



Full wwPDB EM Validation Report ⓘ

Mar 22, 2026 – 06:41 PM UTC

PDB ID : 4AQ5 / pdb_00004aq5
EMDB ID : EMD-2071
Title : Gating movement in acetylcholine receptor analysed by time-resolved electron cryo-microscopy (closed class)
Authors : Unwin, N.; Fujiyoshi, Y.
Deposited on : 2012-04-12
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

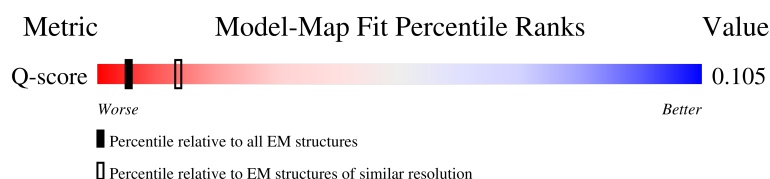
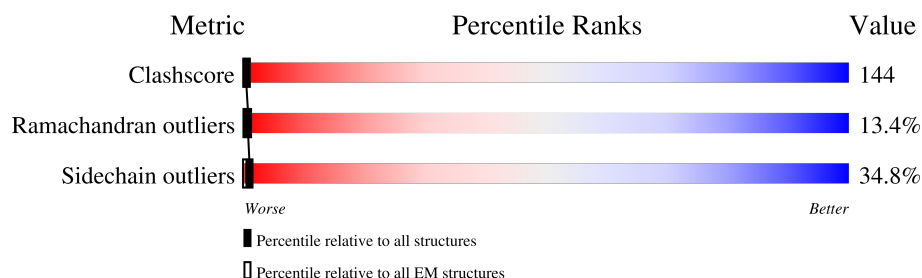
1 Overall quality at a glance

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	31% 14% 29% 36% 20%
1	D	461	30% 14% 29% 36% 20%
2	B	493	32% 15% 29% 29% 25%
3	C	522	31% 13% 26% 30% 29%

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Mol	Chain	Length	Quality of chain
4	E	488	28% 16% 25% 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		

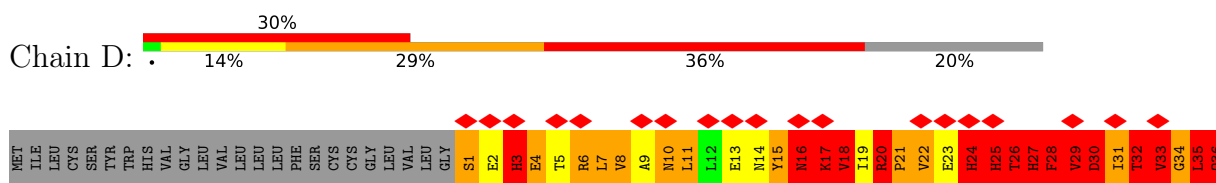
3 Residue-property plots

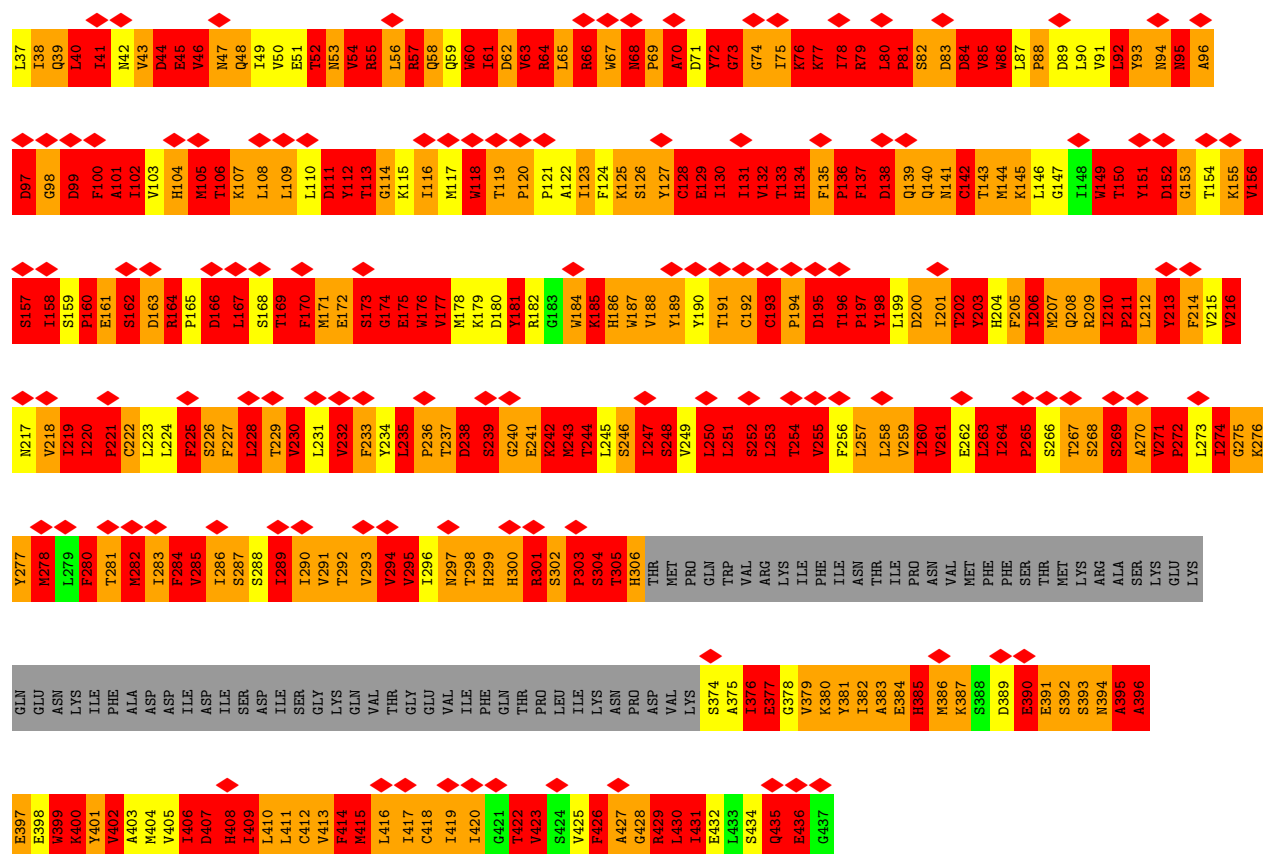
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

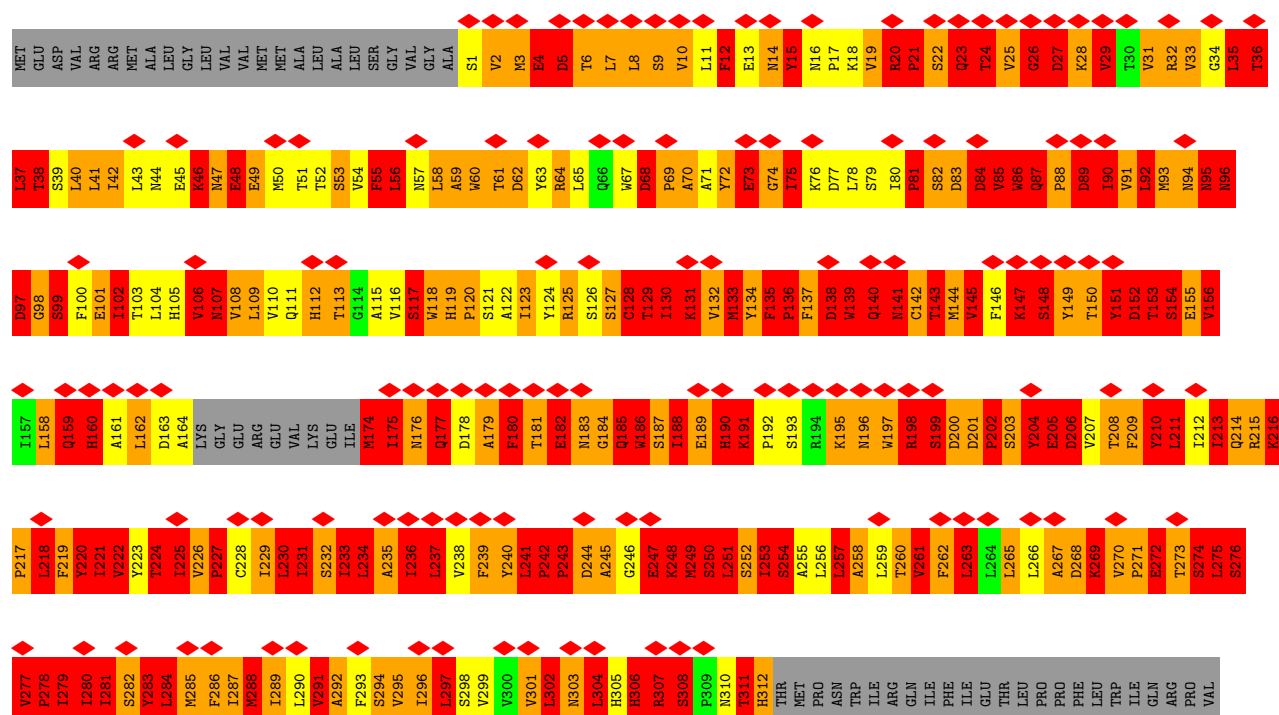


• Molecule 1: ACETYLCHOLINE RECEPTOR SUBUNIT ALPHA





• Molecule 2: ACETYLCHOLINE RECEPTOR BETA SUBUNIT



GLY	ASP	PRO	ARG	LYS	TYR	VAL	PRO	F421	I422	A423	K424	S425	T426	K427	E428	Q429	M430	M431	S432	G433	S434	E435	M436	E437	N438	M439	M440	L441	I442	G443	K444	V445	I446	D447	K448	A449	C450	F451	M452	I453	A454	L455	L456	L457	F458	S459	L460	G461	T462	L463	A464	I465	F466	L467	T468	G469	H470	L471	M472	Q473	C419	V474	P475	E476	F477	PRO	PHE	PRO			
GLU	GLU	TYR	ILE	LEU	LYS	LYS	PRO	V301	I302	V303	L304	N305	V306	S307	L308	R309	T310	P311	N312	T313	H314	SER	LEU	SER	GLU	LYS	LYS	ILE	GLY	LEU	HIS	LEU	PHE	LEU	GLU	THR	PRO	LYS	LYS	ASP	TYR	Q270	K271	V272	T273	E274	T275	S276	L277	N278	V279	P280	L281	G283	K284	Y285	L286	I287	F288	V289	M290	F291	V292	S293	L294	V295	I296	V297	T298	M299	C300
GLU	GLU	TYR	ILE	LEU	LYS	LYS	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	L268	A269	Q270	K271	V272	T273	E274	T275	S276	L277	N278	V279	P280	L281	G283	K284	Y285	L286	I287	F288	V289	M290	F291	V292	S293	L294	V295	I296	V297	T298	M299	C300					
D61	Y62	R63	L64	S65	M66	N67	T68	S69	E70	Y71	E72	G73	I74	Y14	D15	K16	R17	I18	K19	P20	A21	E22	K23	L24	D25	L26	P27	D88	V89	D90	L91	E92	N93	N94	V95	D96	C97	D98	F99	E100	V101	A102	E103	Y104	A105	M106	V107	L108	T109	Y110	N111	D112	G113	S114	E115	M116	W117	L118	P119	P120											
M1	E2	E3	G4	S5	L6	I7	E8	K9	L10	L11	G12	D13	Y14	D15	K16	R17	I18	K19	P20	A21	E22	K23	L24	D25	L26	P27	D88	V89	D90	L91	E92	N93	N94	V95	D96	C97	D98	F99	E100	V101	A102	E103	Y104	A105	M106	V107	L108	T109	Y110	N111	D112	G113	S114	E115	M116	W117	L118	P119	P120												
A121	I122	Y123	R124	S125	T126	C127	P128	I129	A130	V131	T132	Y133	F134	P135	F136	D137	W138	Q139	N140	C141	S142	I143	V144	F145	W146	S147	Q148	T149	Y150	M151	A152	H153	E154	V155	M156	L157	Q158	L159	S160	A161	E162	E163	G164	VAL	VAL	GLU	TRP	ILE	HIS	I172	D173	P174	E175	D176	F177	T178	E179	N180													
G181	E182	M183	T184	I185	R186	H187	R188	P189	A190	K191	K192	N193	T194	W196	Q197	L198	T199	K200	D201	D202	I203	D204	F205	Q206	E207	I208	L209	F210	F211	L212	L213	I214	D215	R216	R217	P218	L219	F220	T221	I222	I223	M224	I225	A227	P228	C229	V230	L231	I232	S233	S234	L235	V236	V237	L238	I239	V297	M299	C300												
A121	I122	Y123	R124	S125	T126	C127	P128	I129	A130	V131	T132	Y133	F134	P135	F136	D137	W138	Q139	N140	C141	S142	I143	V144	F145	W146	S147	Q148	T149	Y150	M151	A152	H153	E154	V155	M156	L157	Q158	L159	S160	A161	E162	E163	G164	VAL	VAL	GLU	TRP	ILE	HIS	I172	D173	P174	E175	D176	F177	T178	E179	N180													
D61	Y62	R63	L64	S65	M66	N67	T68	S69	E70	Y71	E72	G73	I74	Y14	D15	K16	R17	I18	K19	P20	A21	E22	K23	L24	D25	L26	P27	D88	V89	D90	L91	E92	N93	N94	V95	D96	C97	D98	F99	E100	V101	A102	E103	Y104	A105	M106	V107	L108	T109	Y110	N111	D112	G113	S114	E115	M116	W117	L118	P119	P120											
M1	E2	E3	G4	S5	L6	I7	E8	K9	L10	L11	G12	D13	Y14	D15	K16	R17	I18	K19	P20	A21	E22	K23	L24	D25	L26	P27	D88	V89	D90	L91	E92	N93	N94	V95	D96	C97	D98	F99	E100	V101	A102	E103	Y104	A105	M106	V107	L108	T109	Y110	N111	D112	G113	S114	E115	M116	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	4.906	Depositor
Minimum map value	-3.900	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.2	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	2.17	66/3069 (2.2%)	3.36	523/4186 (12.5%)
1	D	2.24	71/3069 (2.3%)	3.37	550/4186 (13.1%)
2	B	2.24	67/3048 (2.2%)	3.31	508/4162 (12.2%)
3	C	2.14	61/3059 (2.0%)	3.38	536/4175 (12.8%)
4	E	2.16	64/3057 (2.1%)	3.37	554/4174 (13.3%)
All	All	2.19	329/15302 (2.2%)	3.36	2671/20883 (12.8%)

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	7	116
1	D	6	125
2	B	6	112
3	C	6	125
4	E	12	107
All	All	37	585

All (329) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	129	THR	C-N	-16.83	1.12	1.33
1	D	208	GLN	C-N	16.34	1.48	1.32
4	E	77	VAL	CA-CB	-12.20	1.46	1.55
2	B	225	ILE	CA-CB	10.58	1.67	1.54
4	E	306	VAL	C-N	-10.50	1.19	1.33
4	E	309	ARG	C-N	-9.99	1.20	1.33
4	E	224	ASN	C-O	-9.58	1.11	1.24
4	E	126	THR	C-N	-9.33	1.19	1.33
3	C	449	VAL	CA-CB	9.22	1.67	1.54
2	B	16	ASN	CA-C	9.11	1.60	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	209	ARG	CA-C	9.08	1.58	1.53
3	C	265	LEU	C-N	9.06	1.45	1.33
1	A	126	SER	C-N	-9.02	1.22	1.33
1	A	282	MET	SD-CE	8.89	2.01	1.79
2	B	159	GLN	C-N	8.81	1.45	1.33
2	B	161	ALA	N-CA	-8.81	1.40	1.46
2	B	143	THR	CA-CB	8.68	1.65	1.53
4	E	287	ILE	CA-CB	8.48	1.65	1.54
1	D	211	PRO	C-O	8.44	1.34	1.24
1	D	106	THR	N-CA	-8.39	1.40	1.46
1	D	176	TRP	CA-C	8.28	1.63	1.52
3	C	183	ALA	CA-CB	-8.09	1.47	1.53
1	A	205	PHE	C-N	-7.87	1.21	1.33
2	B	270	VAL	CA-CB	-7.80	1.50	1.54
1	A	211	PRO	CA-C	7.74	1.63	1.52
4	E	182	GLU	C-N	7.70	1.44	1.33
1	D	158	ILE	CA-CB	7.57	1.66	1.54
2	B	137	PHE	C-N	-7.49	1.22	1.33
3	C	310	LEU	C-N	-7.41	1.24	1.34
1	D	133	THR	CA-CB	7.39	1.63	1.53
2	B	29	VAL	CA-CB	7.32	1.62	1.54
1	D	176	TRP	NE1-CE2	-7.31	1.29	1.37
3	C	303	VAL	CA-CB	7.29	1.62	1.54
2	B	221	ILE	CA-C	7.28	1.62	1.52
1	D	54	VAL	CA-CB	7.28	1.64	1.54
2	B	161	ALA	CA-C	7.23	1.57	1.53
2	B	145	VAL	C-O	-7.20	1.16	1.24
1	A	136	PRO	N-CA	-7.20	1.38	1.47
3	C	125	ILE	N-CA	7.20	1.54	1.46
1	A	247	ILE	CA-CB	7.17	1.64	1.54
1	A	174	GLY	C-N	-7.15	1.24	1.34
3	C	129	SER	C-N	7.14	1.46	1.33
3	C	430	VAL	CA-CB	7.11	1.64	1.54
1	D	156	VAL	CA-C	7.07	1.61	1.52
3	C	97	ASN	C-O	6.97	1.33	1.24
2	B	160	HIS	C-N	6.96	1.38	1.33
3	C	312	PHE	C-N	6.96	1.43	1.34
3	C	227	PHE	C-N	6.94	1.42	1.33
4	E	35	THR	C-N	-6.89	1.24	1.33
1	D	176	TRP	C-N	6.85	1.43	1.33
1	D	237	THR	CA-CB	6.81	1.64	1.53
2	B	232	SER	C-O	-6.80	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	140	GLN	C-N	-6.78	1.24	1.33
1	A	295	VAL	CA-CB	6.77	1.61	1.54
1	D	243	MET	SD-CE	-6.76	1.62	1.79
4	E	115	MET	N-CA	-6.75	1.38	1.46
2	B	214	GLN	C-O	-6.69	1.16	1.24
2	B	287	ILE	CA-C	6.66	1.60	1.52
2	B	85	VAL	CA-C	-6.63	1.45	1.52
3	C	285	VAL	CA-C	6.61	1.59	1.52
1	A	122	ALA	C-N	-6.60	1.24	1.33
4	E	129	ILE	CA-CB	6.58	1.63	1.54
3	C	104	VAL	N-CA	6.57	1.54	1.46
3	C	266	ALA	N-CA	-6.55	1.38	1.46
3	C	462	THR	C-O	-6.54	1.18	1.24
2	B	245	ALA	CA-CB	-6.54	1.42	1.53
1	D	43	VAL	CA-CB	6.53	1.62	1.55
3	C	319	THR	N-CA	6.51	1.53	1.46
1	D	163	ASP	N-CA	-6.49	1.37	1.46
3	C	286	PRO	CA-C	6.46	1.58	1.52
1	D	293	VAL	CA-C	-6.42	1.45	1.52
1	A	207	MET	C-O	-6.42	1.16	1.23
1	D	289	ILE	C-O	-6.40	1.17	1.24
1	A	293	VAL	N-CA	-6.37	1.38	1.46
2	B	292	ALA	N-CA	-6.34	1.38	1.46
4	E	271	LYS	C-O	6.33	1.31	1.24
2	B	454	ILE	CA-CB	6.32	1.61	1.54
1	A	292	THR	CA-CB	-6.30	1.42	1.53
3	C	456	LEU	N-CA	-6.27	1.38	1.46
4	E	34	LEU	C-N	-6.26	1.24	1.33
1	D	168	SER	C-N	-6.25	1.25	1.33
3	C	226	LEU	C-N	-6.25	1.25	1.33
4	E	311	PRO	N-CD	6.22	1.56	1.47
3	C	315	ARG	NE-CZ	6.22	1.39	1.33
2	B	134	TYR	N-CA	6.22	1.52	1.46
3	C	229	VAL	N-CA	6.22	1.54	1.46
2	B	179	ALA	C-O	-6.20	1.18	1.24
2	B	82	SER	CA-C	-6.18	1.50	1.53
4	E	465	ILE	CA-CB	6.17	1.63	1.54
1	D	251	LEU	CA-C	6.16	1.61	1.52
1	A	209	ARG	C-N	6.13	1.40	1.33
3	C	130	CYS	C-N	6.12	1.48	1.33
2	B	135	PHE	C-N	6.10	1.41	1.33
2	B	213	ILE	CA-CB	6.08	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	58	GLN	C-N	-6.07	1.26	1.33
4	E	175	GLU	C-O	-6.06	1.17	1.24
2	B	242	PRO	CA-C	6.05	1.57	1.52
1	D	250	LEU	N-CA	-6.05	1.39	1.46
1	A	47	ASN	CA-CB	6.03	1.61	1.53
4	E	26	HIS	CE1-NE2	6.01	1.38	1.32
1	A	285	VAL	C-N	-6.01	1.26	1.33
4	E	151	ASN	CA-C	6.00	1.59	1.52
2	B	296	ILE	CA-CB	6.00	1.61	1.54
3	C	315	ARG	N-CA	6.00	1.53	1.46
3	C	295	ILE	CA-CB	-5.99	1.47	1.54
1	D	397	GLU	CA-C	5.98	1.60	1.52
1	A	82	SER	N-CA	5.97	1.53	1.46
1	D	211	PRO	C-N	-5.96	1.25	1.33
4	E	57	ILE	C-O	-5.95	1.17	1.24
3	C	97	ASN	N-CA	-5.95	1.40	1.46
3	C	27	ASN	CA-CB	5.94	1.60	1.53
1	D	105	MET	C-N	5.93	1.38	1.33
3	C	202	TYR	CA-C	-5.91	1.45	1.52
1	D	263	LEU	N-CA	-5.91	1.38	1.46
1	D	380	LYS	N-CA	5.91	1.53	1.46
1	D	181	TYR	CA-C	5.91	1.59	1.52
4	E	209	ILE	CA-CB	5.91	1.61	1.54
2	B	124	TYR	N-CA	5.91	1.53	1.46
1	D	36	GLN	CA-C	-5.90	1.46	1.53
1	D	295	VAL	N-CA	5.89	1.53	1.46
2	B	133	MET	C-N	-5.89	1.25	1.34
3	C	220	ILE	C-N	-5.89	1.25	1.33
3	C	318	SER	CA-C	5.89	1.57	1.52
1	D	282	MET	C-N	-5.88	1.26	1.33
1	D	166	ASP	N-CA	-5.87	1.39	1.46
1	D	196	THR	CA-C	5.87	1.60	1.52
4	E	118	LEU	CA-C	-5.87	1.45	1.52
1	A	130	ILE	CA-CB	5.84	1.62	1.54
1	A	180	ASP	C-O	-5.83	1.16	1.24
3	C	104	VAL	CA-CB	-5.83	1.46	1.54
4	E	155	VAL	CA-CB	5.83	1.61	1.54
1	D	280	PHE	C-O	-5.82	1.16	1.24
3	C	198	LYS	CA-C	5.81	1.58	1.52
1	A	57	ARG	NE-CZ	5.80	1.39	1.33
1	A	117	MET	SD-CE	5.80	1.94	1.79
4	E	268	ILE	CA-CB	5.79	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	139	PHE	C-N	-5.78	1.26	1.33
1	A	140	GLN	C-N	-5.77	1.25	1.33
1	A	25	HIS	CE1-NE2	5.76	1.38	1.32
4	E	183	TRP	CA-C	-5.74	1.45	1.53
1	A	3	HIS	CE1-NE2	5.74	1.38	1.32
1	A	250	LEU	N-CA	-5.73	1.39	1.46
3	C	33	ILE	CA-C	5.73	1.59	1.52
4	E	109	VAL	C-O	-5.73	1.18	1.24
1	A	255	VAL	CA-C	5.73	1.59	1.52
1	D	144	MET	CA-C	5.73	1.59	1.52
1	A	27	HIS	CG-CD2	5.72	1.42	1.35
3	C	27	ASN	N-CA	5.71	1.53	1.46
1	A	61	ILE	CA-C	5.71	1.59	1.52
1	D	35	LEU	N-CA	5.71	1.52	1.45
3	C	313	HIS	CE1-NE2	-5.71	1.26	1.32
2	B	185	GLN	C-N	5.70	1.41	1.33
4	E	312	ASN	C-O	5.70	1.30	1.24
1	D	126	SER	CA-C	-5.69	1.45	1.52
4	E	416	VAL	CA-CB	5.69	1.62	1.54
2	B	306	HIS	CG-CD2	-5.68	1.29	1.35
1	A	226	SER	C-O	-5.67	1.17	1.24
1	A	391	GLU	CA-CB	5.65	1.62	1.53
1	A	139	GLN	CA-C	5.64	1.60	1.52
4	E	39	LEU	C-N	-5.64	1.26	1.33
3	C	286	PRO	C-O	-5.63	1.19	1.24
3	C	236	CYS	N-CA	-5.62	1.39	1.46
1	D	174	GLY	C-N	-5.62	1.26	1.33
4	E	61	ASP	N-CA	-5.61	1.39	1.46
1	A	215	VAL	CA-C	5.61	1.59	1.52
1	A	299	HIS	CG-ND1	-5.60	1.32	1.38
4	E	222	ILE	CA-CB	5.60	1.62	1.54
1	D	86	TRP	CA-CB	5.60	1.60	1.52
1	A	101	ALA	CA-CB	-5.60	1.46	1.53
1	A	401	TYR	CA-CB	5.59	1.61	1.53
3	C	305	ASN	C-O	-5.59	1.16	1.24
1	A	48	GLN	C-O	5.59	1.31	1.24
1	D	143	THR	CA-C	-5.59	1.46	1.52
1	A	89	ASP	C-N	5.58	1.40	1.33
4	E	55	ILE	CA-CB	5.58	1.62	1.54
2	B	222	VAL	CA-C	-5.58	1.45	1.52
4	E	232	ILE	CA-CB	5.58	1.62	1.54
1	A	414	PHE	CA-C	5.57	1.60	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	235	PRO	C-O	-5.57	1.16	1.24
1	A	28	PHE	CA-C	5.56	1.60	1.52
3	C	261	ILE	N-CA	-5.55	1.40	1.46
1	A	6	ARG	C-O	-5.54	1.17	1.24
1	A	263	LEU	N-CA	-5.54	1.39	1.46
2	B	91	VAL	CA-C	-5.54	1.45	1.52
4	E	8	GLU	CB-CG	5.54	1.69	1.52
4	E	153	HIS	CG-ND1	5.54	1.44	1.38
2	B	447	CYS	N-CA	-5.53	1.39	1.46
1	A	148	ILE	C-O	-5.51	1.17	1.24
4	E	228	PRO	C-O	-5.49	1.17	1.24
1	D	28	PHE	C-N	-5.48	1.28	1.33
4	E	453	ILE	N-CA	-5.48	1.39	1.46
2	B	209	PHE	N-CA	5.48	1.52	1.46
2	B	221	ILE	N-CA	-5.46	1.40	1.46
1	D	125	LYS	C-O	-5.46	1.17	1.23
4	E	222	ILE	C-N	-5.46	1.28	1.34
2	B	71	ALA	N-CA	5.46	1.53	1.46
1	A	109	LEU	C-N	-5.45	1.25	1.33
1	A	389	ASP	N-CA	-5.44	1.39	1.46
1	D	32	THR	C-N	5.44	1.38	1.33
2	B	250	SER	C-O	-5.43	1.19	1.23
1	A	153	GLY	C-O	-5.43	1.18	1.24
3	C	135	LEU	N-CA	5.42	1.52	1.46
1	D	203	TYR	N-CA	-5.42	1.39	1.46
3	C	222	ARG	NE-CZ	5.42	1.39	1.33
2	B	24	THR	CA-C	5.42	1.60	1.52
2	B	228	CYS	CA-CB	5.42	1.61	1.53
1	D	60	TRP	NE1-CE2	5.41	1.43	1.37
4	E	281	LEU	C-N	5.41	1.40	1.33
4	E	441	LEU	C-O	5.41	1.32	1.23
1	A	72	TYR	C-O	-5.41	1.17	1.24
4	E	205	PHE	N-CA	-5.40	1.39	1.46
1	A	238	ASP	CA-C	5.40	1.59	1.52
4	E	201	ASP	CA-C	5.39	1.59	1.52
4	E	446	ILE	C-N	-5.39	1.27	1.33
1	A	204	HIS	N-CA	-5.38	1.40	1.46
1	D	158	ILE	CA-C	5.37	1.59	1.52
3	C	43	ILE	C-O	-5.37	1.17	1.24
4	E	258	LEU	CA-C	-5.37	1.45	1.52
1	D	140	GLN	C-O	5.36	1.30	1.23
1	D	417	ILE	CA-CB	5.36	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	24	HIS	CE1-NE2	-5.36	1.27	1.32
2	B	68	ASP	CA-C	5.35	1.59	1.52
2	B	105	HIS	ND1-CE1	5.35	1.37	1.32
3	C	83	ARG	CA-C	5.34	1.59	1.52
4	E	221	TYR	C-O	5.34	1.30	1.24
1	A	163	ASP	C-N	-5.34	1.22	1.33
3	C	29	GLU	N-CA	-5.34	1.40	1.46
1	D	220	ILE	CA-C	-5.33	1.47	1.52
4	E	454	ALA	CA-C	-5.32	1.46	1.52
1	D	216	VAL	CA-CB	-5.31	1.46	1.54
3	C	140	ASP	N-CA	-5.31	1.40	1.46
4	E	136	PHE	C-N	-5.31	1.25	1.33
1	D	286	ILE	N-CA	-5.30	1.40	1.46
3	C	67	LEU	N-CA	5.30	1.53	1.46
4	E	314	HIS	ND1-CE1	5.29	1.37	1.32
1	A	61	ILE	C-O	5.29	1.29	1.23
1	A	292	THR	CA-C	-5.29	1.45	1.52
2	B	260	THR	N-CA	-5.29	1.40	1.46
3	C	222	ARG	CA-C	5.28	1.59	1.52
1	D	30	ASP	CA-C	5.28	1.59	1.52
1	A	401	TYR	N-CA	5.28	1.53	1.46
1	A	419	ILE	CA-CB	5.27	1.61	1.54
3	C	480	ARG	C-N	5.27	1.39	1.33
1	D	290	ILE	CA-CB	5.26	1.60	1.54
1	D	294	VAL	CA-CB	5.26	1.60	1.54
2	B	204	TYR	C-O	5.25	1.30	1.24
1	D	232	VAL	CA-CB	5.25	1.61	1.54
4	E	77	VAL	CA-C	-5.24	1.46	1.52
1	D	6	ARG	C-O	-5.24	1.17	1.24
4	E	52	ASN	CA-CB	5.23	1.59	1.52
4	E	54	TRP	N-CA	-5.23	1.40	1.46
4	E	287	ILE	C-O	-5.23	1.18	1.24
1	D	193	CYS	CA-C	5.22	1.59	1.52
2	B	15	TYR	C-N	5.22	1.39	1.33
2	B	437	ARG	C-O	5.22	1.30	1.24
3	C	20	HIS	ND1-CE1	5.21	1.37	1.32
2	B	86	TRP	NE1-CE2	-5.20	1.31	1.37
3	C	51	THR	C-O	-5.20	1.18	1.23
1	D	435	GLN	CA-C	-5.20	1.45	1.52
4	E	110	TYR	N-CA	-5.19	1.39	1.46
2	B	460	HIS	N-CA	5.19	1.52	1.46
1	D	160	PRO	N-CA	5.19	1.51	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	261	GLN	C-O	-5.18	1.18	1.24
1	A	28	PHE	CA-CB	5.18	1.62	1.53
1	A	387	LYS	C-N	-5.18	1.27	1.33
1	A	218	VAL	C-O	-5.18	1.18	1.24
4	E	314	HIS	CD2-NE2	-5.17	1.32	1.37
2	B	112	HIS	CD2-NE2	-5.17	1.32	1.37
2	B	460	HIS	CG-CD2	5.17	1.41	1.35
4	E	128	PRO	CA-CB	-5.16	1.46	1.53
1	A	44	ASP	C-O	-5.16	1.18	1.24
2	B	251	LEU	CA-C	-5.15	1.45	1.52
4	E	423	ALA	CA-CB	5.15	1.61	1.53
4	E	416	VAL	CA-C	5.14	1.59	1.52
1	A	85	VAL	CA-C	5.14	1.58	1.53
1	A	306	HIS	CE1-NE2	-5.14	1.27	1.32
2	B	144	MET	C-N	5.14	1.40	1.33
3	C	467	LEU	CA-CB	5.14	1.61	1.53
1	A	118	TRP	CB-CG	5.13	1.66	1.50
4	E	263	ILE	CA-CB	5.13	1.60	1.54
1	D	292	THR	C-N	-5.13	1.27	1.33
1	D	229	THR	C-N	-5.12	1.27	1.33
1	D	66	ARG	NE-CZ	5.12	1.38	1.33
2	B	8	LEU	N-CA	-5.12	1.40	1.46
3	C	161	ASP	CA-C	-5.12	1.46	1.53
3	C	265	LEU	N-CA	5.11	1.52	1.46
1	A	245	LEU	C-N	-5.11	1.27	1.33
2	B	277	VAL	CA-CB	5.10	1.60	1.54
3	C	32	ASN	CA-CB	5.10	1.59	1.52
1	D	128	CYS	CA-CB	5.10	1.61	1.53
4	E	116	TYR	CA-C	5.10	1.58	1.52
4	E	130	ALA	N-CA	-5.10	1.39	1.46
1	D	72	TYR	C-O	-5.10	1.18	1.24
4	E	162	GLU	N-CA	5.10	1.52	1.46
2	B	291	VAL	CA-C	-5.09	1.46	1.52
4	E	239	VAL	CA-C	-5.09	1.46	1.52
4	E	224	ASN	N-CA	-5.09	1.39	1.46
4	E	452	TRP	C-O	-5.08	1.18	1.24
4	E	156	ASN	C-O	-5.08	1.17	1.24
2	B	98	GLY	CA-C	5.08	1.59	1.52
2	B	181	THR	CA-CB	5.07	1.60	1.53
1	D	204	HIS	CD2-NE2	-5.07	1.32	1.37
2	B	160	HIS	CD2-NE2	5.07	1.43	1.37
1	A	182	ARG	NE-CZ	5.07	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	413	GLU	CA-CB	5.07	1.62	1.53
1	A	424	SER	C-N	5.07	1.40	1.33
3	C	256	LYS	CA-CB	5.07	1.59	1.52
3	C	464	VAL	N-CA	5.07	1.52	1.46
2	B	231	ILE	N-CA	-5.06	1.40	1.46
1	D	214	PHE	C-N	-5.06	1.27	1.33
1	D	247	ILE	C-O	-5.06	1.18	1.24
1	D	248	SER	C-O	5.05	1.29	1.24
1	D	175	GLU	CD-OE1	5.05	1.34	1.25
1	A	422	THR	N-CA	-5.05	1.40	1.46
2	B	241	LEU	CA-CB	5.05	1.60	1.53
3	C	210	THR	C-N	5.04	1.38	1.33
2	B	59	ALA	CA-CB	5.04	1.61	1.53
2	B	421	PHE	C-O	-5.04	1.17	1.24
2	B	460	HIS	CA-C	5.03	1.59	1.52
3	C	473	PHE	CA-C	5.03	1.59	1.52
2	B	242	PRO	C-O	-5.03	1.18	1.24
1	D	40	LEU	C-N	-5.03	1.27	1.33
3	C	127	ARG	N-CA	5.02	1.52	1.46
1	A	425	VAL	N-CA	-5.02	1.39	1.46
1	A	281	THR	CA-CB	5.02	1.61	1.53
2	B	206	ASP	C-N	5.01	1.40	1.33
3	C	181	PRO	N-CD	5.01	1.54	1.47
1	A	409	ILE	CA-CB	5.01	1.61	1.54
2	B	445	THR	CA-CB	5.00	1.61	1.53

