:HG23	2.14	0.46
3:C:60:HIS:HE1	3:C:160:MET:CE	2.27	0.46
1:D:37:LEU:CD1	1:D:54:VAL:HG22	2.45	0.46
1:D:132:VAL:O	1:D:274:ILE:CG1	2.62	0.46
4:E:26:HIS:CD2	4:E:26:HIS:C	2.86	0.46
4:E:35:THR:CB	4:E:54:TRP:HE3	2.25	0.46
4:E:182:GLU:HA	4:E:218:PRO:CG	2.45	0.46
1:A:136:PRO:HD3	1:A:274:ILE:CG2	2.38	0.46
1:A:137:PHE:HD1	1:A:137:PHE:HA	1.65	0.46
1:A:137:PHE:CB	1:A:435:GLN:HG3	2.40	0.46
2:B:43:LEU:HD12	2:B:43:LEU:HA	1.78	0.46
2:B:106:VAL:HG12	2:B:118:TRP:NE1	2.31	0.46
1:D:95:ASN:ND2	1:D:127:TYR:C	2.74	0.46
1:D:166:ASP:HB3	1:D:167:LEU:HD12	1.96	0.46
1:D:291:VAL:HG12	1:D:295:VAL:HG11	1.97	0.46
1:D:411:LEU:O	1:D:415:MET:HE2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:44:GLU:CG	4:E:129:ILE:CB	2.76	0.46
4:E:55:ILE:HG23	4:E:119:PRO:CG	2.45	0.46
4:E:284:LYS:N	4:E:284:LYS:CD	2.72	0.46
1:A:41:ILE:CG2	1:A:123:ILE:HD11	2.46	0.46
1:A:145:LYS:HZ3	1:A:202:THR:HG21	1.80	0.46
1:A:148:ILE:CG2	1:A:148:ILE:O	2.60	0.46
1:A:255:VAL:HG12	1:A:256:PHE:CD1	2.51	0.46
2:B:132:VAL:HG12	2:B:280:ILE:N	2.31	0.46
2:B:147:LYS:CD	2:B:148:SER:H	2.28	0.46
3:C:242:LEU:HD22	3:C:267:GLN:HG2	1.89	0.46
3:C:316:THR:HB	3:C:319:THR:HG22	1.97	0.46
3:C:471:PHE:CD1	3:C:472:ILE:N	2.84	0.46
4:E:26:HIS:O	4:E:26:HIS:ND1	2.40	0.46
4:E:38:ASN:O	4:E:51:THR:CA	2.63	0.46
4:E:159:LEU:HD23	4:E:159:LEU:HA	1.60	0.46
4:E:239:VAL:O	4:E:243:PRO:HD3	2.16	0.46
4:E:272:VAL:N	4:E:273:PRO:HD2	2.29	0.46
1:A:245:LEU:HD13	2:B:250:SER:CA	2.46	0.46
2:B:36:THR:O	2:B:55:PHE:CD1	2.69	0.46
2:B:129:THR:N	2:B:142:CYS:SG	2.88	0.46
3:C:249:LEU:N	3:C:249:LEU:CD1	2.79	0.46
1:D:32:THR:O	1:D:58:GLN:HA	2.15	0.46
1:D:78:ILE:CD1	1:D:78:ILE:C	2.89	0.46
1:D:132:VAL:CB	1:D:274:ILE:HG23	2.45	0.46
4:E:27:VAL:HB	4:E:154:GLU:C	2.41	0.46
4:E:39:LEU:CD2	4:E:183:TRP:HZ2	2.19	0.46
4:E:44:GLU:CB	4:E:280:PRO:CG	2.82	0.46
4:E:472:ASN:ND2	4:E:472:ASN:O	2.49	0.46
1:A:92:LEU:CD2	1:A:92:LEU:N	2.79	0.46
1:A:192:CYS:SG	1:A:193:CYS:N	2.89	0.46
1:A:238:ASP:CB	2:B:306:HIS:NE2	2.78	0.46
2:B:101:GLU:OE1	2:B:123:ILE:HG21	2.16	0.46
2:B:218:LEU:CD1	2:B:221:ILE:HD11	2.46	0.46
2:B:248:LYS:HA	2:B:251:LEU:CD2	2.46	0.46
2:B:254:SER:OG	3:C:265:LEU:HD11	2.16	0.46
3:C:191:GLU:CD	3:C:222:ARG:HB3	2.40	0.46
3:C:267:GLN:HE21	3:C:267:GLN:HB2	1.51	0.46
1:D:26:THR:HG22	1:D:27:HIS:N	2.11	0.46
1:D:44:ASP:OD1	1:D:46:VAL:HG12	2.16	0.46
1:D:57:ARG:CD	1:D:117:MET:SD	3.04	0.46
1:D:117:MET:HE3	1:D:119:THR:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:209:ILE:CG1	4:E:211:PHE:CE1	2.99	0.46
1:A:5:THR:HA	1:A:8:VAL:HG22	1.98	0.46
1:A:79:ARG:HH11	1:A:107:LYS:HZ2	1.62	0.46
1:A:284:PHE:N	1:A:284:PHE:HD1	2.13	0.46
2:B:240:TYR:O	2:B:240:TYR:CD1	2.67	0.46
2:B:281:ILE:HG22	2:B:285:MET:H	1.79	0.46
3:C:10:ASP:O	3:C:16:LYS:HG3	2.15	0.46
3:C:138:PRO:CG	3:C:290:LYS:HE2	2.44	0.46
3:C:212:TYR:O	3:C:212:TYR:HD1	1.94	0.46
1:D:79:ARG:HH12	4:E:154:GLU:CD	2.23	0.46
1:D:92:LEU:H	1:D:92:LEU:HD22	1.63	0.46
1:D:412:CYS:C	1:D:415:MET:HE2	2.41	0.46
1:A:305:THR:O	1:A:306:HIS:CG	2.69	0.46
2:B:78:LEU:HD23	2:B:80:ILE:HD11	1.97	0.46
2:B:201:ASP:CG	2:B:202:PRO:HD2	2.40	0.46
2:B:298:SER:O	2:B:301:VAL:CG2	2.64	0.46
3:C:110:VAL:CG2	3:C:120:TRP:HB2	2.46	0.46
3:C:482:PRO:CG	3:C:483:ALA:N	2.78	0.46
4:E:45:LYS:CG	4:E:277:LEU:O	2.64	0.46
1:A:54:VAL:HG22	1:A:122:ALA:CB	2.46	0.46
1:A:77:LYS:CB	1:A:111:ASP:HA	2.45	0.46
1:A:139:GLN:HE21	1:A:206:ILE:HG23	1.80	0.46
1:A:187:TRP:CD1	1:A:199:LEU:CD2	2.98	0.46
2:B:31:VAL:HG12	2:B:158:LEU:HD23	1.94	0.46
2:B:465:ASP:CG	2:B:466:ASN:H	2.23	0.46
3:C:58:MET:HE1	3:C:120:TRP:CZ2	2.51	0.46
3:C:63:TYR:HD1	3:C:64:ASP:H	1.64	0.46
3:C:288:ILE:CD1	3:C:290:LYS:CD	2.94	0.46
3:C:471:PHE:C	3:C:473:PHE:N	2.74	0.46
1:D:280:PHE:N	1:D:280:PHE:HD1	2.13	0.46
4:E:116:TYR:CD1	4:E:117:TRP:N	2.84	0.46
4:E:184:THR:CG2	4:E:215:GLN:CG	2.77	0.46
1:A:46:VAL:HB	1:A:270:ALA:O	2.16	0.45
1:A:152:ASP:OD1	1:A:152:ASP:N	2.47	0.45
1:A:409:ILE:CA	1:A:412:CYS:HB2	2.46	0.45
2:B:248:LYS:O	2:B:249:MET:C	2.58	0.45
3:C:154:ASN:CB	3:C:211:ASN:CB	2.94	0.45
3:C:316:THR:HG21	3:C:447:ASN:CG	2.41	0.45
1:D:149:TRP:CG	1:D:150:THR:N	2.85	0.45
1:D:184:TRP:HE3	1:D:185:LYS:O	1.98	0.45
1:D:260:ILE:O	1:D:264:ILE:CD1	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:146:ARG:CD	4:E:206:GLN:O	2.62	0.45
1:A:29:VAL:CG2	1:A:86:TRP:HZ3	2.29	0.45
1:A:160:PRO:CG	1:A:185:LYS:CB	2.73	0.45
1:A:255:VAL:HG12	1:A:256:PHE:N	2.30	0.45
2:B:220:TYR:CG	2:B:223:TYR:CE2	3.04	0.45
3:C:93:VAL:HG11	3:C:151:LEU:CD1	2.41	0.45
1:D:46:VAL:HG21	1:D:270:ALA:CA	2.46	0.45
1:D:117:MET:HE3	1:D:119:THR:CG2	2.46	0.45
1:D:410:LEU:O	1:D:414:PHE:CB	2.63	0.45
4:E:49:LEU:HD12	4:E:49:LEU:C	2.41	0.45
4:E:59:TRP:CZ2	4:E:115:MET:CB	2.99	0.45
4:E:146:ARG:NH1	4:E:205:PHE:C	2.74	0.45
1:A:184:TRP:CE3	1:A:185:LYS:O	2.70	0.45
2:B:153:THR:CB	2:B:204:TYR:HB2	2.13	0.45
2:B:175:ILE:HD13	2:B:177:GLN:HB3	1.97	0.45
2:B:251:LEU:HG	2:B:252:SER:N	2.31	0.45
3:C:20:HIS:O	3:C:20:HIS:ND1	2.49	0.45
3:C:153:TYR:HB2	3:C:158:ILE:CB	2.46	0.45
3:C:474:VAL:O	3:C:474:VAL:CG1	2.64	0.45
4:E:138:TRP:CD2	4:E:215:GLN:HA	2.52	0.45
4:E:183:TRP:HB2	4:E:214:ILE:HD13	1.97	0.45
1:A:76:LYS:CG	1:A:77:LYS:N	2.76	0.45
1:A:244:THR:HG23	1:A:245:LEU:N	2.30	0.45
1:A:270:ALA:O	1:A:271:VAL:CG1	2.64	0.45
2:B:111:GLN:NE2	2:B:115:ALA:CB	2.79	0.45
2:B:136:PRO:N	2:B:280:ILE:HD11	2.32	0.45
3:C:63:TYR:O	3:C:65:HIS:CD2	2.69	0.45
3:C:81:ARG:HH12	3:C:111:LEU:HB2	1.79	0.45
3:C:475:MET:HA	3:C:478:PHE:CZ	2.51	0.45
1:D:132:VAL:O	1:D:274:ILE:CG2	2.63	0.45
1:D:229:THR:HA	1:D:232:VAL:HG21	1.95	0.45
1:D:426:PHE:CG	1:D:427:ALA:N	2.84	0.45
4:E:13:ASP:C	4:E:13:ASP:OD1	2.60	0.45
4:E:27:VAL:HG12	4:E:154:GLU:N	2.31	0.45
4:E:77:VAL:HG12	4:E:78:ARG:N	2.31	0.45
4:E:173:ASP:H	4:E:188:ARG:HH11	1.64	0.45
1:A:50:VAL:CG1	1:A:52:THR:CG2	2.95	0.45
1:A:166:ASP:OD2	1:A:178:MET:HE1	2.16	0.45
1:A:245:LEU:HD12	1:A:245:LEU:HA	1.78	0.45
4:E:38:ASN:ND2	4:E:40:ILE:HG12	2.32	0.45
4:E:255:ILE:O	4:E:256:SER:C	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:258:LEU:O	4:E:258:LEU:HG	2.15	0.45
1:A:245:LEU:CD1	2:B:250:SER:HA	2.47	0.45
1:A:260:ILE:CG2	1:A:261:VAL:N	2.79	0.45
2:B:48:GLU:HB2	2:B:128:CYS:O	2.15	0.45
2:B:53:SER:HA	2:B:122:ALA:O	2.16	0.45
2:B:92:LEU:HD12	2:B:95:ASN:HB2	1.99	0.45
2:B:136:PRO:C	2:B:138:ASP:N	2.74	0.45
2:B:409:LYS:CE	3:C:423:ILE:HA	2.47	0.45
3:C:30:VAL:HG21	3:C:158:ILE:H	1.79	0.45
3:C:139:PHE:CE2	3:C:224:LYS:NZ	2.83	0.45
3:C:482:PRO:CD	3:C:483:ALA:H	2.30	0.45
1:D:46:VAL:O	1:D:272:PRO:HD3	2.15	0.45
1:D:227:PHE:C	1:D:227:PHE:CD1	2.92	0.45
1:D:305:THR:CG2	1:D:400:LYS:HG2	2.47	0.45
4:E:202:ASP:C	4:E:203:ILE:HG13	2.41	0.45
4:E:283:GLY:O	4:E:286:LEU:HB2	2.15	0.45
1:A:118:TRP:C	1:A:120:PRO:HD3	2.41	0.45
1:A:165:PRO:HA	1:A:181:TYR:O	2.17	0.45
1:A:176:TRP:HB3	1:A:209:ARG:CD	2.38	0.45
1:A:256:PHE:CD1	1:A:256:PHE:N	2.85	0.45
1:A:376:ILE:HG22	1:A:377:GLU:N	2.29	0.45
1:A:381:TYR:O	1:A:385:HIS:CB	2.65	0.45
2:B:34:GLY:C	2:B:35:LEU:CD2	2.79	0.45
2:B:35:LEU:N	2:B:35:LEU:CD2	2.79	0.45
2:B:438:LEU:O	2:B:442:ILE:HD12	2.17	0.45
3:C:25:LYS:HB3	3:C:28:ASN:ND2	2.29	0.45
3:C:194:HIS:HB3	3:C:220:ILE:HG12	1.98	0.45
1:D:44:ASP:OD2	1:D:46:VAL:HG13	2.17	0.45
1:D:217:ASN:CA	1:D:220:ILE:CD1	2.85	0.45
1:D:302:SER:HB3	1:D:305:THR:HG22	1.98	0.45
4:E:75:ASP:HB3	4:E:110:TYR:CZ	2.52	0.45
4:E:131:VAL:HG12	4:E:131:VAL:O	2.16	0.45
1:A:146:LEU:N	1:A:146:LEU:CD1	2.78	0.45
1:A:171:MET:HG2	1:A:171:MET:O	2.15	0.45
1:A:381:TYR:CD1	1:A:381:TYR:N	2.84	0.45
2:B:91:VAL:HG22	2:B:92:LEU:N	2.31	0.45
2:B:220:TYR:CE2	3:C:279:PRO:HB2	2.48	0.45
2:B:284:LEU:HA	2:B:287:ILE:HG13	1.99	0.45
2:B:439:PHE:O	2:B:442:ILE:CG2	2.63	0.45
3:C:50:GLU:C	3:C:132:ILE:HD13	2.41	0.45
3:C:290:LYS:HB2	3:C:291:TYR:CD1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:242:LYS:CD	1:D:245:LEU:HD13	2.44	0.45
4:E:94:ASN:HD22	4:E:125:SER:CB	2.14	0.45
4:E:135:PRO:CG	4:E:137:ASP:OD1	2.65	0.45
4:E:222:ILE:C	4:E:226:ILE:HG13	2.40	0.45
1:A:145:LYS:CG	1:A:202:THR:HG22	2.16	0.45
2:B:35:LEU:CD1	2:B:56:LEU:HA	2.47	0.45
2:B:91:VAL:HG23	2:B:96:ASN:HB3	1.98	0.45
2:B:132:VAL:CG1	2:B:279:ILE:C	2.89	0.45
2:B:281:ILE:HG23	2:B:284:LEU:HB3	1.98	0.45
3:C:16:LYS:HE3	3:C:16:LYS:CA	2.31	0.45
3:C:48:THR:CB	3:C:285:VAL:N	2.78	0.45
3:C:469:THR:O	3:C:473:PHE:CB	2.63	0.45
1:D:3:HIS:O	1:D:7:LEU:HG	2.17	0.45
1:D:57:ARG:CZ	1:D:117:MET:CE	2.84	0.45
1:D:80:LEU:HD12	1:D:80:LEU:HA	1.75	0.45
1:D:227:PHE:O	1:D:227:PHE:HD1	1.99	0.45
1:D:411:LEU:HD23	1:D:411:LEU:HA	1.74	0.45
4:E:20:PRO:CB	4:E:61:ASP:OD1	2.60	0.45
4:E:45:LYS:CB	4:E:277:LEU:O	2.65	0.45
1:A:15:TYR:CD1	1:A:15:TYR:C	2.94	0.45
1:A:174:GLY:CA	1:A:176:TRP:CE3	3.00	0.45
1:A:188:VAL:O	1:A:197:PRO:HB2	2.16	0.45
1:A:268:SER:C	1:A:270:ALA:H	2.24	0.45
2:B:220:TYR:CD2	2:B:223:TYR:CE2	3.05	0.45
3:C:135:LEU:C	3:C:138:PRO:CD	2.90	0.45
3:C:137:PHE:N	3:C:138:PRO:CD	2.78	0.45
1:D:176:TRP:HB3	1:D:209:ARG:HG3	1.98	0.45
4:E:101:VAL:O	4:E:101:VAL:HG23	2.12	0.45
4:E:273:PRO:CG	4:E:274:GLU:N	2.80	0.45
1:D:160:PRO:HA	1:D:201:ILE:HD11	1.99	0.44
1:D:218:VAL:O	1:D:221:PRO:HG2	2.17	0.44
1:D:257:LEU:HA	1:D:260:ILE:CG1	2.47	0.44
1:D:411:LEU:O	1:D:415:MET:HG3	2.17	0.44
4:E:255:ILE:HG22	4:E:256:SER:N	2.32	0.44
1:A:93:TYR:CD2	1:A:145:LYS:HB3	2.52	0.44
1:A:267:THR:HA	1:A:270:ALA:HB3	1.99	0.44
1:A:285:VAL:HG13	1:A:286:ILE:HG13	1.99	0.44
2:B:3:MET:HB3	2:B:6:THR:HB	1.99	0.44
2:B:101:GLU:OE1	2:B:123:ILE:CG2	2.65	0.44
2:B:239:PHE:HB3	2:B:442:ILE:HG12	1.98	0.44
3:C:64:ASP:O	3:C:116:GLY:HA3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:138:PRO:O	3:C:141:TRP:CD1	2.71	0.44
3:C:162:LEU:HB2	3:C:215:VAL:HG12	1.98	0.44
3:C:179:ILE:CG2	3:C:181:PRO:CD	2.87	0.44
3:C:206:PHE:N	3:C:207:PRO:HD2	2.31	0.44
3:C:288:ILE:HG23	3:C:290:LYS:H	1.82	0.44
1:D:37:LEU:HB2	1:D:54:VAL:CG1	2.46	0.44
1:D:60:TRP:HZ3	1:D:116:ILE:HG13	1.80	0.44
1:D:228:LEU:HD21	4:E:258:LEU:HD21	2.00	0.44
1:D:238:ASP:CB	4:E:308:LEU:HD22	2.46	0.44
1:D:292:THR:O	1:D:296:ILE:HG12	2.17	0.44
4:E:470:HIS:C	4:E:472:ASN:H	2.26	0.44
1:A:181:TYR:HB2	1:A:204:HIS:O	2.16	0.44
2:B:270:VAL:N	2:B:271:PRO:CD	2.81	0.44
1:D:77:LYS:HA	1:D:110:LEU:O	2.18	0.44
1:D:91:VAL:HG21	1:D:96:ALA:HB1	2.00	0.44
1:D:175:GLU:HA	1:D:211:PRO:HB3	1.99	0.44
1:D:187:TRP:CH2	1:D:189:TYR:CG	3.06	0.44
1:D:415:MET:HB2	1:D:415:MET:HE3	1.49	0.44
1:D:430:LEU:C	1:D:430:LEU:HD23	2.41	0.44
4:E:146:ARG:HG3	4:E:147:SER:O	2.18	0.44
4:E:173:ASP:HB3	4:E:185:ILE:CG2	2.41	0.44
4:E:304:LEU:O	4:E:308:LEU:HB2	2.17	0.44
1:A:31:ILE:HA	1:A:59:GLN:O	2.18	0.44
1:A:166:ASP:HB2	1:A:181:TYR:CD1	2.49	0.44
2:B:79:SER:HB2	3:C:153:TYR:HE1	1.82	0.44
2:B:106:VAL:HG12	2:B:118:TRP:HE1	1.83	0.44
2:B:158:LEU:HD23	2:B:158:LEU:HA	1.61	0.44
3:C:80:LEU:O	3:C:112:VAL:CG2	2.65	0.44
1:D:52:THR:O	1:D:123:ILE:HA	2.18	0.44
1:D:76:LYS:HE2	1:D:76:LYS:HB3	1.59	0.44
1:D:145:LYS:CA	1:D:146:LEU:HD12	2.44	0.44
4:E:66:TRP:HD1	4:E:111:ASN:CA	2.24	0.44
4:E:140:ASN:ND2	4:E:212:LEU:H	2.15	0.44
4:E:267:LEU:HD12	4:E:270:GLN:NE2	2.32	0.44
4:E:267:LEU:HA	4:E:270:GLN:CD	2.43	0.44
4:E:284:LYS:O	4:E:288:PHE:CE2	2.71	0.44
4:E:441:LEU:C	4:E:441:LEU:CD1	2.91	0.44
1:A:227:PHE:CA	1:A:230:VAL:HB	2.46	0.44
1:A:274:ILE:HG12	1:A:277:TYR:CE1	2.50	0.44
1:D:51:GLU:HG3	1:D:125:LYS:HG3	2.00	0.44
1:D:64:ARG:CG	1:D:64:ARG:NH1	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:116:ILE:O	1:D:116:ILE:HG12	2.17	0.44
1:D:426:PHE:HE1	1:D:430:LEU:HD12	1.83	0.44
4:E:79:ILE:HA	4:E:80:PRO:HD3	1.67	0.44
4:E:91:LEU:HA	4:E:145:PHE:CB	2.47	0.44
4:E:240:TYR:O	4:E:243:PRO:HD2	2.17	0.44
1:A:46:VAL:CG2	1:A:270:ALA:N	2.79	0.44
1:A:152:ASP:HB3	1:A:196:THR:O	2.17	0.44
1:A:291:VAL:O	1:A:294:VAL:HG12	2.18	0.44
1:A:376:ILE:C	1:A:380:LYS:HE2	2.42	0.44
2:B:40:LEU:CB	2:B:52:THR:HG23	2.46	0.44
2:B:146:PHE:O	2:B:147:LYS:HB2	2.17	0.44
3:C:11:LEU:C	3:C:16:LYS:CG	2.91	0.44
3:C:132:ILE:CG2	3:C:133:ASN:N	2.81	0.44
1:D:188:VAL:HG23	1:D:198:TYR:O	2.18	0.44
1:D:229:THR:CG2	1:D:253:LEU:HD12	2.48	0.44
1:D:238:ASP:OD1	4:E:309:ARG:C	2.61	0.44
1:D:257:LEU:HD22	1:D:285:VAL:HG22	2.00	0.44
1:A:107:LYS:NZ	2:B:151:TYR:CD2	2.86	0.44
1:A:118:TRP:NE1	1:A:120:PRO:HG3	2.33	0.44
1:A:123:ILE:O	1:A:123:ILE:HG23	2.17	0.44
1:A:129:GLU:O	1:A:142:CYS:SG	2.76	0.44
1:A:262:GLU:O	1:A:265:PRO:HD2	2.17	0.44
2:B:28:LYS:HD2	2:B:156:VAL:C	2.43	0.44
2:B:49:GLU:HA	2:B:127:SER:HA	2.00	0.44
3:C:110:VAL:CG1	3:C:111:LEU:N	2.81	0.44
3:C:288:ILE:HD13	3:C:288:ILE:HG21	1.57	0.44
1:D:146:LEU:CD1	1:D:146:LEU:N	2.80	0.44
1:D:283:ILE:N	1:D:286:ILE:HD12	2.32	0.44
4:E:45:LYS:HE2	4:E:278:ASN:HA	1.95	0.44
4:E:195:ASN:CB	4:E:205:PHE:H	2.27	0.44
1:A:145:LYS:NZ	1:A:202:THR:HG21	2.31	0.44
1:A:215:VAL:O	1:A:218:VAL:HG12	2.17	0.44
1:A:237:THR:HB	1:A:406:ILE:HG22	2.00	0.44