All (2671) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	140	GLN	OE1-CD-NE2	-19.09	103.51	122.60
4	E	175	GLU	O-C-N	18.12	140.94	122.09
1	D	106	THR	N-CA-C	17.89	123.45	108.78
3	C	130	CYS	CA-C-N	16.92	140.99	119.84
3	C	130	CYS	C-N-CA	16.92	140.99	119.84
2	B	161	ALA	CA-C-O	15.82	127.11	117.94
1	D	271	VAL	CA-C-N	15.67	135.92	119.78
1	D	271	VAL	C-N-CA	15.67	135.92	119.78
2	B	135	PHE	CA-C-N	-15.56	104.13	119.85
2	B	135	PHE	C-N-CA	-15.56	104.13	119.85
1	A	394	ASN	CA-CB-CG	15.24	127.84	112.60
4	E	224	ASN	CA-C-N	14.93	139.37	120.56
4	E	224	ASN	C-N-CA	14.93	139.37	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	299	HIS	CA-CB-CG	14.79	128.59	113.80
2	B	307	ARG	NE-CZ-NH2	14.76	132.48	119.20
2	B	446	MET	N-CA-C	14.71	127.03	111.14
3	C	130	CYS	O-C-N	-14.43	106.85	121.28
2	B	468	PHE	CA-CB-CG	14.38	128.18	113.80
1	A	140	GLN	OE1-CD-NE2	-14.18	108.42	122.60
1	D	84	ASP	CA-CB-CG	14.14	126.74	112.60
1	D	408	HIS	N-CA-CB	13.35	129.83	109.94
3	C	277	ARG	NE-CZ-NH2	13.32	131.19	119.20
3	C	432	GLN	OE1-CD-NE2	13.13	135.74	122.60
2	B	463	PRO	N-CA-C	12.98	126.53	110.70
1	A	73	GLY	CA-C-N	12.80	134.15	119.94
1	A	73	GLY	C-N-CA	12.80	134.15	119.94
3	C	29	GLU	CA-C-O	-12.64	107.68	120.70
1	A	234	TYR	N-CA-C	12.51	124.45	111.07
1	D	295	VAL	CA-C-O	-12.50	107.19	120.57
4	E	3	GLU	CA-C-N	12.45	133.51	119.94
4	E	3	GLU	C-N-CA	12.45	133.51	119.94
3	C	306	CYS	N-CA-C	-12.45	95.15	112.45
4	E	289	VAL	N-CA-C	12.45	123.17	110.23
3	C	101	GLN	OE1-CD-NE2	-12.43	110.17	122.60
2	B	19	VAL	CA-C-N	12.33	141.14	121.17
2	B	19	VAL	C-N-CA	12.33	141.14	121.17
2	B	275	LEU	CA-C-O	-12.27	107.41	120.42
2	B	188	ILE	N-CA-C	12.23	125.87	107.77
3	C	121	LEU	N-CA-C	12.17	127.43	109.30
1	A	84	ASP	O-C-N	-12.16	108.33	122.20
3	C	265	LEU	O-C-N	12.14	134.71	122.09
1	A	238	ASP	CA-CB-CG	12.11	124.71	112.60
3	C	98	ASN	OD1-CG-ND2	-12.06	110.54	122.60
3	C	92	ILE	CA-C-N	12.00	138.07	123.19
3	C	92	ILE	C-N-CA	12.00	138.07	123.19
1	D	150	THR	N-CA-C	11.97	129.90	113.37
1	D	381	TYR	CA-C-O	-11.94	107.76	120.42
4	E	156	ASN	OD1-CG-ND2	11.94	134.53	122.60
2	B	85	VAL	CB-CA-C	-11.93	100.53	111.74
2	B	204	TYR	CA-C-O	-11.89	106.70	120.49
4	E	98	GLN	OE1-CD-NE2	-11.88	110.72	122.60
1	A	263	LEU	N-CA-C	11.77	125.38	111.02
4	E	309	ARG	NE-CZ-NH1	11.74	133.24	121.50
1	D	250	LEU	CB-CA-C	11.69	130.15	110.86
4	E	77	VAL	CA-C-N	11.58	138.51	121.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	77	VAL	C-N-CA	11.58	138.51	121.26
4	E	278	ASN	OD1-CG-ND2	-11.56	111.04	122.60
1	D	411	LEU	O-C-N	11.52	134.53	122.09
2	B	142	CYS	CA-C-N	11.51	138.41	121.72
2	B	142	CYS	C-N-CA	11.51	138.41	121.72
1	A	209	ARG	N-CA-C	11.49	127.67	109.86
4	E	71	TYR	CA-C-O	11.49	133.71	121.07
3	C	481	PRO	N-CA-C	11.46	124.68	110.70
4	E	238	LEU	N-CA-C	-11.40	94.12	111.56
3	C	113	ARG	NE-CZ-NH2	11.38	129.44	119.20
4	E	136	PHE	CA-C-N	11.37	137.65	122.30
4	E	136	PHE	C-N-CA	11.37	137.65	122.30
1	A	276	LYS	CA-C-N	11.25	136.27	120.29
1	A	276	LYS	C-N-CA	11.25	136.27	120.29
1	A	89	ASP	CA-CB-CG	-11.23	101.37	112.60
3	C	295	ILE	N-CA-C	-11.13	99.96	110.42
3	C	443	VAL	CA-C-N	11.12	132.06	119.94
3	C	443	VAL	C-N-CA	11.12	132.06	119.94
4	E	311	PRO	O-C-N	11.12	137.65	122.64
4	E	268	ILE	N-CA-C	-11.10	100.06	110.82
1	A	28	PHE	CA-C-N	-11.09	108.35	123.10
1	A	28	PHE	C-N-CA	-11.09	108.35	123.10
4	E	420	ASN	CA-C-N	11.07	136.17	120.79
4	E	420	ASN	C-N-CA	11.07	136.17	120.79
4	E	224	ASN	OD1-CG-ND2	10.98	133.58	122.60
2	B	404	ALA	O-C-N	10.90	135.67	122.27
4	E	127	CYS	N-CA-CB	10.88	122.76	109.59
4	E	83	LEU	N-CA-C	10.81	127.42	112.72
1	A	174	GLY	CA-C-N	10.81	135.84	120.28
1	A	174	GLY	C-N-CA	10.81	135.84	120.28
2	B	429	GLN	OE1-CD-NE2	10.81	133.41	122.60
3	C	15	ASN	OD1-CG-ND2	-10.80	111.80	122.60
2	B	56	LEU	CA-C-O	-10.78	109.71	120.92
2	B	306	HIS	CA-CB-CG	-10.77	103.03	113.80
4	E	258	LEU	N-CA-CB	10.74	127.97	109.72
1	A	187	TRP	CA-C-O	-10.68	108.73	120.38
1	D	95	ASN	OD1-CG-ND2	-10.68	111.92	122.60
3	C	101	GLN	CG-CD-NE2	10.65	132.37	116.40
4	E	112	ASP	CA-CB-CG	-10.63	101.97	112.60
3	C	276	GLN	CA-C-O	10.62	131.92	120.55
1	A	29	VAL	O-C-N	-10.62	111.94	123.20
3	C	201	ILE	CA-C-O	-10.60	110.28	121.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	215	GLN	OE1-CD-NE2	-10.53	112.07	122.60
2	B	16	ASN	CA-C-N	10.50	132.97	119.84
2	B	16	ASN	C-N-CA	10.50	132.97	119.84
3	C	156	ASN	OD1-CG-ND2	10.49	133.09	122.60
4	E	263	ILE	CA-C-N	10.49	135.19	120.29
4	E	263	ILE	C-N-CA	10.49	135.19	120.29
3	C	426	THR	O-C-N	-10.48	111.27	122.07
3	C	115	ASN	OD1-CG-ND2	10.48	133.08	122.60
2	B	90	ILE	CA-C-O	10.45	133.84	120.78
1	D	395	ALA	N-CA-C	-10.41	98.42	111.75
4	E	281	LEU	O-C-N	-10.39	111.25	123.41
3	C	274	THR	N-CA-C	10.39	122.61	111.28
3	C	313	HIS	CB-CA-C	10.37	129.81	110.63
1	A	412	CYS	N-CA-CB	10.34	125.00	110.01
3	C	109	ASN	CA-C-O	-10.34	110.61	120.95
4	E	225	ILE	N-CA-C	10.33	120.34	110.42
1	A	389	ASP	O-C-N	-10.31	111.19	122.12
3	C	142	GLN	CG-CD-NE2	10.26	131.80	116.40
1	A	129	GLU	CA-C-O	-10.26	110.36	121.44
3	C	122	PRO	CA-C-N	10.26	132.66	119.84
3	C	122	PRO	C-N-CA	10.26	132.66	119.84
3	C	426	THR	N-CA-C	10.23	122.02	111.07
1	D	260	ILE	N-CA-C	-10.23	100.60	110.42
1	D	414	PHE	CA-CB-CG	10.23	124.03	113.80
3	C	202	TYR	N-CA-C	10.22	126.87	108.48
1	D	403	ALA	CA-C-N	10.20	136.19	120.89
1	D	403	ALA	C-N-CA	10.20	136.19	120.89
1	A	22	VAL	N-CA-CB	10.18	124.28	111.46
1	D	380	LYS	N-CA-C	-10.18	100.00	111.71
1	D	67	TRP	N-CA-C	10.15	124.56	109.24
4	E	98	GLN	CG-CD-NE2	10.15	131.62	116.40
4	E	25	ASP	CA-CB-CG	10.13	122.73	112.60
4	E	215	GLN	CG-CD-NE2	10.13	131.60	116.40
2	B	201	ASP	CA-CB-CG	-10.11	102.49	112.60
3	C	75	SER	CA-C-O	-10.10	110.30	120.70
4	E	178	THR	N-CA-C	10.02	125.33	110.30
1	D	61	ILE	CA-C-O	10.01	131.46	121.45
1	A	303	PRO	CA-N-CD	-9.98	98.03	112.00
1	D	300	HIS	O-C-N	9.97	136.21	122.46
3	C	104	VAL	O-C-N	9.94	135.00	122.57
3	C	267	GLN	CA-C-N	9.93	133.76	120.65
3	C	267	GLN	C-N-CA	9.93	133.76	120.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	7	LEU	CA-C-O	-9.86	110.44	120.80
1	A	297	ASN	OD1-CG-ND2	-9.86	112.74	122.60
1	A	102	ILE	CA-C-N	9.86	139.72	121.97
1	A	102	ILE	C-N-CA	9.86	139.72	121.97
4	E	309	ARG	CD-NE-CZ	9.85	138.19	124.40
3	C	113	ARG	CA-C-O	-9.85	109.85	120.88
2	B	20	ARG	NH1-CZ-NH2	9.83	132.08	119.30
3	C	139	PHE	CA-C-N	9.82	134.45	120.79
3	C	139	PHE	C-N-CA	9.82	134.45	120.79
1	A	277	TYR	CA-C-O	9.81	130.82	120.42
1	D	427	ALA	O-C-N	9.81	132.51	122.12
2	B	95	ASN	O-C-N	-9.78	109.58	122.59
4	E	29	ASP	N-CA-C	9.77	123.82	108.67
1	A	12	LEU	CA-C-O	-9.77	110.45	120.90
1	D	63	VAL	CA-C-O	-9.76	111.12	121.27
1	A	428	GLY	CA-C-N	9.75	133.12	120.44
1	A	428	GLY	C-N-CA	9.75	133.12	120.44
1	D	112	TYR	CA-C-N	9.74	140.15	121.54
1	D	112	TYR	C-N-CA	9.74	140.15	121.54
2	B	89	ASP	CA-C-O	9.73	131.38	119.31
1	D	209	ARG	N-CA-C	9.69	118.05	108.75
4	E	80	PRO	CB-CA-C	9.69	123.95	111.46
4	E	24	LEU	N-CA-C	9.68	124.64	113.02
1	D	209	ARG	CA-C-N	9.67	140.01	122.13
1	D	209	ARG	C-N-CA	9.67	140.01	122.13
1	A	399	TRP	CA-C-N	9.66	136.84	120.71
1	A	399	TRP	C-N-CA	9.66	136.84	120.71
3	C	28	ASN	CA-C-N	9.66	133.58	120.44
3	C	28	ASN	C-N-CA	9.66	133.58	120.44
3	C	150	ALA	CA-C-N	9.65	136.54	121.19
3	C	150	ALA	C-N-CA	9.65	136.54	121.19
3	C	206	PHE	CA-CB-CG	-9.65	104.15	113.80
1	A	218	VAL	CA-C-O	9.64	131.39	121.17
1	A	287	SER	N-CA-CB	9.63	124.29	109.94
1	A	101	ALA	CA-C-N	9.62	139.29	121.97
1	A	101	ALA	C-N-CA	9.62	139.29	121.97
1	D	58	GLN	OE1-CD-NE2	-9.60	113.00	122.60
2	B	47	ASN	CA-CB-CG	9.57	122.17	112.60
4	E	155	VAL	O-C-N	-9.57	112.79	122.93
1	A	104	HIS	ND1-CG-CD2	9.56	115.66	106.10
1	A	169	THR	CA-C-O	-9.54	112.80	121.67
4	E	147	SER	N-CA-C	-9.53	95.66	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	211	ASN	CA-C-N	9.52	139.73	121.54
3	C	211	ASN	C-N-CA	9.52	139.73	121.54
1	A	267	THR	N-CA-CB	9.52	125.18	110.14
1	A	382	ILE	O-C-N	9.49	131.61	121.83
3	C	30	VAL	O-C-N	-9.49	110.70	122.57
4	E	260	ALA	O-C-N	-9.49	112.29	122.07
4	E	118	LEU	CA-C-N	9.49	130.15	120.38
4	E	118	LEU	C-N-CA	9.49	130.15	120.38
3	C	266	ALA	N-CA-CB	9.48	123.76	110.01
4	E	430	ASN	N-CA-C	-9.47	100.92	111.14
1	D	399	TRP	N-CA-C	-9.46	100.84	112.38
1	D	218	VAL	CA-C-N	9.46	132.48	120.56
1	D	218	VAL	C-N-CA	9.46	132.48	120.56
4	E	193	ASN	O-C-N	9.45	134.60	123.17
4	E	132	THR	CA-C-N	9.45	139.58	121.54
4	E	132	THR	C-N-CA	9.45	139.58	121.54
1	A	416	LEU	CA-C-O	9.44	130.42	120.42
1	D	301	ARG	N-CA-C	9.44	130.90	110.80
3	C	21	VAL	CA-C-O	-9.43	110.44	120.53
1	A	177	VAL	CG1-CB-CG2	9.42	131.52	110.80
2	B	205	GLU	N-CA-C	9.40	123.64	109.63
4	E	134	PHE	CA-C-N	-9.39	108.10	119.84
4	E	134	PHE	C-N-CA	-9.39	108.10	119.84
2	B	95	ASN	OD1-CG-ND2	-9.38	113.22	122.60
2	B	441	TYR	N-CA-C	-9.38	100.41	112.23
1	D	266	SER	O-C-N	9.38	132.16	122.03
4	E	27	VAL	N-CA-C	9.37	128.82	109.34
1	A	128	CYS	CA-C-O	-9.36	110.50	120.99
1	D	166	ASP	CA-C-O	-9.36	110.54	120.55
3	C	79	ILE	CA-C-O	-9.34	110.25	120.43
1	D	63	VAL	N-CA-CB	9.33	120.86	110.51
3	C	288	ILE	O-C-N	9.32	134.23	122.57
4	E	65	SER	CA-C-O	-9.32	111.37	121.44
3	C	140	ASP	CA-CB-CG	9.31	121.91	112.60
1	D	266	SER	CA-C-O	-9.31	111.31	120.90
3	C	304	VAL	CA-C-O	-9.29	111.61	121.27
2	B	302	LEU	CA-C-O	-9.28	110.97	120.90
1	D	14	ASN	OD1-CG-ND2	-9.26	113.34	122.60
1	D	376	ILE	CA-C-O	-9.25	110.82	120.71
3	C	18	ASN	CA-C-O	-9.24	111.23	121.58
2	B	302	LEU	O-C-N	9.23	131.69	122.09
4	E	154	GLU	CA-C-N	9.22	136.10	122.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	154	GLU	C-N-CA	9.22	136.10	122.91
1	D	85	VAL	N-CA-C	9.22	123.69	109.12
4	E	17	ARG	NE-CZ-NH2	-9.21	110.91	119.20
3	C	451	GLN	CA-C-N	9.21	134.30	120.31
3	C	451	GLN	C-N-CA	9.21	134.30	120.31
3	C	319	THR	O-C-N	-9.20	111.07	122.20
1	A	248	SER	O-C-N	-9.19	110.36	122.59
1	A	85	VAL	N-CA-C	9.18	120.06	110.05
4	E	152	ALA	N-CA-C	9.18	130.36	110.80
2	B	85	VAL	N-CA-C	9.18	118.90	107.70
1	A	436	GLU	O-C-N	9.17	134.79	122.59
2	B	274	SER	N-CA-C	-9.17	102.27	113.19
2	B	215	ARG	NH1-CZ-NH2	-9.16	107.39	119.30
1	A	209	ARG	NH1-CZ-NH2	-9.16	107.39	119.30
1	D	300	HIS	CA-CB-CG	-9.15	104.65	113.80
2	B	269	LYS	CA-C-N	9.14	129.21	120.43
2	B	269	LYS	C-N-CA	9.14	129.21	120.43
4	E	26	HIS	N-CA-C	9.13	125.54	113.30
1	A	79	ARG	NE-CZ-NH2	9.13	127.42	119.20
1	D	60	TRP	CA-C-O	-9.13	111.30	121.25
1	D	66	ARG	CA-C-O	-9.10	110.97	121.16
1	D	211	PRO	CB-CA-C	-9.10	96.55	111.56
1	A	116	ILE	N-CA-C	9.09	121.71	108.53
1	D	379	VAL	CB-CA-C	-9.08	98.08	112.16
1	D	17	LYS	CA-C-O	-9.08	108.25	118.69
2	B	278	PRO	CA-C-O	-9.08	110.16	122.15
1	A	302	SER	N-CA-C	9.08	121.09	109.65
4	E	134	PHE	O-C-N	9.08	131.76	121.32
1	A	255	VAL	CA-C-N	-9.06	107.96	120.38
1	A	255	VAL	C-N-CA	-9.06	107.96	120.38
4	E	260	ALA	CA-C-O	9.01	130.28	120.82
4	E	118	LEU	N-CA-C	9.01	129.71	109.81
4	E	288	PHE	N-CA-C	-9.00	101.47	111.28
3	C	285	VAL	CA-C-O	-8.99	107.90	119.95
1	D	58	GLN	CG-CD-NE2	8.97	129.85	116.40
1	A	435	GLN	CA-C-O	-8.97	111.59	121.00
2	B	132	VAL	CA-C-N	8.96	138.84	122.54
2	B	132	VAL	C-N-CA	8.96	138.84	122.54
4	E	176	ASP	CA-CB-CG	-8.96	103.64	112.60
2	B	257	LEU	O-C-N	8.95	132.40	122.11
2	B	443	PHE	CA-CB-CG	8.94	122.74	113.80
1	D	378	GLY	CA-C-O	-8.93	111.36	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	68	ASN	OD1-CG-ND2	-8.93	113.67	122.60
1	A	6	ARG	NE-CZ-NH2	8.91	127.22	119.20
1	A	77	LYS	CA-C-O	-8.91	111.20	121.72
4	E	177	PHE	CA-CB-CG	8.91	122.72	113.80
1	A	196	THR	CA-C-N	8.91	129.04	120.31
1	A	196	THR	C-N-CA	8.91	129.04	120.31
1	A	254	THR	N-CA-CB	8.91	124.22	110.14
3	C	46	LYS	N-CA-C	-8.91	94.36	109.24
4	E	88	ASP	CA-CB-CG	-8.91	103.69	112.60
3	C	66	ARG	CA-C-O	-8.90	109.73	119.97
1	D	157	SER	O-C-N	-8.90	112.50	123.44
4	E	421	PHE	N-CA-CB	8.90	123.34	109.82
1	D	301	ARG	O-C-N	8.88	134.39	122.59
2	B	94	ASN	O-C-N	8.87	131.67	122.09
1	A	421	GLY	CA-C-N	8.86	132.87	120.29
1	A	421	GLY	C-N-CA	8.86	132.87	120.29
3	C	113	ARG	NE-CZ-NH1	-8.86	112.64	121.50
2	B	20	ARG	NE-CZ-NH2	-8.83	111.26	119.20
2	B	280	ILE	N-CA-CB	8.81	125.76	111.23
4	E	87	PRO	O-C-N	-8.80	113.70	123.03
1	A	432	GLU	CA-C-O	8.79	128.81	119.14
2	B	297	LEU	CA-C-N	8.79	131.87	120.44
2	B	297	LEU	C-N-CA	8.79	131.87	120.44
1	A	149	TRP	CB-CA-C	8.77	125.33	110.86
2	B	195	LYS	CA-C-O	-8.77	110.41	120.58
1	D	141	ASN	OD1-CG-ND2	-8.74	113.86	122.60
1	A	241	GLU	O-C-N	-8.74	111.52	122.27
4	E	263	ILE	CB-CA-C	-8.73	100.60	112.04
3	C	49	ASP	O-C-N	-8.73	110.98	122.59
1	D	251	LEU	CA-C-O	-8.72	111.21	120.63
1	D	19	ILE	O-C-N	-8.72	113.11	122.61
1	D	140	GLN	CG-CD-NE2	8.72	129.47	116.40
2	B	286	PHE	CA-C-O	-8.71	110.57	120.24
3	C	122	PRO	O-C-N	-8.71	111.18	121.46
1	A	3	HIS	CA-CB-CG	8.71	122.50	113.80
4	E	436	ASN	N-CA-C	-8.70	100.40	111.02
2	B	85	VAL	CA-C-O	-8.70	114.83	120.66
1	D	258	LEU	N-CA-C	-8.70	101.80	111.28
1	A	388	SER	N-CA-C	8.69	121.62	111.02
4	E	5	ARG	CD-NE-CZ	8.69	136.56	124.40
3	C	129	SER	N-CA-CB	8.67	123.26	110.25
3	C	235	PRO	O-C-N	8.66	134.32	122.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	240	GLY	CA-C-O	-8.65	112.33	120.80
4	E	437	GLU	CA-C-O	-8.64	111.25	120.92
1	D	29	VAL	O-C-N	-8.63	112.78	122.36
2	B	256	LEU	CA-C-O	-8.63	109.47	120.00
1	A	432	GLU	O-C-N	-8.62	110.94	122.49
3	C	263	VAL	CA-C-O	-8.62	111.48	121.05
1	A	208	GLN	OE1-CD-NE2	-8.62	113.98	122.60
1	D	44	ASP	CA-C-O	8.61	129.51	120.30
2	B	94	ASN	CA-C-N	8.60	137.97	121.54
2	B	94	ASN	C-N-CA	8.60	137.97	121.54
1	D	96	ALA	CB-CA-C	8.60	123.03	110.04
2	B	424	LEU	CA-C-N	8.60	132.15	120.54
2	B	424	LEU	C-N-CA	8.60	132.15	120.54
3	C	115	ASN	CA-C-N	8.59	138.25	121.41
3	C	115	ASN	C-N-CA	8.59	138.25	121.41
1	D	16	ASN	CA-CB-CG	8.58	121.18	112.60
4	E	233	SER	N-CA-C	-8.58	100.93	111.40
1	A	170	PHE	CA-CB-CG	8.56	122.36	113.80
2	B	270	VAL	CA-C-O	8.55	125.21	118.71
3	C	142	GLN	OE1-CD-NE2	-8.55	114.05	122.60
4	E	205	PHE	N-CA-CB	8.55	124.47	110.37
1	A	84	ASP	CA-CB-CG	8.55	121.15	112.60
1	A	99	ASP	CA-C-N	8.54	132.86	120.82
1	A	99	ASP	C-N-CA	8.54	132.86	120.82
1	D	188	VAL	N-CA-C	8.54	119.86	106.88
4	E	73	GLY	CA-C-O	-8.54	111.74	120.45
1	A	3	HIS	CE1-NE2-CD2	-8.53	100.47	109.00
1	A	301	ARG	CA-C-O	-8.53	108.32	120.51
1	D	18	VAL	CB-CA-C	-8.52	101.07	111.97
1	A	300	HIS	N-CA-C	8.51	120.55	111.28
4	E	62	TYR	CG-CD1-CE1	8.50	133.95	121.20
2	B	70	ALA	N-CA-C	8.50	123.77	113.23
3	C	142	GLN	CA-C-N	8.50	135.97	123.13
3	C	142	GLN	C-N-CA	8.50	135.97	123.13
2	B	307	ARG	NE-CZ-NH1	-8.49	113.01	121.50
1	A	217	ASN	OD1-CG-ND2	8.48	131.08	122.60
3	C	282	ALA	CA-C-O	-8.48	109.68	119.60
4	E	80	PRO	CA-C-N	8.46	134.64	121.19
4	E	80	PRO	C-N-CA	8.46	134.64	121.19
4	E	187	HIS	ND1-CE1-NE2	-8.46	99.94	108.40
1	D	198	TYR	N-CA-C	8.45	121.24	110.33
1	D	393	SER	O-C-N	-8.45	113.03	122.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	104	HIS	CA-CB-CG	-8.44	105.36	113.80
1	A	218	VAL	O-C-N	-8.44	113.64	121.91
2	B	404	ALA	CA-C-N	8.44	137.16	121.97
2	B	404	ALA	C-N-CA	8.44	137.16	121.97
2	B	218	LEU	CA-C-O	-8.43	111.73	120.84
2	B	252	SER	CA-C-O	-8.43	111.97	120.82
1	A	269	SER	CA-C-N	8.42	137.85	121.18
1	A	269	SER	C-N-CA	8.42	137.85	121.18
1	D	32	THR	O-C-N	-8.40	112.27	123.10
2	B	149	TYR	O-C-N	-8.40	110.73	122.15
1	D	431	ILE	N-CA-CB	8.40	125.09	111.23
1	D	54	VAL	O-C-N	8.40	132.14	123.07
1	A	171	MET	CB-CA-C	-8.39	98.08	110.16
2	B	418	ALA	N-CA-C	8.38	121.17	111.11
4	E	131	VAL	O-C-N	-8.38	112.09	122.57
4	E	95	VAL	O-C-N	8.38	133.05	122.57
2	B	210	TYR	N-CA-C	8.38	122.68	110.28
1	A	175	GLU	CA-C-N	8.38	137.85	122.02
1	A	175	GLU	C-N-CA	8.38	137.85	122.02
1	A	297	ASN	N-CA-C	-8.38	101.39	111.69
1	A	404	MET	CA-C-O	-8.38	110.01	118.97
2	B	466	ASN	CA-C-N	-8.36	109.39	119.84
2	B	466	ASN	C-N-CA	-8.36	109.39	119.84
4	E	175	GLU	CA-C-O	-8.36	111.95	120.90
1	A	110	LEU	O-C-N	8.36	132.72	123.10
1	A	385	HIS	CA-C-N	8.36	132.16	120.29
1	A	385	HIS	C-N-CA	8.36	132.16	120.29
2	B	426	LYS	CA-C-O	-8.36	110.66	120.10
1	A	289	ILE	N-CA-C	8.35	118.40	110.30
3	C	18	ASN	N-CA-CB	-8.35	98.14	110.49
3	C	211	ASN	CA-C-O	-8.35	112.46	120.56
1	A	106	THR	O-C-N	-8.34	114.20	123.13
1	D	170	PHE	O-C-N	-8.34	113.34	122.85
2	B	140	GLN	CA-C-O	-8.32	112.19	121.51
2	B	46	LYS	O-C-N	8.31	131.07	122.09
3	C	1	VAL	CA-C-N	8.31	137.41	121.54
3	C	1	VAL	C-N-CA	8.31	137.41	121.54
3	C	264	LEU	CA-C-O	-8.31	111.74	120.55
1	D	427	ALA	CA-C-O	-8.31	111.66	120.63
3	C	306	CYS	CA-C-N	8.30	129.15	119.94
3	C	306	CYS	C-N-CA	8.30	129.15	119.94
1	A	209	ARG	NE-CZ-NH2	8.30	126.67	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	195	ASN	CA-CB-CG	8.30	120.90	112.60
1	D	100	PHE	CA-C-O	-8.29	111.14	120.43
4	E	205	PHE	CA-CB-CG	-8.29	105.51	113.80
3	C	258	SER	CA-C-O	8.28	129.58	120.63
1	A	162	SER	CA-C-O	-8.27	111.39	120.33
2	B	141	ASN	OD1-CG-ND2	8.27	130.87	122.60
1	A	238	ASP	O-C-N	-8.27	112.23	122.24
3	C	428	TYR	O-C-N	-8.26	111.50	122.23
4	E	128	PRO	CB-CA-C	8.25	125.18	111.56
1	A	389	ASP	N-CA-C	8.25	120.27	111.28
2	B	453	SER	CA-C-N	8.25	131.24	120.60
2	B	453	SER	C-N-CA	8.25	131.24	120.60
1	D	171	MET	CA-C-O	-8.25	110.92	120.49
2	B	406	GLU	CA-C-N	8.24	134.70	120.68
2	B	406	GLU	C-N-CA	8.24	134.70	120.68
3	C	464	VAL	CB-CA-C	-8.24	99.38	112.16
1	A	72	TYR	N-CA-C	-8.24	101.35	111.40
1	D	391	GLU	CA-C-O	8.23	129.14	120.42
1	A	136	PRO	CB-CA-C	8.22	122.08	111.64
2	B	97	ASP	N-CA-C	-8.22	103.75	113.21
3	C	2	ASN	OD1-CG-ND2	-8.22	114.38	122.60
2	B	148	SER	O-C-N	-8.22	111.59	121.79
1	A	168	SER	N-CA-C	-8.21	102.41	111.36
1	D	143	THR	CA-C-N	-8.21	111.42	123.00
1	D	143	THR	C-N-CA	-8.21	111.42	123.00
2	B	291	VAL	CA-C-N	8.20	132.36	120.38
2	B	291	VAL	C-N-CA	8.20	132.36	120.38
1	D	429	ARG	NE-CZ-NH1	-8.20	113.30	121.50
3	C	89	ILE	CA-C-O	-8.19	111.75	119.62
3	C	293	MET	N-CA-CB	8.19	122.25	110.13
3	C	244	ALA	O-C-N	-8.19	110.73	122.36
3	C	250	PRO	CA-C-N	8.19	134.14	120.88
3	C	250	PRO	C-N-CA	8.19	134.14	120.88
1	A	117	MET	O-C-N	8.18	133.30	123.24
1	D	136	PRO	N-CA-C	8.18	129.32	112.47
1	A	272	PRO	O-C-N	-8.18	114.36	123.03
1	A	229	THR	N-CA-C	-8.17	101.05	111.02
2	B	427	ASP	N-CA-CB	8.17	121.86	110.01
4	E	257	VAL	CB-CA-C	-8.17	101.29	112.24
1	A	424	SER	CA-C-O	8.17	129.21	120.55
2	B	163	ASP	N-CA-C	8.16	124.93	114.56
1	D	429	ARG	O-C-N	-8.16	113.47	122.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	126	THR	N-CA-C	8.16	121.07	107.20
1	D	99	ASP	N-CA-CB	8.15	124.26	110.49
4	E	61	ASP	CA-CB-CG	8.15	120.75	112.60
1	A	198	TYR	O-C-N	8.14	133.42	122.59
3	C	459	PHE	CA-CB-CG	-8.14	105.66	113.80
3	C	32	ASN	N-CA-C	8.14	121.65	108.63
1	A	226	SER	N-CA-C	-8.14	101.09	111.02
2	B	205	GLU	O-C-N	-8.14	113.25	122.20
2	B	289	ILE	N-CA-C	-8.13	102.14	111.00
1	A	38	ILE	N-CA-CB	8.13	122.77	110.58
4	E	29	ASP	CA-C-O	8.13	129.78	120.60
1	A	301	ARG	CA-C-N	8.12	136.37	120.94
1	A	301	ARG	C-N-CA	8.12	136.37	120.94
1	A	109	LEU	O-C-N	8.11	132.76	123.27
3	C	153	TYR	O-C-N	8.10	132.23	122.75
1	D	243	MET	CA-C-N	8.10	132.20	120.38
1	D	243	MET	C-N-CA	8.10	132.20	120.38
2	B	3	MET	O-C-N	8.10	133.36	122.59
3	C	449	VAL	CA-C-O	-8.10	110.66	120.78
3	C	299	VAL	N-CA-C	-8.08	100.94	111.05
1	D	94	ASN	O-C-N	8.08	133.34	122.59
4	E	446	ILE	O-C-N	8.07	130.29	121.90
2	B	152	ASP	CA-CB-CG	-8.07	104.53	112.60
2	B	125	ARG	NE-CZ-NH1	8.06	129.56	121.50
3	C	190	TRP	O-C-N	8.06	134.37	122.76
3	C	263	VAL	N-CA-C	-8.06	102.95	110.53
1	A	224	LEU	CA-C-N	8.06	131.08	120.28
1	A	224	LEU	C-N-CA	8.06	131.08	120.28
1	D	189	TYR	O-C-N	-8.05	114.04	123.06
3	C	122	PRO	CA-C-O	8.05	132.24	120.56
4	E	420	ASN	CA-CB-CG	8.05	120.65	112.60
1	A	394	ASN	OD1-CG-ND2	-8.04	114.56	122.60
4	E	93	ASN	N-CA-CB	8.04	124.09	110.49
1	A	262	GLU	CA-C-N	8.04	131.97	120.79
1	A	262	GLU	C-N-CA	8.04	131.97	120.79
1	A	149	TRP	CG-CD2-CE3	-8.03	125.87	133.90
1	A	250	LEU	CA-C-N	-8.03	109.70	120.63
1	A	250	LEU	C-N-CA	-8.03	109.70	120.63
3	C	237	VAL	N-CA-C	-8.03	103.03	110.82
2	B	29	VAL	CA-C-O	-8.03	111.97	120.48
1	D	99	ASP	O-C-N	-8.02	111.93	122.59
4	E	89	VAL	N-CA-C	8.01	120.45	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	197	GLN	CA-C-O	-8.00	111.47	121.88
1	D	415	MET	N-CA-C	-8.00	102.50	111.14
4	E	310	THR	CA-C-N	8.00	129.84	119.84
4	E	310	THR	C-N-CA	8.00	129.84	119.84
1	D	79	ARG	NH1-CZ-NH2	8.00	129.69	119.30
2	B	215	ARG	CA-CB-CG	7.99	130.07	114.10
2	B	220	TYR	O-C-N	7.98	132.17	122.35
2	B	306	HIS	N-CA-C	7.98	127.80	110.80
2	B	242	PRO	CA-C-N	-7.98	109.86	119.84
2	B	242	PRO	C-N-CA	-7.98	109.86	119.84
1	A	408	HIS	N-CA-CB	7.98	122.03	110.06
1	D	274	ILE	CA-C-O	-7.98	111.33	120.74
2	B	457	ASP	CA-C-O	-7.97	112.10	120.55
2	B	44	ASN	O-C-N	7.97	132.36	122.63
1	D	95	ASN	CA-CB-CG	7.97	120.57	112.60
1	D	210	ILE	O-C-N	7.97	130.18	121.10
3	C	104	VAL	CA-C-N	7.96	134.74	122.08
3	C	104	VAL	C-N-CA	7.96	134.74	122.08
1	D	230	VAL	N-CA-C	-7.95	103.06	110.53
2	B	213	ILE	N-CA-C	7.95	120.37	109.80
4	E	312	ASN	CA-C-O	-7.95	109.41	118.47
4	E	303	VAL	N-CA-CB	7.93	121.33	110.54
4	E	266	PHE	CA-CB-CG	-7.93	105.87	113.80
3	C	112	VAL	CB-CA-C	-7.91	100.23	111.31
4	E	39	LEU	O-C-N	7.91	132.34	122.84
1	A	224	LEU	CB-CA-C	-7.91	98.34	110.92
1	A	431	ILE	CA-C-O	-7.91	110.89	120.78
1	A	387	LYS	CA-C-N	7.91	131.78	120.79
1	A	387	LYS	C-N-CA	7.91	131.78	120.79
1	D	156	VAL	CA-C-O	-7.90	112.90	121.28
1	D	417	ILE	CA-C-N	7.90	131.66	120.28
1	D	417	ILE	C-N-CA	7.90	131.66	120.28
1	A	290	ILE	O-C-N	7.90	129.85	121.87
1	A	118	TRP	CA-C-N	-7.89	114.05	122.89
1	A	118	TRP	C-N-CA	-7.89	114.05	122.89
2	B	411	ILE	O-C-N	-7.89	112.70	122.57
1	D	151	TYR	N-CA-CB	7.89	123.16	110.77
1	D	230	VAL	O-C-N	-7.89	113.69	121.90
4	E	195	ASN	OD1-CG-ND2	-7.88	114.72	122.60
3	C	202	TYR	O-C-N	-7.87	113.76	123.44
4	E	188	ARG	CA-C-O	7.86	130.93	120.16
1	A	145	LYS	CA-C-O	7.86	129.52	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	436	ASN	CA-CB-CG	7.85	120.45	112.60
3	C	269	VAL	CA-C-O	7.84	128.94	120.47
1	A	299	HIS	ND1-CG-CD2	7.84	113.94	106.10
1	D	93	TYR	CA-C-O	-7.84	109.30	120.51
3	C	248	TYR	O-C-N	-7.83	113.22	122.15
1	D	88	PRO	CA-C-O	-7.82	112.12	121.03
1	A	136	PRO	N-CA-C	7.82	124.00	111.26
4	E	227	ALA	CA-C-O	-7.81	109.46	120.16
4	E	440	VAL	O-C-N	-7.81	114.26	121.91
1	A	229	THR	O-C-N	7.81	130.44	122.08
3	C	426	THR	CB-CA-C	-7.81	98.62	110.88
4	E	69	SER	CA-C-O	-7.81	109.63	119.31
3	C	17	TYR	CB-CG-CD1	-7.80	109.11	120.80
1	D	9	ALA	O-C-N	7.79	130.10	122.07
3	C	19	LYS	N-CA-CB	7.79	123.66	110.49
1	A	229	THR	CA-C-O	-7.79	112.50	121.07
1	D	41	ILE	N-CA-C	7.79	117.85	110.53
2	B	7	LEU	CA-C-O	7.78	129.17	121.00
3	C	152	ASN	N-CA-C	7.78	119.54	111.14
2	B	272	GLU	CA-C-O	-7.77	111.03	119.97
1	D	176	TRP	CA-CB-CG	7.77	128.37	113.60
1	A	383	ALA	CA-C-O	-7.76	112.24	120.55
1	D	408	HIS	O-C-N	-7.76	114.02	122.09
3	C	91	ASP	CA-C-O	-7.75	111.08	121.86
3	C	245	LEU	O-C-N	-7.75	112.79	122.17
2	B	89	ASP	CA-C-N	7.75	135.91	121.97
2	B	89	ASP	C-N-CA	7.75	135.91	121.97
1	A	375	ALA	CA-C-N	7.74	130.91	120.77
1	A	375	ALA	C-N-CA	7.74	130.91	120.77
1	D	47	ASN	CA-C-O	-7.74	110.45	119.59
3	C	145	SER	N-CA-C	7.74	122.31	109.46
4	E	151	ASN	OD1-CG-ND2	7.74	130.34	122.60
2	B	461	ASN	CA-CB-CG	-7.73	104.87	112.60
1	D	130	ILE	CA-C-N	7.73	135.89	121.97
1	D	130	ILE	C-N-CA	7.73	135.89	121.97
3	C	459	PHE	CA-C-N	7.73	135.88	121.97
3	C	459	PHE	C-N-CA	7.73	135.88	121.97
1	A	288	SER	O-C-N	7.73	130.31	122.12
4	E	255	ILE	CB-CA-C	-7.73	101.90	111.87
4	E	193	ASN	N-CA-C	7.72	120.90	109.24
1	D	88	PRO	O-C-N	7.72	131.75	123.10
1	A	147	GLY	CA-C-O	-7.72	114.00	121.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	384	GLU	CA-C-O	-7.72	112.37	120.55
1	D	55	ARG	O-C-N	-7.72	113.67	122.93
3	C	268	ALA	CB-CA-C	7.71	122.84	110.96
1	D	408	HIS	ND1-CE1-NE2	-7.71	100.69	108.40
1	A	8	VAL	N-CA-C	7.70	118.48	110.62
2	B	82	SER	O-C-N	7.70	127.25	121.47
3	C	186	GLU	O-C-N	7.70	133.68	122.43
1	A	162	SER	N-CA-C	7.70	121.72	108.02
2	B	303	ASN	CB-CA-C	7.70	123.16	110.92
2	B	229	ILE	CA-C-N	7.70	130.81	120.65
2	B	229	ILE	C-N-CA	7.70	130.81	120.65
2	B	462	VAL	CB-CA-C	7.70	125.37	111.36
1	A	4	GLU	CA-C-N	7.70	133.56	120.71
1	A	4	GLU	C-N-CA	7.70	133.56	120.71
3	C	158	ILE	N-CA-C	7.69	120.02	108.80
3	C	115	ASN	CA-CB-CG	-7.67	104.93	112.60
4	E	106	ASN	OD1-CG-ND2	7.67	130.27	122.60
4	E	16	LYS	CA-C-N	7.67	135.26	120.99
4	E	16	LYS	C-N-CA	7.67	135.26	120.99
2	B	414	GLN	N-CA-CB	7.67	121.35	110.07
3	C	157	GLU	N-CA-CB	7.67	123.45	110.49
1	A	159	SER	CA-C-N	-7.67	110.26	119.84
1	A	159	SER	C-N-CA	-7.67	110.26	119.84
3	C	137	PHE	CA-C-N	-7.66	110.26	119.84
3	C	137	PHE	C-N-CA	-7.66	110.26	119.84
3	C	462	THR	CA-C-O	7.66	126.24	118.73
2	B	458	ALA	CA-C-N	7.66	136.16	121.54
2	B	458	ALA	C-N-CA	7.66	136.16	121.54
3	C	101	GLN	CA-C-N	7.66	131.62	120.82
3	C	101	GLN	C-N-CA	7.66	131.62	120.82
4	E	425	SER	CA-C-N	7.65	130.86	120.38
4	E	425	SER	C-N-CA	7.65	130.86	120.38
2	B	7	LEU	O-C-N	-7.64	114.08	122.03
3	C	285	VAL	O-C-N	-7.64	112.39	121.10
1	D	419	ILE	CA-C-O	-7.64	111.92	120.32
1	D	47	ASN	N-CA-C	-7.64	103.03	112.88
2	B	434	VAL	N-CA-C	7.63	117.69	110.74
3	C	425	SER	CA-C-N	7.63	130.36	120.44
3	C	425	SER	C-N-CA	7.63	130.36	120.44
3	C	103	ASN	O-C-N	7.63	132.58	123.27
2	B	240	TYR	CA-C-N	7.63	129.63	120.09
2	B	240	TYR	C-N-CA	7.63	129.63	120.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	9	SER	N-CA-C	7.63	119.67	111.36
1	D	150	THR	CA-C-N	7.62	133.52	122.77
1	D	150	THR	C-N-CA	7.62	133.52	122.77
1	A	376	ILE	CA-C-O	-7.62	113.49	121.41
1	D	198	TYR	CA-C-O	-7.62	113.42	122.03
3	C	447	ASN	OD1-CG-ND2	-7.62	114.98	122.60
4	E	107	VAL	O-C-N	-7.62	113.05	122.57
4	E	207	GLU	O-C-N	7.61	131.14	122.99
1	A	300	HIS	CA-C-N	7.61	136.08	121.54
1	A	300	HIS	C-N-CA	7.61	136.08	121.54
4	E	23	THR	O-C-N	-7.61	116.56	123.41
1	A	261	VAL	CA-C-O	-7.61	112.35	120.64
3	C	483	ALA	CA-C-N	7.61	135.40	121.70
3	C	483	ALA	C-N-CA	7.61	135.40	121.70
4	E	176	ASP	CA-C-N	7.61	136.07	121.54
4	E	176	ASP	C-N-CA	7.61	136.07	121.54
2	B	159	GLN	CA-C-N	7.61	136.27	121.66
2	B	159	GLN	C-N-CA	7.61	136.27	121.66
3	C	430	VAL	CB-CA-C	-7.61	102.05	112.24
3	C	309	VAL	CA-C-O	7.60	130.28	120.78
4	E	112	ASP	O-C-N	-7.59	112.49	122.59
2	B	253	ILE	O-C-N	7.59	129.33	121.89
4	E	460	LEU	N-CA-C	-7.59	102.70	110.97
1	A	133	THR	N-CA-C	7.58	122.73	113.17
4	E	451	PHE	CA-CB-CG	7.58	121.39	113.80
1	A	213	TYR	CA-C-O	7.58	128.66	120.55
1	A	422	THR	O-C-N	-7.58	113.51	122.15
4	E	113	GLY	CA-C-N	-7.58	111.51	122.19
4	E	113	GLY	C-N-CA	-7.58	111.51	122.19
1	A	14	ASN	N-CA-C	7.57	121.43	109.39
4	E	28	ILE	CA-C-N	7.57	133.26	121.99
4	E	28	ILE	C-N-CA	7.57	133.26	121.99
1	A	434	SER	CA-C-N	7.56	130.63	120.65
1	A	434	SER	C-N-CA	7.56	130.63	120.65
1	A	99	ASP	CA-CB-CG	7.56	120.16	112.60
1	D	155	LYS	N-CA-C	7.56	122.73	112.68
4	E	71	TYR	N-CA-C	-7.55	101.81	111.02
1	D	376	ILE	CA-C-N	7.55	130.40	120.28
1	D	376	ILE	C-N-CA	7.55	130.40	120.28
3	C	282	ALA	CA-C-N	7.54	131.78	120.31
3	C	282	ALA	C-N-CA	7.54	131.78	120.31
2	B	130	ILE	O-C-N	-7.54	114.52	121.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	473	PHE	N-CA-C	-7.54	103.00	111.14
1	D	149	TRP	CG-CD1-NE1	7.54	120.00	110.20
1	A	186	HIS	CA-CB-CG	7.54	121.34	113.80
2	B	14	ASN	CA-CB-CG	-7.53	105.07	112.60
2	B	426	LYS	CA-C-N	7.53	130.24	120.44
2	B	426	LYS	C-N-CA	7.53	130.24	120.44
4	E	157	LEU	CA-C-O	-7.53	112.40	121.28
1	A	80	LEU	CA-C-N	-7.53	112.99	120.21
1	A	80	LEU	C-N-CA	-7.53	112.99	120.21
2	B	128	CYS	CA-C-N	7.52	135.91	121.54
2	B	128	CYS	C-N-CA	7.52	135.91	121.54
3	C	310	LEU	CA-C-N	7.52	131.36	120.38
3	C	310	LEU	C-N-CA	7.52	131.36	120.38
4	E	473	GLN	N-CA-C	7.52	122.27	113.18
1	A	67	TRP	CA-C-O	-7.51	113.19	121.23
1	A	169	THR	CB-CA-C	-7.51	100.50	112.07
1	D	184	TRP	CA-CB-CG	7.51	127.88	113.60
1	D	77	LYS	CA-C-O	7.51	128.29	120.40
3	C	49	ASP	CA-C-O	-7.51	109.77	120.51
3	C	316	THR	N-CA-CB	7.51	119.12	110.03
1	D	176	TRP	CB-CG-CD2	-7.51	116.29	126.80
1	D	211	PRO	CA-C-O	-7.50	106.94	120.60
1	D	265	PRO	CA-N-CD	-7.50	101.50	112.00
2	B	303	ASN	O-C-N	-7.50	114.05	122.08
3	C	112	VAL	CA-C-O	-7.50	112.04	120.74
3	C	313	HIS	CA-CB-CG	7.50	121.30	113.80
4	E	313	THR	N-CA-CB	7.50	121.77	110.22
2	B	12	PHE	O-C-N	-7.50	111.30	122.39
2	B	108	VAL	CA-C-N	7.50	132.39	122.42
2	B	108	VAL	C-N-CA	7.50	132.39	122.42
2	B	152	ASP	CA-C-O	-7.50	111.12	120.57
4	E	199	THR	CA-C-O	-7.50	110.26	119.18
1	D	102	ILE	CB-CG1-CD1	7.49	129.54	113.80
1	D	209	ARG	O-C-N	7.49	127.87	121.65
1	A	414	PHE	O-C-N	7.48	131.47	122.27
4	E	17	ARG	N-CA-C	7.48	121.85	112.87
3	C	89	ILE	N-CA-C	7.48	116.26	107.73
4	E	195	ASN	O-C-N	-7.48	114.47	123.29
2	B	130	ILE	CA-C-O	-7.48	113.25	121.17
4	E	148	GLN	N-CA-C	7.47	122.24	113.20
2	B	230	LEU	N-CA-C	-7.47	102.83	110.97
1	D	266	SER	CA-C-N	7.47	130.51	120.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	266	SER	C-N-CA	7.47	130.51	120.65
1	A	12	LEU	O-C-N	7.47	129.85	122.09
1	A	46	VAL	CA-C-O	7.46	128.56	120.57
1	D	235	LEU	O-C-N	7.46	129.89	121.32
4	E	111	ASN	CA-CB-CG	-7.45	105.15	112.60
2	B	84	ASP	N-CA-C	7.45	122.06	113.19
3	C	213	GLN	OE1-CD-NE2	7.45	130.05	122.60
1	D	151	TYR	CB-CG-CD1	7.45	131.98	120.80
1	A	134	HIS	N-CA-C	7.45	119.18	111.14
3	C	101	GLN	O-C-N	7.44	132.34	122.82
3	C	291	TYR	CA-C-O	-7.44	112.59	120.55
4	E	309	ARG	CA-C-O	-7.44	109.87	120.51
1	A	86	TRP	CA-C-O	7.43	128.53	120.58
2	B	203	SER	CA-C-N	-7.43	110.94	121.72
2	B	203	SER	C-N-CA	-7.43	110.94	121.72
1	A	264	ILE	N-CA-C	7.42	124.91	108.88
3	C	301	GLY	CA-C-N	7.42	130.06	120.56
3	C	301	GLY	C-N-CA	7.42	130.06	120.56
1	D	20	ARG	NE-CZ-NH1	7.42	128.92	121.50
4	E	434	SER	CA-C-O	7.42	128.41	120.55
1	A	3	HIS	CA-C-N	7.41	130.08	120.44
1	A	3	HIS	C-N-CA	7.41	130.08	120.44
1	A	301	ARG	N-CA-C	7.41	126.59	110.80
1	A	225	PHE	N-CA-C	-7.40	103.21	111.28
1	D	219	ILE	O-C-N	-7.40	114.66	121.91
3	C	88	TRP	CB-CA-C	-7.40	98.36	109.90
1	D	134	HIS	N-CA-C	7.40	119.13	111.14
4	E	65	SER	CA-C-N	-7.39	108.74	123.09
4	E	65	SER	C-N-CA	-7.39	108.74	123.09
1	D	112	TYR	N-CA-C	-7.39	103.21	111.71
1	A	64	ARG	NE-CZ-NH1	-7.39	114.11	121.50
2	B	288	MET	N-CA-C	-7.39	103.31	111.36
4	E	185	ILE	O-C-N	7.39	130.66	122.98
1	A	140	GLN	CG-CD-NE2	7.38	127.47	116.40
1	D	238	ASP	CA-C-O	-7.38	110.71	119.35
1	A	379	VAL	CB-CA-C	-7.38	102.36	112.24
3	C	224	LYS	O-C-N	-7.38	112.84	121.32
1	D	95	ASN	O-C-N	-7.37	112.79	122.59
3	C	280	GLU	O-C-N	-7.37	114.20	122.08
4	E	92	GLU	CA-C-N	7.37	135.61	121.54
4	E	92	GLU	C-N-CA	7.37	135.61	121.54
1	A	246	SER	CA-C-O	-7.36	113.12	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	219	PHE	CA-C-N	-7.36	110.55	122.26
2	B	219	PHE	C-N-CA	-7.36	110.55	122.26
2	B	5	ASP	N-CA-CB	7.36	122.93	110.49
4	E	63	ARG	NH1-CZ-NH2	-7.36	109.73	119.30
1	D	73	GLY	CA-C-N	7.35	135.82	121.41
1	D	73	GLY	C-N-CA	7.35	135.82	121.41
4	E	25	ASP	CA-C-O	7.35	127.86	119.18
2	B	144	MET	CA-C-N	-7.35	113.12	123.11
2	B	144	MET	C-N-CA	-7.35	113.12	123.11
2	B	188	ILE	O-C-N	-7.35	115.54	123.18
2	B	306	HIS	N-CA-CB	7.34	122.90	110.49
1	D	94	ASN	CA-C-O	-7.34	110.01	120.51
4	E	70	GLU	CA-C-O	-7.34	110.01	120.51
4	E	245	GLN	N-CA-C	7.34	118.98	110.97
4	E	460	LEU	CA-C-O	-7.34	113.29	121.00
1	A	87	LEU	CA-C-O	7.33	125.52	119.36
3	C	65	HIS	ND1-CE1-NE2	-7.33	101.07	108.40
1	D	48	GLN	OE1-CD-NE2	-7.33	115.27	122.60
4	E	226	ILE	N-CA-C	7.32	117.45	110.42
1	D	392	SER	CA-C-N	7.31	130.95	120.79
1	D	392	SER	C-N-CA	7.31	130.95	120.79
1	D	385	HIS	N-CA-C	-7.30	103.01	110.97
2	B	3	MET	CA-C-O	-7.30	110.07	120.51
4	E	219	LEU	O-C-N	7.29	131.90	122.93
1	D	128	CYS	O-C-N	-7.29	113.08	122.78
3	C	315	ARG	NH1-CZ-NH2	-7.29	109.83	119.30
4	E	297	VAL	N-CA-CB	7.28	123.25	111.23
2	B	156	VAL	O-C-N	-7.28	113.47	122.57
1	A	235	LEU	CA-C-N	7.28	128.93	119.84
1	A	235	LEU	C-N-CA	7.28	128.93	119.84
3	C	232	PHE	N-CA-C	7.27	121.39	112.23
4	E	161	ALA	N-CA-CB	7.27	122.78	110.49
3	C	60	HIS	CA-CB-CG	-7.27	106.53	113.80
3	C	118	VAL	O-C-N	-7.26	115.23	123.00
3	C	207	PRO	O-C-N	-7.26	113.92	123.06
1	D	243	MET	CA-CB-CG	7.25	128.60	114.10
2	B	242	PRO	N-CA-C	7.25	119.55	110.70
3	C	257	MET	CA-C-O	7.25	128.16	120.70
1	D	203	TYR	CA-C-O	7.24	129.23	121.55
3	C	79	ILE	CB-CA-C	-7.24	98.85	110.28
1	D	20	ARG	CA-C-O	-7.23	110.85	121.27
4	E	431	ASP	O-C-N	7.23	130.43	122.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	72	TYR	CA-CB-CG	7.23	126.92	113.90
1	D	253	LEU	CA-C-O	7.23	130.85	120.51
3	C	228	TYR	CA-CB-CG	7.23	126.91	113.90
1	A	111	ASP	N-CA-CB	7.23	121.15	109.95
2	B	95	ASN	CA-C-N	7.23	135.34	121.54
2	B	95	ASN	C-N-CA	7.23	135.34	121.54
3	C	7	LEU	O-C-N	-7.23	114.29	122.09
3	C	69	TRP	O-C-N	7.22	133.16	122.76
1	D	172	GLU	CA-C-O	7.22	128.26	119.38
3	C	17	TYR	CA-C-O	7.22	129.12	120.81
4	E	274	GLU	CA-C-O	7.22	128.43	120.63
3	C	285	VAL	CB-CA-C	-7.22	98.22	111.36
1	A	426	PHE	O-C-N	-7.22	112.99	122.59
2	B	162	LEU	N-CA-CB	7.22	120.34	110.38
1	D	139	GLN	N-CA-C	7.22	126.17	110.80
1	A	258	LEU	CA-C-N	7.21	131.87	120.47
1	A	258	LEU	C-N-CA	7.21	131.87	120.47
4	E	457	LEU	CA-C-O	7.21	128.13	120.70
1	D	235	LEU	CA-C-N	7.21	128.85	119.84
1	D	235	LEU	C-N-CA	7.21	128.85	119.84
1	A	290	ILE	CA-C-O	-7.21	112.86	120.57
2	B	61	THR	O-C-N	-7.20	113.87	123.23
1	D	385	HIS	CA-C-O	-7.20	113.44	121.00
1	A	216	VAL	O-C-N	-7.20	113.58	122.57
3	C	28	ASN	CA-CB-CG	7.20	119.80	112.60
4	E	190	ALA	N-CA-CB	7.19	121.72	110.71
1	A	260	ILE	CB-CA-C	-7.19	102.60	112.02
4	E	471	LEU	CA-C-N	7.18	135.57	122.79
4	E	471	LEU	C-N-CA	7.18	135.57	122.79
2	B	252	SER	O-C-N	7.18	129.47	122.07
2	B	307	ARG	N-CA-C	7.17	126.06	110.80
1	A	209	ARG	CD-NE-CZ	7.17	134.43	124.40
1	A	375	ALA	CA-C-O	7.17	127.13	119.03
3	C	308	ILE	CA-C-O	-7.16	111.83	120.78
3	C	19	LYS	CB-CG-CD	7.16	127.77	111.30
3	C	223	ARG	CB-CA-C	-7.16	98.40	110.43
2	B	186	TRP	CB-CG-CD1	7.16	137.64	126.90
2	B	428	TRP	CA-C-O	-7.16	112.97	120.55
3	C	236	CYS	N-CA-CB	7.15	121.44	109.78
1	A	104	HIS	CB-CG-ND1	-7.15	111.97	122.70
1	D	160	PRO	CA-N-CD	-7.15	101.99	112.00
2	B	446	MET	CA-C-O	-7.15	113.34	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	178	ILE	CA-C-O	-7.15	108.65	120.80
3	C	16	LYS	CA-C-N	7.14	130.94	120.95
3	C	16	LYS	C-N-CA	7.14	130.94	120.95
4	E	119	PRO	N-CA-C	7.14	119.41	110.70
4	E	140	ASN	CA-C-O	7.14	128.82	120.69
1	A	412	CYS	CA-CB-SG	7.13	130.81	114.40
2	B	306	HIS	CB-CG-ND1	-7.13	112.00	122.70
2	B	20	ARG	CA-C-N	7.13	128.76	119.84
2	B	20	ARG	C-N-CA	7.13	128.76	119.84
4	E	12	GLY	CA-C-N	7.13	131.15	120.31
4	E	12	GLY	C-N-CA	7.13	131.15	120.31
1	A	383	ALA	CA-C-N	7.13	129.83	120.28
1	A	383	ALA	C-N-CA	7.13	129.83	120.28
1	A	180	ASP	CA-CB-CG	7.13	119.73	112.60
1	A	423	VAL	CA-C-N	7.12	129.83	120.28
1	A	423	VAL	C-N-CA	7.12	129.83	120.28
1	D	114	GLY	O-C-N	-7.12	113.45	122.70
1	D	265	PRO	N-CA-CB	-7.12	95.33	103.30
3	C	69	TRP	CD2-CE2-CZ2	7.12	129.52	122.40
3	C	11	LEU	CA-C-O	-7.12	112.94	120.55
1	D	288	SER	CA-C-N	-7.11	111.81	120.70
1	D	288	SER	C-N-CA	-7.11	111.81	120.70
2	B	437	ARG	CD-NE-CZ	7.11	134.35	124.40
3	C	116	GLY	N-CA-C	7.11	130.03	113.18
3	C	104	VAL	CA-CB-CG1	7.11	122.49	110.40
4	E	94	ASN	O-C-N	7.11	132.04	122.59
4	E	425	SER	CA-C-O	-7.11	113.58	120.90
3	C	26	HIS	CA-CB-CG	-7.10	106.70	113.80
3	C	481	PRO	CA-C-N	7.10	128.72	119.84
3	C	481	PRO	C-N-CA	7.10	128.72	119.84
2	B	139	TRP	CD2-CE2-CZ2	7.10	129.50	122.40
2	B	77	ASP	CA-CB-CG	7.09	119.69	112.60
1	D	47	ASN	OD1-CG-ND2	7.09	129.69	122.60
4	E	443	GLY	N-CA-C	7.09	129.98	113.18
4	E	151	ASN	CA-C-N	7.08	135.06	121.54
4	E	151	ASN	C-N-CA	7.08	135.06	121.54
2	B	271	PRO	O-C-N	7.07	130.72	122.23
1	D	162	SER	CA-C-N	7.07	132.50	121.26
1	D	162	SER	C-N-CA	7.07	132.50	121.26
2	B	211	LEU	CA-C-O	-7.07	110.69	120.52
2	B	81	PRO	CA-C-N	-7.07	115.41	123.04
2	B	81	PRO	C-N-CA	-7.07	115.41	123.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	198	ARG	NE-CZ-NH2	7.07	125.56	119.20
4	E	114	SER	CA-C-N	-7.07	112.81	122.77
4	E	114	SER	C-N-CA	-7.07	112.81	122.77
4	E	206	GLN	OE1-CD-NE2	-7.06	115.54	122.60
1	A	110	LEU	CA-C-O	-7.06	112.95	121.28
3	C	122	PRO	N-CA-C	7.06	119.31	110.70
4	E	445	VAL	N-CA-C	7.05	117.84	110.72
4	E	299	ASN	CA-CB-CG	7.05	119.65	112.60
1	A	159	SER	O-C-N	7.04	129.41	121.32
1	A	217	ASN	CA-CB-CG	-7.04	105.56	112.60
1	A	232	VAL	CA-CB-CG1	7.03	122.36	110.40
1	A	61	ILE	N-CA-CB	7.03	124.00	111.63
2	B	61	THR	N-CA-C	7.03	120.86	109.40
1	A	68	ASN	CA-CB-CG	7.03	119.63	112.60
2	B	3	MET	CA-C-N	7.02	134.96	121.54
2	B	3	MET	C-N-CA	7.02	134.96	121.54
2	B	142	CYS	CB-CA-C	-7.02	97.31	110.16
3	C	65	HIS	CA-C-N	7.02	130.98	120.31
3	C	65	HIS	C-N-CA	7.02	130.98	120.31
4	E	299	ASN	N-CA-C	-7.02	103.98	112.54
1	A	6	ARG	NH1-CZ-NH2	-7.01	110.19	119.30
1	A	48	GLN	CG-CD-NE2	7.00	126.91	116.40
1	A	165	PRO	N-CA-C	7.00	122.25	111.11
1	A	99	ASP	N-CA-C	7.00	120.46	109.96
2	B	16	ASN	OD1-CG-ND2	7.00	129.60	122.60
1	D	142	CYS	CA-C-O	7.00	128.75	120.70
1	D	137	PHE	O-C-N	-7.00	113.59	122.34
4	E	183	TRP	CA-C-N	7.00	134.91	121.54
4	E	183	TRP	C-N-CA	7.00	134.91	121.54
2	B	428	TRP	N-CA-C	-7.00	103.65	111.28
3	C	41	ASN	CA-CB-CG	-7.00	105.60	112.60
4	E	126	THR	O-C-N	7.00	130.76	123.62
1	D	129	GLU	O-C-N	-6.99	113.29	122.59
1	A	163	ASP	CA-CB-CG	6.99	119.59	112.60
3	C	244	ALA	N-CA-C	-6.99	103.74	112.90
1	D	221	PRO	N-CD-CG	-6.98	92.72	103.20
1	A	172	GLU	O-C-N	6.98	131.78	122.43
2	B	291	VAL	CA-C-O	-6.97	112.06	120.78
1	A	280	PHE	CA-CB-CG	6.97	120.77	113.80
3	C	260	ALA	CA-C-N	6.97	129.35	120.56
3	C	260	ALA	C-N-CA	6.97	129.35	120.56
4	E	238	LEU	CA-C-O	-6.97	112.12	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	196	THR	CA-C-N	6.97	128.38	120.85
1	D	196	THR	C-N-CA	6.97	128.38	120.85
2	B	449	ILE	CA-C-N	6.97	127.54	119.94
2	B	449	ILE	C-N-CA	6.97	127.54	119.94
3	C	102	TYR	O-C-N	-6.97	114.31	122.95
1	D	79	ARG	NE-CZ-NH1	-6.97	114.53	121.50
1	A	22	VAL	CA-CB-CG2	6.97	122.25	110.40
3	C	76	ASP	CA-C-O	-6.97	110.55	120.51
1	A	48	GLN	OE1-CD-NE2	-6.96	115.64	122.60
1	D	68	ASN	CA-CB-CG	6.96	119.56	112.60
3	C	478	PHE	O-C-N	6.96	130.34	122.27
1	D	219	ILE	N-CA-CB	6.96	118.69	110.55
4	E	125	SER	O-C-N	-6.95	113.99	122.68
1	D	80	LEU	N-CA-CB	6.95	117.80	109.74
1	A	113	THR	CB-CA-C	-6.94	98.58	109.34
2	B	89	ASP	CA-CB-CG	6.94	119.54	112.60
1	A	150	THR	CA-C-N	-6.94	110.67	122.33
1	A	150	THR	C-N-CA	-6.94	110.67	122.33
1	D	15	TYR	O-C-N	-6.94	114.93	123.33
2	B	190	HIS	CB-CA-C	-6.94	96.61	110.42
1	D	10	ASN	CA-C-N	6.94	129.89	120.38
1	D	10	ASN	C-N-CA	6.94	129.89	120.38
1	D	252	SER	CA-C-N	6.93	134.78	121.54
1	D	252	SER	C-N-CA	6.93	134.78	121.54
2	B	456	LEU	O-C-N	-6.93	114.88	122.09
1	A	64	ARG	N-CA-C	-6.93	104.71	113.02
1	A	256	PHE	CA-C-O	-6.93	113.15	120.63
4	E	420	ASN	CA-C-O	-6.92	111.62	119.79
4	E	446	ILE	CA-C-O	-6.92	113.36	121.05
1	A	300	HIS	CA-CB-CG	-6.92	106.88	113.80
4	E	138	TRP	O-C-N	6.92	131.29	123.19
1	A	115	LYS	CA-C-N	-6.92	114.18	123.10
1	A	115	LYS	C-N-CA	-6.92	114.18	123.10
1	D	244	THR	CA-CB-OG1	-6.91	99.23	109.60
3	C	125	ILE	O-C-N	-6.91	115.15	122.68
1	D	176	TRP	N-CA-CB	6.91	122.17	110.49
4	E	225	ILE	CA-C-N	6.91	129.27	120.56
4	E	225	ILE	C-N-CA	6.91	129.27	120.56
4	E	304	LEU	N-CA-C	-6.91	103.68	111.14
2	B	219	PHE	O-C-N	6.91	131.78	122.59
1	D	267	THR	N-CA-C	6.90	118.49	110.97
1	A	77	LYS	N-CA-C	-6.90	100.31	110.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	130	ILE	CB-CA-C	6.90	120.80	111.97
3	C	300	THR	CA-C-N	6.89	134.92	121.41
3	C	300	THR	C-N-CA	6.89	134.92	121.41
2	B	278	PRO	O-C-N	-6.89	114.77	123.04
3	C	304	VAL	N-CA-C	-6.89	103.12	110.36
1	D	202	THR	CA-C-N	6.89	131.16	120.75
1	D	202	THR	C-N-CA	6.89	131.16	120.75
2	B	162	LEU	CA-C-N	6.89	132.62	122.08
2	B	162	LEU	C-N-CA	6.89	132.62	122.08
4	E	232	ILE	CA-C-O	-6.88	113.04	120.47
2	B	137	PHE	CA-C-O	6.88	127.77	119.10
3	C	253	SER	CA-CB-OG	6.88	124.86	111.10
1	A	195	ASP	CA-CB-CG	6.88	119.48	112.60
1	A	231	LEU	CA-C-O	-6.88	113.81	120.90
2	B	16	ASN	CA-C-O	-6.88	114.22	119.59
3	C	250	PRO	O-C-N	-6.88	113.02	122.24
4	E	119	PRO	CA-C-N	-6.88	111.24	119.84
4	E	119	PRO	C-N-CA	-6.88	111.24	119.84
2	B	37	LEU	N-CA-CB	-6.88	100.27	110.17
2	B	240	TYR	N-CA-C	-6.88	105.02	113.41
4	E	4	GLY	CA-C-N	6.87	130.76	120.31
4	E	4	GLY	C-N-CA	6.87	130.76	120.31
1	D	138	ASP	CA-C-O	-6.87	111.53	119.56
1	A	168	SER	O-C-N	-6.87	114.32	122.15
2	B	447	CYS	CB-CA-C	6.87	124.08	110.42
2	B	112	HIS	ND1-CE1-NE2	-6.86	101.54	108.40
4	E	439	TRP	O-C-N	6.86	131.71	122.59
1	A	398	GLU	CA-C-O	-6.86	111.70	119.79
1	D	407	ASP	O-C-N	6.85	130.70	122.27
4	E	306	VAL	CG1-CB-CG2	6.85	125.88	110.80
1	A	4	GLU	O-C-N	-6.85	115.02	122.07
1	D	98	GLY	CA-C-O	-6.85	108.65	120.57
1	D	9	ALA	CA-C-N	-6.84	111.54	120.44
1	D	9	ALA	C-N-CA	-6.84	111.54	120.44
4	E	70	GLU	CA-CB-CG	6.84	127.78	114.10
3	C	463	PRO	N-CA-CB	-6.84	97.10	103.46
2	B	105	HIS	N-CA-C	6.84	120.92	111.90
4	E	415	CYS	CA-C-N	6.83	134.27	121.97
4	E	415	CYS	C-N-CA	6.83	134.27	121.97
3	C	141	TRP	CB-CG-CD1	6.83	137.15	126.90
4	E	313	THR	CA-C-O	-6.83	112.38	120.10
1	D	272	PRO	O-C-N	-6.82	114.55	123.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	273	LEU	N-CA-C	6.82	118.71	111.28
1	D	127	TYR	O-C-N	-6.82	114.41	123.14
4	E	186	ARG	NE-CZ-NH1	-6.82	114.68	121.50
3	C	479	ASN	CA-C-N	6.81	138.42	121.80
3	C	479	ASN	C-N-CA	6.81	138.42	121.80
1	D	31	ILE	O-C-N	6.81	130.72	122.95
3	C	275	SER	O-C-N	-6.81	113.06	122.46
1	A	24	HIS	CA-CB-CG	-6.81	106.99	113.80
2	B	236	ILE	CA-C-N	6.81	129.71	120.38
2	B	236	ILE	C-N-CA	6.81	129.71	120.38
1	D	137	PHE	CB-CA-C	6.81	121.46	110.09
4	E	136	PHE	CA-C-O	6.81	126.33	118.77
1	D	15	TYR	CB-CG-CD1	-6.81	110.59	120.80
1	D	28	PHE	CA-CB-CG	6.81	120.61	113.80
2	B	426	LYS	N-CA-C	-6.80	103.88	111.71
1	A	74	GLY	N-CA-C	6.80	120.39	112.50
1	A	24	HIS	ND1-CE1-NE2	-6.80	101.60	108.40
1	A	209	ARG	CA-C-N	6.80	134.72	122.13
1	A	209	ARG	C-N-CA	6.80	134.72	122.13
3	C	446	TRP	O-C-N	6.80	129.35	122.08
4	E	285	TYR	O-C-N	6.79	131.06	122.23
3	C	272	LEU	CA-C-O	-6.79	113.28	120.55
2	B	87	GLN	OE1-CD-NE2	-6.79	115.81	122.60
2	B	247	GLU	CA-C-N	6.79	134.50	121.54
2	B	247	GLU	C-N-CA	6.79	134.50	121.54
3	C	92	ILE	O-C-N	6.78	131.05	122.57
2	B	162	LEU	CA-C-O	6.78	129.54	121.88
2	B	36	THR	O-C-N	-6.78	115.49	123.22
4	E	273	PRO	O-C-N	6.78	131.79	122.64
1	D	411	LEU	N-CA-CB	6.78	119.90	110.07
4	E	11	LEU	O-C-N	-6.78	113.42	122.43
4	E	41	SER	CA-C-N	-6.77	113.12	123.14
4	E	41	SER	C-N-CA	-6.77	113.12	123.14
4	E	66	TRP	CA-C-O	-6.77	112.99	121.46
2	B	203	SER	N-CA-C	6.77	119.54	109.59
1	A	398	GLU	CA-C-N	6.76	131.52	120.63
1	A	398	GLU	C-N-CA	6.76	131.52	120.63
1	D	25	HIS	CA-CB-CG	-6.76	107.04	113.80
4	E	435	GLU	CB-CG-CD	6.76	124.09	112.60
3	C	107	PHE	O-C-N	-6.76	113.60	122.59
1	A	251	LEU	O-C-N	-6.75	114.74	122.03
2	B	46	LYS	N-CA-C	-6.75	103.85	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	LYS	CA-C-O	6.75	129.79	121.89
4	E	181	GLY	O-C-N	-6.75	113.92	122.70
1	A	3	HIS	CG-CD2-NE2	6.75	113.95	107.20
2	B	214	GLN	CA-C-N	6.75	131.83	122.79
2	B	214	GLN	C-N-CA	6.75	131.83	122.79
3	C	277	ARG	O-C-N	-6.75	112.40	122.39
3	C	302	VAL	N-CA-CB	6.75	119.20	110.57
4	E	421	PHE	CA-CB-CG	6.74	120.54	113.80
2	B	261	VAL	N-CA-C	-6.74	103.28	110.36
2	B	308	SER	CB-CA-C	6.74	119.12	109.08
1	A	15	TYR	CB-CA-C	-6.74	101.43	110.79
1	A	436	GLU	CA-C-O	-6.74	110.88	120.51
2	B	277	VAL	CA-C-N	6.74	127.19	120.52
2	B	277	VAL	C-N-CA	6.74	127.19	120.52
1	D	240	GLY	CA-C-N	6.74	134.40	121.54
1	D	240	GLY	C-N-CA	6.74	134.40	121.54
4	E	474	VAL	N-CA-CB	6.73	120.63	111.21
1	A	274	ILE	N-CA-CB	6.73	118.23	110.49
2	B	466	ASN	CA-CB-CG	6.73	119.33	112.60
3	C	96	ASN	OD1-CG-ND2	6.73	129.33	122.60
4	E	215	GLN	CA-C-O	-6.72	113.46	121.66
3	C	303	VAL	O-C-N	6.72	128.50	121.91
1	A	97	ASP	O-C-N	-6.72	113.65	122.59
1	A	161	GLU	CA-C-N	6.72	132.40	122.86
1	A	161	GLU	C-N-CA	6.72	132.40	122.86
3	C	14	VAL	N-CA-C	6.72	123.31	109.34
3	C	480	ARG	CA-C-O	-6.72	110.96	120.16
4	E	244	ALA	N-CA-CB	6.72	120.69	110.28
2	B	253	ILE	CA-C-O	-6.71	114.07	121.05
2	B	106	VAL	CB-CA-C	-6.71	100.61	110.81
1	D	197	PRO	CA-N-CD	-6.71	102.60	112.00
1	A	16	ASN	OD1-CG-ND2	6.70	129.30	122.60
1	A	253	LEU	CA-C-O	-6.70	113.76	120.80
3	C	467	LEU	N-CA-C	6.70	118.28	110.97
1	A	204	HIS	ND1-CE1-NE2	-6.70	101.70	108.40
1	D	4	GLU	O-C-N	6.70	131.50	122.59
4	E	182	GLU	CA-C-O	-6.70	110.93	120.51
4	E	116	TYR	N-CA-CB	-6.69	98.88	111.00
3	C	319	THR	CA-C-O	-6.69	113.19	121.02
1	A	78	ILE	N-CA-CB	-6.69	104.96	112.45
4	E	5	ARG	NE-CZ-NH1	-6.69	114.81	121.50
2	B	427	ASP	CB-CA-C	-6.68	100.39	110.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	427	ALA	N-CA-CB	6.68	120.09	110.06
4	E	308	LEU	CA-C-N	6.68	134.31	121.54
4	E	308	LEU	C-N-CA	6.68	134.31	121.54
1	A	283	ILE	N-CA-CB	6.68	119.63	110.54
4	E	17	ARG	NH1-CZ-NH2	6.68	127.99	119.30
2	B	6	THR	O-C-N	-6.68	114.09	122.17
4	E	105	ALA	O-C-N	-6.68	115.35	123.30
1	D	62	ASP	CA-C-O	-6.67	113.12	120.33
1	D	297	ASN	N-CA-C	-6.67	103.93	111.07
1	A	187	TRP	O-C-N	6.67	131.16	123.29
2	B	71	ALA	CA-C-O	6.67	127.25	119.32
1	D	272	PRO	CA-N-CD	-6.67	102.67	112.00
4	E	84	LEU	CA-C-O	-6.67	110.98	120.51
2	B	15	TYR	O-C-N	-6.66	114.61	122.81
1	D	295	VAL	N-CA-C	6.66	119.38	111.05
1	A	249	VAL	CB-CA-C	-6.66	100.36	111.29
3	C	277	ARG	N-CA-CB	-6.66	99.63	110.42
1	D	384	GLU	CA-C-O	6.66	127.57	119.38
1	D	234	TYR	N-CA-C	6.66	118.54	111.28
1	D	255	VAL	O-C-N	-6.66	114.47	122.06
2	B	150	THR	O-C-N	6.65	131.44	122.59
4	E	214	ILE	CA-C-N	6.65	134.85	122.74
4	E	214	ILE	C-N-CA	6.65	134.85	122.74
2	B	44	ASN	N-CA-C	-6.65	94.67	107.57
1	A	252	SER	CA-C-O	-6.65	112.76	120.20
1	D	423	VAL	N-CA-CB	6.65	122.20	111.23
1	A	234	TYR	O-C-N	-6.64	115.23	122.07
4	E	426	THR	N-CA-CB	6.64	120.03	110.06
3	C	222	ARG	CA-C-O	-6.64	113.59	120.89
1	D	47	ASN	CA-C-N	6.64	131.57	122.07
1	D	47	ASN	C-N-CA	6.64	131.57	122.07
1	D	190	TYR	O-C-N	-6.64	114.80	123.16
1	D	233	PHE	CA-C-N	6.63	129.17	120.28
1	D	233	PHE	C-N-CA	6.63	129.17	120.28
4	E	24	LEU	CA-C-O	-6.63	111.40	119.43
4	E	302	ILE	CB-CA-C	-6.63	102.36	112.05
1	D	185	LYS	O-C-N	6.63	130.44	122.68
1	A	20	ARG	O-C-N	6.63	132.47	121.59
1	A	227	PHE	O-C-N	6.63	129.98	122.22
2	B	453	SER	N-CA-C	-6.63	104.67	112.89
1	A	272	PRO	N-CA-CB	6.62	108.60	103.30
1	A	132	VAL	CB-CA-C	6.62	121.72	112.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	218	PRO	CA-N-CD	-6.62	102.73	112.00
1	A	39	GLN	O-C-N	-6.62	117.04	123.26
1	D	209	ARG	NE-CZ-NH1	6.62	128.12	121.50
2	B	215	ARG	CB-CA-C	6.62	121.84	111.72
1	D	127	TYR	CG-CD1-CE1	-6.62	111.28	121.20
1	D	76	LYS	CA-C-N	6.61	132.72	123.07
1	D	76	LYS	C-N-CA	6.61	132.72	123.07
3	C	224	LYS	N-CA-CB	6.60	122.12	110.37
3	C	31	VAL	CB-CA-C	-6.60	101.86	110.84
1	D	219	ILE	N-CA-C	6.60	116.76	110.42
4	E	298	THR	N-CA-CB	6.60	121.64	110.49
3	C	113	ARG	CD-NE-CZ	6.59	133.63	124.40
2	B	217	PRO	CA-C-N	-6.59	113.69	122.85
2	B	217	PRO	C-N-CA	-6.59	113.69	122.85
1	A	231	LEU	N-CA-C	-6.59	103.72	111.03
1	D	61	ILE	O-C-N	-6.59	115.64	122.82
4	E	288	PHE	CB-CG-CD2	6.59	131.90	120.70
4	E	223	ILE	O-C-N	6.58	130.68	122.05
3	C	152	ASN	N-CA-CB	-6.58	100.53	110.07
3	C	459	PHE	O-C-N	6.58	132.12	122.39
4	E	220	PHE	CA-C-O	6.58	127.23	119.67
1	A	77	LYS	O-C-N	-6.57	115.58	122.94
1	D	422	THR	OG1-CB-CG2	6.57	122.45	109.30
2	B	230	LEU	CA-C-N	6.57	133.80	121.97
2	B	230	LEU	C-N-CA	6.57	133.80	121.97
4	E	106	ASN	CA-CB-CG	6.57	119.17	112.60
4	E	456	LEU	CA-C-N	6.57	129.37	120.44
4	E	456	LEU	C-N-CA	6.57	129.37	120.44
1	A	154	THR	CA-CB-OG1	6.57	119.45	109.60
1	D	30	ASP	CA-CB-CG	-6.56	106.04	112.60
1	D	392	SER	O-C-N	-6.56	114.20	122.27
2	B	29	VAL	O-C-N	-6.56	116.29	123.18
4	E	117	TRP	O-C-N	-6.56	116.00	123.48
1	A	27	HIS	CB-CG-ND1	6.56	132.53	122.70
4	E	454	ALA	CB-CA-C	6.56	121.06	110.96
2	B	442	ILE	CA-C-N	6.56	131.61	121.19
2	B	442	ILE	C-N-CA	6.56	131.61	121.19
2	B	180	PHE	CA-C-O	-6.55	113.98	121.19
1	A	257	LEU	CA-C-O	6.55	127.50	119.97
1	A	292	THR	OG1-CB-CG2	6.55	122.40	109.30
3	C	246	ALA	CA-C-N	6.55	129.72	120.28
3	C	246	ALA	C-N-CA	6.55	129.72	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	129	THR	N-CA-C	6.55	124.75	110.80
4	E	423	ALA	O-C-N	6.55	130.75	122.23
2	B	88	PRO	CB-CA-C	6.54	122.36	111.56
2	B	234	LEU	N-CA-C	-6.54	104.15	111.28
1	A	250	LEU	CD1-CG-CD2	6.54	125.19	110.80
3	C	84	PRO	N-CA-C	6.54	123.29	113.81
3	C	40	SER	O-C-N	6.53	131.64	122.36
1	D	407	ASP	CA-C-N	6.53	129.36	120.54
1	D	407	ASP	C-N-CA	6.53	129.36	120.54
3	C	136	TYR	CA-CB-CG	6.53	125.66	113.90
1	A	61	ILE	N-CA-C	6.53	117.22	108.27
3	C	190	TRP	CE2-CD2-CE3	-6.53	112.27	118.80
4	E	299	ASN	CA-C-N	6.53	129.51	120.63
4	E	299	ASN	C-N-CA	6.53	129.51	120.63
1	D	27	HIS	O-C-N	6.53	131.27	122.59
3	C	236	CYS	N-CA-C	6.53	122.14	111.37
1	D	376	ILE	O-C-N	6.52	130.45	121.84
2	B	99	SER	CA-C-N	6.52	132.38	122.93
2	B	99	SER	C-N-CA	6.52	132.38	122.93
2	B	215	ARG	NE-CZ-NH1	6.52	128.02	121.50
1	A	279	LEU	O-C-N	6.52	129.63	122.20
1	A	217	ASN	CA-C-N	6.52	128.77	120.56
1	A	217	ASN	C-N-CA	6.52	128.77	120.56
1	D	206	ILE	O-C-N	6.51	130.72	123.10
2	B	110	VAL	N-CA-CB	-6.51	103.25	111.46
1	D	136	PRO	CB-CA-C	6.51	122.31	111.56
1	D	414	PHE	N-CA-C	-6.51	103.29	111.11
1	A	232	VAL	CA-CB-CG2	6.51	121.47	110.40
2	B	220	TYR	CA-C-O	-6.51	111.89	119.05
4	E	312	ASN	N-CA-C	-6.51	106.55	114.75
1	A	149	TRP	CA-CB-CG	6.51	125.97	113.60
1	D	419	ILE	CA-C-N	-6.51	110.25	121.97
1	D	419	ILE	C-N-CA	-6.51	110.25	121.97
3	C	68	THR	CB-CA-C	-6.51	97.47	110.42
3	C	151	LEU	CA-C-O	6.51	128.63	121.02
1	D	396	ALA	O-C-N	-6.51	112.93	122.43
4	E	69	SER	N-CA-CB	6.50	120.99	110.40
4	E	435	GLU	CA-C-O	-6.50	111.22	120.51
1	D	226	SER	CA-C-O	6.50	127.45	119.79
3	C	282	ALA	O-C-N	-6.50	113.14	122.36
1	D	301	ARG	CA-C-O	-6.50	111.22	120.51
1	A	297	ASN	CA-C-O	6.49	127.45	120.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	92	LEU	O-C-N	6.49	132.48	122.87
2	B	197	TRP	N-CA-C	6.49	118.44	109.54
2	B	468	PHE	N-CA-CB	6.49	121.45	110.49
4	E	13	ASP	N-CA-C	6.48	119.34	111.82
2	B	421	PHE	CD1-CG-CD2	6.48	128.32	118.60
3	C	320	HIS	ND1-CG-CD2	-6.48	99.62	106.10
1	D	78	ILE	CA-C-N	-6.48	113.86	123.00
1	D	78	ILE	C-N-CA	-6.48	113.86	123.00
1	D	137	PHE	CA-CB-CG	6.48	120.28	113.80
4	E	304	LEU	CA-C-O	-6.48	114.02	120.70
1	A	150	THR	CA-C-O	-6.48	113.69	121.34
3	C	279	PRO	CA-C-N	6.48	129.80	120.79
3	C	279	PRO	C-N-CA	6.48	129.80	120.79
3	C	299	VAL	CA-C-O	-6.48	113.64	120.57
1	D	426	PHE	CA-C-N	6.48	129.25	120.38
1	D	426	PHE	C-N-CA	6.48	129.25	120.38
2	B	250	SER	CA-C-O	6.47	127.83	120.71
1	D	404	MET	CA-C-O	-6.47	114.09	120.89
1	D	232	VAL	CB-CA-C	-6.47	100.68	111.29
4	E	439	TRP	CG-CD2-CE3	6.47	140.37	133.90
1	D	13	GLU	CA-C-O	-6.47	111.26	120.51
3	C	425	SER	CB-CA-C	-6.47	100.73	110.88
1	D	166	ASP	O-C-N	-6.47	114.35	122.17
1	A	188	VAL	N-CA-C	6.46	116.03	106.85
4	E	186	ARG	NE-CZ-NH2	6.46	125.02	119.20
3	C	14	VAL	O-C-N	-6.46	114.50	122.57
3	C	275	SER	CA-C-O	6.46	127.44	119.05
1	A	111	ASP	N-CA-C	6.45	120.02	109.76
1	D	104	HIS	ND1-CG-CD2	6.45	112.55	106.10
4	E	438	ASN	OD1-CG-ND2	6.45	129.05	122.60
2	B	138	ASP	CA-C-O	6.45	127.31	119.31
1	D	165	PRO	N-CA-CB	6.45	110.03	103.25
3	C	75	SER	N-CA-C	6.45	118.10	111.14
3	C	206	PHE	CA-C-N	6.45	126.95	119.99
3	C	206	PHE	C-N-CA	6.45	126.95	119.99
1	D	390	GLU	CA-C-O	-6.45	113.70	120.92
2	B	131	LYS	N-CA-C	6.45	117.54	108.00
1	D	275	GLY	CA-C-O	6.44	127.25	119.65
3	C	87	ILE	N-CA-CB	6.44	121.86	111.23
1	A	164	ARG	CA-C-O	-6.44	111.34	120.16
1	D	406	ILE	CB-CA-C	6.44	120.83	112.14
2	B	237	LEU	N-CA-C	6.44	119.12	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	251	CYS	N-CA-CB	6.44	120.66	109.72
1	A	129	GLU	N-CA-C	-6.43	101.88	110.24
3	C	29	GLU	CA-CB-CG	6.43	126.97	114.10
4	E	74	ILE	CA-CB-CG1	6.43	121.34	110.40
1	A	229	THR	CB-CA-C	6.43	121.15	110.92
1	D	67	TRP	O-C-N	6.43	130.95	123.17
2	B	139	TRP	CE2-CD2-CG	6.43	114.91	107.20
1	D	395	ALA	CA-C-O	-6.43	113.00	120.20
4	E	272	VAL	CA-C-N	-6.43	111.81	119.84
4	E	272	VAL	C-N-CA	-6.43	111.81	119.84
4	E	433	GLY	O-C-N	-6.42	114.35	122.70
3	C	203	GLY	N-CA-C	-6.42	102.74	112.89
1	D	8	VAL	N-CA-CB	6.42	119.28	110.54
1	A	216	VAL	N-CA-C	6.42	122.69	109.34
1	A	265	PRO	CA-C-O	-6.42	108.92	120.60
3	C	478	PHE	N-CA-CB	6.42	119.74	110.88
1	A	422	THR	CA-C-N	6.42	133.52	121.97
1	A	422	THR	C-N-CA	6.42	133.52	121.97
3	C	480	ARG	NE-CZ-NH2	6.42	124.98	119.20
4	E	86	LEU	N-CA-C	6.42	120.84	108.45
3	C	69	TRP	CA-C-O	-6.42	113.07	121.73
2	B	403	GLU	CA-C-N	6.42	130.06	120.31
2	B	403	GLU	C-N-CA	6.42	130.06	120.31
3	C	423	ILE	CA-CB-CG2	6.42	121.41	110.50
1	D	15	TYR	CA-C-N	6.41	133.20	121.85
1	D	15	TYR	C-N-CA	6.41	133.20	121.85
1	A	166	ASP	N-CA-CB	6.41	119.62	110.13
1	A	262	GLU	O-C-N	6.41	129.46	122.15
2	B	197	TRP	CH2-CZ2-CE2	-6.41	109.17	117.50
1	D	88	PRO	N-CA-CB	-6.41	97.72	103.36
4	E	435	GLU	O-C-N	6.40	131.11	122.59
1	A	268	SER	CA-C-O	6.40	127.33	119.97
3	C	213	GLN	CG-CD-NE2	-6.40	106.80	116.40
2	B	145	VAL	N-CA-C	6.39	116.83	107.37
2	B	448	SER	CA-C-O	-6.39	113.68	120.71
1	D	205	PHE	CA-C-N	-6.39	114.81	123.12
1	D	205	PHE	C-N-CA	-6.39	114.81	123.12
4	E	250	LYS	N-CA-C	6.39	122.03	113.72
1	A	278	MET	CA-C-O	-6.39	113.78	120.55
1	D	163	ASP	CA-C-O	-6.39	113.90	120.80
2	B	460	HIS	CB-CG-ND1	6.38	132.27	122.70
4	E	237	VAL	O-C-N	-6.38	113.77	122.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	PRO	N-CA-C	-6.38	99.32	112.47
4	E	185	ILE	CA-C-O	-6.38	113.30	121.40
1	D	397	GLU	CA-C-N	6.38	130.01	120.31
1	D	397	GLU	C-N-CA	6.38	130.01	120.31
1	D	83	ASP	CA-C-O	-6.38	111.39	120.51
4	E	452	TRP	CG-CD2-CE3	6.38	140.28	133.90
3	C	195	LYS	CA-C-N	6.38	126.60	119.90
3	C	195	LYS	C-N-CA	6.38	126.60	119.90
3	C	267	GLN	CA-C-O	-6.37	113.79	120.55
1	D	411	LEU	CA-C-O	-6.37	114.14	120.70
2	B	102	ILE	CA-C-O	6.37	128.74	120.78
2	B	4	GLU	CA-C-O	-6.37	111.40	120.51
2	B	469	ALA	N-CA-CB	-6.37	100.85	110.40
3	C	6	ARG	NE-CZ-NH2	-6.37	113.47	119.20
3	C	154	ASN	O-C-N	-6.37	113.99	122.14
2	B	143	THR	O-C-N	-6.36	115.19	123.02
4	E	451	PHE	CA-C-O	6.36	127.20	119.31
3	C	481	PRO	CA-C-O	-6.36	111.33	120.56
4	E	106	ASN	CB-CA-C	6.36	123.08	110.42
1	A	200	ASP	N-CA-C	6.36	119.87	109.06
1	D	127	TYR	N-CA-CB	-6.36	99.95	110.95
4	E	451	PHE	CA-C-N	6.36	129.04	120.65
4	E	451	PHE	C-N-CA	6.36	129.04	120.65
1	D	286	ILE	CA-C-O	-6.35	114.34	120.95
3	C	187	ASN	CA-C-N	6.35	126.79	120.31
3	C	187	ASN	C-N-CA	6.35	126.79	120.31
3	C	308	ILE	O-C-N	6.35	130.50	122.57
1	D	300	HIS	N-CA-C	6.34	120.76	112.89
3	C	18	ASN	OD1-CG-ND2	-6.34	116.26	122.60
1	D	217	ASN	CA-C-N	-6.34	110.41	120.55
1	D	217	ASN	C-N-CA	-6.34	110.41	120.55
1	A	229	THR	N-CA-CB	6.34	119.46	109.82
2	B	287	ILE	O-C-N	6.34	130.93	122.31
4	E	136	PHE	CB-CA-C	6.33	119.66	109.02
4	E	140	ASN	OD1-CG-ND2	6.33	128.94	122.60
1	A	14	ASN	CA-C-N	6.33	131.32	121.76
1	A	14	ASN	C-N-CA	6.33	131.32	121.76
2	B	26	GLY	CA-C-N	6.33	133.63	121.54
2	B	26	GLY	C-N-CA	6.33	133.63	121.54
2	B	176	ASN	CB-CG-ND2	6.33	125.89	116.40
3	C	438	ALA	CA-C-N	6.33	129.59	120.79
3	C	438	ALA	C-N-CA	6.33	129.59	120.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	52	THR	CA-CB-OG1	6.33	119.10	109.60
1	A	260	ILE	CA-CB-CG2	6.33	121.26	110.50
2	B	465	ASP	N-CA-C	6.33	121.15	112.04
1	D	151	TYR	CD1-CG-CD2	-6.33	108.61	118.10
4	E	241	PHE	CA-C-N	6.33	127.59	120.06
4	E	241	PHE	C-N-CA	6.33	127.59	120.06
2	B	82	SER	N-CA-CB	6.32	121.17	110.49
1	D	412	CYS	CA-C-O	6.32	129.55	120.51
4	E	188	ARG	NE-CZ-NH1	6.32	127.82	121.50
1	A	245	LEU	N-CA-CB	6.32	119.36	109.94
1	D	63	VAL	CB-CA-C	-6.32	103.79	111.88
4	E	219	LEU	N-CA-CB	-6.32	100.44	109.85
3	C	179	ILE	N-CA-C	6.32	117.73	109.58
1	D	264	ILE	CA-C-N	6.31	126.79	119.47
1	D	264	ILE	C-N-CA	6.31	126.79	119.47
1	D	254	THR	O-C-N	-6.31	115.57	122.07
4	E	183	TRP	O-C-N	-6.31	115.90	122.84
2	B	231	ILE	CA-C-O	-6.31	112.89	120.78
3	C	433	ILE	CA-C-N	6.31	133.59	121.54
3	C	433	ILE	C-N-CA	6.31	133.59	121.54
1	A	5	THR	CA-C-O	6.31	127.30	120.55
2	B	19	VAL	N-CA-C	6.31	118.88	109.17
2	B	119	HIS	CA-CB-CG	6.31	120.11	113.80
1	A	113	THR	N-CA-C	6.30	121.50	113.55
3	C	156	ASN	CB-CG-OD1	-6.30	108.19	120.80
3	C	277	ARG	NE-CZ-NH1	-6.30	115.20	121.50
1	D	46	VAL	CB-CA-C	-6.30	103.52	112.22
2	B	411	ILE	CA-C-N	6.30	133.58	121.54
2	B	411	ILE	C-N-CA	6.30	133.58	121.54
1	D	8	VAL	N-CA-C	6.30	117.05	110.62
4	E	26	HIS	CG-CD2-NE2	-6.30	100.90	107.20
1	A	210	ILE	CA-C-N	-6.30	111.97	119.84
1	A	210	ILE	C-N-CA	-6.30	111.97	119.84
2	B	254	SER	N-CA-C	-6.30	104.52	111.82
3	C	151	LEU	CA-CB-CG	6.30	138.34	116.30
2	B	453	SER	O-C-N	-6.29	113.77	122.46
1	D	399	TRP	CE2-CD2-CE3	-6.29	112.51	118.80
4	E	246	ALA	O-C-N	-6.29	114.22	122.59
2	B	129	THR	O-C-N	6.29	130.96	122.59
1	D	69	PRO	CA-N-CD	-6.29	103.19	112.00
1	D	127	TYR	CD1-CG-CD2	6.29	127.53	118.10
4	E	159	LEU	CA-C-O	-6.29	114.40	120.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	3	GLU	O-C-N	6.28	128.78	122.12
1	A	375	ALA	O-C-N	-6.28	115.38	122.23
3	C	109	ASN	CA-CB-CG	-6.28	106.32	112.60
3	C	41	ASN	OD1-CG-ND2	6.28	128.88	122.60
4	E	19	LYS	CB-CA-C	6.28	118.49	109.26
2	B	181	THR	CA-C-N	6.28	128.69	120.28
2	B	181	THR	C-N-CA	6.28	128.69	120.28
1	D	159	SER	CA-C-N	6.28	127.63	120.85
1	D	159	SER	C-N-CA	6.28	127.63	120.85
1	D	299	HIS	N-CA-C	-6.27	104.52	111.36
1	A	376	ILE	CA-C-N	6.27	133.52	121.54
1	A	376	ILE	C-N-CA	6.27	133.52	121.54
1	A	379	VAL	CA-C-N	6.27	129.31	120.28
1	A	379	VAL	C-N-CA	6.27	129.31	120.28
2	B	468	PHE	CA-C-O	6.27	129.47	120.51
4	E	288	PHE	CG-CD2-CE2	6.27	131.36	120.70
3	C	108	CYS	O-C-N	-6.27	114.26	122.97
4	E	187	HIS	O-C-N	6.27	129.84	123.26
4	E	450	CYS	CA-C-N	-6.27	110.17	121.14
4	E	450	CYS	C-N-CA	-6.27	110.17	121.14
1	A	273	LEU	CA-C-N	-6.26	111.62	120.77
1	A	273	LEU	C-N-CA	-6.26	111.62	120.77
1	D	42	ASN	OD1-CG-ND2	6.26	128.86	122.60
4	E	26	HIS	CA-CB-CG	-6.26	107.54	113.80
1	D	67	TRP	CE2-CD2-CE3	-6.26	112.54	118.80
4	E	239	VAL	N-CA-CB	6.26	121.56	111.23
1	A	7	LEU	CA-C-N	6.26	129.03	120.46
1	A	7	LEU	C-N-CA	6.26	129.03	120.46
3	C	208	ASN	OD1-CG-ND2	-6.26	116.34	122.60
1	D	248	SER	CA-C-O	-6.25	113.92	120.92
3	C	23	PRO	N-CA-CB	6.25	109.81	103.25
2	B	62	ASP	O-C-N	-6.25	114.89	123.01
1	A	240	GLY	O-C-N	-6.25	114.58	122.70
1	A	69	PRO	O-C-N	6.25	131.07	122.64
1	A	167	LEU	CA-C-N	6.25	129.16	120.29
1	A	167	LEU	C-N-CA	6.25	129.16	120.29
3	C	201	ILE	O-C-N	6.25	129.87	123.00
1	D	149	TRP	CB-CG-CD1	6.25	136.27	126.90
4	E	241	PHE	CA-CB-CG	6.24	120.04	113.80
3	C	208	ASN	O-C-N	-6.24	114.38	122.37
1	A	129	GLU	O-C-N	6.24	130.80	122.82
3	C	270	PHE	CA-CB-CG	-6.24	107.56	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	32	THR	N-CA-C	-6.24	100.47	110.14
2	B	272	GLU	N-CA-CB	6.23	119.94	110.28
2	B	410	TYR	O-C-N	-6.23	114.30	122.59
1	A	128	CYS	N-CA-C	6.23	118.77	108.99
4	E	45	LYS	N-CA-C	-6.23	104.57	111.36
2	B	86	TRP	O-C-N	-6.23	114.31	122.59
3	C	141	TRP	CG-CD1-NE1	6.23	118.30	110.20
3	C	241	PHE	N-CA-CB	6.23	119.98	110.14
3	C	320	HIS	CB-CG-ND1	6.23	132.04	122.70
4	E	431	ASP	CA-C-O	-6.23	113.95	120.92
1	D	396	ALA	CA-C-N	-6.22	110.95	122.09
1	D	396	ALA	C-N-CA	-6.22	110.95	122.09
4	E	273	PRO	N-CA-CB	-6.22	96.72	103.25
2	B	133	MET	CA-CB-CG	6.22	126.55	114.10
1	D	132	VAL	CA-C-N	-6.22	112.65	122.79
1	D	132	VAL	C-N-CA	-6.22	112.65	122.79
1	A	52	THR	N-CA-C	6.21	119.15	109.52
2	B	22	SER	O-C-N	-6.21	115.15	123.23
4	E	162	GLU	N-CA-C	-6.21	105.83	113.41
3	C	9	ASN	N-CA-C	-6.21	103.81	112.45
3	C	315	ARG	NE-CZ-NH2	6.21	124.79	119.20
2	B	198	ARG	CD-NE-CZ	6.21	133.10	124.40
1	D	298	THR	CA-C-O	6.21	127.13	120.55
3	C	478	PHE	CA-C-O	-6.21	112.07	118.90
1	A	29	VAL	CB-CA-C	6.21	119.58	110.77
3	C	57	TRP	CB-CG-CD1	6.20	136.20	126.90
1	A	227	PHE	CA-CB-CG	-6.20	107.60	113.80
2	B	186	TRP	CA-CB-CG	6.20	125.38	113.60
3	C	26	HIS	ND1-CE1-NE2	-6.20	102.20	108.40
3	C	229	VAL	CA-C-N	-6.20	112.62	120.56
3	C	229	VAL	C-N-CA	-6.20	112.62	120.56
3	C	288	ILE	CA-CB-CG2	6.20	121.04	110.50
1	D	85	VAL	O-C-N	6.20	130.36	122.61
4	E	185	ILE	CA-C-N	-6.20	112.32	121.99
4	E	185	ILE	C-N-CA	-6.20	112.32	121.99
4	E	451	PHE	O-C-N	-6.20	113.91	122.46
1	A	152	ASP	CA-C-O	-6.19	115.51	122.01
2	B	177	GLN	CA-C-N	6.19	129.72	120.31
2	B	177	GLN	C-N-CA	6.19	129.72	120.31
3	C	267	GLN	OE1-CD-NE2	-6.19	116.41	122.60
1	D	382	ILE	O-C-N	-6.19	115.86	121.87
1	A	300	HIS	CA-C-O	-6.19	113.99	120.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	150	THR	CA-C-N	6.19	130.92	122.19
2	B	150	THR	C-N-CA	6.19	130.92	122.19
1	D	67	TRP	CB-CG-CD2	6.19	135.47	126.80
1	D	380	LYS	CA-C-N	6.19	129.08	120.29
1	D	380	LYS	C-N-CA	6.19	129.08	120.29
2	B	234	LEU	N-CA-CB	6.19	119.22	110.12
1	D	408	HIS	CA-CB-CG	6.19	119.99	113.80
4	E	427	LYS	CA-CB-CG	6.19	126.47	114.10
1	A	297	ASN	CB-CG-ND2	6.18	125.67	116.40
4	E	63	ARG	NE-CZ-NH1	6.18	127.68	121.50
1	A	283	ILE	O-C-N	6.18	127.86	121.87
4	E	259	LEU	CA-C-O	6.18	127.51	120.90
1	A	256	PHE	O-C-N	6.17	128.66	122.12
3	C	262	CYS	N-CA-C	-6.17	104.61	111.71
2	B	74	GLY	CA-C-N	6.17	133.08	121.97
2	B	74	GLY	C-N-CA	6.17	133.08	121.97
1	D	261	VAL	CA-C-O	-6.17	112.56	120.03
1	D	80	LEU	CA-C-O	-6.17	114.23	120.96
1	D	429	ARG	N-CA-C	6.17	118.01	111.28
4	E	164	GLY	CA-C-O	6.17	133.76	120.80
4	E	202	ASP	CA-CB-CG	6.17	118.77	112.60
4	E	466	PHE	CB-CA-C	-6.17	100.54	110.79
4	E	267	LEU	N-CA-C	-6.17	105.02	112.54
2	B	193	SER	N-CA-CB	-6.16	101.28	110.71
2	B	306	HIS	CB-CG-CD2	6.16	139.21	131.20
3	C	445	ASN	CA-C-O	6.16	126.96	119.38
4	E	242	LEU	N-CA-C	-6.16	105.07	113.57
2	B	197	TRP	CZ3-CH2-CZ2	6.16	129.51	121.50
1	A	47	ASN	CA-C-O	-6.16	114.07	121.34
1	A	164	ARG	NE-CZ-NH2	-6.16	113.66	119.20
2	B	25	VAL	N-CA-CB	6.16	121.39	111.23
2	B	10	VAL	N-CA-C	6.16	116.27	110.30
3	C	311	ASN	OD1-CG-ND2	6.16	128.75	122.60
1	D	302	SER	CA-C-N	6.16	127.53	119.84
1	D	302	SER	C-N-CA	6.16	127.53	119.84
2	B	63	TYR	CA-C-O	6.15	128.71	119.23
2	B	422	ASP	O-C-N	-6.15	115.60	122.12
1	D	283	ILE	O-C-N	-6.15	115.79	121.94
1	A	8	VAL	O-C-N	6.15	127.83	121.87
3	C	480	ARG	CD-NE-CZ	6.15	133.00	124.40
4	E	436	ASN	OD1-CG-ND2	-6.15	116.45	122.60
3	C	84	PRO	O-C-N	-6.14	114.73	122.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	130	ILE	CG1-CB-CG2	6.14	129.12	110.70
4	E	99	PHE	CA-CB-CG	6.14	119.94	113.80
2	B	452	PHE	CA-CB-CG	-6.14	107.66	113.80
3	C	159	SER	CB-CA-C	-6.14	103.08	110.94
1	D	70	ALA	CA-C-O	-6.14	112.35	119.59
3	C	98	ASN	N-CA-C	6.13	120.38	113.02
4	E	78	ARG	CD-NE-CZ	-6.13	115.81	124.40
3	C	94	LEU	CB-CA-C	6.13	121.87	112.00
1	D	250	LEU	CD1-CG-CD2	6.13	124.28	110.80
1	A	9	ALA	CA-C-O	-6.13	114.39	120.70
1	D	209	ARG	NH1-CZ-NH2	-6.13	111.34	119.30
1	D	5	THR	CA-C-O	6.12	127.02	119.79
3	C	484	LYS	O-C-N	-6.12	113.21	123.00
4	E	313	THR	N-CA-C	6.12	118.75	111.71
4	E	197	GLN	N-CA-C	6.12	119.41	110.17
2	B	233	ILE	CA-C-N	6.11	128.47	120.28
2	B	233	ILE	C-N-CA	6.11	128.47	120.28
1	D	191	THR	CA-CB-OG1	6.11	118.77	109.60
2	B	284	LEU	CA-C-N	6.11	133.21	121.54
2	B	284	LEU	C-N-CA	6.11	133.21	121.54
2	B	460	HIS	CG-CD2-NE2	6.11	113.31	107.20
3	C	236	CYS	O-C-N	-6.11	115.09	122.11
1	D	177	VAL	CA-C-O	6.11	128.41	120.78
3	C	426	THR	CA-C-O	-6.10	114.41	120.82
2	B	36	THR	CB-CA-C	6.10	119.80	109.80
1	D	3	HIS	CE1-NE2-CD2	-6.10	102.90	109.00
3	C	141	TRP	CA-C-N	6.10	133.19	121.54
3	C	141	TRP	C-N-CA	6.10	133.19	121.54
4	E	105	ALA	CA-C-O	-6.10	113.77	120.36
2	B	445	THR	CB-CA-C	-6.10	101.06	110.81
1	A	176	TRP	N-CA-C	6.09	119.81	110.36
3	C	276	GLN	O-C-N	-6.09	114.80	122.17
1	D	197	PRO	O-C-N	-6.09	116.46	123.23
4	E	260	ALA	CA-C-N	6.09	128.76	120.54
4	E	260	ALA	C-N-CA	6.09	128.76	120.54
2	B	278	PRO	CA-N-CD	-6.09	103.47	112.00
4	E	111	ASN	O-C-N	-6.09	114.49	122.59
3	C	161	ASP	CA-C-O	-6.09	114.13	120.89
1	D	53	ASN	N-CA-C	6.09	119.74	109.76
1	D	82	SER	N-CA-C	6.09	117.91	111.28
3	C	190	TRP	CD2-CE3-CZ3	6.08	126.51	118.60
4	E	272	VAL	N-CA-CB	6.08	119.73	111.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	176	TRP	CA-CB-CG	6.08	125.16	113.60
2	B	10	VAL	CA-C-N	6.08	130.86	121.19
2	B	10	VAL	C-N-CA	6.08	130.86	121.19
4	E	447	ASP	CA-C-O	6.08	127.76	121.07
1	A	95	ASN	CA-C-O	-6.08	111.81	120.51
2	B	287	ILE	CA-C-N	6.08	128.92	120.29
2	B	287	ILE	C-N-CA	6.08	128.92	120.29
1	D	81	PRO	N-CA-C	-6.08	102.33	111.57
1	D	378	GLY	O-C-N	6.08	128.01	122.18
4	E	272	VAL	N-CA-C	6.08	122.01	108.88
3	C	102	TYR	CB-CA-C	6.08	119.38	109.90
4	E	104	TYR	CA-CB-CG	6.07	124.83	113.90
2	B	177	GLN	O-C-N	-6.07	114.88	122.35
3	C	288	ILE	CA-C-N	6.07	127.73	120.14
3	C	288	ILE	C-N-CA	6.07	127.73	120.14
1	A	38	ILE	CB-CA-C	-6.07	103.84	112.22
1	A	250	LEU	CB-CA-C	6.07	120.86	110.79
3	C	277	ARG	CD-NE-CZ	6.07	132.89	124.40
2	B	135	PHE	O-C-N	6.07	128.30	121.32
3	C	286	PRO	N-CA-CB	6.07	106.32	102.92
4	E	76	LEU	CA-C-O	-6.07	114.22	121.56
1	A	257	LEU	O-C-N	-6.06	114.81	122.27
2	B	177	GLN	CG-CD-NE2	-6.06	107.31	116.40
2	B	211	LEU	CB-CA-C	-6.06	101.83	111.17
1	D	162	SER	N-CA-CB	6.06	120.74	110.49
4	E	244	ALA	CA-C-N	6.06	128.65	120.65
4	E	244	ALA	C-N-CA	6.06	128.65	120.65
1	D	72	TYR	CA-C-O	-6.06	114.46	120.70
4	E	82	GLU	CB-CG-CD	6.06	122.89	112.60
4	E	193	ASN	CA-C-O	-6.05	114.56	121.40
1	A	4	GLU	CB-CA-C	-6.05	101.38	110.88
4	E	416	VAL	CA-C-O	6.05	128.34	120.78
3	C	143	ASN	N-CA-C	6.04	119.84	107.69
1	D	26	THR	O-C-N	6.04	130.63	122.59
1	A	389	ASP	CA-C-O	6.04	126.95	120.55
2	B	64	ARG	CB-CA-C	6.04	120.16	109.65
1	D	15	TYR	CB-CG-CD2	6.04	129.86	120.80
4	E	218	PRO	O-C-N	6.04	130.80	122.64
1	D	173	SER	CA-C-N	6.04	133.25	121.41
1	D	173	SER	C-N-CA	6.04	133.25	121.41
1	A	170	PHE	CA-C-O	-6.04	114.17	121.05
1	D	18	VAL	N-CA-CB	6.04	117.62	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	160	HIS	CA-CB-CG	-6.04	107.76	113.80
1	A	80	LEU	N-CA-C	-6.03	99.75	109.40
3	C	114	PRO	N-CA-C	6.03	124.90	112.47
2	B	276	SER	CA-C-N	6.03	133.29	122.13
2	B	276	SER	C-N-CA	6.03	133.29	122.13
2	B	55	PHE	CB-CA-C	-6.03	99.29	109.72
3	C	66	ARG	O-C-N	6.03	129.68	122.27
1	D	11	LEU	N-CA-C	6.02	118.62	111.33
2	B	310	ASN	N-CA-CB	6.02	119.66	110.39
2	B	312	HIS	CG-CD2-NE2	6.02	113.22	107.20
3	C	108	CYS	CA-C-N	6.02	130.95	121.56
3	C	108	CYS	C-N-CA	6.02	130.95	121.56
3	C	69	TRP	CE3-CZ3-CH2	6.02	128.93	121.10
3	C	458	MET	N-CA-C	-6.02	105.02	112.90
4	E	310	THR	CA-CB-OG1	-6.02	100.57	109.60
3	C	35	LEU	O-C-N	-6.02	115.58	123.16
3	C	482	PRO	N-CA-CB	6.02	109.57	103.25
1	D	396	ALA	N-CA-C	6.02	120.46	113.18
3	C	54	THR	CA-C-N	6.01	130.67	122.19
3	C	54	THR	C-N-CA	6.01	130.67	122.19
3	C	316	THR	CA-C-N	6.01	125.22	118.97
3	C	316	THR	C-N-CA	6.01	125.22	118.97
1	D	299	HIS	CA-CB-CG	6.01	119.81	113.80
1	D	382	ILE	CA-C-O	6.01	127.20	120.95
4	E	74	ILE	CA-CB-CG2	6.01	120.72	110.50
1	A	260	ILE	N-CA-CB	6.01	118.26	110.57
2	B	118	TRP	CA-C-O	-6.01	112.87	120.20
1	D	284	PHE	CB-CA-C	-6.01	99.52	110.63
1	D	36	GLN	OE1-CD-NE2	-6.01	116.59	122.60
1	D	118	TRP	CD2-CE2-CZ2	6.01	128.41	122.40
4	E	43	ASN	N-CA-CB	6.01	121.73	110.56
4	E	73	GLY	CA-C-N	6.01	132.78	121.97
4	E	73	GLY	C-N-CA	6.01	132.78	121.97
4	E	26	HIS	CB-CA-C	6.00	120.32	110.17
4	E	3	GLU	CA-C-O	-6.00	114.19	120.55
4	E	78	ARG	NE-CZ-NH1	-6.00	115.50	121.50
1	A	21	PRO	O-C-N	6.00	130.74	122.64
1	D	422	THR	O-C-N	-6.00	115.31	122.15
4	E	458	PHE	CG-CD2-CE2	6.00	130.90	120.70
3	C	99	ASP	CA-C-N	6.00	133.16	121.41
3	C	99	ASP	C-N-CA	6.00	133.16	121.41
1	D	436	GLU	O-C-N	-5.99	114.62	122.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	80	LEU	CD1-CG-CD2	5.99	123.98	110.80
2	B	215	ARG	NE-CZ-NH2	5.99	124.59	119.20
3	C	86	LEU	CA-C-N	5.99	132.75	121.97
3	C	86	LEU	C-N-CA	5.99	132.75	121.97
3	C	480	ARG	NE-CZ-NH1	-5.99	115.51	121.50
3	C	473	PHE	CA-CB-CG	5.99	119.79	113.80
1	A	155	LYS	N-CA-C	-5.99	103.52	111.24
1	A	412	CYS	O-C-N	5.99	128.24	122.07
1	D	118	TRP	CE2-CD2-CE3	-5.98	112.82	118.80
4	E	81	SER	CA-C-N	5.98	132.12	120.99
4	E	81	SER	C-N-CA	5.98	132.12	120.99
1	A	430	LEU	N-CA-C	5.98	123.54	110.80
3	C	189	GLU	N-CA-CB	-5.98	100.36	110.41
4	E	227	ALA	O-C-N	5.98	128.19	121.32
4	E	246	ALA	N-CA-C	5.98	123.53	110.80
2	B	205	GLU	CA-C-N	5.97	132.95	121.54
2	B	205	GLU	C-N-CA	5.97	132.95	121.54
1	A	76	LYS	N-CA-C	5.97	123.52	110.80
3	C	243	ALA	CA-C-O	-5.97	113.35	120.10
1	D	33	VAL	CA-C-N	-5.97	111.66	121.04
1	D	33	VAL	C-N-CA	-5.97	111.66	121.04
1	D	306	HIS	CA-CB-CG	5.97	119.77	113.80
1	D	264	ILE	CB-CA-C	5.97	122.22	111.36
2	B	272	GLU	CA-C-N	5.97	134.35	121.64
2	B	272	GLU	C-N-CA	5.97	134.35	121.64
2	B	150	THR	CA-C-O	-5.96	111.98	120.51
3	C	207	PRO	CA-C-N	5.96	132.55	122.65
3	C	207	PRO	C-N-CA	5.96	132.55	122.65
3	C	300	THR	O-C-N	5.96	128.29	122.09
1	A	221	PRO	O-C-N	-5.96	115.38	122.24
1	A	249	VAL	N-CA-C	5.96	121.74	109.34
3	C	272	LEU	N-CA-C	5.96	118.67	111.40
1	A	293	VAL	CA-C-O	-5.96	113.33	120.78
4	E	420	ASN	N-CA-C	-5.96	104.72	112.23
3	C	17	TYR	O-C-N	-5.96	115.60	122.93
1	D	45	GLU	CB-CA-C	5.96	122.28	110.42
1	D	82	SER	CA-C-O	5.96	126.87	120.55
1	D	56	LEU	CA-C-O	-5.96	111.99	120.51
2	B	249	MET	CB-CA-C	5.95	122.26	110.42
1	D	239	SER	CA-C-N	5.95	126.69	120.03
1	D	239	SER	C-N-CA	5.95	126.69	120.03
1	D	194	PRO	CA-C-N	5.95	130.93	122.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	194	PRO	C-N-CA	5.95	130.93	122.72
4	E	87	PRO	CA-C-O	5.95	127.88	120.92
4	E	101	VAL	O-C-N	-5.95	115.14	122.57
2	B	414	GLN	O-C-N	-5.94	115.22	122.11
3	C	25	LYS	CA-C-O	5.94	128.35	121.28
1	A	99	ASP	CA-C-O	-5.94	113.98	120.81
3	C	229	VAL	CA-C-O	5.94	128.21	120.78
1	D	422	THR	CA-CB-OG1	5.94	118.51	109.60
2	B	427	ASP	CA-C-N	5.94	128.24	120.28
2	B	427	ASP	C-N-CA	5.94	128.24	120.28
1	A	202	THR	CA-C-N	5.94	129.91	121.42
1	A	202	THR	C-N-CA	5.94	129.91	121.42
1	D	176	TRP	CZ3-CH2-CZ2	5.93	129.22	121.50
4	E	23	THR	CB-CA-C	5.93	120.23	110.03
2	B	153	THR	O-C-N	-5.93	114.70	122.59
1	D	400	LYS	CA-C-N	-5.93	113.64	123.37
1	D	400	LYS	C-N-CA	-5.93	113.64	123.37
3	C	240	SER	CA-C-O	-5.93	114.08	121.02
1	D	425	VAL	CA-C-O	-5.93	113.85	120.25
3	C	224	LYS	CG-CD-CE	5.93	124.94	111.30
1	D	422	THR	CA-C-N	5.93	132.64	121.97
1	D	422	THR	C-N-CA	5.93	132.64	121.97
2	B	197	TRP	CG-CD2-CE3	-5.93	127.97	133.90
3	C	178	ILE	O-C-N	-5.93	113.52	123.00
4	E	19	LYS	CA-CB-CG	5.93	125.95	114.10
3	C	286	PRO	CA-N-CD	-5.92	103.70	112.00
1	D	119	THR	CA-C-N	5.92	126.48	120.38
1	D	119	THR	C-N-CA	5.92	126.48	120.38
2	B	82	SER	CA-C-O	-5.92	114.51	117.94
1	D	66	ARG	NE-CZ-NH2	5.92	124.53	119.20
1	D	205	PHE	CA-CB-CG	5.92	119.72	113.80
1	D	250	LEU	CA-C-N	5.92	128.49	120.38
1	D	250	LEU	C-N-CA	5.92	128.49	120.38
1	A	149	TRP	CE2-CD2-CE3	5.92	124.72	118.80
4	E	40	ILE	CA-C-N	-5.92	112.51	121.86
4	E	40	ILE	C-N-CA	-5.92	112.51	121.86
2	B	460	HIS	N-CA-C	5.92	118.52	111.71
3	C	29	GLU	N-CA-CB	5.92	118.65	110.07
1	D	286	ILE	N-CA-C	-5.92	104.58	110.62
1	A	275	GLY	CA-C-O	5.92	126.48	120.45
1	D	389	ASP	O-C-N	-5.92	115.25	122.11
1	A	126	SER	N-CA-C	5.91	118.86	109.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	272	PRO	N-CA-C	5.91	120.61	111.21
4	E	472	ASN	CA-C-N	5.91	133.11	121.58
4	E	472	ASN	C-N-CA	5.91	133.11	121.58
1	A	265	PRO	O-C-N	-5.91	114.66	122.64
1	A	210	ILE	CB-CG1-CD1	5.91	126.20	113.80
3	C	443	VAL	N-CA-CB	5.91	120.97	111.23
4	E	265	LEU	CB-CA-C	-5.91	101.87	110.96
4	E	304	LEU	N-CA-CB	5.90	118.63	110.07
4	E	310	THR	O-C-N	-5.90	116.14	121.39
2	B	6	THR	CA-C-O	5.90	126.86	120.55
3	C	207	PRO	CA-N-CD	-5.90	103.74	112.00
1	D	242	LYS	N-CA-C	5.90	118.43	110.88
4	E	280	PRO	CA-C-N	-5.90	111.56	121.94
4	E	280	PRO	C-N-CA	-5.90	111.56	121.94
4	E	460	LEU	CA-C-N	5.90	132.97	121.41
4	E	460	LEU	C-N-CA	5.90	132.97	121.41
2	B	8	LEU	CA-C-N	5.90	128.66	120.29
2	B	8	LEU	C-N-CA	5.90	128.66	120.29
3	C	299	VAL	CA-C-N	5.90	128.50	120.54
3	C	299	VAL	C-N-CA	5.90	128.50	120.54
3	C	104	VAL	CA-CB-CG2	5.89	120.42	110.40
3	C	440	ASP	CA-CB-CG	5.89	118.50	112.60
1	D	111	ASP	CB-CA-C	5.89	121.32	110.24
1	A	86	TRP	CG-CD1-NE1	5.89	117.86	110.20
3	C	466	VAL	CA-C-O	-5.89	114.41	120.71
1	D	167	LEU	CA-C-N	5.89	132.79	121.54
1	D	167	LEU	C-N-CA	5.89	132.79	121.54
4	E	311	PRO	CA-C-O	-5.89	109.88	120.60
2	B	100	PHE	O-C-N	-5.88	115.74	123.21
1	D	413	VAL	CA-C-N	5.88	128.48	120.54
1	D	413	VAL	C-N-CA	5.88	128.48	120.54
3	C	55	ASN	N-CA-C	5.88	119.23	109.46
3	C	75	SER	N-CA-CB	5.88	118.60	110.07
4	E	30	VAL	N-CA-C	5.88	116.34	108.11
1	D	195	ASP	CA-C-O	-5.88	114.02	120.43
1	D	282	MET	CA-C-N	5.88	128.18	120.60
1	D	282	MET	C-N-CA	5.88	128.18	120.60
2	B	303	ASN	N-CA-CB	5.87	118.74	109.82
3	C	468	GLY	N-CA-C	-5.87	105.67	112.83
1	D	436	GLU	CB-CG-CD	5.87	122.58	112.60
4	E	159	LEU	O-C-N	5.87	129.56	122.75
1	A	3	HIS	CB-CA-C	5.87	121.06	111.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	233	ILE	N-CA-C	-5.87	104.61	111.00
2	B	277	VAL	CA-C-O	-5.86	112.09	119.95
3	C	432	GLN	O-C-N	5.86	129.26	122.17
1	D	294	VAL	CA-C-O	-5.86	114.55	121.05
4	E	277	LEU	CA-C-N	5.86	128.61	120.29
4	E	277	LEU	C-N-CA	5.86	128.61	120.29
3	C	255	GLU	CB-CG-CD	-5.86	102.64	112.60
2	B	277	VAL	N-CA-C	5.86	121.53	108.88
1	D	185	LYS	N-CA-C	5.86	119.08	110.59
3	C	75	SER	CB-CA-C	-5.86	101.65	110.90
4	E	470	HIS	CB-CG-CD2	5.85	138.81	131.20
1	D	85	VAL	CB-CA-C	-5.85	102.96	111.68
3	C	225	PRO	CA-N-CD	-5.85	103.81	112.00
1	D	293	VAL	N-CA-C	-5.85	104.63	110.30
1	A	117	MET	CA-C-O	-5.84	114.27	121.11
2	B	46	LYS	CA-C-O	-5.84	114.68	120.70
1	D	406	ILE	CG1-CB-CG2	5.84	128.23	110.70
1	A	306	HIS	CB-CG-CD2	5.84	138.79	131.20
3	C	474	VAL	CA-C-N	5.84	129.58	120.82
3	C	474	VAL	C-N-CA	5.84	129.58	120.82
2	B	8	LEU	CB-CA-C	-5.84	101.47	110.81
1	D	304	SER	CB-CA-C	5.84	119.95	110.96
2	B	304	LEU	N-CA-CB	5.84	120.36	110.49
3	C	320	HIS	CA-CB-CG	5.84	119.64	113.80
1	D	256	PHE	N-CA-CB	5.84	118.44	109.98
1	D	292	THR	CA-CB-OG1	-5.84	100.85	109.60
2	B	187	SER	CA-C-N	5.83	131.26	122.98
2	B	187	SER	C-N-CA	5.83	131.26	122.98
2	B	461	ASN	N-CA-CB	5.83	118.77	110.13
1	D	407	ASP	CA-C-O	-5.83	113.26	119.97
4	E	69	SER	N-CA-C	5.83	120.12	112.89
1	A	20	ARG	CA-C-N	5.83	127.12	119.84
1	A	20	ARG	C-N-CA	5.83	127.12	119.84
2	B	461	ASN	O-C-N	5.83	129.22	122.17
4	E	64	LEU	N-CA-C	5.82	123.20	110.80
4	E	60	ASN	CB-CG-ND2	5.82	125.13	116.40
1	D	69	PRO	N-CD-CG	5.82	111.93	103.20
1	A	244	THR	CA-C-O	5.82	126.66	119.97
3	C	17	TYR	CB-CG-CD2	5.82	129.53	120.80
3	C	196	PRO	CA-C-O	-5.82	114.40	121.03
3	C	208	ASN	CB-CA-C	5.82	120.87	110.81
2	B	49	GLU	N-CA-CB	-5.81	101.33	110.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	131	PRO	CA-N-CD	-5.81	103.86	112.00
3	C	302	VAL	CA-CB-CG2	5.81	120.28	110.40
1	A	176	TRP	CG-CD2-CE3	5.81	139.71	133.90
2	B	432	ALA	O-C-N	-5.81	114.86	122.59
1	D	169	THR	O-C-N	-5.81	110.94	121.63
1	D	304	SER	CA-C-N	-5.81	111.26	122.06