1:A:261:VAL:O	1:A:261:VAL:HG13	2.18	0.44
2:B:10:VAL:HG13	2:B:11:LEU:N	2.33	0.44
2:B:153:THR:O	2:B:204:TYR:CD2	2.65	0.44
2:B:197:TRP:HD1	2:B:204:TYR:HB3	1.79	0.44
2:B:203:SER:O	2:B:205:GLU:HG2	2.17	0.44
2:B:269:LYS:CG	2:B:270:VAL:H	2.31	0.44
3:C:3:GLU:O	3:C:7:LEU:HB2	2.17	0.44
3:C:61:ALA:HB1	3:C:113:ARG:HH22	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:137:PHE:HD1	3:C:288:ILE:CB	2.28	0.44
1:D:53:ASN:CB	1:D:123:ILE:HG12	2.46	0.44
1:D:76:LYS:HG2	1:D:112:TYR:HE2	1.79	0.44
1:D:260:ILE:HG22	1:D:264:ILE:CD1	2.43	0.44
4:E:18:ILE:HD13	4:E:18:ILE:HG21	1.84	0.44
4:E:90:VAL:HG22	4:E:99:PHE:HE1	1.82	0.44
4:E:294:LEU:HA	4:E:297:VAL:HG23	2.00	0.44
1:A:121:PRO:HB2	2:B:149:TYR:CZ	2.53	0.44
1:A:397:GLU:O	1:A:400:LYS:HB2	2.18	0.44
2:B:7:LEU:HD11	2:B:69:PRO:HD2	2.00	0.44
2:B:135:PHE:H	2:B:136:PRO:CD	2.30	0.44
2:B:284:LEU:HA	2:B:287:ILE:CG1	2.47	0.44
3:C:41:ASN:HD22	3:C:41:ASN:HA	1.36	0.44
1:D:28:PHE:CZ	1:D:153:GLY:O	2.71	0.44
1:D:53:ASN:HD22	1:D:123:ILE:HG13	1.83	0.44
1:D:167:LEU:H	1:D:167:LEU:HD13	1.82	0.44
1:D:432:GLU:HG2	1:D:435:GLN:HE21	1.77	0.44
1:A:35:LEU:HD13	1:A:203:TYR:CE2	2.52	0.43
1:A:136:PRO:CA	1:A:277:TYR:OH	2.59	0.43
1:A:207:MET:N	1:A:207:MET:SD	2.91	0.43
2:B:35:LEU:CD2	2:B:56:LEU:CA	2.95	0.43
2:B:35:LEU:HD21	2:B:56:LEU:HA	1.99	0.43
2:B:145:VAL:HG13	2:B:208:THR:HA	2.00	0.43
2:B:185:GLN:CD	2:B:219:PHE:CE2	2.96	0.43
3:C:161:ASP:HA	3:C:199:LYS:CG	2.43	0.43
1:D:166:ASP:OD2	1:D:181:TYR:CG	2.70	0.43
1:D:233:PHE:CZ	1:D:417:ILE:CD1	3.01	0.43
1:D:244:THR:CG2	1:D:245:LEU:H	2.27	0.43
4:E:182:GLU:HG3	4:E:221:TYR:OH	2.17	0.43
4:E:212:LEU:N	4:E:212:LEU:CD1	2.81	0.43
4:E:284:LYS:CE	4:E:284:LYS:CA	2.91	0.43
1:A:62:ASP:OD1	1:A:64:ARG:HB2	2.17	0.43
1:A:77:LYS:CA	1:A:110:LEU:O	2.66	0.43
1:A:93:TYR:CZ	1:A:198:TYR:CE2	3.06	0.43
1:A:203:TYR:HB3	1:A:205:PHE:HE1	1.82	0.43
2:B:20:ARG:H	2:B:20:ARG:CD	2.25	0.43
3:C:113:ARG:NE	3:C:119:THR:CG2	2.77	0.43
3:C:228:TYR:CE1	3:C:229:VAL:HG22	2.53	0.43
1:D:78:ILE:O	1:D:78:ILE:HD13	2.13	0.43
1:D:103:VAL:HG13	1:D:118:TRP:CZ2	2.53	0.43
4:E:42:LEU:HD22	4:E:183:TRP:CH2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:123:TYR:HD1	4:E:123:TYR:H	1.66	0.43
4:E:129:ILE:HG13	4:E:129:ILE:O	2.18	0.43
1:A:128:CYS:CB	1:A:144:MET:HE2	2.47	0.43
1:A:137:PHE:O	1:A:208:GLN:HB2	2.18	0.43
2:B:248:LYS:HE2	2:B:248:LYS:HB2	1.70	0.43
3:C:68:THR:N	3:C:116:GLY:N	2.67	0.43
3:C:94:LEU:O	3:C:98:ASN:CB	2.66	0.43
3:C:223:ARG:CG	3:C:224:LYS:H	2.31	0.43
1:D:93:TYR:C	1:D:95:ASN:H	2.25	0.43
1:D:250:LEU:CD2	1:D:292:THR:HB	2.47	0.43
4:E:56:GLU:CG	4:E:118:LEU:HD22	2.46	0.43
1:A:38:ILE:CD1	1:A:38:ILE:H	2.31	0.43
1:A:79:ARG:HH11	1:A:107:LYS:HZ1	1.63	0.43
1:A:220:ILE:O	1:A:220:ILE:HG22	2.17	0.43
1:A:376:ILE:O	1:A:380:LYS:CE	2.65	0.43
2:B:140:GLN:O	2:B:213:ILE:CD1	2.65	0.43
2:B:232:SER:O	2:B:233:ILE:C	2.59	0.43
3:C:45:LEU:HD23	3:C:52:LEU:HD12	2.00	0.43
3:C:106:TYR:O	3:C:107:PHE:CD1	2.70	0.43
3:C:257:MET:HE1	3:C:314:PHE:HB3	1.98	0.43
3:C:283:LEU:C	3:C:285:VAL:N	2.74	0.43
1:D:86:TRP:HE3	1:D:86:TRP:H	1.65	0.43
4:E:20:PRO:HG3	4:E:61:ASP:CA	2.41	0.43
4:E:136:PHE:HZ	4:E:217:LYS:HD2	1.75	0.43
4:E:195:ASN:CB	4:E:205:PHE:O	2.66	0.43
4:E:275:THR:O	4:E:279:VAL:HG23	2.18	0.43
1:A:46:VAL:CB	1:A:270:ALA:C	2.92	0.43
1:A:74:GLY:C	1:A:75:ILE:HG23	2.43	0.43
1:A:92:LEU:O	1:A:93:TYR:C	2.60	0.43
1:A:287:SER:O	1:A:291:VAL:HG23	2.19	0.43
2:B:10:VAL:HG12	2:B:11:LEU:HD23	2.00	0.43
2:B:290:LEU:HD11	2:B:453:SER:CB	2.49	0.43
2:B:411:ILE:HG13	2:B:411:ILE:H	1.69	0.43
2:B:434:VAL:HG12	2:B:438:LEU:HD12	1.98	0.43
3:C:273:LEU:CD2	3:C:276:GLN:CB	2.92	0.43
1:D:283:ILE:CA	1:D:286:ILE:HD12	2.46	0.43
1:D:377:GLU:CG	4:E:415:CYS:HB2	2.48	0.43
4:E:30:VAL:HG22	4:E:59:TRP:CB	2.48	0.43
4:E:59:TRP:HE3	4:E:59:TRP:N	2.16	0.43
1:A:72:TYR:CB	1:A:112:TYR:CB	2.83	0.43
1:A:107:LYS:CE	2:B:150:THR:CB	2.94	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:ILE:HG22	1:A:203:TYR:CE1	2.54	0.43
1:A:267:THR:O	1:A:268:SER:C	2.62	0.43
2:B:35:LEU:CD2	2:B:56:LEU:C	2.92	0.43
2:B:105:HIS:N	2:B:118:TRP:CH2	2.86	0.43
2:B:187:SER:OG	2:B:216:LYS:HE2	2.19	0.43
2:B:431:VAL:CG2	2:B:433:MET:HG2	2.49	0.43
3:C:141:TRP:HH2	3:C:223:ARG:HD3	1.80	0.43
1:D:36:GLN:O	1:D:54:VAL:HA	2.19	0.43
1:D:68:ASN:HB2	1:D:69:PRO:HD3	1.99	0.43
1:D:92:LEU:HG	1:D:124:PHE:CE1	2.53	0.43
1:D:411:LEU:HD23	1:D:414:PHE:HD2	1.82	0.43
4:E:76:LEU:C	4:E:77:VAL:CG2	2.91	0.43
4:E:139:GLN:O	4:E:213:ILE:HA	2.17	0.43
1:A:134:HIS:CD2	1:A:207:MET:HE3	2.54	0.43
1:A:167:LEU:HA	1:A:170:PHE:HB2	2.01	0.43
1:A:227:PHE:HD1	1:A:230:VAL:HB	1.83	0.43
1:A:410:LEU:HD13	1:A:414:PHE:HD2	1.84	0.43
2:B:38:THR:CG2	2:B:55:PHE:HE1	2.27	0.43
2:B:238:VAL:HG21	2:B:255:ALA:HB1	1.99	0.43
2:B:251:LEU:C	2:B:251:LEU:CD1	2.75	0.43
2:B:274:SER:O	2:B:278:PRO:CD	2.66	0.43
2:B:468:PHE:O	2:B:469:ALA:HB2	2.18	0.43
3:C:40:SER:O	3:C:41:ASN:HB2	2.19	0.43
3:C:89:ILE:HD13	3:C:89:ILE:HG21	1.62	0.43
3:C:232:PHE:O	3:C:235:PRO:HD2	2.18	0.43
3:C:288:ILE:HD13	3:C:290:LYS:CD	2.48	0.43
1:D:40:LEU:HD22	1:D:52:THR:HG1	1.82	0.43
1:D:75:ILE:CD1	4:E:24:LEU:HD12	2.49	0.43
1:D:114:GLY:O	1:D:116:ILE:HD13	2.19	0.43
4:E:35:THR:HG23	4:E:175:GLU:OE2	2.18	0.43
4:E:58:GLN:HA	4:E:59:TRP:CE3	2.54	0.43
4:E:103:TYR:HD2	4:E:104:TYR:CD1	2.37	0.43
4:E:213:ILE:O	4:E:213:ILE:CG2	2.66	0.43
4:E:287:ILE:HG13	4:E:291:PHE:CD2	2.54	0.43
1:A:247:ILE:CD1	1:A:247:ILE:C	2.91	0.43
1:A:265:PRO:CD	1:A:266:SER:N	2.81	0.43
3:C:251:ALA:C	3:C:253:SER:N	2.76	0.43
1:D:16:ASN:HD22	1:D:16:ASN:N	2.17	0.43
1:D:128:CYS:SG	1:D:144:MET:HE2	2.59	0.43
1:D:160:PRO:HD3	1:D:185:LYS:HB2	1.91	0.43
1:D:240:GLY:O	1:D:243:MET:SD	2.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:416:LEU:O	1:D:420:ILE:HG23	2.19	0.43
4:E:231:LEU:HG	4:E:232:ILE:N	2.19	0.43
1:A:7:LEU:HD22	1:A:70:ALA:HA	2.01	0.43
1:A:28:PHE:CD1	1:A:154:THR:O	2.72	0.43
1:A:80:LEU:CD2	1:A:110:LEU:HB2	2.48	0.43
1:A:131:ILE:CG1	1:A:140:GLN:HG2	2.48	0.43
1:A:179:LYS:CE	1:A:208:GLN:OE1	2.66	0.43
1:A:237:THR:HB	1:A:406:ILE:CG2	2.49	0.43
2:B:35:LEU:O	2:B:174:MET:CE	2.63	0.43
2:B:92:LEU:HD22	2:B:146:PHE:CG	2.54	0.43
2:B:105:HIS:H	2:B:118:TRP:HH2	1.65	0.43
3:C:284:ALA:O	3:C:285:VAL:HG12	2.18	0.43
1:D:37:LEU:N	1:D:54:VAL:HG12	2.34	0.43
4:E:5:ARG:H	4:E:5:ARG:HG2	1.44	0.43
4:E:152:ALA:CB	4:E:204:ASP:O	2.63	0.43
4:E:273:PRO:O	4:E:277:LEU:HG	2.19	0.43
4:E:287:ILE:HG13	4:E:291:PHE:HE2	1.83	0.43
1:A:35:LEU:HD13	1:A:203:TYR:CZ	2.54	0.43
1:A:41:ILE:CD1	1:A:51:GLU:OE1	2.60	0.43
1:A:77:LYS:HD2	1:A:111:ASP:OD2	2.19	0.43
1:A:139:GLN:HB2	1:A:207:MET:O	2.19	0.43
1:A:409:ILE:H	1:A:409:ILE:HG13	1.54	0.43
2:B:38:THR:HG23	2:B:54:VAL:HA	2.00	0.43
2:B:281:ILE:HG22	2:B:285:MET:CA	2.48	0.43
2:B:296:ILE:O	2:B:296:ILE:CG2	2.67	0.43
3:C:247:PHE:HE1	3:C:309:VAL:HG23	1.77	0.43
1:D:15:TYR:HE2	1:D:84:ASP:HB3	1.81	0.43
1:D:189:TYR:N	1:D:197:PRO:HD2	2.33	0.43
4:E:104:TYR:HD1	4:E:104:TYR:N	2.16	0.43
4:E:151:ASN:HA	4:E:205:PHE:CG	2.54	0.43
4:E:173:ASP:OD2	4:E:185:ILE:HD13	2.18	0.43
4:E:453:ILE:HD12	4:E:454:ALA:N	2.34	0.43
2:B:93:MET:CG	2:B:206:ASP:HB3	2.49	0.42
2:B:226:VAL:CG2	2:B:227:PRO:CD	2.95	0.42
2:B:277:VAL:N	2:B:278:PRO:CD	2.79	0.42
2:B:415:LEU:HD13	2:B:415:LEU:O	2.16	0.42
3:C:35:LEU:HD22	3:C:215:VAL:CG2	2.46	0.42
3:C:54:THR:O	3:C:126:PHE:CD2	2.72	0.42
3:C:72:SER:HA	3:C:76:ASP:HB2	1.99	0.42
3:C:125:ILE:O	3:C:125:ILE:HG22	2.19	0.42
3:C:449:VAL:HG12	3:C:452:THR:CB	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:VAL:O	1:D:18:VAL:HG12	2.19	0.42
1:D:38:ILE:C	1:D:39:GLN:HG3	2.44	0.42
4:E:44:GLU:CB	4:E:280:PRO:CB	2.58	0.42
4:E:242:LEU:N	4:E:243:PRO:HD2	2.34	0.42
4:E:242:LEU:HA	4:E:245:GLN:OE1	2.19	0.42
4:E:267:LEU:HA	4:E:270:GLN:HG3	2.00	0.42
1:A:67:TRP:HB2	1:A:112:TYR:O	2.19	0.42
1:A:171:MET:CE	1:A:176:TRP:CZ2	2.89	0.42
1:A:241:GLU:O	1:A:241:GLU:HG2	2.19	0.42
1:A:267:THR:HG23	1:A:271:VAL:HG21	1.99	0.42
2:B:32:ARG:HH21	2:B:60:TRP:CA	2.31	0.42
2:B:198:ARG:HH11	2:B:198:ARG:CG	2.29	0.42
2:B:216:LYS:O	2:B:216:LYS:CD	2.59	0.42
2:B:223:TYR:C	2:B:226:VAL:HG22	2.44	0.42
2:B:256:LEU:O	2:B:257:LEU:C	2.63	0.42
2:B:422:ASP:C	2:B:422:ASP:OD1	2.63	0.42
3:C:30:VAL:HG23	3:C:157:GLU:N	2.30	0.42
3:C:116:GLY:O	3:C:117:TYR:C	2.61	0.42
3:C:463:PRO:C	3:C:467:LEU:HD23	2.43	0.42
3:C:474:VAL:O	3:C:474:VAL:HG12	2.19	0.42
1:D:60:TRP:CD2	1:D:86:TRP:HH2	2.37	0.42
1:D:89:ASP:OD1	1:D:89:ASP:O	2.36	0.42
1:D:176:TRP:HB2	1:D:209:ARG:HA	2.02	0.42
1:D:178:MET:HE1	1:D:207:MET:SD	2.58	0.42
4:E:91:LEU:HB3	4:E:94:ASN:N	2.27	0.42
4:E:127:CYS:SG	4:E:128:PRO:CD	3.02	0.42
4:E:140:ASN:OD1	4:E:211:PHE:CG	2.72	0.42
4:E:296:ILE:CG1	4:E:297:VAL:N	2.81	0.42
1:A:305:THR:CB	1:A:400:LYS:CB	2.97	0.42
2:B:34:GLY:O	2:B:35:LEU:CD2	2.68	0.42
2:B:202:PRO:HG2	2:B:203:SER:N	2.33	0.42
2:B:240:TYR:CD1	2:B:240:TYR:C	2.95	0.42
2:B:276:SER:O	2:B:276:SER:OG	2.35	0.42
2:B:287:ILE:N	2:B:290:LEU:HD12	2.34	0.42
3:C:52:LEU:HD22	3:C:52:LEU:H	1.84	0.42
3:C:59:ASP:OD1	3:C:121:LEU:CD1	2.65	0.42
3:C:106:TYR:O	3:C:107:PHE:C	2.62	0.42
1:D:45:GLU:CD	1:D:271:VAL:HG22	2.44	0.42
1:D:305:THR:O	1:D:306:HIS:C	2.62	0.42
1:D:398:GLU:HB2	1:D:401:TYR:CE1	2.54	0.42
4:E:100:GLU:CD	4:E:122:ILE:HG12	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:188:ARG:N	4:E:189:PRO:HD3	2.32	0.42
4:E:450:CYS:O	4:E:454:ALA:HB2	2.19	0.42
1:A:36:GLN:OE1	1:A:37:LEU:C	2.62	0.42
1:A:57:ARG:HD3	1:A:161:GLU:CD	2.44	0.42
1:A:160:PRO:HG2	1:A:185:LYS:CD	2.47	0.42
1:A:195:ASP:OD1	1:A:197:PRO:HG3	2.19	0.42
1:A:380:LYS:HB2	1:A:381:TYR:HD1	1.84	0.42
1:A:382:ILE:HG12	1:A:382:ILE:H	1.66	0.42
1:A:410:LEU:O	1:A:414:PHE:HB2	2.19	0.42
1:A:426:PHE:CD1	1:A:427:ALA:N	2.76	0.42
3:C:11:LEU:C	3:C:16:LYS:HG3	2.44	0.42
3:C:59:ASP:HA	3:C:121:LEU:HB2	1.97	0.42
1:D:49:ILE:HA	1:D:49:ILE:HD13	1.72	0.42
1:D:181:TYR:CE1	1:D:203:TYR:HB3	2.46	0.42
1:D:187:TRP:CH2	1:D:189:TYR:CB	2.96	0.42
1:D:256:PHE:CZ	4:E:263:ILE:HA	2.54	0.42
1:D:295:VAL:HG23	1:D:296:ILE:N	2.34	0.42
4:E:91:LEU:HD13	4:E:145:PHE:N	2.34	0.42
4:E:242:LEU:HG	4:E:243:PRO:HD3	2.01	0.42
4:E:418:ALA:HA	4:E:421:PHE:HD2	1.84	0.42
1:A:7:LEU:HD22	1:A:70:ALA:CA	2.50	0.42
1:A:131:ILE:HG12	1:A:140:GLN:HG2	2.01	0.42
2:B:40:LEU:HB2	2:B:52:THR:HG23	2.00	0.42
2:B:96:ASN:C	2:B:98:GLY:N	2.77	0.42
2:B:463:PRO:HB2	2:B:464:PRO:CD	2.49	0.42
3:C:7:LEU:C	3:C:9:ASN:H	2.26	0.42
3:C:74:TYR:O	3:C:78:SER:HA	2.18	0.42
3:C:111:LEU:O	3:C:118:VAL:HG13	2.20	0.42
1:D:37:LEU:HA	1:D:54:VAL:HG13	2.00	0.42
1:D:252:SER:HB2	4:E:259:LEU:CD2	2.49	0.42
1:A:389:ASP:C	1:A:392:SER:HB3	2.45	0.42
1:A:410:LEU:C	1:A:410:LEU:CD1	2.92	0.42
2:B:128:CYS:SG	2:B:144:MET:CG	3.06	0.42
2:B:135:PHE:HB2	2:B:279:ILE:HG21	2.01	0.42
2:B:211:LEU:HB3	2:B:213:ILE:HG23	2.00	0.42
3:C:69:TRP:HB2	3:C:74:TYR:H	1.84	0.42
3:C:80:LEU:O	3:C:112:VAL:CB	2.66	0.42
1:D:47:ASN:O	1:D:49:ILE:HG12	2.19	0.42
1:D:212:LEU:O	1:D:216:VAL:CG2	2.67	0.42
1:D:240:GLY:C	1:D:242:LYS:N	2.76	0.42
1:D:407:ASP:HA	1:D:410:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:58:GLN:HA	4:E:59:TRP:HE3	1.84	0.42
4:E:128:PRO:HD2	4:E:141:CYS:HA	2.02	0.42
1:A:20:ARG:CG	1:A:20:ARG:O	2.67	0.42
1:A:148:ILE:O	1:A:198:TYR:CE2	2.73	0.42
1:A:166:ASP:OD1	1:A:166:ASP:C	2.60	0.42
1:A:235:LEU:HA	2:B:306:HIS:CD2	2.55	0.42
1:A:251:LEU:CG	4:E:260:ALA:CB	2.98	0.42
2:B:160:HIS:HE1	2:B:207:VAL:HG21	1.85	0.42
2:B:269:LYS:C	2:B:271:PRO:CD	2.90	0.42
3:C:154:ASN:CA	3:C:211:ASN:CB	2.95	0.42
3:C:179:ILE:HD11	3:C:195:LYS:HB3	2.02	0.42
3:C:429:ILE:HG13	3:C:430:VAL:CG2	2.50	0.42
3:C:470:ILE:HD13	3:C:470:ILE:HA	1.84	0.42
1:D:60:TRP:O	1:D:116:ILE:HG12	2.20	0.42
1:D:179:LYS:HB2	1:D:206:ILE:HG22	2.01	0.42
1:D:251:LEU:C	1:D:254:THR:HG22	2.45	0.42
4:E:66:TRP:CE3	4:E:70:GLU:HG2	2.54	0.42
1:A:12:LEU:HD12	1:A:12:LEU:O	2.20	0.42
1:A:185:LYS:O	1:A:186:HIS:HB2	2.20	0.42
2:B:46:LYS:HB2	2:B:276:SER:O	2.19	0.42
2:B:186:TRP:CG	2:B:215:ARG:HD2	2.55	0.42
2:B:286:PHE:C	2:B:290:LEU:HD12	2.44	0.42
3:C:180:ASP:HB2	3:C:195:LYS:CB	2.50	0.42
3:C:261:ILE:O	3:C:262:CYS:C	2.61	0.42
3:C:269:VAL:HA	3:C:272:LEU:HD11	2.02	0.42
3:C:431:LYS:HE2	1:D:379:VAL:HG22	1.97	0.42
3:C:476:GLY:HA2	3:C:479:ASN:HB3	2.01	0.42
1:D:7:LEU:HD22	1:D:70:ALA:O	2.19	0.42
1:D:36:GLN:HB3	1:D:55:ARG:CB	2.48	0.42
1:D:149:TRP:CZ2	1:D:150:THR:HB	2.55	0.42
1:D:231:LEU:HD23	1:D:231:LEU:HA	1.70	0.42
1:D:398:GLU:CB	1:D:401:TYR:CZ	3.03	0.42
4:E:24:LEU:HA	4:E:24:LEU:HD23	1.48	0.42
4:E:45:LYS:HZ1	4:E:278:ASN:HA	1.82	0.42
4:E:76:LEU:O	4:E:77:VAL:HG23	2.20	0.42
1:A:57:ARG:CG	1:A:57:ARG:O	2.67	0.42
1:A:130:ILE:CD1	1:A:130:ILE:N	2.81	0.42
1:A:148:ILE:HG21	1:A:198:TYR:HB3	1.99	0.42
1:A:279:LEU:HD13	1:A:282:MET:HB3	2.01	0.42
1:A:395:ALA:O	1:A:399:TRP:CB	2.68	0.42
2:B:95:ASN:HA	2:B:127:SER:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:139:TRP:O	2:B:140:GLN:CG	2.68	0.42
2:B:456:LEU:N	2:B:456:LEU:CD2	2.82	0.42
3:C:159:SER:C	3:C:213:GLN:HG3	2.45	0.42
3:C:192:ILE:CD1	3:C:221:ILE:HG21	2.49	0.42
1:D:58:GLN:HE22	1:D:87:LEU:HD11	1.85	0.42
1:D:90:LEU:HD23	1:D:90:LEU:HA	1.69	0.42
1:D:429:ARG:N	1:D:429:ARG:NE	2.67	0.42
4:E:26:HIS:CA	4:E:27:VAL:HG13	2.50	0.42
4:E:62:TYR:C	4:E:64:LEU:N	2.78	0.42
4:E:76:LEU:O	4:E:77:VAL:CG2	2.68	0.42
4:E:91:LEU:O	4:E:92:GLU:C	2.63	0.42
4:E:267:LEU:C	4:E:270:GLN:HG3	2.42	0.42
1:A:157:SER:HB2	1:A:199:LEU:HD11	2.00	0.42
1:A:185:LYS:HB3	1:A:185:LYS:HE2	1.79	0.42
1:A:220:ILE:O	1:A:220:ILE:CG2	2.67	0.42
1:A:231:LEU:HD23	1:A:231:LEU:HA	1.94	0.42
1:A:238:ASP:HB3	2:B:306:HIS:HE1	1.74	0.42
2:B:136:PRO:C	2:B:138:ASP:H	2.27	0.42
2:B:439:PHE:C	2:B:442:ILE:HB	2.45	0.42
3:C:149:THR:HA	3:C:160:MET:HE2	2.02	0.42
3:C:247:PHE:CD2	3:C:460:ILE:CD1	3.02	0.42
1:D:19:ILE:H	1:D:19:ILE:HG13	1.66	0.42
1:D:247:ILE:HA	1:D:247:ILE:HD13	1.61	0.42
1:D:429:ARG:NE	1:D:429:ARG:CA	2.83	0.42
4:E:63:ARG:O	4:E:64:LEU:HG	2.20	0.42
4:E:75:ASP:HB3	4:E:110:TYR:OH	2.20	0.42
4:E:94:ASN:ND2	4:E:126:THR:H	2.18	0.42
4:E:172:ILE:CG2	4:E:174:PRO:HD2	2.49	0.42
4:E:267:LEU:CD1	4:E:270:GLN:OE1	2.65	0.42
4:E:462:THR:O	4:E:463:LEU:C	2.62	0.42
1:A:85:VAL:HG12	1:A:86:TRP:N	2.34	0.41
1:A:136:PRO:HG3	1:A:274:ILE:HG23	2.01	0.41
1:A:159:SER:HB2	1:A:160:PRO:CD	2.50	0.41
1:A:163:ASP:O	1:A:164:ARG:HG3	2.19	0.41
1:A:189:TYR:CA	1:A:197:PRO:HD2	2.32	0.41
1:A:245:LEU:HD21	2:B:250:SER:HA	1.93	0.41
2:B:409:LYS:HE2	3:C:423:ILE:HA	2.02	0.41
1:D:2:GLU:C	1:D:4:GLU:N	2.78	0.41
1:D:106:THR:HG23	1:D:107:LYS:NZ	2.35	0.41
1:D:128:CYS:O	1:D:129:GLU:C	2.63	0.41
4:E:59:TRP:CH2	4:E:107:VAL:CG1	3.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:CYS:C	1:A:195:ASP:H	2.28	0.41
1:A:232:VAL:O	1:A:236:PRO:HG3	2.20	0.41
2:B:456:LEU:CD2	2:B:456:LEU:H	2.33	0.41
3:C:110:VAL:HG22	3:C:120:TRP:CG	2.55	0.41
3:C:139:PHE:C	3:C:141:TRP:HD1	2.28	0.41
3:C:303:VAL:O	3:C:306:CYS:HB2	2.20	0.41
3:C:435:GLU:O	3:C:439:TYR:HD1	2.03	0.41
1:D:176:TRP:HB3	1:D:209:ARG:CG	2.50	0.41
4:E:44:GLU:CG	4:E:129:ILE:CG1	2.89	0.41
4:E:133:TYR:CG	4:E:139:GLN:CB	3.03	0.41
4:E:262:THR:O	4:E:263:ILE:C	2.63	0.41
1:A:103:VAL:HG12	1:A:104:HIS:N	2.35	0.41
1:A:213:TYR:CG	1:A:214:PHE:N	2.88	0.41
3:C:58:MET:SD	3:C:92:ILE:HD12	2.58	0.41
3:C:76:ASP:C	3:C:77:ILE:HG23	2.45	0.41
3:C:261:ILE:C	3:C:263:VAL:N	2.79	0.41
1:D:63:VAL:CG1	1:D:64:ARG:N	2.81	0.41
1:D:250:LEU:O	1:D:254:THR:HG22	2.20	0.41
1:D:419:ILE:CD1	1:D:420:ILE:CG2	2.98	0.41
4:E:17:ARG:NH1	4:E:18:ILE:HG22	2.33	0.41
4:E:66:TRP:CD1	4:E:66:TRP:N	2.88	0.41
4:E:103:TYR:HD1	4:E:117:TRP:HH2	1.68	0.41
4:E:181:GLY:HA2	4:E:183:TRP:CE3	2.55	0.41
4:E:297:VAL:O	4:E:300:CYS:HB3	2.20	0.41
1:A:157:SER:HB2	1:A:199:LEU:HD12	2.00	0.41
1:A:257:LEU:O	1:A:260:ILE:HG22	2.20	0.41
1:A:384:GLU:OE2	1:A:387:LYS:HG3	2.21	0.41
2:B:22:SER:C	2:B:23:GLN:HE21	2.27	0.41
3:C:149:THR:HB	3:C:214:ASP:HA	2.02	0.41
3:C:431:LYS:NZ	1:D:382:ILE:CD1	2.83	0.41
1:D:45:GLU:CB	1:D:271:VAL:CG2	2.86	0.41
1:D:46:VAL:HG21	1:D:270:ALA:HA	2.02	0.41
4:E:44:GLU:CG	4:E:280:PRO:CB	2.65	0.41
1:A:136:PRO:HB3	1:A:138:ASP:OD1	2.20	0.41
1:A:166:ASP:N	1:A:181:TYR:HD1	2.17	0.41
1:A:420:ILE:CG1	1:A:421:GLY:H	2.26	0.41
2:B:198:ARG:HG3	2:B:198:ARG:NH1	2.33	0.41
2:B:248:LYS:CD	2:B:252:SER:CB	2.62	0.41
3:C:84:PRO:HG3	3:C:107:PHE:C	2.45	0.41
3:C:148:PHE:N	3:C:148:PHE:HD1	2.18	0.41
3:C:201:ILE:HA	3:C:213:GLN:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:37:LEU:HD12	1:D:53:ASN:C	2.43	0.41
1:D:137:PHE:HE1	1:D:210:ILE:HD12	1.86	0.41
1:D:188:VAL:C	1:D:197:PRO:HD2	2.46	0.41
1:D:216:VAL:O	1:D:220:ILE:CG1	2.64	0.41
1:D:291:VAL:HG12	1:D:295:VAL:CG1	2.50	0.41
4:E:2:GLU:HB3	4:E:6:LEU:HG	2.01	0.41
4:E:19:LYS:HZ1	4:E:154:GLU:CB	2.31	0.41
4:E:74:ILE:C	4:E:76:LEU:N	2.79	0.41
4:E:91:LEU:HB2	4:E:95:VAL:HG23	2.03	0.41
4:E:159:LEU:CD1	4:E:192:LYS:HA	2.47	0.41
4:E:237:VAL:O	4:E:237:VAL:HG12	2.21	0.41
4:E:242:LEU:HG	4:E:243:PRO:CD	2.51	0.41
1:A:92:LEU:HD23	1:A:92:LEU:H	1.86	0.41
1:A:398:GLU:HA	1:A:401:TYR:CE1	2.56	0.41
2:B:56:LEU:O	2:B:57:ASN:C	2.63	0.41
2:B:138:ASP:OD1	2:B:464:PRO:HB2	2.21	0.41
2:B:186:TRP:HB2	2:B:187:SER:H	1.66	0.41
2:B:258:ALA:CB	3:C:265:LEU:HD13	2.50	0.41
2:B:439:PHE:CD1	2:B:439:PHE:C	2.97	0.41
2:B:440:LEU:C	2:B:443:PHE:HB3	2.44	0.41
3:C:135:LEU:C	3:C:137:PHE:N	2.79	0.41
3:C:222:ARG:NH2	3:C:224:LYS:N	2.68	0.41
3:C:446:TRP:HA	3:C:446:TRP:CE3	2.55	0.41
1:D:92:LEU:H	1:D:92:LEU:HD23	1.80	0.41
1:D:107:LYS:HE3	4:E:149:THR:CA	2.47	0.41
1:D:295:VAL:HG13	1:D:295:VAL:H	1.44	0.41
1:D:420:ILE:HA	1:D:423:VAL:CB	2.51	0.41
4:E:55:ILE:HG13	4:E:55:ILE:O	2.20	0.41
4:E:58:GLN:HA	4:E:115:MET:O	2.21	0.41
4:E:88:ASP:OD2	4:E:149:THR:HB	2.20	0.41
4:E:133:TYR:CD1	4:E:139:GLN:N	2.77	0.41
4:E:133:TYR:HA	4:E:135:PRO:HD2	2.03	0.41
1:A:45:GLU:O	1:A:46:VAL:C	2.62	0.41
1:A:51:GLU:HG3	1:A:125:LYS:HD2	2.02	0.41
1:A:137:PHE:HE1	1:A:210:ILE:HB	1.84	0.41
1:A:287:SER:O	1:A:288:SER:C	2.62	0.41
1:A:293:VAL:O	1:A:297:ASN:HB3	2.20	0.41
1:A:387:LYS:H	1:A:387:LYS:HG2	1.55	0.41
2:B:40:LEU:CD2	2:B:52:THR:OG1	2.63	0.41
2:B:437:ARG:HG2	2:B:437:ARG:HH11	1.86	0.41
3:C:121:LEU:O	3:C:121:LEU:CG	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:130:CYS:SG	3:C:131:PRO:HD2	2.60	0.41
3:C:139:PHE:O	3:C:141:TRP:HD1	2.02	0.41
3:C:474:VAL:HA	3:C:477:ASN:CG	2.46	0.41
4:E:45:LYS:HB3	4:E:277:LEU:O	2.21	0.41
4:E:81:SER:C	4:E:86:LEU:HD11	2.46	0.41
4:E:270:GLN:O	4:E:273:PRO:HG2	2.21	0.41
4:E:297:VAL:HB	4:E:298:THR:H	1.57	0.41
1:A:92:LEU:CB	1:A:95:ASN:HD22	2.34	0.41
1:A:133:THR:O	1:A:140:GLN:HB2	2.20	0.41
1:A:134:HIS:C	1:A:134:HIS:ND1	2.79	0.41
1:A:245:LEU:CD1	2:B:250:SER:CA	2.98	0.41
1:A:305:THR:O	1:A:306:HIS:HB3	2.20	0.41
2:B:53:SER:C	2:B:54:VAL:HG13	2.46	0.41
2:B:147:LYS:HE2	2:B:148:SER:OG	2.20	0.41
2:B:232:SER:HA	2:B:235:ALA:CB	2.48	0.41
2:B:260:THR:O	2:B:264:LEU:HG	2.20	0.41
2:B:286:PHE:CD1	2:B:287:ILE:HG23	2.54	0.41
2:B:403:GLU:CD	2:B:403:GLU:C	2.88	0.41
3:C:132:ILE:O	3:C:133:ASN:HB2	2.18	0.41
3:C:201:ILE:CG1	3:C:211:ASN:O	2.59	0.41
3:C:465:MET:O	3:C:465:MET:HG2	2.09	0.41
1:D:137:PHE:HE1	1:D:210:ILE:CD1	2.32	0.41
1:D:257:LEU:C	1:D:260:ILE:H	2.29	0.41
1:D:264:ILE:HA	1:D:267:THR:HG22	2.02	0.41
1:D:423:VAL:HA	1:D:426:PHE:HB3	2.02	0.41
4:E:177:PHE:CD1	4:E:178:THR:O	2.74	0.41
4:E:436:ASN:HA	4:E:439:TRP:CD1	2.54	0.41
1:A:41:ILE:HG21	1:A:123:ILE:HD11	2.01	0.41
1:A:56:LEU:CD1	1:A:90:LEU:HD13	2.51	0.41
1:A:146:LEU:HD22	1:A:203:TYR:CZ	2.55	0.41
1:A:168:SER:C	1:A:169:THR:HG23	2.46	0.41
1:A:217:ASN:O	1:A:221:PRO:CD	2.68	0.41
1:A:293:VAL:CG1	1:A:294:VAL:N	2.84	0.41
2:B:28:LYS:CD	2:B:156:VAL:N	2.84	0.41
2:B:92:LEU:O	2:B:93:MET:C	2.63	0.41
2:B:95:ASN:O	2:B:96:ASN:C	2.63	0.41
2:B:184:GLY:C	2:B:186:TRP:N	2.78	0.41
2:B:185:GLN:CB	2:B:219:PHE:CE2	2.83	0.41
2:B:202:PRO:HG2	2:B:203:SER:H	1.86	0.41
2:B:227:PRO:O	2:B:231:ILE:CG1	2.67	0.41
2:B:242:PRO:HG2	2:B:243:PRO:HD2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:249:MET:HE2	2:B:250:SER:HB3	2.03	0.41
2:B:424:LEU:HD23	2:B:424:LEU:HA	1.81	0.41
2:B:431:VAL:HG23	2:B:433:MET:H	1.86	0.41
3:C:69:TRP:HB2	3:C:74:TYR:CA	2.51	0.41
3:C:98:ASN:C	3:C:100:GLY:H	2.29	0.41
3:C:288:ILE:CG1	3:C:289:GLY:H	2.21	0.41
3:C:291:TYR:O	3:C:295:ILE:HG13	2.21	0.41
3:C:295:ILE:HG22	3:C:296:MET:HE3	2.02	0.41
3:C:462:THR:N	3:C:463:PRO:HD2	2.35	0.41
1:D:32:THR:HG21	1:D:59:GLN:HE21	1.86	0.41
1:D:38:ILE:O	1:D:39:GLN:CG	2.66	0.41
1:D:109:LEU:O	1:D:116:ILE:HA	2.21	0.41
1:D:135:PHE:N	1:D:136:PRO:CD	2.84	0.41
1:D:192:CYS:SG	1:D:193:CYS:N	2.93	0.41
4:E:32:LEU:HD12	4:E:208:ILE:CD1	2.49	0.41
4:E:47:GLU:HA	4:E:129:ILE:CD1	2.26	0.41
4:E:103:TYR:CD2	4:E:104:TYR:N	2.89	0.41
4:E:225:ILE:HD12	4:E:225:ILE:HA	1.38	0.41
4:E:269:ALA:O	4:E:273:PRO:CG	2.69	0.41
4:E:453:ILE:HA	4:E:456:LEU:HB3	2.02	0.41
1:A:39:GLN:O	1:A:40:LEU:HD23	2.21	0.41
1:A:110:LEU:CD1	1:A:114:GLY:C	2.93	0.41
1:A:146:LEU:HD22	1:A:203:TYR:OH	2.21	0.41
1:A:245:LEU:HD21	2:B:253:ILE:HB	2.03	0.41
2:B:35:LEU:HD22	2:B:56:LEU:C	2.46	0.41
2:B:36:THR:HB	2:B:55:PHE:CD2	2.57	0.41
2:B:68:ASP:CB	2:B:69:PRO:HD2	2.51	0.41
2:B:72:TYR:HD1	2:B:112:HIS:HB2	1.85	0.41
2:B:87:GLN:HB3	2:B:104:LEU:CD1	2.23	0.41
2:B:152:ASP:CG	2:B:203:SER:HB2	2.45	0.41
2:B:235:ALA:O	2:B:236:ILE:C	2.64	0.41
2:B:262:PHE:HA	2:B:265:LEU:HD12	2.03	0.41
3:C:1:VAL:HA	3:C:4:GLU:CG	2.35	0.41
3:C:19:LYS:O	3:C:19:LYS:CE	2.69	0.41
3:C:26:HIS:CE1	3:C:66:ARG:NH2	2.84	0.41
3:C:192:ILE:CD1	3:C:221:ILE:HG22	2.50	0.41
3:C:431:LYS:O	3:C:434:LYS:HB3	2.20	0.41
1:D:220:ILE:HG13	1:D:220:ILE:H	1.72	0.41
1:D:220:ILE:HB	1:D:221:PRO:CD	2.51	0.41
1:D:229:THR:CG2	1:D:253:LEU:CD1	2.96	0.41
4:E:35:THR:CG2	4:E:175:GLU:OE1	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:150:TYR:O	4:E:205:PHE:CD1	2.74	0.41
4:E:182:GLU:OE1	4:E:182:GLU:CA	2.69	0.41
4:E:264:PHE:N	4:E:264:PHE:HD1	2.19	0.41
2:B:40:LEU:C	2:B:40:LEU:CD1	2.89	0.40
2:B:104:LEU:CA	2:B:118:TRP:HH2	2.18	0.40
2:B:286:PHE:HD1	2:B:290:LEU:CD1	2.33	0.40
3:C:26:HIS:ND1	3:C:26:HIS:N	2.66	0.40
3:C:69:TRP:NE1	3:C:114:PRO:CA	2.81	0.40
3:C:78:SER:HA	3:C:114:PRO:HB2	1.99	0.40
1:D:132:VAL:O	1:D:274:ILE:CB	2.69	0.40
1:D:153:GLY:HA3	1:D:196:THR:O	2.21	0.40
1:D:225:PHE:CZ	1:D:285:VAL:HG23	2.56	0.40
1:D:231:LEU:O	1:D:232:VAL:C	2.62	0.40
1:D:259:VAL:HA	1:D:262:GLU:OE1	2.22	0.40
1:D:264:ILE:HG13	1:D:264:ILE:H	1.18	0.40
1:D:274:ILE:HG22	1:D:276:LYS:HZ2	1.83	0.40
1:D:274:ILE:CB	1:D:276:LYS:HD3	2.39	0.40
1:D:305:THR:HG21	1:D:400:LYS:C	2.45	0.40
4:E:262:THR:CG2	4:E:265:LEU:HB2	2.44	0.40
1:A:58:GLN:HB2	1:A:118:TRP:HB3	2.02	0.40
1:A:166:ASP:CA	1:A:181:TYR:CD1	3.04	0.40
1:A:380:LYS:HB2	1:A:381:TYR:CD1	2.56	0.40
2:B:56:LEU:N	2:B:56:LEU:CD2	2.84	0.40
2:B:417:SER:HB2	2:B:421:PHE:HZ	1.86	0.40
3:C:42:LEU:HD23	3:C:42:LEU:C	2.46	0.40
3:C:46:LYS:HG3	3:C:49:ASP:CG	2.45	0.40
3:C:446:TRP:HA	3:C:446:TRP:HE3	1.86	0.40
1:D:188:VAL:CG1	1:D:190:TYR:CE1	3.04	0.40
4:E:10:LEU:HD22	4:E:64:LEU:HD21	2.02	0.40
4:E:66:TRP:NE1	4:E:111:ASN:CA	2.67	0.40
4:E:70:GLU:O	4:E:74:ILE:HD13	2.21	0.40
4:E:187:HIS:ND1	4:E:188:ARG:N	2.66	0.40
4:E:242:LEU:C	4:E:242:LEU:CD1	2.84	0.40
4:E:255:ILE:HD13	4:E:255:ILE:HA	1.61	0.40
1:A:34:GLY:O	1:A:57:ARG:HG2	2.22	0.40
1:A:228:LEU:HD23	1:A:228:LEU:HA	1.96	0.40
2:B:414:GLN:O	2:B:418:ALA:CB	2.69	0.40
3:C:3:GLU:O	3:C:3:GLU:HG2	2.21	0.40
3:C:50:GLU:HB3	3:C:132:ILE:HB	2.03	0.40
3:C:180:ASP:HB2	3:C:195:LYS:HB3	2.04	0.40
3:C:427:ASN:O	3:C:431:LYS:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:36:GLN:NE2	1:D:36:GLN:CA	2.81	0.40
1:D:134:HIS:C	1:D:134:HIS:HD1	2.29	0.40
1:D:252:SER:CB	4:E:259:LEU:HD22	2.51	0.40
1:D:274:ILE:HG13	1:D:277:TYR:HD2	1.86	0.40
1:D:301:ARG:NH1	1:D:406:ILE:CD1	2.80	0.40
4:E:59:TRP:CE2	4:E:115:MET:CB	3.04	0.40
4:E:60:ASN:N	4:E:60:ASN:ND2	2.68	0.40
4:E:145:PHE:O	4:E:208:ILE:CD1	2.70	0.40
4:E:271:LYS:N	4:E:273:PRO:HD2	2.35	0.40
1:A:43:VAL:CG1	1:A:50:VAL:CG2	2.90	0.40
1:A:218:VAL:HG13	1:A:219:ILE:H	1.77	0.40
1:A:255:VAL:HG12	1:A:256:PHE:HD1	1.86	0.40
2:B:24:THR:HG22	2:B:25:VAL:N	2.25	0.40
2:B:425:LYS:CA	2:B:428:TRP:CD1	2.86	0.40
2:B:429:GLN:HA	2:B:429:GLN:NE2	2.34	0.40
3:C:195:LYS:HD2	3:C:218:TYR:O	2.21	0.40
3:C:204:ASP:C	3:C:207:PRO:HD2	2.47	0.40
3:C:211:ASN:HB2	3:C:212:TYR:H	1.67	0.40
1:D:72:TYR:HA	1:D:112:TYR:CB	2.52	0.40
1:D:267:THR:HG23	1:D:268:SER:H	1.86	0.40
4:E:91:LEU:CG	4:E:145:PHE:HB3	2.50	0.40
4:E:117:TRP:NE1	4:E:119:PRO:HD3	2.35	0.40
4:E:133:TYR:CD2	4:E:139:GLN:HB3	2.56	0.40
2:B:143:THR:CG2	2:B:145:VAL:HG22	2.50	0.40
2:B:160:HIS:NE2	2:B:209:PHE:CE1	2.89	0.40
2:B:218:LEU:CD1	2:B:221:ILE:HG12	2.50	0.40
2:B:269:LYS:CE	2:B:270:VAL:CG2	2.69	0.40
2:B:269:LYS:CD	2:B:270:VAL:N	2.83	0.40
2:B:310:ASN:O	2:B:311:THR:C	2.61	0.40
3:C:102:TYR:CD1	3:C:102:TYR:C	3.00	0.40
3:C:110:VAL:CG1	3:C:111:LEU:H	2.34	0.40
3:C:219:LEU:CD1	3:C:221:ILE:HG22	2.51	0.40
3:C:241:PHE:CD1	3:C:242:LEU:N	2.89	0.40
3:C:249:LEU:HB3	3:C:256:LYS:HZ1	1.75	0.40
1:D:280:PHE:O	1:D:284:PHE:CD1	2.75	0.40
1:D:412:CYS:O	1:D:415:MET:CE	2.68	0.40
4:E:44:GLU:OE1	4:E:129:ILE:HD12	2.22	0.40
4:E:59:TRP:CE3	4:E:115:MET:HB2	2.56	0.40
4:E:67:ASN:O	4:E:71:TYR:HD2	2.05	0.40
4:E:133:TYR:CA	4:E:135:PRO:HD2	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	366/461 (79%)	251 (69%)	68 (19%)	47 (13%)	0	4
1	D	366/461 (79%)	265 (72%)	54 (15%)	47 (13%)	0	4
2	B	364/493 (74%)	238 (65%)	85 (23%)	41 (11%)	0	5
3	C	364/522 (70%)	244 (67%)	74 (20%)	46 (13%)	0	4
4	E	365/488 (75%)	239 (66%)	76 (21%)	50 (14%)	0	4
All	All	1825/2425 (75%)	1237 (68%)	357 (20%)	231 (13%)	0	4