1	D	304	SER	C-N-CA	-5.81	111.26	122.06
4	E	80	PRO	N-CA-C	5.81	120.20	111.14
4	E	278	ASN	CB-CG-ND2	5.81	125.11	116.40
1	A	26	THR	O-C-N	5.81	130.31	122.59
1	A	66	ARG	O-C-N	-5.80	115.51	122.65
1	D	270	ALA	CB-CA-C	5.80	119.40	109.24
1	D	271	VAL	CA-C-O	-5.80	112.17	119.95
4	E	267	LEU	CA-C-N	5.80	129.04	120.74
4	E	267	LEU	C-N-CA	5.80	129.04	120.74
1	A	223	LEU	N-CA-C	-5.80	104.56	111.69
1	D	22	VAL	CA-C-N	-5.80	114.60	123.07
1	D	22	VAL	C-N-CA	-5.80	114.60	123.07
4	E	188	ARG	NH1-CZ-NH2	-5.80	111.76	119.30
2	B	214	GLN	OE1-CD-NE2	5.80	128.40	122.60
3	C	109	ASN	OD1-CG-ND2	-5.79	116.81	122.60
1	D	250	LEU	N-CA-C	-5.79	103.77	111.24
3	C	247	PHE	N-CA-C	5.79	118.37	111.71
4	E	138	TRP	N-CA-C	5.79	119.26	109.76
1	A	225	PHE	CA-C-N	5.79	128.84	120.79
1	A	225	PHE	C-N-CA	5.79	128.84	120.79
1	A	104	HIS	CG-CD2-NE2	-5.79	101.41	107.20
1	A	267	THR	CA-C-O	-5.79	113.72	120.20
1	A	8	VAL	CB-CA-C	-5.79	104.33	112.14
1	D	251	LEU	O-C-N	5.78	128.25	122.12
1	D	265	PRO	CA-CB-CG	-5.78	93.51	104.50
2	B	112	HIS	CA-C-O	-5.78	114.94	120.90
2	B	133	MET	N-CA-C	5.78	117.83	110.61
1	D	275	GLY	N-CA-C	5.78	121.39	113.99
2	B	9	SER	CA-C-N	5.78	127.92	120.70
2	B	9	SER	C-N-CA	5.78	127.92	120.70
2	B	24	THR	CA-C-N	5.78	132.37	121.97
2	B	24	THR	C-N-CA	5.78	132.37	121.97
4	E	469	GLY	O-C-N	-5.78	116.65	122.19
3	C	242	LEU	CA-C-N	5.77	128.59	120.28
3	C	242	LEU	C-N-CA	5.77	128.59	120.28
4	E	268	ILE	N-CA-CB	5.77	118.83	110.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	153	GLY	O-C-N	-5.77	116.27	122.73
2	B	81	PRO	N-CA-CB	5.77	109.31	103.25
4	E	39	LEU	CA-C-O	-5.77	114.02	121.11
2	B	287	ILE	N-CA-C	-5.77	105.50	113.00
1	D	133	THR	CA-C-N	5.76	128.28	120.44
1	D	133	THR	C-N-CA	5.76	128.28	120.44
4	E	278	ASN	CB-CA-C	-5.76	101.05	110.85
3	C	433	ILE	N-CA-CB	5.76	118.38	110.54
3	C	194	HIS	O-C-N	-5.76	116.25	122.88
4	E	446	ILE	CB-CA-C	-5.76	104.48	112.02
4	E	448	LYS	CA-C-O	-5.76	114.41	120.63
1	D	217	ASN	O-C-N	5.76	129.54	122.34
1	A	45	GLU	N-CA-C	5.76	118.04	111.02
3	C	83	ARG	NH1-CZ-NH2	5.75	126.78	119.30
3	C	125	ILE	CB-CA-C	-5.75	105.02	111.23
1	A	286	ILE	CA-C-O	-5.75	112.62	119.58
3	C	5	GLU	CA-C-O	-5.75	112.28	120.51
3	C	272	LEU	CA-C-N	-5.75	112.57	120.28
3	C	272	LEU	C-N-CA	-5.75	112.57	120.28
4	E	65	SER	N-CA-C	-5.75	102.76	110.24
2	B	432	ALA	CA-C-N	5.75	128.56	120.28
2	B	432	ALA	C-N-CA	5.75	128.56	120.28
1	D	140	GLN	N-CA-C	5.75	117.92	109.24
1	D	191	THR	N-CA-CB	5.75	120.10	110.32
4	E	155	VAL	N-CA-C	5.75	117.28	108.71
1	A	220	ILE	O-C-N	5.75	127.65	121.10
2	B	152	ASP	CB-CA-C	-5.75	101.58	111.23
4	E	14	TYR	CG-CD1-CE1	-5.75	112.58	121.20
1	D	84	ASP	CB-CA-C	5.75	121.85	110.42
4	E	10	LEU	CA-C-O	-5.75	113.36	119.97
4	E	441	LEU	N-CA-CB	-5.75	102.55	110.42
1	A	432	GLU	CB-CA-C	5.74	119.75	109.29
1	D	383	ALA	CA-C-O	-5.74	114.41	120.55
1	D	13	GLU	CA-C-N	5.74	130.69	122.08
1	D	13	GLU	C-N-CA	5.74	130.69	122.08
1	D	411	LEU	CA-C-N	5.74	132.50	121.54
1	D	411	LEU	C-N-CA	5.74	132.50	121.54
1	A	217	ASN	CA-C-O	-5.74	114.31	121.02
3	C	270	PHE	CA-C-N	5.74	129.03	120.31
3	C	270	PHE	C-N-CA	5.74	129.03	120.31
2	B	220	TYR	CA-C-N	5.74	128.32	120.46
2	B	220	TYR	C-N-CA	5.74	128.32	120.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	16	ASN	CA-C-O	-5.73	114.57	120.99
1	D	28	PHE	CA-C-N	5.73	128.81	122.22
1	D	28	PHE	C-N-CA	5.73	128.81	122.22
1	D	232	VAL	CA-C-O	-5.73	113.61	120.78
4	E	26	HIS	CA-C-N	-5.73	111.65	121.97
4	E	26	HIS	C-N-CA	-5.73	111.65	121.97
2	B	23	GLN	OE1-CD-NE2	-5.73	116.87	122.60
3	C	466	VAL	CA-CB-CG1	5.73	120.14	110.40
4	E	129	ILE	O-C-N	-5.73	115.41	122.57
1	A	184	TRP	CZ3-CH2-CZ2	-5.73	114.06	121.50
1	A	40	LEU	CA-C-O	-5.72	114.52	120.70
3	C	66	ARG	N-CA-CB	5.72	119.15	110.28
4	E	205	PHE	O-C-N	-5.72	116.24	123.05
1	A	101	ALA	N-CA-CB	5.72	119.31	110.21
1	D	381	TYR	CA-C-N	5.72	128.30	120.46
1	D	381	TYR	C-N-CA	5.72	128.30	120.46
4	E	100	GLU	CA-C-N	5.72	132.26	121.97
4	E	100	GLU	C-N-CA	5.72	132.26	121.97
4	E	312	ASN	O-C-N	5.72	128.67	121.64
3	C	212	TYR	CA-C-O	5.71	128.68	120.51
4	E	140	ASN	O-C-N	-5.71	116.36	123.04
2	B	421	PHE	CG-CD1-CE1	-5.71	111.00	120.70
4	E	290	MET	CA-C-N	-5.71	111.02	121.52
4	E	290	MET	C-N-CA	-5.71	111.02	121.52
2	B	446	MET	CA-C-N	5.71	132.44	121.54
2	B	446	MET	C-N-CA	5.71	132.44	121.54
3	C	142	GLN	CB-CG-CD	5.71	122.30	112.60
2	B	60	TRP	O-C-N	-5.70	115.37	122.73
2	B	198	ARG	N-CA-CB	5.70	120.13	110.49
4	E	140	ASN	N-CA-CB	-5.70	101.11	109.95
1	A	16	ASN	O-C-N	-5.70	115.67	122.63
4	E	181	GLY	CA-C-N	5.70	132.43	121.54
4	E	181	GLY	C-N-CA	5.70	132.43	121.54
1	A	122	ALA	CA-C-N	5.70	132.23	121.97
1	A	122	ALA	C-N-CA	5.70	132.23	121.97
3	C	291	TYR	N-CA-CB	5.70	118.57	110.13
3	C	471	PHE	CE1-CZ-CE2	5.70	130.26	120.00
1	A	396	ALA	O-C-N	5.70	130.17	122.59
3	C	137	PHE	CG-CD2-CE2	5.70	130.38	120.70
4	E	191	LYS	O-C-N	5.70	130.25	123.24
2	B	213	ILE	CB-CA-C	-5.69	103.42	111.28
1	A	176	TRP	CD2-CE3-CZ3	5.69	126.00	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	140	ASP	N-CA-CB	5.69	118.47	109.82
1	D	305	THR	O-C-N	-5.69	114.33	122.41
1	D	401	TYR	CA-C-O	5.69	131.28	121.09
4	E	47	GLU	O-C-N	-5.69	115.02	122.59
4	E	233	SER	CA-C-O	-5.69	114.46	120.55
1	D	62	ASP	CA-C-N	5.69	127.94	120.60
1	D	62	ASP	C-N-CA	5.69	127.94	120.60
4	E	472	ASN	N-CA-CB	5.69	118.65	110.40
2	B	417	SER	CA-C-O	-5.69	114.49	120.63
4	E	439	TRP	CA-C-N	5.69	127.73	120.56
4	E	439	TRP	C-N-CA	5.69	127.73	120.56
3	C	76	ASP	O-C-N	5.69	130.16	122.59
1	D	381	TYR	O-C-N	5.69	128.63	122.15
4	E	68	THR	N-CA-CB	5.69	120.10	110.49
2	B	197	TRP	CD2-CE2-CZ2	5.68	128.09	122.40
2	B	258	ALA	O-C-N	-5.68	116.21	122.07
4	E	124	ARG	NE-CZ-NH2	-5.68	114.08	119.20
4	E	111	ASN	OD1-CG-ND2	5.68	128.28	122.60
4	E	467	LEU	N-CA-CB	5.68	119.05	110.30
1	A	24	HIS	O-C-N	-5.68	115.04	122.59
1	A	96	ALA	N-CA-CB	5.68	120.09	110.49
1	A	384	GLU	CA-C-N	5.68	128.46	120.28
1	A	384	GLU	C-N-CA	5.68	128.46	120.28
4	E	163	GLU	CB-CG-CD	5.68	122.25	112.60
1	D	278	MET	N-CA-C	5.67	119.01	111.75
1	D	54	VAL	CA-C-O	-5.67	114.25	120.43
1	A	227	PHE	N-CA-C	5.67	118.23	111.71
2	B	120	PRO	N-CA-CB	-5.67	97.30	103.25
1	A	79	ARG	CA-C-O	5.67	126.56	120.32
3	C	65	HIS	N-CA-CB	-5.67	100.68	110.32
1	D	409	ILE	CA-C-O	-5.67	112.72	119.58
4	E	156	ASN	N-CA-C	-5.67	98.73	110.80
4	E	435	GLU	CA-CB-CG	5.67	125.44	114.10
3	C	243	ALA	O-C-N	5.67	128.85	122.22
2	B	17	PRO	CA-C-N	5.66	132.39	121.18
2	B	17	PRO	C-N-CA	5.66	132.39	121.18
3	C	228	TYR	O-C-N	5.66	127.90	122.07
1	A	297	ASN	CA-CB-CG	5.66	118.26	112.60
1	D	264	ILE	N-CA-CB	-5.66	103.28	111.21
4	E	309	ARG	NH1-CZ-NH2	-5.66	111.94	119.30
4	E	196	TRP	CA-C-O	-5.66	112.42	120.51
1	A	28	PHE	CA-C-O	-5.66	112.42	120.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	65	HIS	CE1-NE2-CD2	5.66	114.66	109.00
3	C	317	PRO	N-CA-CB	5.66	109.28	103.23
3	C	462	THR	N-CA-CB	-5.66	101.87	110.30
4	E	310	THR	N-CA-C	-5.66	100.35	109.40
3	C	451	GLN	CA-C-O	-5.65	111.87	119.11
2	B	301	VAL	N-CA-C	-5.65	105.01	110.72
3	C	447	ASN	CA-C-O	5.65	126.53	120.20
1	D	45	GLU	O-C-N	-5.65	115.07	122.59
1	D	131	ILE	CB-CA-C	-5.65	102.02	111.29
1	A	425	VAL	CA-C-O	-5.65	114.37	120.47
1	D	189	TYR	CA-CB-CG	5.65	124.06	113.90
1	A	262	GLU	N-CA-C	5.64	117.51	111.36
2	B	136	PRO	CB-CA-C	5.64	118.37	110.98
4	E	308	LEU	CA-CB-CG	5.64	136.04	116.30
3	C	31	VAL	N-CA-CB	-5.64	104.22	110.99
1	A	132	VAL	CA-CB-CG2	5.64	119.98	110.40
4	E	217	LYS	CA-C-O	-5.63	112.44	120.16
1	A	96	ALA	CA-C-O	-5.63	112.45	120.51
1	D	152	ASP	N-CA-CB	-5.63	101.77	110.56
2	B	220	TYR	CD1-CE1-CZ	-5.63	109.46	119.60
4	E	68	THR	CA-C-O	5.63	128.56	120.51
1	A	136	PRO	CA-C-N	5.63	128.60	120.38
1	A	136	PRO	C-N-CA	5.63	128.60	120.38
2	B	280	ILE	N-CA-C	5.63	121.05	109.34
3	C	237	VAL	CA-C-O	-5.63	114.26	120.96
2	B	220	TYR	CG-CD1-CE1	5.63	129.64	121.20
2	B	451	THR	N-CA-C	-5.63	106.45	113.15
3	C	74	TYR	CA-C-N	5.63	128.09	120.44
3	C	74	TYR	C-N-CA	5.63	128.09	120.44
3	C	152	ASN	O-C-N	-5.63	116.01	122.09
4	E	172	ILE	CB-CG1-CD1	5.63	125.62	113.80
1	D	6	ARG	NE-CZ-NH2	5.63	124.26	119.20
1	D	237	THR	CA-CB-OG1	5.62	118.03	109.60
2	B	14	ASN	O-C-N	-5.62	115.68	122.48
2	B	124	TYR	CA-CB-CG	5.62	124.02	113.90
3	C	214	ASP	N-CA-C	5.62	117.61	109.07
2	B	70	ALA	O-C-N	-5.61	114.77	122.46
2	B	127	SER	CA-CB-OG	5.61	122.33	111.10
4	E	269	ALA	CA-C-O	-5.61	112.48	119.38
1	D	84	ASP	CA-C-O	-5.61	112.49	120.51
1	D	425	VAL	CA-C-N	5.61	132.25	121.54
1	D	425	VAL	C-N-CA	5.61	132.25	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	235	LEU	CA-C-O	-5.61	113.52	119.97
3	C	11	LEU	CB-CA-C	-5.60	101.38	110.79
3	C	102	TYR	CA-CB-CG	5.60	123.98	113.90
2	B	56	LEU	CD1-CG-CD2	5.60	123.12	110.80
1	D	248	SER	CA-CB-OG	5.60	122.30	111.10
1	A	409	ILE	CB-CA-C	-5.59	104.74	112.24
2	B	285	MET	CA-CB-CG	5.59	125.29	114.10
1	D	39	GLN	OE1-CD-NE2	-5.59	117.01	122.60
1	A	27	HIS	N-CA-C	5.59	122.71	110.80
3	C	40	SER	CA-C-O	-5.59	113.06	119.60
1	A	384	GLU	O-C-N	5.59	128.04	122.12
2	B	191	LYS	CA-C-N	5.59	125.58	120.21
2	B	191	LYS	C-N-CA	5.59	125.58	120.21
1	D	275	GLY	O-C-N	-5.59	116.39	122.54
3	C	63	TYR	CB-CG-CD1	5.59	129.18	120.80
4	E	314	HIS	CA-CB-CG	5.59	119.39	113.80
2	B	117	SER	O-C-N	-5.58	116.65	123.30
2	B	106	VAL	O-C-N	-5.58	117.44	123.14
1	A	245	LEU	CB-CA-C	5.58	119.74	110.81
3	C	187	ASN	N-CA-C	-5.58	104.90	112.26
4	E	16	LYS	N-CA-C	5.58	122.68	110.80
4	E	104	TYR	CA-C-N	-5.58	115.13	122.99
4	E	104	TYR	C-N-CA	-5.58	115.13	122.99
4	E	117	TRP	N-CA-CB	-5.58	101.12	110.99
4	E	256	SER	O-C-N	5.58	130.00	122.59
1	A	395	ALA	CA-C-O	-5.57	114.61	120.63
2	B	84	ASP	CB-CA-C	5.57	121.08	110.27
4	E	68	THR	N-CA-C	5.57	122.67	110.80
3	C	275	SER	CA-C-N	5.57	130.01	120.71
3	C	275	SER	C-N-CA	5.57	130.01	120.71
3	C	295	ILE	CA-C-N	-5.57	111.39	121.14
3	C	295	ILE	C-N-CA	-5.57	111.39	121.14
3	C	313	HIS	N-CA-C	5.57	118.11	111.71
2	B	267	ALA	CA-C-O	5.56	126.28	119.05
1	D	227	PHE	N-CA-C	-5.56	105.13	111.14
4	E	117	TRP	CE2-CD2-CE3	5.56	124.36	118.80
1	A	2	GLU	O-C-N	5.56	129.99	122.59
4	E	199	THR	CA-CB-OG1	5.56	117.94	109.60
3	C	29	GLU	CA-C-N	5.56	131.98	121.97
3	C	29	GLU	C-N-CA	5.56	131.98	121.97
1	D	290	ILE	O-C-N	-5.56	116.44	121.89
1	D	104	HIS	N-CA-CB	-5.56	102.31	110.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	190	ALA	CA-C-N	-5.56	113.95	122.62
4	E	190	ALA	C-N-CA	-5.56	113.95	122.62
1	A	65	LEU	CD1-CG-CD2	5.56	123.03	110.80
2	B	42	ILE	CA-C-O	5.56	126.58	120.64
2	B	307	ARG	CD-NE-CZ	-5.56	116.62	124.40
1	A	39	GLN	CG-CD-OE1	-5.55	109.69	120.80
1	A	209	ARG	CG-CD-NE	5.55	124.22	112.00
1	A	408	HIS	CA-CB-CG	5.55	119.36	113.80
4	E	266	PHE	N-CA-CB	5.55	119.61	110.39
1	A	120	PRO	N-CA-CB	5.55	108.47	103.08
1	D	41	ILE	CA-C-N	-5.55	112.83	122.37
1	D	41	ILE	C-N-CA	-5.55	112.83	122.37
1	D	151	TYR	CA-CB-CG	5.55	123.88	113.90
1	A	18	VAL	CB-CA-C	-5.54	102.20	111.29
1	A	113	THR	CA-C-O	-5.54	113.29	119.67
2	B	84	ASP	CA-C-N	-5.54	116.42	121.97
2	B	84	ASP	C-N-CA	-5.54	116.42	121.97
2	B	466	ASN	N-CA-C	5.54	122.06	109.81
3	C	190	TRP	CG-CD2-CE3	5.54	139.44	133.90
3	C	223	ARG	NH1-CZ-NH2	-5.54	112.09	119.30
2	B	133	MET	CA-C-O	5.54	126.96	121.20
1	A	411	LEU	N-CA-CB	5.54	118.83	110.30
1	D	218	VAL	CB-CA-C	-5.54	104.82	112.24
4	E	139	GLN	O-C-N	-5.54	116.76	123.13
2	B	190	HIS	N-CA-CB	5.54	119.85	110.49
2	B	278	PRO	N-CA-C	5.54	119.38	111.13
1	A	44	ASP	N-CA-CB	5.53	119.25	110.84
2	B	107	ASN	OD1-CG-ND2	5.53	128.13	122.60
1	D	24	HIS	ND1-CE1-NE2	5.53	113.93	108.40
1	A	128	CYS	CA-CB-SG	5.53	127.12	114.40
1	A	230	VAL	CB-CA-C	-5.53	104.67	112.14
3	C	100	GLY	CA-C-O	-5.53	110.95	120.57
1	A	227	PHE	CB-CG-CD1	5.53	130.10	120.70
3	C	99	ASP	CA-C-O	5.53	128.42	120.51
1	A	81	PRO	N-CA-CB	-5.53	96.12	103.42
1	A	292	THR	CA-CB-CG2	5.53	119.89	110.50
4	E	190	ALA	CB-CA-C	-5.53	103.11	110.79
2	B	434	VAL	CB-CA-C	-5.52	104.65	111.94
1	A	252	SER	O-C-N	5.52	128.50	122.20
2	B	182	GLU	CA-C-N	5.52	132.09	121.54
2	B	182	GLU	C-N-CA	5.52	132.09	121.54
3	C	128	SER	CA-C-N	5.52	132.49	122.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	128	SER	C-N-CA	5.52	132.49	122.27
3	C	294	PHE	CZ-CE2-CD2	-5.52	110.06	120.00
1	D	434	SER	O-C-N	5.52	129.50	122.10
4	E	291	PHE	CB-CA-C	5.52	120.77	109.67
2	B	208	THR	CB-CA-C	-5.52	101.70	110.81
2	B	72	TYR	O-C-N	5.52	129.75	122.30
3	C	157	GLU	CA-C-N	-5.52	114.97	122.92
3	C	157	GLU	C-N-CA	-5.52	114.97	122.92
1	A	232	VAL	N-CA-CB	5.52	120.33	111.23
4	E	232	ILE	CA-CB-CG1	-5.52	101.02	110.40
4	E	88	ASP	CA-C-N	5.52	128.80	120.75
4	E	88	ASP	C-N-CA	5.52	128.80	120.75
2	B	154	SER	CA-CB-OG	5.51	122.12	111.10
3	C	195	LYS	N-CA-C	5.51	121.99	109.81
4	E	22	LYS	CA-C-N	5.51	134.86	122.19
4	E	22	LYS	C-N-CA	5.51	134.86	122.19
1	D	16	ASN	CA-C-N	-5.51	113.55	121.98
1	D	16	ASN	C-N-CA	-5.51	113.55	121.98
3	C	312	PHE	CA-CB-CG	5.51	119.31	113.80
4	E	82	GLU	N-CA-CB	-5.50	100.30	110.32
1	A	260	ILE	N-CA-C	-5.50	105.36	110.53
3	C	120	TRP	CA-C-N	5.50	128.70	122.59
3	C	120	TRP	C-N-CA	5.50	128.70	122.59
1	D	31	ILE	N-CA-CB	5.50	116.72	110.72
1	D	72	TYR	CB-CG-CD2	5.50	129.05	120.80
3	C	300	THR	CA-CB-CG2	-5.50	101.15	110.50
3	C	307	GLY	O-C-N	-5.50	116.90	122.18
1	A	260	ILE	CB-CG1-CD1	5.50	125.34	113.80
1	A	265	PRO	N-CA-CB	5.50	109.02	103.25
3	C	257	MET	N-CA-CB	-5.50	102.10	110.07
1	D	93	TYR	O-C-N	5.50	129.90	122.59
1	A	272	PRO	CA-N-CD	-5.50	104.31	112.00
3	C	22	ARG	CG-CD-NE	-5.50	99.91	112.00
1	A	407	ASP	CA-C-O	-5.49	114.73	120.55
1	D	112	TYR	CE1-CZ-CE2	-5.49	109.31	120.30
1	D	164	ARG	CA-C-O	-5.49	114.62	120.28
1	D	177	VAL	CB-CA-C	5.49	120.30	111.29
4	E	95	VAL	CA-C-O	-5.49	113.91	120.78
2	B	292	ALA	CA-C-N	5.49	127.90	120.65
2	B	292	ALA	C-N-CA	5.49	127.90	120.65
2	B	288	MET	CA-C-O	-5.49	114.60	120.42
3	C	27	ASN	CB-CA-C	-5.49	101.60	110.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	26	HIS	ND1-CE1-NE2	-5.49	102.91	108.40
4	E	163	GLU	O-C-N	5.49	129.89	122.59
1	A	140	GLN	CA-C-O	-5.49	114.78	120.70
3	C	150	ALA	O-C-N	-5.49	115.29	122.59
1	A	60	TRP	CG-CD1-NE1	-5.48	103.07	110.20
3	C	286	PRO	N-CD-CG	5.48	111.42	103.20
1	D	62	ASP	CA-CB-CG	5.48	118.08	112.60
4	E	66	TRP	CD2-CE2-CZ2	5.48	127.88	122.40
1	A	255	VAL	CA-C-O	-5.48	114.97	121.05
4	E	44	GLU	N-CA-C	5.48	120.03	113.23
2	B	462	VAL	O-C-N	-5.48	114.86	121.10
2	B	127	SER	CA-C-O	-5.47	114.56	120.09
4	E	9	LYS	O-C-N	5.47	129.87	122.59
1	A	233	PHE	CA-C-N	5.47	127.56	120.44
1	A	233	PHE	C-N-CA	5.47	127.56	120.44
1	A	390	GLU	CA-C-N	5.47	128.07	120.63
1	A	390	GLU	C-N-CA	5.47	128.07	120.63
4	E	28	ILE	O-C-N	-5.47	116.48	122.83
1	A	436	GLU	CA-CB-CG	5.47	125.04	114.10
4	E	446	ILE	N-CA-CB	-5.47	103.57	110.57
1	A	78	ILE	N-CA-C	5.47	115.49	108.82
4	E	25	ASP	N-CA-CB	5.47	118.95	110.80
1	A	191	THR	N-CA-C	-5.46	106.45	113.01
1	A	235	LEU	CA-C-O	-5.46	112.67	120.16
1	A	426	PHE	CA-CB-CG	5.46	119.26	113.80
3	C	185	THR	N-CA-C	5.46	117.01	109.15
1	D	176	TRP	CB-CG-CD1	5.46	135.09	126.90
2	B	307	ARG	CA-CB-CG	5.46	125.02	114.10
1	D	83	ASP	CA-C-N	5.46	131.97	121.54
1	D	83	ASP	C-N-CA	5.46	131.97	121.54
4	E	148	GLN	CA-C-N	5.46	131.97	121.54
4	E	148	GLN	C-N-CA	5.46	131.97	121.54
2	B	294	SER	O-C-N	-5.46	114.93	122.46
3	C	259	THR	O-C-N	-5.46	114.98	122.46
4	E	414	SER	N-CA-CB	-5.46	101.22	110.50
1	A	138	ASP	N-CA-C	5.46	119.65	112.89
1	A	262	GLU	CA-C-O	5.46	126.20	120.42
1	A	86	TRP	CB-CG-CD1	5.45	135.08	126.90
1	A	87	LEU	N-CA-C	5.45	118.51	108.69
4	E	175	GLU	N-CA-CB	5.45	118.07	109.94
2	B	42	ILE	N-CA-C	5.45	115.74	108.27
4	E	26	HIS	CA-C-O	-5.45	112.83	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	66	TRP	CG-CD1-NE1	5.45	117.28	110.20
1	A	281	THR	CA-C-O	-5.45	114.77	120.55
3	C	63	TYR	CG-CD2-CE2	5.45	129.37	121.20
1	D	57	ARG	CA-C-O	-5.45	112.72	120.51
1	A	411	LEU	CA-CB-CG	5.45	135.36	116.30
4	E	223	ILE	CA-C-O	-5.45	113.10	119.85
4	E	279	VAL	O-C-N	5.45	127.31	121.10
4	E	281	LEU	N-CA-CB	-5.44	101.28	111.13
2	B	224	THR	CA-C-N	5.44	128.21	120.53
2	B	224	THR	C-N-CA	5.44	128.21	120.53
3	C	230	ILE	CB-CA-C	-5.44	104.89	112.02
4	E	297	VAL	CB-CA-C	-5.44	102.36	111.29
3	C	97	ASN	OD1-CG-ND2	5.44	128.04	122.60
4	E	430	ASN	CA-CB-CG	-5.44	107.16	112.60
4	E	296	ILE	CA-C-N	5.44	131.76	121.97
4	E	296	ILE	C-N-CA	5.44	131.76	121.97
4	E	255	ILE	N-CA-C	-5.44	105.31	110.42
1	A	427	ALA	O-C-N	-5.43	115.96	122.15
2	B	129	THR	N-CA-CB	5.43	119.67	110.49
1	D	278	MET	CA-C-N	5.43	128.31	120.38
1	D	278	MET	C-N-CA	5.43	128.31	120.38
4	E	75	ASP	CA-CB-CG	5.43	118.03	112.60
4	E	249	GLN	CB-CG-CD	5.43	121.83	112.60
3	C	103	ASN	OD1-CG-ND2	5.43	128.03	122.60
2	B	21	PRO	CA-N-CD	-5.42	104.41	112.00
1	A	168	SER	CA-CB-OG	5.42	121.95	111.10
4	E	468	THR	N-CA-C	-5.42	106.17	112.89
4	E	127	CYS	CA-C-O	-5.42	111.97	121.67
1	A	67	TRP	N-CA-C	5.42	117.08	108.79
1	A	81	PRO	CB-CA-C	5.42	119.40	111.22
2	B	159	GLN	N-CA-CB	-5.42	101.32	111.13
2	B	434	VAL	CG1-CB-CG2	5.42	122.72	110.80
3	C	135	LEU	CA-C-N	5.42	131.89	121.54
3	C	135	LEU	C-N-CA	5.42	131.89	121.54
1	D	191	THR	O-C-N	5.42	129.43	122.39
2	B	63	TYR	CB-CG-CD1	5.42	128.93	120.80
2	B	117	SER	CA-C-O	-5.42	114.51	120.36
1	D	430	LEU	CA-C-O	5.42	127.36	121.02
1	D	300	HIS	CG-CD2-NE2	-5.42	101.78	107.20
4	E	94	ASN	CA-C-O	-5.41	112.77	120.51
4	E	111	ASN	N-CA-C	5.41	122.33	110.80
2	B	118	TRP	CD2-CE2-CZ2	-5.41	116.99	122.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	452	THR	CB-CA-C	-5.41	100.28	110.67
1	D	86	TRP	O-C-N	-5.41	115.32	122.57
4	E	103	TYR	CG-CD1-CE1	5.41	129.31	121.20
4	E	225	ILE	O-C-N	5.41	127.21	121.91
4	E	288	PHE	CB-CA-C	-5.41	101.81	110.79
1	A	208	GLN	O-C-N	-5.41	115.46	122.97
1	D	227	PHE	CA-CB-CG	-5.41	108.39	113.80
4	E	4	GLY	N-CA-C	-5.41	105.95	112.49
1	A	178	MET	CA-C-O	5.40	128.10	121.72
1	A	424	SER	N-CA-C	5.40	117.17	111.28
2	B	136	PRO	CA-CB-CG	-5.40	94.23	104.50
1	D	300	HIS	CA-C-N	5.40	131.86	121.54
1	D	300	HIS	C-N-CA	5.40	131.86	121.54
3	C	132	ILE	CA-CB-CG2	5.40	119.68	110.50
1	D	63	VAL	O-C-N	5.40	127.34	121.94
4	E	470	HIS	CB-CA-C	-5.40	102.41	110.88
2	B	187	SER	O-C-N	5.40	128.33	123.26
3	C	41	ASN	N-CA-C	5.39	122.29	110.80
4	E	5	ARG	NE-CZ-NH2	5.39	124.06	119.20
4	E	130	ALA	N-CA-C	5.39	122.29	110.80
2	B	442	ILE	N-CA-C	-5.39	105.12	111.00
4	E	159	LEU	N-CA-C	5.39	114.95	107.73
4	E	289	VAL	O-C-N	-5.39	116.14	121.96
1	A	394	ASN	N-CA-C	-5.39	105.10	110.97
1	A	401	TYR	CA-C-O	5.39	126.84	120.70
1	A	401	TYR	CB-CA-C	-5.39	101.96	111.22
3	C	437	ASN	CB-CA-C	5.38	120.67	109.95
4	E	236	VAL	CA-C-O	-5.38	113.00	119.36
4	E	78	ARG	N-CA-CB	5.38	120.84	111.74
1	A	136	PRO	O-C-N	-5.38	116.28	122.85
1	A	414	PHE	CA-C-O	-5.38	113.78	119.97
1	D	304	SER	CA-C-O	-5.38	115.35	121.00
4	E	64	LEU	O-C-N	-5.38	115.44	122.59
1	A	152	ASP	CA-CB-CG	-5.38	107.22	112.60
2	B	219	PHE	CD1-CG-CD2	-5.38	110.54	118.60
3	C	115	ASN	O-C-N	5.37	129.74	122.59
4	E	91	LEU	O-C-N	5.37	129.41	122.43
2	B	181	THR	CA-C-O	-5.37	114.26	120.49
2	B	218	LEU	O-C-N	5.37	129.47	122.87
3	C	300	THR	CA-CB-OG1	-5.36	101.56	109.60
1	D	305	THR	N-CA-C	-5.36	106.74	113.28
4	E	23	THR	CA-C-O	5.36	127.01	121.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	304	SER	O-C-N	-5.36	115.46	122.59
2	B	403	GLU	CA-C-O	-5.36	111.69	120.80
1	D	377	GLU	CA-C-O	-5.36	114.87	120.55
4	E	468	THR	O-C-N	-5.36	115.06	122.46
1	D	43	VAL	O-C-N	5.36	128.34	123.19
1	D	6	ARG	CA-C-O	5.36	126.13	119.97
1	D	258	LEU	N-CA-CB	5.36	118.00	110.12
1	A	292	THR	CA-C-N	5.36	131.61	121.97
1	A	292	THR	C-N-CA	5.36	131.61	121.97
1	A	431	ILE	CA-CB-CG1	5.36	119.50	110.40
4	E	93	ASN	CA-CB-CG	5.36	117.95	112.60
4	E	466	PHE	N-CA-CB	5.36	117.99	110.12
2	B	273	THR	N-CA-CB	5.35	118.23	110.26
1	A	400	LYS	O-C-N	-5.35	115.69	122.17
2	B	240	TYR	CA-C-O	-5.35	113.36	119.41
1	A	20	ARG	NH1-CZ-NH2	-5.35	112.35	119.30
2	B	102	ILE	CA-CB-CG1	5.35	119.49	110.40
2	B	64	ARG	NE-CZ-NH1	5.34	126.84	121.50
1	D	29	VAL	CA-C-O	-5.34	116.03	121.70
2	B	20	ARG	CA-C-O	-5.34	114.20	119.49
4	E	240	TYR	CG-CD1-CE1	-5.34	113.19	121.20
2	B	274	SER	N-CA-CB	5.34	119.82	110.42
3	C	95	GLN	OE1-CD-NE2	5.34	127.94	122.60
1	D	82	SER	N-CA-CB	5.34	117.97	110.12
1	D	196	THR	CA-CB-CG2	5.34	119.58	110.50
4	E	61	ASP	O-C-N	-5.34	117.37	123.40
4	E	439	TRP	NE1-CE2-CZ2	-5.34	122.09	130.10
4	E	424	LYS	CA-C-N	5.34	127.89	120.63
4	E	424	LYS	C-N-CA	5.34	127.89	120.63
1	D	176	TRP	O-C-N	5.34	129.69	122.59
1	D	184	TRP	CE2-CD2-CE3	-5.33	113.47	118.80
4	E	207	GLU	CA-C-O	-5.33	115.60	121.31
3	C	186	GLU	CA-C-O	-5.33	112.29	119.11
1	D	402	VAL	CA-C-O	-5.33	112.55	119.53
1	A	376	ILE	N-CA-CB	-5.33	105.03	110.62
1	A	435	GLN	N-CA-CB	5.33	117.69	109.91
3	C	20	HIS	CA-CB-CG	-5.33	108.47	113.80
4	E	75	ASP	O-C-N	-5.33	115.11	122.46
1	D	250	LEU	CA-C-O	-5.33	115.21	120.80
2	B	216	LYS	N-CA-C	5.33	121.58	109.81
4	E	464	ALA	N-CA-C	5.33	122.14	110.80
3	C	239	ILE	CA-C-N	5.32	129.65	121.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	239	ILE	C-N-CA	5.32	129.65	121.19
1	A	98	GLY	CA-C-N	5.32	128.40	120.95
1	A	98	GLY	C-N-CA	5.32	128.40	120.95
1	A	260	ILE	CA-C-O	-5.32	115.15	121.05
2	B	454	ILE	CA-C-O	5.32	126.80	121.27
1	D	208	GLN	CG-CD-NE2	5.31	124.37	116.40
2	B	408	ILE	N-CA-C	-5.31	105.67	110.82
3	C	24	VAL	O-C-N	-5.31	115.93	122.57
1	D	264	ILE	CA-C-O	-5.31	112.84	119.95
4	E	75	ASP	CA-C-O	5.31	125.95	119.05
3	C	211	ASN	OD1-CG-ND2	5.30	127.91	122.60
1	D	102	ILE	CG1-CB-CG2	-5.30	94.79	110.70
1	A	59	GLN	OE1-CD-NE2	5.30	127.90	122.60
1	A	214	PHE	CG-CD1-CE1	-5.30	111.69	120.70
1	A	270	ALA	N-CA-C	5.30	119.37	113.01
2	B	74	GLY	CA-C-O	-5.30	111.34	120.57
3	C	192	ILE	N-CA-C	5.30	115.41	107.51
1	D	92	LEU	CA-C-O	-5.30	115.95	122.36
4	E	193	ASN	CA-C-N	5.30	132.45	121.32
4	E	193	ASN	C-N-CA	5.30	132.45	121.32
4	E	470	HIS	N-CA-C	5.30	116.74	111.07
1	D	291	VAL	N-CA-CB	5.29	118.52	110.58
1	D	86	TRP	CG-CD1-NE1	-5.29	103.32	110.20
4	E	96	ASP	N-CA-C	-5.29	107.37	113.88
1	A	7	LEU	N-CA-CB	5.29	119.43	110.49
2	B	109	LEU	O-C-N	5.29	129.28	122.93
2	B	117	SER	N-CA-CB	-5.29	101.80	110.68
1	D	429	ARG	NH1-CZ-NH2	5.29	126.18	119.30
3	C	97	ASN	CA-C-O	-5.29	114.01	119.51
4	E	66	TRP	CA-CB-CG	5.29	123.64	113.60
4	E	29	ASP	N-CA-CB	5.29	118.40	109.94
1	A	119	THR	N-CA-CB	5.28	119.04	110.75
2	B	141	ASN	O-C-N	-5.28	116.71	122.84
1	D	14	ASN	CA-C-N	5.28	131.46	122.37
1	D	14	ASN	C-N-CA	5.28	131.46	122.37
4	E	271	LYS	O-C-N	-5.28	115.56	122.59
2	B	99	SER	O-C-N	-5.28	115.57	122.59
1	A	23	GLU	O-C-N	5.28	131.01	122.99
1	A	4	GLU	CA-C-O	5.28	126.36	120.82
2	B	221	ILE	O-C-N	5.28	126.99	121.87
3	C	32	ASN	O-C-N	-5.28	115.30	122.48
1	A	105	MET	O-C-N	-5.28	116.63	122.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	92	GLU	CA-C-O	-5.28	112.97	120.51
3	C	225	PRO	O-C-N	5.27	129.76	122.64
4	E	246	ALA	CA-C-O	5.27	128.04	120.51
4	E	443	GLY	CA-C-N	5.27	127.87	120.28
4	E	443	GLY	C-N-CA	5.27	127.87	120.28
1	A	19	ILE	O-C-N	-5.27	116.87	122.61
1	A	413	VAL	CG1-CB-CG2	5.27	122.39	110.80
4	E	78	ARG	NH1-CZ-NH2	5.27	126.15	119.30
4	E	90	VAL	O-C-N	5.27	129.15	122.57
1	D	406	ILE	N-CA-CB	-5.26	103.38	110.54
4	E	137	ASP	N-CA-C	-5.26	100.59	108.96
1	A	187	TRP	CD2-CE2-CZ2	-5.26	117.14	122.40
2	B	186	TRP	CZ3-CH2-CZ2	-5.26	114.66	121.50
2	B	297	LEU	CA-CB-CG	-5.26	97.89	116.30
1	D	28	PHE	CA-C-O	-5.26	112.99	120.51
1	D	256	PHE	CA-CB-CG	5.26	119.06	113.80
4	E	195	ASN	CA-C-O	5.26	126.11	120.38
4	E	240	TYR	CA-C-N	5.26	129.62	120.68
4	E	240	TYR	C-N-CA	5.26	129.62	120.68
3	C	139	PHE	CB-CG-CD1	5.26	129.64	120.70
1	D	86	TRP	NE1-CE2-CZ2	5.26	137.99	130.10
1	D	274	ILE	CA-CB-CG1	5.26	119.34	110.40
1	A	20	ARG	CD-NE-CZ	5.26	131.76	124.40
4	E	254	SER	N-CA-CB	5.25	119.37	110.49
4	E	424	LYS	N-CA-C	-5.25	106.13	112.54
1	A	108	LEU	CA-C-N	-5.25	115.36	122.77
1	A	108	LEU	C-N-CA	-5.25	115.36	122.77
2	B	75	ILE	O-C-N	-5.25	116.00	122.57
3	C	309	VAL	N-CA-CB	5.25	119.90	111.23
1	A	218	VAL	N-CA-C	5.25	115.46	110.42
2	B	110	VAL	CB-CA-C	5.25	118.63	110.96
2	B	135	PHE	CA-CB-CG	-5.25	108.55	113.80
2	B	151	TYR	N-CA-CB	5.25	118.83	110.16
1	D	157	SER	N-CA-C	5.25	117.93	108.48
1	D	92	LEU	O-C-N	-5.25	114.94	122.29
4	E	117	TRP	CG-CD2-CE3	-5.25	128.65	133.90
3	C	20	HIS	N-CA-C	-5.25	106.72	113.23
1	D	33	VAL	CA-C-O	-5.25	116.79	121.09
4	E	466	PHE	N-CA-C	-5.25	105.56	111.28
4	E	181	GLY	CA-C-O	5.25	129.70	120.57
2	B	416	GLU	N-CA-C	-5.24	104.47	111.24
1	D	270	ALA	N-CA-CB	5.24	118.12	110.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	25	VAL	CA-CB-CG1	5.24	119.31	110.40
1	D	104	HIS	CB-CG-ND1	-5.24	114.84	122.70
1	D	266	SER	N-CA-C	-5.24	105.21	111.03
4	E	189	PRO	CB-CA-C	5.24	120.21	111.56
1	A	106	THR	CB-CA-C	5.24	120.95	114.40
3	C	245	LEU	CA-C-O	5.24	126.15	120.55
2	B	139	TRP	NE1-CE2-CD2	-5.24	100.59	107.40
3	C	47	GLU	CA-C-O	-5.24	114.23	120.56
3	C	240	SER	CA-C-N	5.24	128.03	120.38
3	C	240	SER	C-N-CA	5.24	128.03	120.38
1	A	173	SER	O-C-N	-5.23	115.64	122.39
3	C	187	ASN	OD1-CG-ND2	-5.23	117.37	122.60
1	A	297	ASN	O-C-N	-5.23	115.43	122.23
1	D	291	VAL	CA-C-O	-5.23	115.30	120.85
1	A	435	GLN	OE1-CD-NE2	5.23	127.83	122.60
2	B	286	PHE	CG-CD2-CE2	5.23	129.59	120.70
2	B	254	SER	CA-C-N	5.23	127.24	120.44
2	B	254	SER	C-N-CA	5.23	127.24	120.44
3	C	432	GLN	CA-C-O	-5.23	114.96	120.55
1	D	38	ILE	O-C-N	5.23	127.24	122.06
1	D	155	LYS	CA-C-O	5.23	127.45	120.13
1	D	408	HIS	CE1-NE2-CD2	5.23	114.23	109.00
2	B	409	LYS	CA-C-N	5.23	131.52	121.54
2	B	409	LYS	C-N-CA	5.23	131.52	121.54
3	C	113	ARG	N-CA-C	-5.23	102.55	110.39
1	A	56	LEU	N-CA-CB	5.22	118.52	110.21
3	C	457	SER	N-CA-CB	-5.22	101.63	110.41
1	D	101	ALA	CA-C-N	5.22	131.37	121.97
1	D	101	ALA	C-N-CA	5.22	131.37	121.97
4	E	145	PHE	CA-CB-CG	5.22	119.02	113.80
1	A	211	PRO	CB-CA-C	5.22	120.17	111.56
3	C	454	ASP	CA-C-O	-5.22	113.05	120.51
1	D	301	ARG	CA-C-N	5.22	129.97	121.83
1	D	301	ARG	C-N-CA	5.22	129.97	121.83
1	A	292	THR	CA-CB-OG1	5.22	117.43	109.60
3	C	472	ILE	N-CA-CB	5.22	121.10	110.82
1	D	299	HIS	CE1-NE2-CD2	5.22	114.22	109.00
1	A	210	ILE	O-C-N	5.21	127.04	121.10
3	C	48	THR	N-CA-CB	5.21	119.30	110.49
3	C	283	LEU	N-CA-CB	5.21	118.36	110.28
3	C	438	ALA	CA-C-O	5.21	125.95	120.42
1	A	402	VAL	N-CA-CB	5.21	119.83	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	156	VAL	CA-CB-CG2	5.21	119.26	110.40
1	A	152	ASP	O-C-N	-5.21	115.38	122.36
3	C	432	GLN	CB-CA-C	-5.21	102.04	110.79
1	D	413	VAL	CA-C-O	-5.21	114.20	119.20
2	B	176	ASN	CA-CB-CG	-5.21	107.39	112.60
3	C	69	TRP	CA-C-N	5.21	131.49	121.54
3	C	69	TRP	C-N-CA	5.21	131.49	121.54
3	C	291	TYR	N-CA-C	-5.21	105.05	111.40
1	D	191	THR	CA-C-O	-5.21	113.19	119.49
4	E	12	GLY	O-C-N	5.21	129.47	122.70
1	A	163	ASP	CA-C-O	5.21	126.58	120.80
3	C	421	SER	O-C-N	-5.20	114.68	123.00
4	E	18	ILE	CA-C-O	-5.20	115.00	120.57
1	A	69	PRO	CB-CA-C	-5.20	102.98	111.56
2	B	189	GLU	CA-C-O	-5.20	113.65	119.79
3	C	272	LEU	O-C-N	-5.20	115.88	122.17
2	B	131	LYS	CA-C-O	5.20	127.55	119.80
3	C	423	ILE	CB-CA-C	5.20	119.82	111.29
4	E	87	PRO	N-CA-C	5.20	118.66	110.50
2	B	112	HIS	CA-CB-CG	-5.20	108.60	113.80
3	C	126	PHE	N-CA-C	5.20	117.31	109.41
4	E	213	ILE	CA-C-O	-5.20	114.37	120.76
1	A	402	VAL	N-CA-C	-5.19	98.54	109.34
2	B	199	SER	CA-C-O	5.19	125.35	119.27
4	E	187	HIS	CE1-NE2-CD2	5.19	114.19	109.00
3	C	457	SER	CA-CB-OG	-5.19	100.72	111.10
4	E	137	ASP	OD1-CG-OD2	-5.19	110.44	122.90
1	A	129	GLU	CB-CG-CD	5.19	121.42	112.60
1	D	161	GLU	O-C-N	5.19	128.05	122.34
3	C	64	ASP	O-C-N	-5.19	116.61	122.84
4	E	284	LYS	CB-CA-C	5.19	120.75	110.42
1	A	16	ASN	CB-CG-OD1	-5.19	110.43	120.80
4	E	468	THR	CA-C-N	5.19	125.74	119.98
4	E	468	THR	C-N-CA	5.19	125.74	119.98
2	B	281	ILE	CA-C-O	-5.18	114.30	120.78
1	D	213	TYR	N-CA-C	-5.18	105.71	111.36
4	E	31	THR	CA-CB-OG1	5.18	117.38	109.60
3	C	455	ARG	N-CA-CB	5.18	117.49	109.98
2	B	272	GLU	N-CA-C	5.18	117.83	111.82
1	D	251	LEU	CB-CA-C	-5.18	101.88	110.68
3	C	259	THR	CA-C-N	5.18	127.64	120.29
3	C	259	THR	C-N-CA	5.18	127.64	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	258	ALA	CB-CA-C	-5.17	102.76	110.88
1	D	404	MET	N-CA-CB	5.17	117.45	110.10
4	E	267	LEU	O-C-N	-5.17	115.50	122.43
1	A	65	LEU	O-C-N	5.17	128.40	122.25
2	B	268	ASP	CA-CB-CG	-5.17	107.43	112.60
3	C	29	GLU	CB-CA-C	5.17	119.06	110.90
3	C	234	THR	N-CA-C	-5.17	106.26	113.45
3	C	478	PHE	N-CA-C	-5.17	106.94	114.12
1	A	196	THR	N-CA-CB	-5.17	101.17	110.37
1	A	406	ILE	CA-C-N	5.17	127.20	120.28
1	A	406	ILE	C-N-CA	5.17	127.20	120.28
3	C	247	PHE	CG-CD1-CE1	-5.17	111.92	120.70
1	A	157	SER	N-CA-C	5.16	117.01	108.13
3	C	8	ILE	CA-C-O	-5.16	114.32	120.78
3	C	256	LYS	O-C-N	-5.16	115.80	122.56
1	D	64	ARG	CD-NE-CZ	5.16	131.63	124.40
1	D	67	TRP	CA-C-O	-5.16	115.57	121.40
1	D	134	HIS	N-CA-CB	5.16	117.55	110.07
3	C	196	PRO	N-CA-C	5.16	118.59	110.80
1	A	399	TRP	CG-CD2-CE3	-5.16	128.75	133.90
1	D	186	HIS	O-C-N	5.16	128.05	123.41
4	E	101	VAL	N-CA-CB	5.16	119.74	111.23
2	B	96	ASN	O-C-N	5.15	129.44	122.59
1	D	278	MET	CB-CG-SD	5.15	128.16	112.70
4	E	421	PHE	O-C-N	5.15	127.59	122.08
2	B	164	ALA	N-CA-CB	5.15	118.13	110.40
3	C	6	ARG	N-CA-C	5.15	121.77	110.80
3	C	470	ILE	CA-C-N	5.15	131.38	121.54
3	C	470	ILE	C-N-CA	5.15	131.38	121.54
1	D	225	PHE	CA-C-O	5.15	125.70	119.31
1	D	41	ILE	O-C-N	5.15	127.25	121.90
4	E	312	ASN	CA-CB-CG	5.15	117.75	112.60
1	D	109	LEU	CA-C-O	5.14	126.19	120.43
2	B	123	ILE	CB-CA-C	5.14	118.23	110.98
2	B	461	ASN	CB-CA-C	-5.14	102.15	110.79
4	E	78	ARG	CA-C-N	5.14	131.65	122.13
4	E	78	ARG	C-N-CA	5.14	131.65	122.13
1	A	3	HIS	CB-CG-ND1	5.14	130.41	122.70
1	A	63	VAL	CA-CB-CG1	-5.14	101.66	110.40
1	A	274	ILE	O-C-N	5.14	128.16	122.66
3	C	83	ARG	NE-CZ-NH1	-5.14	116.36	121.50
2	B	73	GLU	N-CA-C	-5.14	107.04	113.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	274	ILE	CB-CA-C	-5.14	105.07	111.08
4	E	103	TYR	O-C-N	-5.14	114.55	122.61
4	E	122	ILE	CA-C-O	-5.14	115.07	120.57
1	A	141	ASN	CA-CB-CG	5.13	117.73	112.60
1	D	287	SER	CA-C-N	-5.13	112.89	120.28
1	D	287	SER	C-N-CA	-5.13	112.89	120.28
4	E	466	PHE	CD1-CE1-CZ	-5.13	110.76	120.00
2	B	241	LEU	N-CA-CB	-5.13	102.48	110.43
4	E	249	GLN	OE1-CD-NE2	5.13	127.73	122.60
1	A	68	ASN	CA-C-N	5.13	126.25	119.84
1	A	68	ASN	C-N-CA	5.13	126.25	119.84
1	A	251	LEU	CA-C-O	5.13	126.18	120.90
1	D	384	GLU	CG-CD-OE2	5.13	130.20	118.40
1	A	151	TYR	CB-CG-CD1	5.12	128.49	120.80
3	C	185	THR	N-CA-CB	5.12	118.00	109.60
2	B	35	LEU	O-C-N	5.12	129.21	123.27
1	D	6	ARG	NH1-CZ-NH2	-5.12	112.64	119.30
1	A	405	VAL	O-C-N	-5.12	116.54	122.17
2	B	62	ASP	CA-CB-CG	5.12	117.72	112.60
2	B	91	VAL	CA-C-N	-5.12	114.93	123.33
2	B	91	VAL	C-N-CA	-5.12	114.93	123.33
2	B	277	VAL	CA-CB-CG1	5.12	119.11	110.40
3	C	10	ASP	N-CA-C	-5.12	105.61	111.14
1	D	187	TRP	CA-C-O	-5.12	114.69	120.32
4	E	172	ILE	N-CA-CB	5.12	120.21	111.50
4	E	124	ARG	CD-NE-CZ	-5.12	117.23	124.40
3	C	230	ILE	O-C-N	-5.12	116.58	121.90
2	B	261	VAL	CB-CA-C	5.12	118.43	111.88
1	D	434	SER	CA-C-O	-5.12	113.55	119.64
4	E	77	VAL	N-CA-C	5.12	113.94	107.70
4	E	110	TYR	N-CA-CB	5.12	119.14	110.49
3	C	227	PHE	CA-C-N	-5.11	113.79	120.44
3	C	227	PHE	C-N-CA	-5.11	113.79	120.44
3	C	308	ILE	CA-C-N	5.11	131.17	121.97
3	C	308	ILE	C-N-CA	5.11	131.17	121.97
1	D	247	ILE	CB-CA-C	-5.11	105.32	112.02
4	E	220	PHE	CB-CA-C	5.11	117.27	109.34
1	A	219	ILE	CA-C-O	-5.11	113.85	120.03
3	C	141	TRP	N-CA-CB	-5.11	104.41	112.13
1	A	271	VAL	CA-C-N	5.11	126.51	120.23
1	A	271	VAL	C-N-CA	5.11	126.51	120.23
2	B	5	ASP	CA-C-N	5.11	129.24	120.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	5	ASP	C-N-CA	5.11	129.24	120.71
2	B	220	TYR	N-CA-C	5.11	120.36	113.72
3	C	226	LEU	N-CA-C	-5.11	104.31	110.44
1	A	118	TRP	CB-CA-C	-5.11	103.98	111.23
3	C	449	VAL	CA-C-N	5.11	131.42	121.41
3	C	449	VAL	C-N-CA	5.11	131.42	121.41
3	C	463	PRO	CA-C-O	-5.11	112.07	118.86
3	C	13	ILE	O-C-N	-5.10	116.19	122.57
3	C	134	VAL	O-C-N	-5.10	116.19	122.57
3	C	241	PHE	CA-C-O	-5.10	114.48	120.20
3	C	426	THR	N-CA-CB	5.10	117.41	110.01
4	E	313	THR	O-C-N	5.10	128.19	122.22
3	C	440	ASP	CA-C-N	5.10	128.47	120.82
3	C	440	ASP	C-N-CA	5.10	128.47	120.82
1	A	14	ASN	CB-CA-C	5.10	120.21	112.00
1	A	420	ILE	N-CA-C	5.10	119.95	109.34
2	B	443	PHE	CA-C-O	-5.10	115.05	121.02
1	A	86	TRP	CD2-CE3-CZ3	-5.10	111.97	118.60
1	A	115	LYS	CA-C-O	-5.10	113.22	120.51
1	A	186	HIS	CG-CD2-NE2	5.10	112.30	107.20
2	B	217	PRO	CA-N-CD	-5.10	104.86	112.00
3	C	139	PHE	CD1-CE1-CZ	-5.10	110.83	120.00
2	B	233	ILE	O-C-N	-5.10	116.20	122.57
3	C	295	ILE	O-C-N	5.09	127.39	121.94
1	D	40	LEU	CA-C-O	-5.09	110.87	120.69
1	D	181	TYR	N-CA-CB	-5.09	101.92	111.13
4	E	26	HIS	ND1-CG-CD2	5.09	111.19	106.10
4	E	199	THR	O-C-N	5.09	129.64	122.41
3	C	460	ILE	CA-CB-CG2	-5.09	101.85	110.50
4	E	93	ASN	N-CA-C	5.09	121.63	110.80
3	C	447	ASN	CA-CB-CG	5.08	117.69	112.60
1	D	399	TRP	O-C-N	-5.08	115.78	122.39
4	E	233	SER	N-CA-CB	5.08	117.66	110.13
1	A	170	PHE	N-CA-C	-5.08	102.17	110.20
3	C	428	TYR	N-CA-C	-5.08	105.44	111.69
1	D	259	VAL	CB-CA-C	5.08	119.23	112.22
1	D	303	PRO	CA-C-O	-5.08	111.36	120.60
4	E	87	PRO	CB-CA-C	5.08	117.09	111.56
1	A	38	ILE	CA-C-N	5.08	133.02	122.41
1	A	38	ILE	C-N-CA	5.08	133.02	122.41
1	A	257	LEU	N-CA-CB	5.08	118.15	110.28
1	A	378	GLY	O-C-N	-5.08	114.35	122.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	101	GLU	CA-C-O	-5.07	112.38	120.85
3	C	9	ASN	CB-CG-ND2	-5.07	108.79	116.40
4	E	26	HIS	CE1-NE2-CD2	5.07	114.07	109.00
4	E	77	VAL	N-CA-CB	5.07	116.54	109.84
2	B	94	ASN	CA-CB-CG	5.07	117.67	112.60
2	B	220	TYR	CA-CB-CG	5.07	123.03	113.90
2	B	248	LYS	CA-C-O	5.07	127.76	120.51
3	C	447	ASN	O-C-N	-5.07	116.42	122.20
1	D	228	LEU	N-CA-CB	5.07	118.13	110.28
3	C	74	TYR	CA-CB-CG	5.06	123.01	113.90
2	B	263	LEU	O-C-N	5.06	129.45	122.46
4	E	258	LEU	O-C-N	-5.06	116.07	122.20
1	A	249	VAL	N-CA-CB	5.06	119.58	111.23
1	A	304	SER	N-CA-C	5.06	121.58	110.80
2	B	178	ASP	CA-CB-CG	5.06	117.66	112.60
3	C	482	PRO	CA-N-CD	-5.06	104.92	112.00
1	D	283	ILE	CA-CB-CG1	5.06	119.00	110.40
3	C	35	LEU	CA-C-N	5.06	129.90	122.77
3	C	35	LEU	C-N-CA	5.06	129.90	122.77
1	D	287	SER	CA-C-O	-5.06	115.49	120.90
4	E	257	VAL	CA-C-O	-5.06	115.30	120.71
1	A	20	ARG	CB-CA-C	-5.06	103.09	109.31
3	C	312	PHE	N-CA-C	-5.06	105.86	112.23
4	E	175	GLU	N-CA-C	5.06	117.18	111.11
3	C	466	VAL	CA-CB-CG2	5.05	118.99	110.40
1	D	374	SER	CB-CA-C	5.05	119.70	110.10
4	E	105	ALA	CA-C-N	5.05	131.20	121.54
4	E	105	ALA	C-N-CA	5.05	131.20	121.54
3	C	107	PHE	CA-C-N	5.05	132.09	123.05
3	C	107	PHE	C-N-CA	5.05	132.09	123.05
1	D	55	ARG	N-CA-C	-5.05	100.28	108.41
1	A	166	ASP	CA-CB-CG	-5.05	107.55	112.60
3	C	62	TRP	CE2-CD2-CE3	5.05	123.85	118.80
1	D	286	ILE	CB-CA-C	-5.05	105.33	112.14
2	B	312	HIS	CB-CG-CD2	5.04	137.76	131.20
2	B	459	SER	O-C-N	-5.04	115.88	122.59
4	E	438	ASN	CA-C-O	-5.04	113.30	120.51
1	A	223	LEU	CB-CG-CD2	5.04	125.82	110.70
1	D	128	CYS	CB-CA-C	-5.04	99.56	111.65
4	E	260	ALA	N-CA-C	5.04	116.46	111.07
4	E	439	TRP	N-CA-C	5.04	121.53	110.80
1	D	219	ILE	CA-C-O	-5.04	115.83	121.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	436	GLU	CB-CA-C	5.04	120.45	110.42
4	E	102	ALA	CB-CA-C	-5.04	102.09	110.81
2	B	38	THR	CA-C-N	5.04	131.16	121.54
2	B	38	THR	C-N-CA	5.04	131.16	121.54
3	C	197	ALA	N-CA-C	5.04	116.62	108.41
1	D	165	PRO	CA-CB-CG	-5.04	94.93	104.50
1	A	15	TYR	CA-CB-CG	-5.04	104.83	113.90
4	E	291	PHE	CA-C-O	-5.04	113.71	119.60
1	A	95	ASN	CB-CA-C	5.03	120.44	110.42
2	B	178	ASP	CA-C-N	5.03	129.23	121.53
2	B	178	ASP	C-N-CA	5.03	129.23	121.53
1	D	104	HIS	O-C-N	-5.03	116.86	122.75
4	E	127	CYS	N-CA-C	5.03	117.11	109.41
1	A	143	THR	CA-C-N	-5.03	115.72	122.86
1	A	143	THR	C-N-CA	-5.03	115.72	122.86
1	A	294	VAL	CB-CA-C	-5.03	105.45	112.04
2	B	301	VAL	N-CA-CB	5.03	118.12	110.58
4	E	1	ASN	CA-CB-CG	-5.03	107.57	112.60
4	E	233	SER	CA-C-N	5.03	127.27	120.38
4	E	233	SER	C-N-CA	5.03	127.27	120.38
2	B	206	ASP	N-CA-C	5.03	121.50	110.80
2	B	424	LEU	O-C-N	5.03	128.45	122.27
4	E	232	ILE	CB-CA-C	-5.02	104.12	112.26
2	B	134	TYR	N-CA-CB	-5.02	103.15	111.49
2	B	454	ILE	O-C-N	-5.02	116.92	121.94
3	C	475	MET	CB-CA-C	-5.02	102.40	110.74
1	D	93	TYR	CA-C-N	5.02	131.13	121.54
1	D	93	TYR	C-N-CA	5.02	131.13	121.54
4	E	71	TYR	CB-CG-CD1	-5.02	113.27	120.80
4	E	280	PRO	N-CA-C	5.02	122.82	112.47
2	B	153	THR	CA-CB-OG1	5.02	117.13	109.60
2	B	216	LYS	CB-CA-C	5.02	120.06	110.17
1	D	205	PHE	N-CA-CB	-5.02	102.67	110.55
2	B	130	ILE	CA-CB-CG1	5.02	118.93	110.40
3	C	238	LEU	CB-CA-C	5.02	120.41	110.42
4	E	298	THR	N-CA-C	5.02	121.49	110.80
1	D	113	THR	CA-C-O	5.02	127.68	120.51
1	D	81	PRO	N-CA-CB	-5.01	97.56	103.23
4	E	208	ILE	N-CA-C	5.01	115.54	106.61
3	C	183	ALA	CB-CA-C	5.01	121.06	112.44
1	D	285	VAL	CA-CB-CG1	5.01	118.92	110.40
4	E	110	TYR	CG-CD1-CE1	-5.01	113.68	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	472	ASN	N-CA-C	-5.01	107.23	113.55
1	A	244	THR	O-C-N	-5.01	116.11	122.27
2	B	227	PRO	N-CD-CG	5.01	110.71	103.20
1	D	297	ASN	CA-C-O	5.01	126.08	120.82
3	C	317	PRO	CA-C-N	5.01	130.07	122.56
3	C	317	PRO	C-N-CA	5.01	130.07	122.56
3	C	153	TYR	N-CA-CB	-5.00	103.10	110.26
1	D	256	PHE	CG-CD2-CE2	5.00	129.21	120.70
4	E	40	ILE	N-CA-C	5.00	115.78	110.72
4	E	122	ILE	N-CA-C	-5.00	101.20	108.36
2	B	447	CYS	N-CA-CB	5.00	118.95	110.49
1	D	22	VAL	CA-C-O	5.00	126.64	120.84