All (231) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	7	LEU
1	A	48	GLN
1	A	83	ASP
1	A	93	TYR
1	A	97	ASP
1	A	102	ILE
1	A	112	TYR
1	A	131	ILE
1	A	149	TRP
1	A	198	TYR
1	A	215	VAL
1	A	248	SER
1	A	249	VAL
1	A	282	MET
1	A	292	THR
1	A	293	VAL
1	A	303	PRO
1	A	304	SER
1	A	392	SER
1	A	420	ILE

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Mol	Chain	Res	Type
2	B	2	VAL
2	B	27	ASP
2	B	48	GLU
2	B	68	ASP
2	B	81	PRO
2	B	89	ASP
2	B	90	ILE
2	B	93	MET
2	B	94	ASN
2	B	99	SER
2	B	107	ASN
2	B	129	THR
2	B	156	VAL
2	B	185	GLN
2	B	206	ASP
2	B	277	VAL
2	B	280	ILE
2	B	306	HIS
2	B	307	ARG
3	C	2	ASN
3	C	13	ILE
3	C	30	VAL
3	C	71	ALA
3	C	99	ASP
3	C	115	ASN
3	C	131	PRO
3	C	132	ILE
3	C	180	ASP
3	C	212	TYR
3	C	224	LYS
3	C	239	ILE
3	C	253	SER
3	C	288	ILE
3	C	301	GLY
3	C	303	VAL
3	C	310	LEU
3	C	434	LYS
3	C	453	ILE
3	C	475	MET
3	C	484	LYS
1	D	3	HIS
1	D	24	HIS

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Mol	Chain	Res	Type
1	D	27	HIS
1	D	30	ASP
1	D	45	GLU
1	D	64	ARG
1	D	74	GLY
1	D	75	ILE
1	D	93	TYR
1	D	94	ASN
1	D	97	ASP
1	D	102	ILE
1	D	113	THR
1	D	130	ILE
1	D	131	ILE
1	D	136	PRO
1	D	153	GLY
1	D	235	LEU
1	D	239	SER
1	D	241	GLU
1	D	276	LYS
1	D	282	MET
1	D	301	ARG
1	D	436	GLU
4	E	2	GLU
4	E	16	LYS
4	E	27	VAL
4	E	68	THR
4	E	82	GLU
4	E	84	LEU
4	E	95	VAL
4	E	98	GLN
4	E	110	TYR
4	E	128	PRO
4	E	152	ALA
4	E	173	ASP
4	E	217	LYS
4	E	222	ILE
4	E	246	ALA
4	E	249	GLN
4	E	253	LEU
4	E	271	LYS
4	E	298	THR
4	E	429	GLN

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Mol	Chain	Res	Type
4	E	438	ASN
1	A	21	PRO
1	A	28	PHE
1	A	75	ILE
1	A	82	SER
1	A	216	VAL
1	A	239	SER
1	A	426	PHE
2	B	86	TRP
2	B	184	GLY
2	B	198	ARG
2	B	249	MET
2	B	281	ILE
2	B	468	PHE
3	C	87	ILE
3	C	116	GLY
3	C	205	LYS
3	C	471	PHE
1	D	2	GLU
1	D	4	GLU
1	D	280	PHE
1	D	423	VAL
1	D	426	PHE
4	E	47	GLU
4	E	101	VAL
4	E	129	ILE
4	E	161	ALA
4	E	443	GLY
4	E	461	GLY
4	E	464	ALA
1	A	4	GLU
1	A	27	HIS
1	A	76	LYS
1	A	148	ILE
1	A	212	LEU
1	A	436	GLU
2	B	76	LYS
2	B	95	ASN
2	B	137	PHE
3	C	240	SER
3	C	440	ASP
3	C	482	PRO