All (37) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1	SER	CA
1	A	209	ARG	CA
1	A	267	THR	CB
1	A	292	THR	CB
1	A	304	SER	CA
1	A	305	THR	CB
1	A	374	SER	CA
2	B	1	SER	CA
2	B	84	ASP	CA
2	B	215	ARG	CA
2	B	280	ILE	CA
2	B	307	ARG	CA
2	B	447	CYS	CA
3	C	19	LYS	CA
3	C	48	THR	CA
3	C	129	SER	CA
3	C	180	ASP	CA
3	C	195	LYS	CA
3	C	236	CYS	CA
1	D	45	GLU	CA
1	D	99	ASP	CA
1	D	130	ILE	CB
1	D	136	PRO	CA
1	D	408	HIS	CA
1	D	431	ILE	CA
4	E	26	HIS	CA

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Mol	Chain	Res	Type	Atom
4	E	29	ASP	CA
4	E	68	THR	CB,CA
4	E	74	ILE	CB
4	E	93	ASN	CA
4	E	106	ASN	CA
4	E	118	LEU	CA
4	E	130	ALA	CA
4	E	161	ALA	CA
4	E	173	ASP	CA
4	E	260	ALA	CA

All (585) 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	112	TYR	Mainchain
1	A	113	THR	Mainchain
1	A	115	LYS	Mainchain
1	A	128	CYS	Mainchain
1	A	129	GLU	Mainchain
1	A	132	VAL	Mainchain
1	A	133	THR	Mainchain
1	A	135	PHE	Peptide,Mainchain
1	A	136	PRO	Mainchain
1	A	137	PHE	Mainchain
1	A	138	ASP	Mainchain
1	A	147	GLY	Mainchain
1	A	150	THR	Mainchain
1	A	151	TYR	Mainchain
1	A	152	ASP	Mainchain
1	A	16	ASN	Mainchain
1	A	161	GLU	Peptide,Mainchain
1	A	162	SER	Peptide,Mainchain
1	A	167	LEU	Mainchain
1	A	170	PHE	Mainchain
1	A	174	GLY	Mainchain
1	A	175	GLU	Mainchain
1	A	187	TRP	Mainchain
1	A	193	CYS	Mainchain
1	A	195	ASP	Mainchain