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Mol	Chain	Res	Type
1	D	28	PHE
1	D	68	ASN
1	D	76	LYS
1	D	84	ASP
1	D	162	SER
1	D	174	GLY
1	D	210	ILE
1	D	252	SER
1	D	399	TRP
1	D	403	ALA
4	E	74	ILE
4	E	92	GLU
4	E	133	TYR
4	E	135	PRO
4	E	200	LYS
4	E	206	GLN
4	E	284	LYS
4	E	309	ARG
4	E	439	TRP
1	A	26	THR
1	A	129	GLU
1	A	135	PHE
1	A	162	SER
1	A	180	ASP
1	A	210	ILE
1	A	214	PHE
2	B	39	SER
2	B	102	ILE
2	B	120	PRO
2	B	139	TRP
2	B	147	LYS
2	B	153	THR
2	B	466	ASN
3	C	72	SER
3	C	76	ASP
3	C	137	PHE
3	C	295	ILE
3	C	458	MET
1	D	148	ILE
1	D	236	PRO
4	E	13	ASP
4	E	63	ARG

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Mol	Chain	Res	Type
4	E	280	PRO
4	E	432	SER
1	A	13	GLU
1	A	17	LYS
1	A	167	LEU
1	A	271	VAL
1	A	419	ILE
2	B	75	ILE
2	B	97	ASP
3	C	5	GLU
3	C	95	GLN
3	C	122	PRO
3	C	134	VAL
3	C	211	ASN
1	D	264	ILE
4	E	184	THR
4	E	203	ILE
4	E	231	LEU
4	E	431	ASP
3	C	77	ILE
3	C	136	TYR
1	D	120	PRO
4	E	120	PRO
4	E	279	VAL
2	B	236	ILE
2	B	295	VAL
3	C	138	PRO
3	C	309	VAL
1	D	114	GLY
4	E	297	VAL
1	D	121	PRO
2	B	135	PHE
2	B	463	PRO
3	C	229	VAL
3	C	302	VAL
3	C	449	VAL
1	D	428	GLY
4	E	257	VAL
4	E	446	ILE
1	A	428	GLY
1	D	135	PHE
3	C	104	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	343/427 (80%)	214 (62%)	129 (38%)	0	1
1	D	343/427 (80%)	219 (64%)	124 (36%)	0	1
2	B	340/449 (76%)	239 (70%)	101 (30%)	0	2
3	C	335/475 (70%)	213 (64%)	122 (36%)	0	1
4	E	337/447 (75%)	211 (63%)	126 (37%)	0	1
All	All	1698/2225 (76%)	1096 (64%)	602 (36%)	1	1

All (602) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	SER
1	A	2	GLU
1	A	6	ARG
1	A	7	LEU
1	A	12	LEU
1	A	20	ARG
1	A	22	VAL
1	A	24	HIS
1	A	25	HIS
1	A	26	THR
1	A	29	VAL
1	A	31	ILE
1	A	33	VAL
1	A	35	LEU
1	A	36	GLN
1	A	46	VAL
1	A	54	VAL
1	A	56	LEU
1	A	61	ILE
1	A	63	VAL
1	A	66	ARG
1	A	68	ASN
1	A	72	TYR

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Mol	Chain	Res	Type
1	A	75	ILE
1	A	77	LYS
1	A	78	ILE
1	A	79	ARG
1	A	87	LEU
1	A	92	LEU
1	A	94	ASN
1	A	95	ASN
1	A	100	PHE
1	A	103	VAL
1	A	105	MET
1	A	108	LEU
1	A	110	LEU
1	A	112	TYR
1	A	113	THR
1	A	116	ILE
1	A	117	MET
1	A	124	PHE
1	A	125	LYS
1	A	126	SER
1	A	130	ILE
1	A	132	VAL
1	A	139	GLN
1	A	141	ASN
1	A	142	CYS
1	A	144	MET
1	A	145	LYS
1	A	149	TRP
1	A	156	VAL
1	A	158	ILE
1	A	162	SER
1	A	164	ARG
1	A	167	LEU
1	A	173	SER
1	A	180	ASP
1	A	181	TYR
1	A	188	VAL
1	A	190	TYR
1	A	191	THR
1	A	193	CYS
1	A	195	ASP
1	A	198	TYR

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Mol	Chain	Res	Type
1	A	200	ASP
1	A	201	ILE
1	A	207	MET
1	A	209	ARG
1	A	224	LEU
1	A	225	PHE
1	A	228	LEU
1	A	230	VAL
1	A	232	VAL
1	A	235	LEU
1	A	243	MET
1	A	246	SER
1	A	247	ILE
1	A	248	SER
1	A	254	THR
1	A	255	VAL
1	A	256	PHE
1	A	257	LEU
1	A	260	ILE
1	A	264	ILE
1	A	265	PRO
1	A	266	SER
1	A	267	THR
1	A	268	SER
1	A	273	LEU
1	A	274	ILE
1	A	278	MET
1	A	279	LEU
1	A	280	PHE
1	A	282	MET
1	A	284	PHE
1	A	290	ILE
1	A	292	THR
1	A	293	VAL
1	A	296	ILE
1	A	297	ASN
1	A	298	THR
1	A	304	SER
1	A	306	HIS
1	A	374	SER
1	A	376	ILE
1	A	381	TYR

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Mol	Chain	Res	Type
1	A	382	ILE
1	A	387	LYS
1	A	389	ASP
1	A	391	GLU
1	A	399	TRP
1	A	401	TYR
1	A	402	VAL
1	A	405	VAL
1	A	408	HIS
1	A	409	ILE
1	A	410	LEU
1	A	414	PHE
1	A	415	MET
1	A	419	ILE
1	A	420	ILE
1	A	425	VAL
1	A	426	PHE
1	A	430	LEU
1	A	431	ILE
1	A	433	LEU
1	A	434	SER
1	A	435	GLN
2	B	15	TYR
2	B	18	LYS
2	B	19	VAL
2	B	20	ARG
2	B	21	PRO
2	B	23	GLN
2	B	25	VAL
2	B	27	ASP
2	B	28	LYS
2	B	29	VAL
2	B	31	VAL
2	B	32	ARG
2	B	33	VAL
2	B	37	LEU
2	B	40	LEU
2	B	41	LEU
2	B	42	ILE
2	B	43	LEU
2	B	53	SER
2	B	55	PHE

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Mol	Chain	Res	Type
2	B	56	LEU
2	B	58	LEU
2	B	64	ARG
2	B	65	LEU
2	B	69	PRO
2	B	73	GLU
2	B	79	SER
2	B	81	PRO
2	B	82	SER
2	B	89	ASP
2	B	95	ASN
2	B	102	ILE
2	B	106	VAL
2	B	107	ASN
2	B	117	SER
2	B	119	HIS
2	B	120	PRO
2	B	129	THR
2	B	133	MET
2	B	135	PHE
2	B	136	PRO
2	B	137	PHE
2	B	138	ASP
2	B	145	VAL
2	B	156	VAL
2	B	158	LEU
2	B	159	GLN
2	B	181	THR
2	B	182	GLU
2	B	188	ILE
2	B	191	LYS
2	B	196	ASN
2	B	200	ASP
2	B	201	ASP
2	B	202	PRO
2	B	208	THR
2	B	213	ILE
2	B	216	LYS
2	B	220	TYR
2	B	221	ILE
2	B	225	ILE
2	B	233	ILE

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Mol	Chain	Res	Type
2	B	236	ILE
2	B	237	LEU
2	B	241	LEU
2	B	248	LYS
2	B	249	MET
2	B	251	LEU
2	B	253	ILE
2	B	261	VAL
2	B	263	LEU
2	B	265	LEU
2	B	269	LYS
2	B	275	LEU
2	B	277	VAL
2	B	280	ILE
2	B	281	ILE
2	B	283	TYR
2	B	284	LEU
2	B	288	MET
2	B	291	VAL
2	B	300	VAL
2	B	304	LEU
2	B	307	ARG
2	B	311	THR
2	B	408	ILE
2	B	411	ILE
2	B	421	PHE
2	B	426	LYS
2	B	429	GLN
2	B	431	VAL
2	B	436	ASP
2	B	437	ARG
2	B	439	PHE
2	B	440	LEU
2	B	442	ILE
2	B	447	CYS
2	B	454	ILE
2	B	462	VAL
2	B	464	PRO
2	B	468	PHE
3	C	2	ASN
3	C	3	GLU
3	C	5	GLU

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Mol	Chain	Res	Type
3	C	7	LEU
3	C	13	ILE
3	C	16	LYS
3	C	22	ARG
3	C	24	VAL
3	C	25	LYS
3	C	27	ASN
3	C	28	ASN
3	C	37	LEU
3	C	41	ASN
3	C	43	ILE
3	C	45	LEU
3	C	46	LYS
3	C	48	THR
3	C	50	GLU
3	C	52	LEU
3	C	54	THR
3	C	55	ASN
3	C	60	HIS
3	C	65	HIS
3	C	66	ARG
3	C	67	LEU
3	C	69	TRP
3	C	78	SER
3	C	85	GLU
3	C	87	ILE
3	C	91	ASP
3	C	92	ILE
3	C	94	LEU
3	C	96	ASN
3	C	99	ASP
3	C	102	TYR
3	C	104	VAL
3	C	106	TYR
3	C	107	PHE
3	C	114	PRO
3	C	115	ASN
3	C	121	LEU
3	C	125	ILE
3	C	130	CYS
3	C	132	ILE
3	C	140	ASP

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Mol	Chain	Res	Type
3	C	148	PHE
3	C	149	THR
3	C	152	ASN
3	C	158	ILE
3	C	160	MET
3	C	162	LEU
3	C	179	ILE
3	C	180	ASP
3	C	185	THR
3	C	199	LYS
3	C	201	ILE
3	C	202	TYR
3	C	205	LYS
3	C	206	PHE
3	C	211	ASN
3	C	214	ASP
3	C	222	ARG
3	C	225	PRO
3	C	228	TYR
3	C	229	VAL
3	C	233	ILE
3	C	237	VAL
3	C	241	PHE
3	C	242	LEU
3	C	245	LEU
3	C	249	LEU
3	C	252	GLU
3	C	256	LYS
3	C	259	THR
3	C	262	CYS
3	C	264	LEU
3	C	267	GLN
3	C	269	VAL
3	C	271	LEU
3	C	272	LEU
3	C	274	THR
3	C	276	GLN
3	C	278	LEU
3	C	279	PRO
3	C	280	GLU
3	C	285	VAL
3	C	291	TYR

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Mol	Chain	Res	Type
3	C	293	MET
3	C	296	MET
3	C	297	SER
3	C	299	VAL
3	C	302	VAL
3	C	303	VAL
3	C	309	VAL
3	C	310	LEU
3	C	311	ASN
3	C	315	ARG
3	C	318	SER
3	C	319	THR
3	C	421	SER
3	C	423	ILE
3	C	426	THR
3	C	429	ILE
3	C	430	VAL
3	C	442	GLU
3	C	446	TRP
3	C	449	VAL
3	C	451	GLN
3	C	452	THR
3	C	455	ARG
3	C	456	LEU
3	C	458	MET
3	C	460	ILE
3	C	465	MET
3	C	470	ILE
3	C	471	PHE
3	C	472	ILE
3	C	475	MET
3	C	478	PHE
3	C	479	ASN
3	C	480	ARG
3	C	482	PRO
1	D	3	HIS
1	D	8	VAL
1	D	16	ASN
1	D	17	LYS
1	D	20	ARG
1	D	22	VAL
1	D	23	GLU

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Mol	Chain	Res	Type
1	D	25	HIS
1	D	26	THR
1	D	30	ASP
1	D	35	LEU
1	D	36	GLN
1	D	40	LEU
1	D	41	ILE
1	D	42	ASN
1	D	46	VAL
1	D	54	VAL
1	D	55	ARG
1	D	56	LEU
1	D	60	TRP
1	D	61	ILE
1	D	62	ASP
1	D	64	ARG
1	D	66	ARG
1	D	72	TYR
1	D	76	LYS
1	D	78	ILE
1	D	79	ARG
1	D	80	LEU
1	D	84	ASP
1	D	86	TRP
1	D	91	VAL
1	D	92	LEU
1	D	94	ASN
1	D	100	PHE
1	D	102	ILE
1	D	105	MET
1	D	106	THR
1	D	107	LYS
1	D	108	LEU
1	D	112	TYR
1	D	116	ILE
1	D	118	TRP
1	D	120	PRO
1	D	123	ILE
1	D	126	SER
1	D	129	GLU
1	D	130	ILE
1	D	133	THR

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Mol	Chain	Res	Type
1	D	135	PHE
1	D	142	CYS
1	D	143	THR
1	D	145	LYS
1	D	149	TRP
1	D	151	TYR
1	D	152	ASP
1	D	154	THR
1	D	156	VAL
1	D	158	ILE
1	D	160	PRO
1	D	164	ARG
1	D	167	LEU
1	D	170	PHE
1	D	176	TRP
1	D	177	VAL
1	D	180	ASP
1	D	185	LYS
1	D	188	VAL
1	D	193	CYS
1	D	198	TYR
1	D	200	ASP
1	D	201	ILE
1	D	202	THR
1	D	203	TYR
1	D	207	MET
1	D	210	ILE
1	D	216	VAL
1	D	219	ILE
1	D	220	ILE
1	D	221	PRO
1	D	222	CYS
1	D	225	PHE
1	D	226	SER
1	D	227	PHE
1	D	228	LEU
1	D	230	VAL
1	D	237	THR
1	D	238	ASP
1	D	243	MET
1	D	244	THR
1	D	245	LEU

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Mol	Chain	Res	Type
1	D	247	ILE
1	D	249	VAL
1	D	250	LEU
1	D	253	LEU
1	D	257	LEU
1	D	265	PRO
1	D	267	THR
1	D	271	VAL
1	D	272	PRO
1	D	273	LEU
1	D	274	ILE
1	D	278	MET
1	D	280	PHE
1	D	281	THR
1	D	285	VAL
1	D	289	ILE
1	D	295	VAL
1	D	377	GLU
1	D	382	ILE
1	D	385	HIS
1	D	387	LYS
1	D	394	ASN
1	D	399	TRP
1	D	400	LYS
1	D	402	VAL
1	D	406	ILE
1	D	407	ASP
1	D	408	HIS
1	D	409	ILE
1	D	414	PHE
1	D	418	CYS
1	D	420	ILE
1	D	422	THR
4	E	5	ARG
4	E	13	ASP
4	E	15	ASP
4	E	18	ILE
4	E	19	LYS
4	E	22	LYS
4	E	23	THR
4	E	25	ASP
4	E	27	VAL

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Mol	Chain	Res	Type
4	E	29	ASP
4	E	31	THR
4	E	44	GLU
4	E	45	LYS
4	E	49	LEU
4	E	52	ASN
4	E	53	VAL
4	E	55	ILE
4	E	60	ASN
4	E	62	TYR
4	E	63	ARG
4	E	66	TRP
4	E	67	ASN
4	E	69	SER
4	E	70	GLU
4	E	71	TYR
4	E	74	ILE
4	E	75	ASP
4	E	76	LEU
4	E	79	ILE
4	E	80	PRO
4	E	81	SER
4	E	82	GLU
4	E	83	LEU
4	E	84	LEU
4	E	86	LEU
4	E	87	PRO
4	E	89	VAL
4	E	90	VAL
4	E	100	GLU
4	E	101	VAL
4	E	104	TYR
4	E	106	ASN
4	E	107	VAL
4	E	108	LEU
4	E	110	TYR
4	E	116	TYR
4	E	120	PRO
4	E	122	ILE
4	E	123	TYR
4	E	124	ARG
4	E	125	SER

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Mol	Chain	Res	Type
4	E	127	CYS
4	E	134	PHE
4	E	135	PRO
4	E	140	ASN
4	E	143	LEU
4	E	147	SER
4	E	148	GLN
4	E	154	GLU
4	E	156	ASN
4	E	158	GLN
4	E	162	GLU
4	E	172	ILE
4	E	177	PHE
4	E	179	GLU
4	E	182	GLU
4	E	184	THR
4	E	188	ARG
4	E	191	LYS
4	E	194	TYR
4	E	195	ASN
4	E	196	TRP
4	E	201	ASP
4	E	204	ASP
4	E	208	ILE
4	E	210	PHE
4	E	212	LEU
4	E	213	ILE
4	E	214	ILE
4	E	217	LYS
4	E	220	PHE
4	E	221	TYR
4	E	223	ILE
4	E	225	ILE
4	E	231	LEU
4	E	232	ILE
4	E	235	LEU
4	E	238	LEU
4	E	239	VAL
4	E	242	LEU
4	E	252	THR
4	E	254	SER
4	E	255	ILE

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Mol	Chain	Res	Type
4	E	256	SER
4	E	257	VAL
4	E	258	LEU
4	E	263	ILE
4	E	268	ILE
4	E	270	GLN
4	E	271	LYS
4	E	275	THR
4	E	276	SER
4	E	279	VAL
4	E	284	LYS
4	E	286	LEU
4	E	287	ILE
4	E	291	PHE
4	E	293	SER
4	E	294	LEU
4	E	296	ILE
4	E	297	VAL
4	E	301	VAL
4	E	303	VAL
4	E	310	THR
4	E	416	VAL
4	E	439	TRP
4	E	444	LYS
4	E	452	TRP
4	E	455	LEU
4	E	456	LEU
4	E	465	ILE
4	E	467	LEU
4	E	471	LEU
4	E	472	ASN
4	E	473	GLN
4	E	474	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (77) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	24	HIS
1	A	27	HIS
1	A	47	ASN
1	A	53	ASN

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Mol	Chain	Res	Type
1	A	58	GLN
1	A	59	GLN
1	A	95	ASN
1	A	104	HIS
1	A	139	GLN
1	A	299	HIS
1	A	300	HIS
1	A	435	GLN
2	B	23	GLN
2	B	44	ASN
2	B	47	ASN
2	B	66	GLN
2	B	95	ASN
2	B	96	ASN
2	B	111	GLN
2	B	140	GLN
2	B	141	ASN
2	B	176	ASN
2	B	303	ASN
2	B	305	HIS
2	B	310	ASN
2	B	429	GLN
2	B	460	HIS
2	B	466	ASN
3	C	15	ASN
3	C	26	HIS
3	C	28	ASN
3	C	41	ASN
3	C	55	ASN
3	C	65	HIS
3	C	95	GLN
3	C	97	ASN
3	C	98	ASN
3	C	103	ASN
3	C	115	ASN
3	C	200	ASN
3	C	211	ASN
3	C	267	GLN
3	C	447	ASN
3	C	479	ASN
1	D	16	ASN
1	D	25	HIS

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Mol	Chain	Res	Type
1	D	36	GLN
1	D	53	ASN
1	D	58	GLN
1	D	59	GLN
1	D	94	ASN
1	D	95	ASN
1	D	408	HIS
1	D	435	GLN
4	E	1	ASN
4	E	26	HIS
4	E	52	ASN
4	E	60	ASN
4	E	67	ASN
4	E	93	ASN
4	E	94	ASN
4	E	98	GLN
4	E	111	ASN
4	E	140	ASN
4	E	156	ASN
4	E	158	GLN
4	E	197	GLN
4	E	206	GLN
4	E	215	GLN
4	E	249	GLN
4	E	261	GLN
4	E	278	ASN
4	E	312	ASN
4	E	420	ASN
4	E	429	GLN
4	E	472	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	E	2
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	126:THR	C	127:CYS	N	1.19
1	E	309:ARG	C	310:THR	N	1.19
1	B	129:THR	C	130:ILE	N	1.12

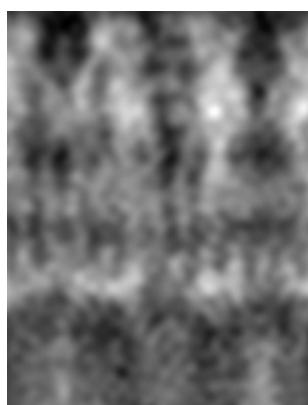
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2072. These allow visual inspection of the internal detail of the map and identification of artifacts.

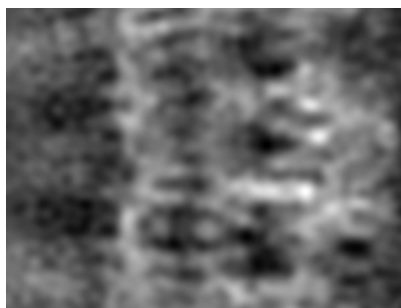
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

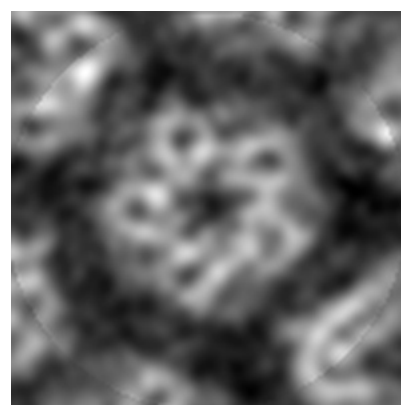
6.1.1 Primary map



X



Y

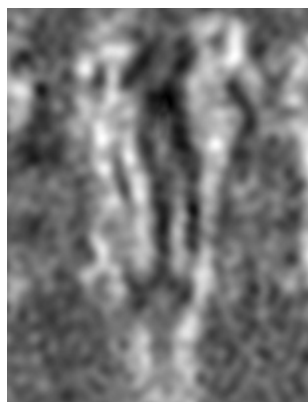


Z

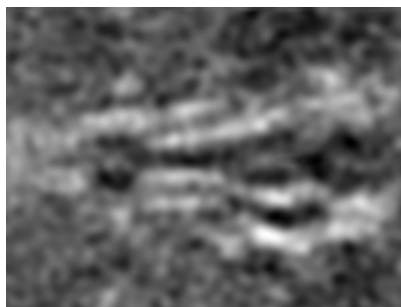
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

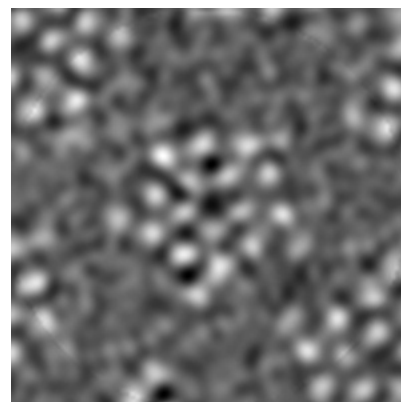
6.2.1 Primary map



X Index: 64



Y Index: 64

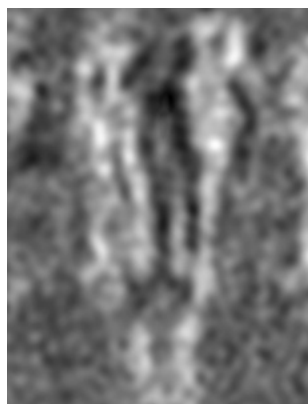


Z Index: 84

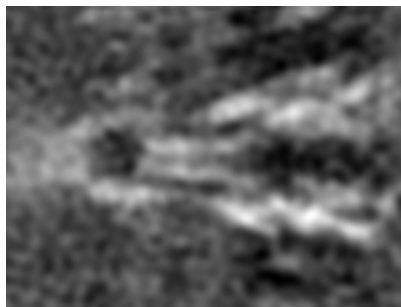
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

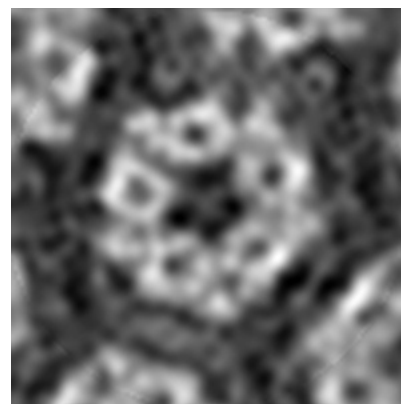
6.3.1 Primary map



X Index: 63



Y Index: 71

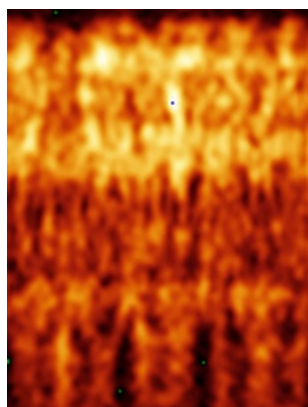


Z Index: 145

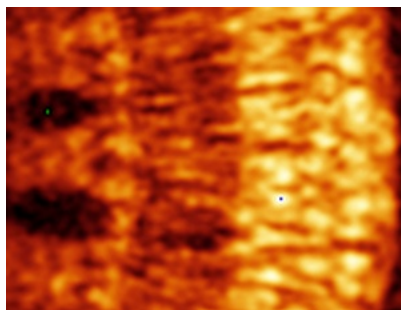
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

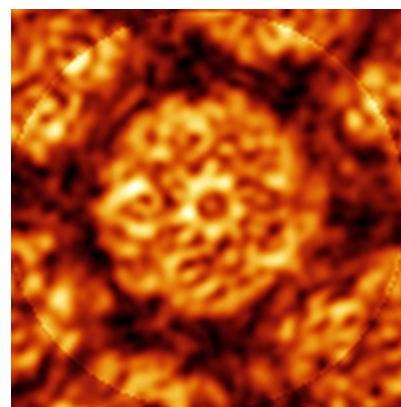
6.4.1 Primary map



X



Y

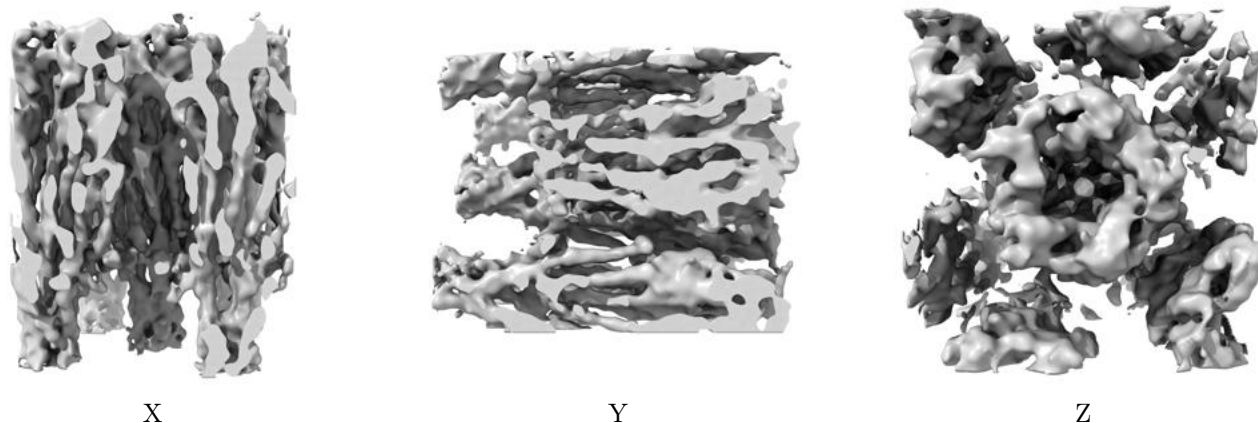


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

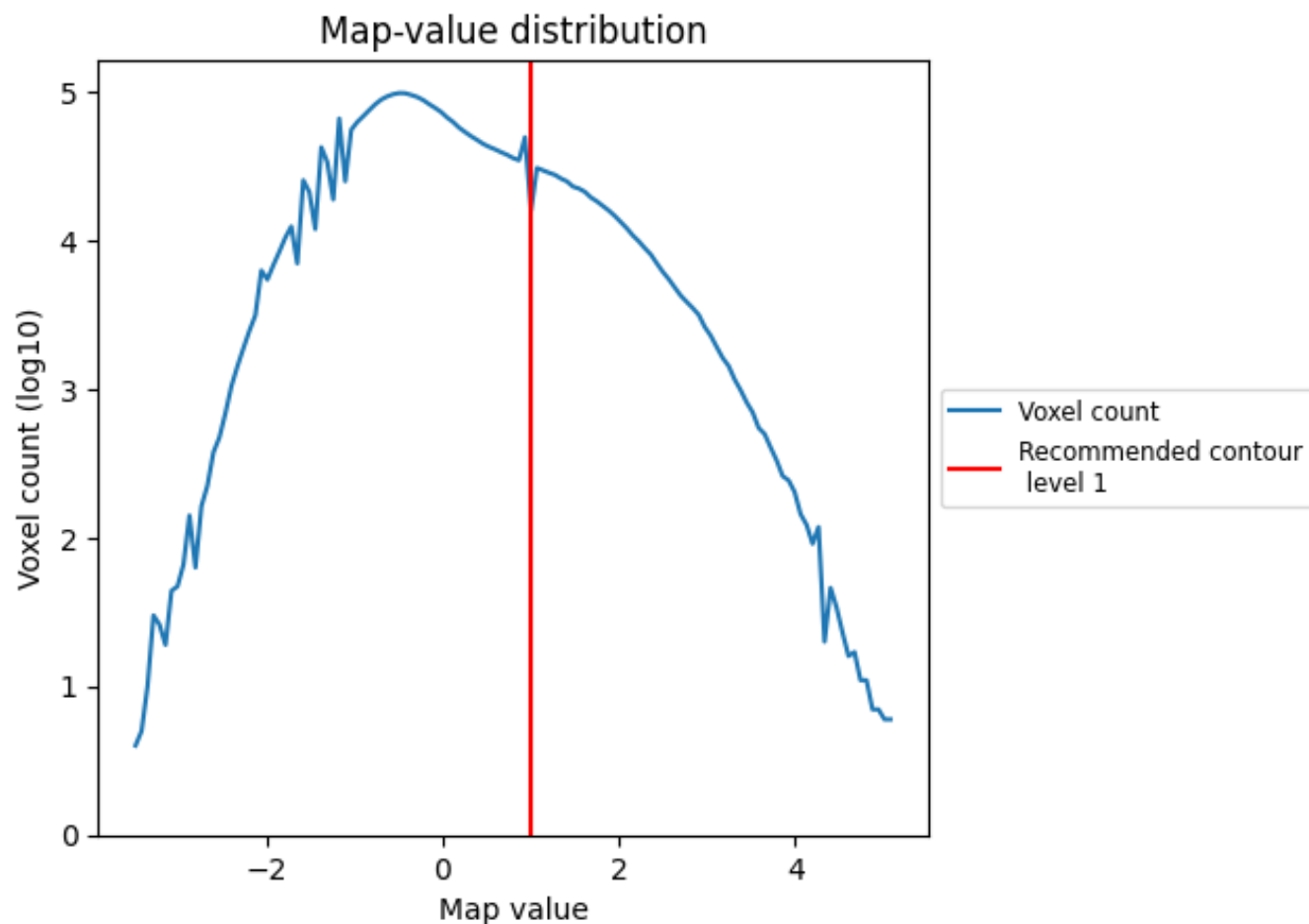
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