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Mol	Chain	Res	Type	Group
1	A	199	LEU	Mainchain
1	A	207	MET	Mainchain
1	A	208	GLN	Mainchain
1	A	209	ARG	Peptide,Mainchain
1	A	210	ILE	Mainchain
1	A	211	PRO	Mainchain
1	A	215	VAL	Mainchain
1	A	217	ASN	Mainchain
1	A	221	PRO	Mainchain
1	A	222	CYS	Mainchain
1	A	223	LEU	Mainchain
1	A	228	LEU	Mainchain
1	A	231	LEU	Mainchain
1	A	235	LEU	Mainchain
1	A	236	PRO	Mainchain
1	A	238	ASP	Peptide,Mainchain
1	A	24	HIS	Mainchain
1	A	240	GLY	Mainchain
1	A	241	GLU	Mainchain
1	A	246	SER	Mainchain
1	A	248	SER	Mainchain
1	A	25	HIS	Mainchain
1	A	251	LEU	Mainchain
1	A	253	LEU	Mainchain
1	A	255	VAL	Mainchain
1	A	260	ILE	Mainchain
1	A	261	VAL	Mainchain
1	A	264	ILE	Mainchain
1	A	265	PRO	Mainchain
1	A	266	SER	Mainchain
1	A	267	THR	Mainchain
1	A	272	PRO	Mainchain
1	A	273	LEU	Mainchain
1	A	276	LYS	Mainchain
1	A	28	PHE	Mainchain
1	A	281	THR	Mainchain
1	A	286	ILE	Mainchain
1	A	289	ILE	Mainchain
1	A	293	VAL	Mainchain
1	A	296	ILE	Mainchain
1	A	3	HIS	Peptide
1	A	300	HIS	Mainchain