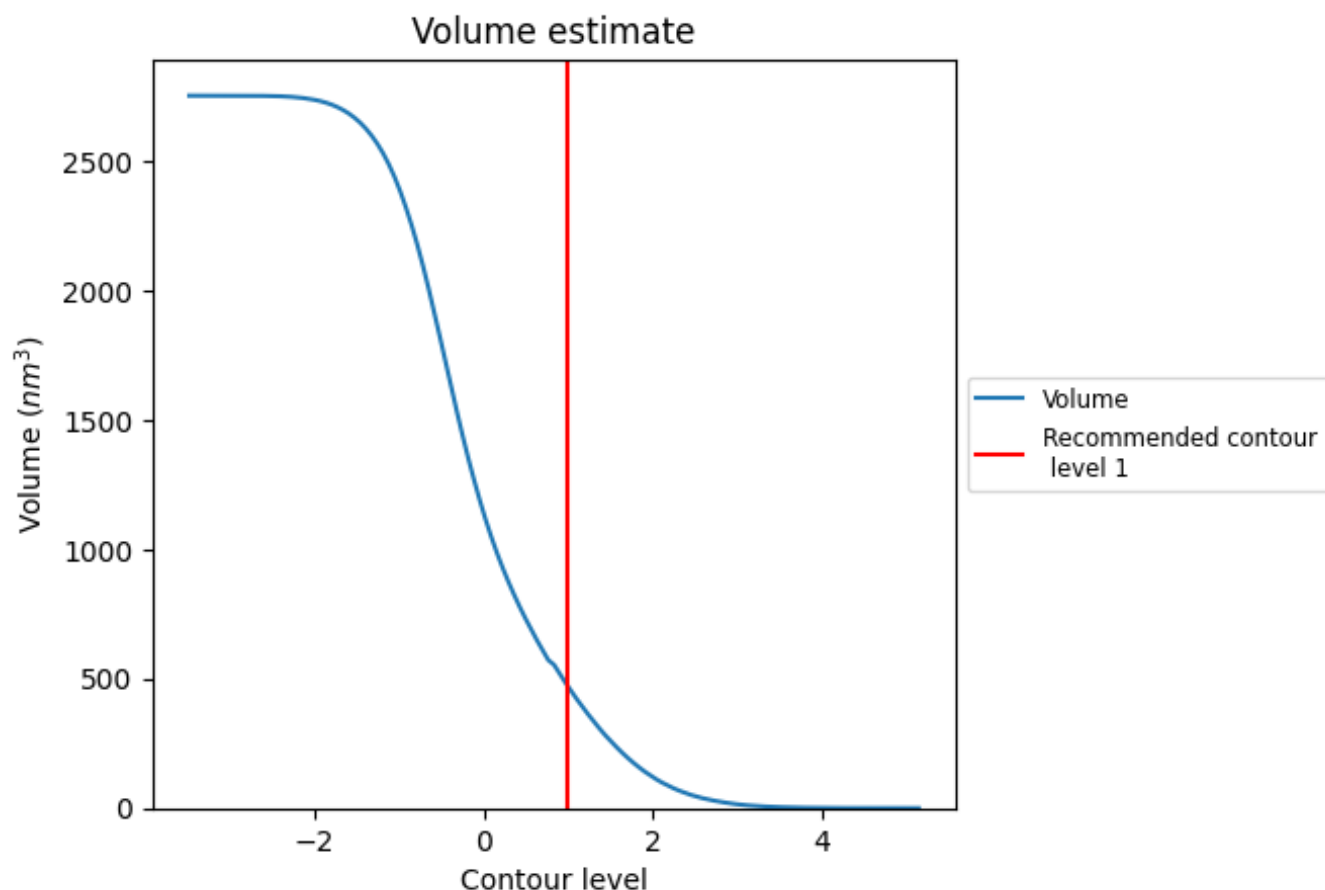
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 469 nm³; this corresponds to an approximate mass of 424 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

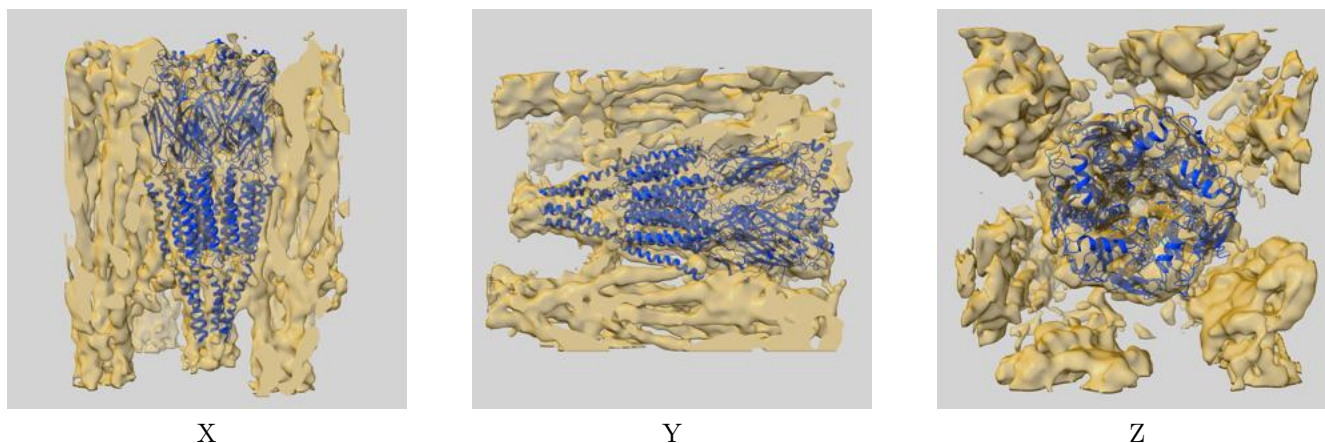
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

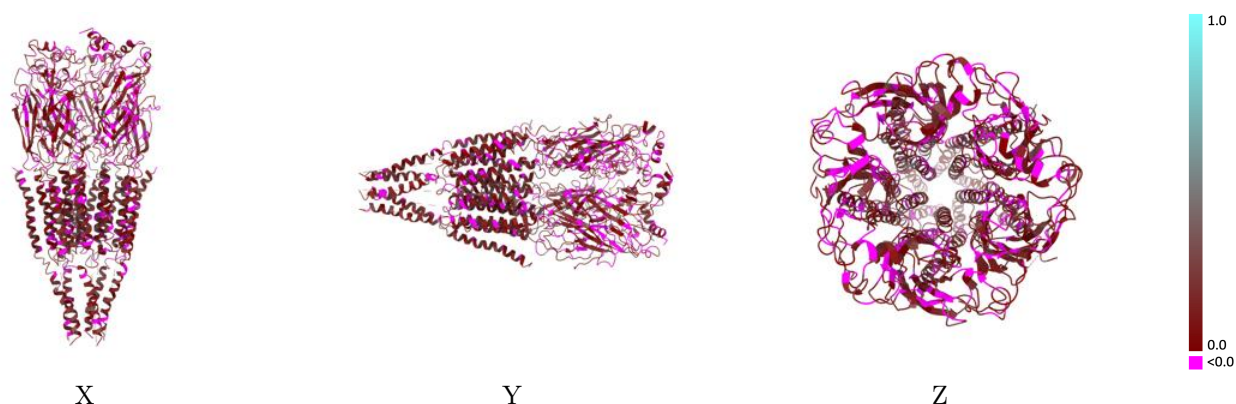
This section contains information regarding the fit between EMDB map EMD-2072 and PDB model 4AQ9. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



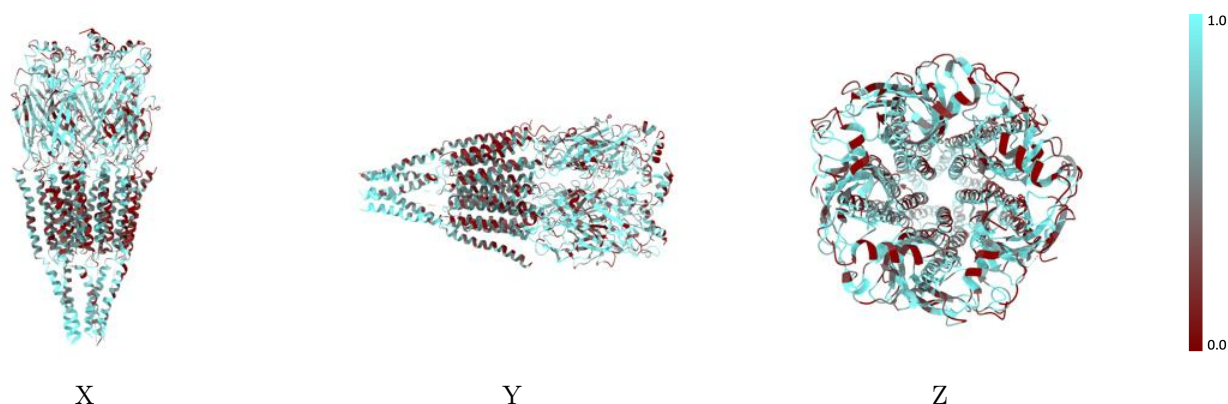
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



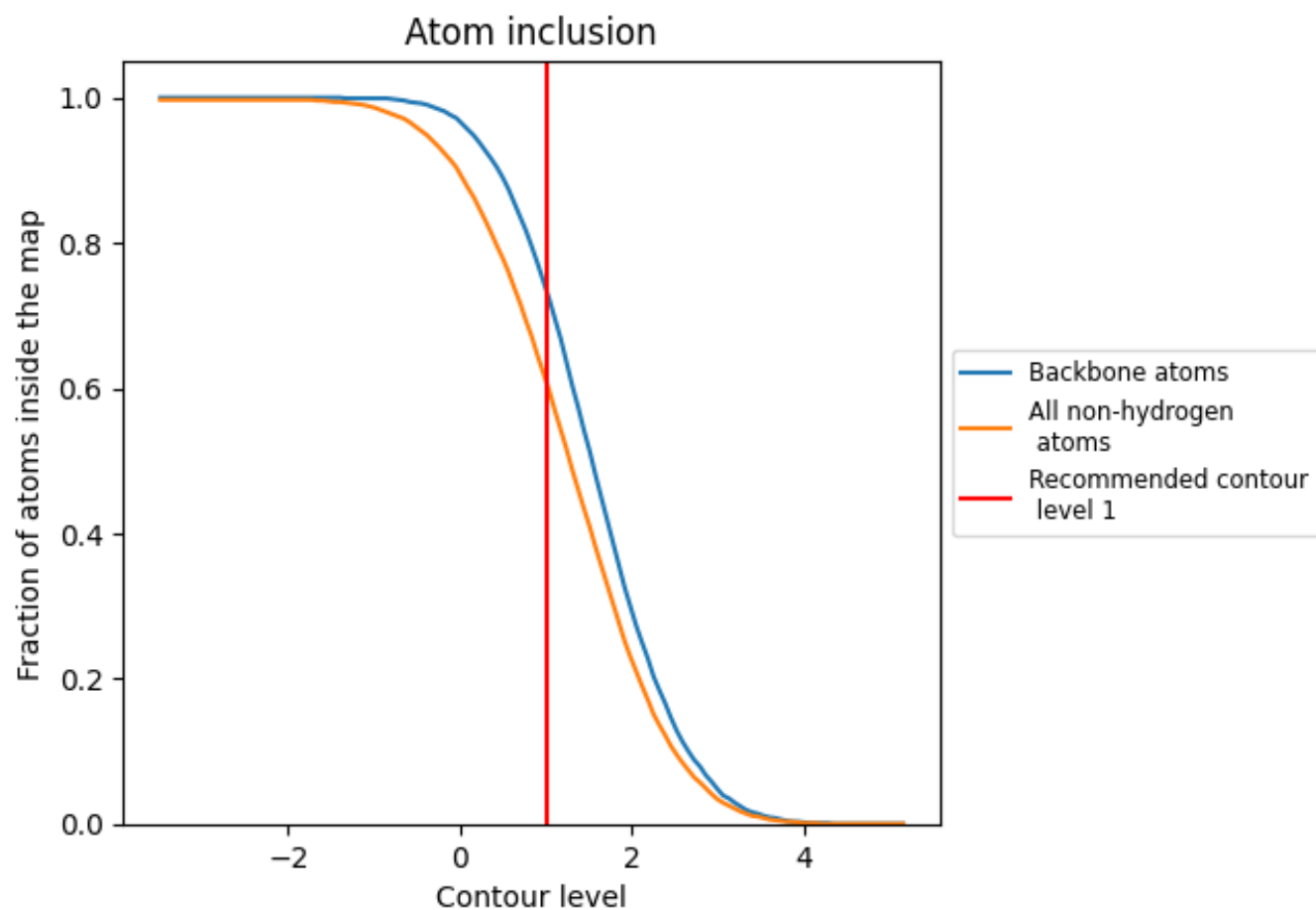
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6100	0.1030
A	0.6080	0.1060
B	0.5780	0.0910
C	0.5740	0.0980
D	0.6270	0.1090
E	0.6610	0.1100