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Mol	Chain	Res	Type	Group
1	A	301	ARG	Mainchain
1	A	302	SER	Mainchain
1	A	303	PRO	Peptide,Mainchain
1	A	304	SER	Peptide,Mainchain
1	A	305	THR	Mainchain
1	A	374	SER	Peptide,Mainchain
1	A	375	ALA	Peptide,Mainchain
1	A	378	GLY	Mainchain
1	A	38	ILE	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	419	ILE	Peptide
1	A	422	THR	Mainchain
1	A	426	PHE	Mainchain
1	A	431	ILE	Mainchain
1	A	435	GLN	Mainchain
1	A	44	ASP	Mainchain
1	A	47	ASN	Mainchain
1	A	48	GLN	Mainchain
1	A	61	ILE	Mainchain
1	A	66	ARG	Mainchain
1	A	67	TRP	Mainchain
1	A	73	GLY	Mainchain
1	A	74	GLY	Mainchain
1	A	77	LYS	Mainchain
1	A	84	ASP	Mainchain
1	A	85	VAL	Mainchain
1	A	94	ASN	Mainchain
1	A	95	ASN	Mainchain
1	A	97	ASP	Peptide,Mainchain
2	B	1	SER	Mainchain
2	B	106	VAL	Mainchain
2	B	107	ASN	Mainchain
2	B	113	THR	Mainchain
2	B	117	SER	Mainchain
2	B	119	HIS	Mainchain

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Mol	Chain	Res	Type	Group
2	B	12	PHE	Mainchain
2	B	130	ILE	Mainchain
2	B	131	LYS	Mainchain
2	B	139	TRP	Mainchain
2	B	14	ASN	Mainchain
2	B	140	GLN	Mainchain
2	B	141	ASN	Mainchain
2	B	143	THR	Mainchain
2	B	147	LYS	Mainchain
2	B	148	SER	Mainchain
2	B	15	TYR	Mainchain
2	B	151	TYR	Mainchain
2	B	152	ASP	Mainchain
2	B	155	GLU	Mainchain
2	B	160	HIS	Mainchain
2	B	174	MET	Mainchain
2	B	175	ILE	Mainchain
2	B	177	GLN	Mainchain
2	B	182	GLU	Mainchain
2	B	184	GLY	Peptide
2	B	186	TRP	Mainchain
2	B	188	ILE	Mainchain
2	B	191	LYS	Mainchain
2	B	199	SER	Mainchain
2	B	202	PRO	Mainchain
2	B	204	TYR	Mainchain
2	B	205	GLU	Mainchain
2	B	210	TYR	Mainchain
2	B	211	LEU	Mainchain
2	B	214	GLN	Mainchain
2	B	216	LYS	Mainchain
2	B	218	LEU	Mainchain
2	B	222	VAL	Mainchain
2	B	224	THR	Mainchain
2	B	226	VAL	Mainchain
2	B	227	PRO	Mainchain
2	B	230	LEU	Mainchain
2	B	231	ILE	Mainchain
2	B	24	THR	Mainchain
2	B	242	PRO	Mainchain
2	B	243	PRO	Mainchain
2	B	244	ASP	Mainchain

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Mol	Chain	Res	Type	Group
2	B	247	GLU	Mainchain
2	B	250	SER	Mainchain
2	B	254	SER	Mainchain
2	B	26	GLY	Peptide
2	B	262	PHE	Mainchain
2	B	269	LYS	Mainchain
2	B	272	GLU	Mainchain
2	B	274	SER	Mainchain
2	B	275	LEU	Mainchain
2	B	276	SER	Peptide
2	B	278	PRO	Mainchain
2	B	279	ILE	Peptide
2	B	280	ILE	Mainchain
2	B	281	ILE	Mainchain
2	B	282	SER	Mainchain
2	B	283	TYR	Peptide,Mainchain
2	B	29	VAL	Mainchain
2	B	294	SER	Mainchain
2	B	297	LEU	Mainchain
2	B	298	SER	Mainchain
2	B	302	LEU	Mainchain
2	B	303	ASN	Mainchain
2	B	306	HIS	Peptide,Mainchain
2	B	311	THR	Peptide,Mainchain
2	B	36	THR	Mainchain
2	B	38	THR	Mainchain
2	B	4	GLU	Mainchain
2	B	405	VAL	Mainchain
2	B	407	ALA	Mainchain
2	B	410	TYR	Mainchain
2	B	412	ALA	Mainchain
2	B	414	GLN	Mainchain
2	B	429	GLN	Mainchain
2	B	430	TYR	Mainchain
2	B	433	MET	Mainchain
2	B	435	ALA	Mainchain
2	B	439	PHE	Mainchain
2	B	440	LEU	Mainchain
2	B	441	TYR	Mainchain
2	B	443	PHE	Mainchain
2	B	445	THR	Mainchain
2	B	446	MET	Mainchain

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Mol	Chain	Res	Type	Group
2	B	447	CYS	Mainchain
2	B	455	PHE	Mainchain
2	B	456	LEU	Mainchain
2	B	461	ASN	Mainchain
2	B	463	PRO	Mainchain
2	B	48	GLU	Mainchain
2	B	56	LEU	Mainchain
2	B	81	PRO	Mainchain
2	B	83	ASP	Mainchain
2	B	84	ASP	Mainchain
2	B	85	VAL	Peptide
2	B	87	GLN	Mainchain
2	B	88	PRO	Mainchain
2	B	92	LEU	Mainchain
2	B	94	ASN	Peptide
2	B	95	ASN	Mainchain
2	B	97	ASP	Peptide,Mainchain
2	B	99	SER	Mainchain
3	C	1	VAL	Peptide
3	C	10	ASP	Mainchain
3	C	105	ALA	Mainchain
3	C	106	TYR	Mainchain
3	C	108	CYS	Mainchain
3	C	11	LEU	Mainchain
3	C	112	VAL	Mainchain
3	C	113	ARG	Mainchain
3	C	118	VAL	Mainchain
3	C	13	ILE	Mainchain
3	C	130	CYS	Mainchain
3	C	133	ASN	Mainchain
3	C	134	VAL	Mainchain
3	C	135	LEU	Mainchain
3	C	152	ASN	Mainchain
3	C	161	ASP	Mainchain
3	C	178	ILE	Mainchain
3	C	179	ILE	Peptide
3	C	18	ASN	Mainchain
3	C	180	ASP	Mainchain
3	C	181	PRO	Mainchain
3	C	182	GLU	Mainchain
3	C	183	ALA	Mainchain
3	C	187	ASN	Peptide

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Mol	Chain	Res	Type	Group
3	C	189	GLU	Mainchain
3	C	193	ILE	Mainchain
3	C	194	HIS	Peptide,Mainchain
3	C	202	TYR	Mainchain
3	C	203	GLY	Mainchain
3	C	204	ASP	Mainchain
3	C	208	ASN	Peptide,Mainchain
3	C	209	GLY	Mainchain
3	C	21	VAL	Mainchain
3	C	211	ASN	Mainchain
3	C	212	TYR	Mainchain
3	C	22	ARG	Mainchain
3	C	222	ARG	Mainchain
3	C	223	ARG	Mainchain
3	C	224	LYS	Mainchain
3	C	225	PRO	Mainchain
3	C	226	LEU	Mainchain
3	C	234	THR	Mainchain
3	C	236	CYS	Mainchain
3	C	237	VAL	Mainchain
3	C	239	ILE	Mainchain
3	C	240	SER	Mainchain
3	C	243	ALA	Mainchain
3	C	244	ALA	Mainchain
3	C	245	LEU	Mainchain
3	C	248	TYR	Mainchain
3	C	249	LEU	Mainchain
3	C	252	GLU	Mainchain
3	C	256	LYS	Peptide
3	C	263	VAL	Mainchain
3	C	266	ALA	Mainchain
3	C	267	GLN	Mainchain
3	C	268	ALA	Mainchain
3	C	27	ASN	Mainchain
3	C	271	LEU	Mainchain
3	C	272	LEU	Mainchain
3	C	273	LEU	Mainchain
3	C	274	THR	Mainchain
3	C	276	GLN	Mainchain
3	C	281	THR	Mainchain
3	C	282	ALA	Mainchain
3	C	283	LEU	Mainchain

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Mol	Chain	Res	Type	Group
3	C	284	ALA	Peptide,Mainchain
3	C	285	VAL	Mainchain
3	C	287	LEU	Mainchain
3	C	29	GLU	Peptide,Mainchain
3	C	290	LYS	Mainchain
3	C	291	TYR	Mainchain
3	C	3	GLU	Mainchain
3	C	30	VAL	Mainchain
3	C	304	VAL	Mainchain
3	C	305	ASN	Mainchain
3	C	310	LEU	Mainchain
3	C	318	SER	Mainchain
3	C	319	THR	Mainchain
3	C	41	ASN	Mainchain
3	C	421	SER	Mainchain
3	C	422	GLY	Peptide
3	C	423	ILE	Mainchain
3	C	425	SER	Mainchain
3	C	426	THR	Mainchain
3	C	427	ASN	Mainchain
3	C	431	LYS	Mainchain
3	C	435	GLU	Mainchain
3	C	440	ASP	Mainchain
3	C	443	VAL	Mainchain
3	C	445	ASN	Mainchain
3	C	451	GLN	Mainchain
3	C	454	ASP	Mainchain
3	C	46	LYS	Mainchain
3	C	463	PRO	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	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

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Mol	Chain	Res	Type	Group
3	C	68	THR	Mainchain
3	C	74	TYR	Mainchain
3	C	78	SER	Mainchain
3	C	8	ILE	Mainchain
3	C	84	PRO	Mainchain
3	C	85	GLU	Mainchain
3	C	87	ILE	Mainchain
3	C	9	ASN	Mainchain
3	C	90	PRO	Mainchain
3	C	94	LEU	Mainchain
3	C	95	GLN	Mainchain
3	C	98	ASN	Peptide,Mainchain
1	D	1	SER	Mainchain
1	D	100	PHE	Mainchain
1	D	101	ALA	Peptide,Mainchain
1	D	105	MET	Mainchain
1	D	106	THR	Mainchain
1	D	111	ASP	Mainchain
1	D	113	THR	Peptide
1	D	114	GLY	Mainchain
1	D	128	CYS	Mainchain
1	D	129	GLU	Mainchain
1	D	132	VAL	Mainchain
1	D	136	PRO	Mainchain
1	D	137	PHE	Mainchain
1	D	138	ASP	Mainchain
1	D	150	THR	Mainchain
1	D	156	VAL	Mainchain
1	D	157	SER	Mainchain
1	D	16	ASN	Mainchain
1	D	160	PRO	Mainchain
1	D	161	GLU	Peptide
1	D	162	SER	Peptide,Mainchain
1	D	163	ASP	Mainchain
1	D	166	ASP	Mainchain
1	D	169	THR	Mainchain
1	D	17	LYS	Mainchain
1	D	172	GLU	Mainchain
1	D	173	SER	Peptide
1	D	175	GLU	Peptide,Mainchain
1	D	176	TRP	Mainchain
1	D	18	VAL	Mainchain

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Mol	Chain	Res	Type	Group
1	D	181	TYR	Mainchain
1	D	194	PRO	Mainchain
1	D	195	ASP	Mainchain
1	D	197	PRO	Peptide,Mainchain
1	D	20	ARG	Mainchain
1	D	202	THR	Mainchain
1	D	21	PRO	Mainchain
1	D	211	PRO	Mainchain
1	D	213	TYR	Mainchain
1	D	216	VAL	Mainchain
1	D	219	ILE	Mainchain
1	D	221	PRO	Mainchain
1	D	228	LEU	Mainchain
1	D	232	VAL	Mainchain
1	D	238	ASP	Peptide,Mainchain
1	D	24	HIS	Mainchain
1	D	242	LYS	Mainchain
1	D	244	THR	Mainchain
1	D	246	SER	Mainchain
1	D	247	ILE	Mainchain
1	D	248	SER	Mainchain
1	D	25	HIS	Mainchain
1	D	251	LEU	Mainchain
1	D	254	THR	Mainchain
1	D	255	VAL	Mainchain
1	D	260	ILE	Mainchain
1	D	261	VAL	Mainchain
1	D	263	LEU	Mainchain
1	D	264	ILE	Mainchain
1	D	265	PRO	Mainchain
1	D	268	SER	Mainchain
1	D	269	SER	Mainchain
1	D	27	HIS	Mainchain
1	D	275	GLY	Mainchain
1	D	277	TYR	Mainchain
1	D	28	PHE	Mainchain
1	D	284	PHE	Mainchain
1	D	29	VAL	Mainchain
1	D	303	PRO	Mainchain
1	D	304	SER	Mainchain
1	D	305	THR	Mainchain
1	D	32	THR	Mainchain

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Mol	Chain	Res	Type	Group
1	D	33	VAL	Mainchain
1	D	34	GLY	Peptide,Mainchain
1	D	375	ALA	Mainchain
1	D	376	ILE	Mainchain
1	D	385	HIS	Mainchain
1	D	386	MET	Mainchain
1	D	390	GLU	Mainchain
1	D	395	ALA	Mainchain
1	D	396	ALA	Mainchain
1	D	399	TRP	Mainchain
1	D	400	LYS	Mainchain
1	D	402	VAL	Mainchain
1	D	408	HIS	Mainchain
1	D	410	LEU	Mainchain
1	D	414	PHE	Mainchain
1	D	416	LEU	Mainchain
1	D	418	CYS	Mainchain
1	D	422	THR	Peptide
1	D	423	VAL	Mainchain
1	D	428	GLY	Mainchain
1	D	429	ARG	Mainchain
1	D	431	ILE	Mainchain
1	D	44	ASP	Peptide
1	D	46	VAL	Mainchain
1	D	52	THR	Mainchain
1	D	57	ARG	Mainchain
1	D	61	ILE	Mainchain
1	D	63	VAL	Mainchain
1	D	65	LEU	Mainchain
1	D	66	ARG	Mainchain
1	D	68	ASN	Mainchain
1	D	70	ALA	Mainchain
1	D	73	GLY	Mainchain
1	D	74	GLY	Mainchain
1	D	76	LYS	Mainchain
1	D	77	LYS	Mainchain
1	D	79	ARG	Mainchain
1	D	80	LEU	Mainchain
1	D	81	PRO	Mainchain
1	D	82	SER	Mainchain
1	D	83	ASP	Mainchain
1	D	84	ASP	Mainchain

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Mol	Chain	Res	Type	Group
1	D	86	TRP	Mainchain
1	D	92	LEU	Mainchain
1	D	97	ASP	Peptide
1	D	98	GLY	Peptide,Mainchain
4	E	10	LEU	Mainchain
4	E	100	GLU	Mainchain
4	E	101	VAL	Mainchain
4	E	105	ALA	Peptide,Mainchain
4	E	107	VAL	Mainchain
4	E	109	VAL	Peptide
4	E	110	TYR	Peptide
4	E	112	ASP	Mainchain
4	E	118	LEU	Peptide
4	E	127	CYS	Mainchain
4	E	128	PRO	Mainchain
4	E	129	ILE	Mainchain
4	E	131	VAL	Mainchain
4	E	132	THR	Peptide
4	E	137	ASP	Mainchain
4	E	139	GLN	Mainchain
4	E	153	HIS	Mainchain
4	E	159	LEU	Peptide,Mainchain
4	E	160	SER	Peptide
4	E	163	GLU	Mainchain
4	E	17	ARG	Mainchain
4	E	172	ILE	Peptide
4	E	180	ASN	Peptide,Mainchain
4	E	181	GLY	Peptide
4	E	182	GLU	Mainchain
4	E	184	THR	Mainchain
4	E	187	HIS	Mainchain
4	E	189	PRO	Mainchain
4	E	190	ALA	Mainchain
4	E	195	ASN	Mainchain
4	E	196	TRP	Mainchain
4	E	198	LEU	Mainchain
4	E	204	ASP	Mainchain
4	E	215	GLN	Mainchain
4	E	217	LYS	Mainchain
4	E	22	LYS	Mainchain
4	E	221	TYR	Mainchain
4	E	223	ILE	Peptide

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Mol	Chain	Res	Type	Group
4	E	224	ASN	Mainchain
4	E	225	ILE	Mainchain
4	E	226	ILE	Mainchain
4	E	227	ALA	Mainchain
4	E	229	CYS	Mainchain
4	E	232	ILE	Mainchain
4	E	233	SER	Mainchain
4	E	235	LEU	Mainchain
4	E	236	VAL	Mainchain
4	E	237	VAL	Mainchain
4	E	238	LEU	Mainchain
4	E	24	LEU	Mainchain
4	E	250	LYS	Mainchain
4	E	252	THR	Peptide
4	E	255	ILE	Mainchain
4	E	256	SER	Mainchain
4	E	257	VAL	Mainchain
4	E	26	HIS	Mainchain
4	E	260	ALA	Mainchain
4	E	264	PHE	Mainchain
4	E	266	PHE	Mainchain
4	E	267	LEU	Mainchain
4	E	271	LYS	Mainchain
4	E	277	LEU	Mainchain
4	E	278	ASN	Mainchain
4	E	280	PRO	Mainchain
4	E	281	LEU	Mainchain
4	E	289	VAL	Mainchain
4	E	297	VAL	Mainchain
4	E	302	ILE	Mainchain
4	E	304	LEU	Mainchain
4	E	307	SER	Mainchain
4	E	309	ARG	Peptide
4	E	310	THR	Mainchain
4	E	416	VAL	Mainchain
4	E	418	ALA	Mainchain
4	E	422	ILE	Mainchain
4	E	425	SER	Mainchain
4	E	426	THR	Mainchain
4	E	427	LYS	Mainchain
4	E	430	ASN	Mainchain
4	E	441	LEU	Mainchain

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Mol	Chain	Res	Type	Group
4	E	442	ILE	Mainchain
4	E	444	LYS	Mainchain
4	E	460	LEU	Mainchain
4	E	465	ILE	Mainchain
4	E	47	GLU	Mainchain
4	E	5	ARG	Mainchain
4	E	61	ASP	Mainchain
4	E	63	ARG	Mainchain
4	E	65	SER	Mainchain
4	E	69	SER	Mainchain
4	E	70	GLU	Mainchain
4	E	73	GLY	Mainchain
4	E	76	LEU	Mainchain
4	E	79	ILE	Peptide,Mainchain
4	E	81	SER	Mainchain
4	E	83	LEU	Mainchain
4	E	84	LEU	Mainchain
4	E	85	TRP	Mainchain
4	E	88	ASP	Mainchain
4	E	92	GLU	Peptide
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	920	0
1	D	2991	0	3006	869	0
2	B	2972	0	2953	859	0
3	C	2983	0	2987	872	0
4	E	2987	0	2994	977	0
All	All	14924	0	14946	4300	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 144.

All (4300) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:MET:CE	1:A:282:MET:SD	2.01	1.46
1:D:86:TRP:CD2	1:D:86:TRP:O	1.71	1.40
2:B:306:HIS:O	2:B:306:HIS:ND1	1.62	1.29
1:A:113:THR:CG2	1:A:113:THR:O	1.76	1.28
1:A:236:PRO:HB3	1:A:299:HIS:CE1	1.69	1.27
2:B:104:LEU:HD12	2:B:118:TRP:CH2	1.71	1.24
1:D:72:TYR:CD1	1:D:72:TYR:C	2.17	1.20
3:C:68:THR:HA	3:C:115:ASN:HA	1.22	1.20
3:C:67:LEU:HB3	3:C:116:GLY:CA	1.71	1.19
2:B:87:GLN:HB3	2:B:104:LEU:HD11	1.20	1.18
2:B:31:VAL:HG21	2:B:86:TRP:CZ3	1.77	1.18
3:C:148:PHE:HB2	3:C:215:VAL:CG2	1.73	1.18
2:B:46:LYS:HA	2:B:278:PRO:HD2	1.18	1.17
3:C:67:LEU:CB	3:C:116:GLY:HA2	1.73	1.17
1:D:29:VAL:HG23	1:D:60:TRP:CD1	1.79	1.17
1:D:86:TRP:O	1:D:86:TRP:CG	1.94	1.17
1:A:72:TYR:HB2	1:A:112:TYR:CD2	1.78	1.17
1:A:145:LYS:HG3	1:A:202:THR:HG22	1.26	1.17
4:E:45:LYS:CA	4:E:280:PRO:HA	1.75	1.17
2:B:9:SER:HA	2:B:12:PHE:CE1	1.80	1.17
2:B:132:VAL:HG13	2:B:279:ILE:HA	1.17	1.16
4:E:255:ILE:HD11	4:E:304:LEU:CD2	1.74	1.16
1:D:62:ASP:HB3	1:D:65:LEU:HD13	1.17	1.16
2:B:37:LEU:CA	2:B:54:VAL:HG12	1.73	1.16
4:E:172:ILE:HD12	4:E:188:ARG:HB3	1.22	1.16
4:E:284:LYS:N	4:E:284:LYS:HE3	1.60	1.16
3:C:463:PRO:HA	3:C:466:VAL:HG23	1.24	1.16
3:C:138:PRO:HG3	3:C:288:ILE:HD11	1.19	1.16
3:C:242:LEU:HD22	3:C:267:GLN:HB3	1.19	1.15
2:B:247:GLU:C	2:B:249:MET:HG3	1.72	1.15
1:A:167:LEU:HD12	1:A:178:MET:HB2	1.26	1.15
1:D:305:THR:HG22	1:D:400:LYS:HB3	1.23	1.15
4:E:138:TRP:HB2	4:E:213:ILE:CG1	1.75	1.14
2:B:176:ASN:HB2	2:B:191:LYS:HB3	1.29	1.14
2:B:248:LYS:CD	2:B:252:SER:HB3	1.78	1.14
3:C:50:GLU:HA	3:C:132:ILE:HD13	1.25	1.13
2:B:191:LYS:O	2:B:191:LYS:CG	1.95	1.13
1:D:32:THR:HB	1:D:59:GLN:HB3	1.30	1.13
1:D:145:LYS:CG	1:D:202:THR:HG23	1.77	1.13
1:D:198:TYR:N	1:D:198:TYR:HD1	1.44	1.13
2:B:56:LEU:HD22	2:B:120:PRO:CG	1.78	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:44:GLU:HB3	4:E:280:PRO:CG	1.79	1.13
1:A:380:LYS:HB3	2:B:408:ILE:HD13	1.24	1.13
4:E:246:ALA:HB1	4:E:250:LYS:HG3	1.23	1.13
2:B:46:LYS:HE2	2:B:278:PRO:HG3	1.20	1.12
1:D:38:ILE:HA	1:D:169:THR:HG21	1.22	1.12
2:B:133:MET:HG2	2:B:140:GLN:HG3	1.24	1.12
3:C:278:LEU:C	3:C:278:LEU:HD12	1.73	1.12
4:E:89:VAL:HG23	4:E:99:PHE:CZ	1.84	1.11
2:B:56:LEU:CD1	2:B:56:LEU:N	2.10	1.11
1:D:48:GLN:HB3	1:D:130:ILE:HD12	1.31	1.11
4:E:66:TRP:NE1	4:E:111:ASN:HA	1.65	1.11
1:A:113:THR:O	1:A:113:THR:HG22	1.31	1.11
2:B:92:LEU:H	2:B:96:ASN:HB2	1.13	1.11
4:E:71:TYR:HA	4:E:111:ASN:HB2	1.25	1.11
1:A:66:ARG:HA	1:A:113:THR:HA	1.24	1.10
1:D:92:LEU:HB3	1:D:95:ASN:HB2	1.29	1.10
2:B:3:MET:HE3	2:B:69:PRO:HG3	1.24	1.10
1:A:65:LEU:HB3	1:A:110:LEU:HD11	1.24	1.10
2:B:56:LEU:N	2:B:56:LEU:HD13	1.59	1.10
1:A:20:ARG:HG2	1:A:20:ARG:HH11	1.15	1.09
1:D:145:LYS:HG3	1:D:202:THR:CG2	1.81	1.09
1:D:61:ILE:HA	1:D:116:ILE:HD11	1.31	1.09
1:D:131:ILE:HG13	1:D:133:THR:H	1.03	1.09
1:A:2:GLU:CD	1:A:74:GLY:HA2	1.76	1.09
2:B:48:GLU:HA	2:B:130:ILE:HD11	1.23	1.09
4:E:44:GLU:HB3	4:E:280:PRO:HG3	1.29	1.09
4:E:255:ILE:HD11	4:E:304:LEU:HD22	1.12	1.09
2:B:308:SER:CB	2:B:311:THR:HG22	1.83	1.09
2:B:186:TRP:HB3	2:B:215:ARG:HG3	1.30	1.08
2:B:311:THR:HB	2:B:430:TYR:HD2	1.17	1.08
1:A:38:ILE:HD11	1:A:55:ARG:CG	1.83	1.08
2:B:186:TRP:HB2	2:B:215:ARG:HB2	1.21	1.08
2:B:241:LEU:HD21	2:B:251:LEU:HD11	1.13	1.08
3:C:31:VAL:O	3:C:31:VAL:HG13	1.47	1.08
2:B:23:GLN:HE21	2:B:23:GLN:N	1.52	1.08
1:A:133:THR:HA	1:A:274:ILE:CG2	1.82	1.08
2:B:131:LYS:HD3	2:B:132:VAL:H	1.03	1.08
1:D:20:ARG:HG2	1:D:20:ARG:HH11	1.19	1.08
1:D:48:GLN:HB3	1:D:130:ILE:CD1	1.83	1.08
4:E:44:GLU:CD	4:E:129:ILE:HB	1.77	1.08
4:E:45:LYS:HA	4:E:280:PRO:HA	1.27	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:302:SER:HB3	1:D:400:LYS:CG	1.84	1.07
1:D:305:THR:HB	1:D:401:TYR:HD2	1.12	1.07
4:E:136:PHE:CZ	4:E:217:LYS:HD2	1.88	1.07
4:E:189:PRO:HD2	4:E:211:PHE:HB2	1.21	1.07
1:A:97:ASP:HB2	1:A:127:TYR:HB2	1.35	1.07
1:A:380:LYS:CB	2:B:408:ILE:HD13	1.84	1.07
2:B:56:LEU:HD22	2:B:120:PRO:HG2	1.20	1.07
1:D:28:PHE:HD2	1:D:157:SER:HB3	1.17	1.07
1:D:377:GLU:HG3	4:E:415:CYS:HB2	1.14	1.07
1:A:2:GLU:O	1:A:2:GLU:HG2	1.49	1.07
1:A:130:ILE:HD13	1:A:131:ILE:H	1.19	1.07
2:B:308:SER:HB2	2:B:311:THR:HG22	1.07	1.07
4:E:94:ASN:HB3	4:E:125:SER:HB3	1.34	1.07
1:D:35:LEU:HD11	1:D:54:VAL:HG11	1.35	1.07
3:C:59:ASP:HA	3:C:121:LEU:HB3	1.37	1.06
3:C:115:ASN:CG	3:C:115:ASN:O	1.94	1.06
2:B:37:LEU:HA	2:B:54:VAL:CG1	1.83	1.06
2:B:241:LEU:HG	2:B:248:LYS:HE2	1.25	1.06
3:C:445:ASN:HA	3:C:448:LEU:HG	1.37	1.06
4:E:75:ASP:HA	4:E:111:ASN:HD22	1.12	1.06
1:A:38:ILE:CD1	1:A:55:ARG:HG3	1.84	1.06
2:B:248:LYS:HD3	2:B:252:SER:HB3	1.10	1.06
3:C:93:VAL:HG11	3:C:151:LEU:HD13	1.06	1.06
4:E:279:VAL:HB	4:E:280:PRO:HD2	1.13	1.06
4:E:211:PHE:C	4:E:212:LEU:HD12	1.81	1.06
1:A:133:THR:HA	1:A:274:ILE:HG22	1.08	1.05
2:B:153:THR:HB	2:B:204:TYR:HB2	1.31	1.05
4:E:19:LYS:HZ3	4:E:154:GLU:HB3	1.19	1.05
4:E:90:VAL:HG22	4:E:95:VAL:CG1	1.86	1.05
2:B:23:GLN:NE2	2:B:23:GLN:H	1.55	1.05
3:C:122:PRO:CB	3:C:123:PRO:HD2	1.82	1.05
1:D:7:LEU:HD21	1:D:70:ALA:HB1	1.36	1.05
1:D:220:ILE:HG21	4:E:294:LEU:HD11	1.33	1.05
4:E:19:LYS:NZ	4:E:154:GLU:HB3	1.70	1.05
4:E:36:LEU:CD2	4:E:51:THR:HG21	1.87	1.05
4:E:235:LEU:HD12	4:E:235:LEU:O	1.55	1.05
2:B:236:ILE:HB	2:B:446:MET:HE1	1.37	1.05
4:E:56:GLU:HA	4:E:118:LEU:HB2	1.38	1.05
4:E:235:LEU:HD12	4:E:235:LEU:C	1.82	1.05
1:A:148:ILE:HG21	1:A:198:TYR:HB2	1.33	1.04
2:B:130:ILE:HB	2:B:134:TYR:CD2	1.92	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:449:VAL:HG12	3:C:452:THR:HB	1.36	1.04
1:D:166:ASP:CG	1:D:178:MET:HE2	1.81	1.04
1:D:233:PHE:CZ	1:D:417:ILE:HD12	1.90	1.04
4:E:219:LEU:HB3	4:E:222:ILE:HB	1.37	1.04
4:E:236:VAL:HA	4:E:239:VAL:HG23	1.34	1.04
4:E:129:ILE:HG22	4:E:133:TYR:CD2	1.90	1.04
3:C:180:ASP:HB3	3:C:181:PRO:HD3	1.35	1.04
1:A:277:TYR:HA	1:A:280:PHE:CZ	1.93	1.04
2:B:220:TYR:HB3	2:B:223:TYR:CE2	1.90	1.04
1:D:106:THR:HG22	1:D:107:LYS:H	1.16	1.04
1:A:379:VAL:HG13	4:E:424:LYS:HE2	1.39	1.04
4:E:55:ILE:C	4:E:118:LEU:HD13	1.83	1.04
4:E:66:TRP:HE1	4:E:111:ASN:HA	1.21	1.04
4:E:36:LEU:HD23	4:E:51:THR:HG21	1.40	1.03
1:A:64:ARG:HA	1:A:66:ARG:NH1	1.71	1.03
1:A:380:LYS:HB3	2:B:408:ILE:CD1	1.88	1.03
2:B:134:TYR:CE1	2:B:213:ILE:HG13	1.92	1.03
4:E:91:LEU:CD1	4:E:145:PHE:HB3	1.87	1.03
4:E:183:TRP:CB	4:E:216:ARG:HG2	1.88	1.03
1:A:16:ASN:HB2	1:A:19:ILE:HD12	1.36	1.03
2:B:56:LEU:HD13	2:B:56:LEU:H	0.93	1.03
4:E:185:ILE:HG12	4:E:214:ILE:HG22	1.40	1.03
2:B:306:HIS:HD1	2:B:306:HIS:C	1.65	1.03
1:A:57:ARG:HA	1:A:119:THR:HG22	1.05	1.03
1:A:66:ARG:HA	1:A:113:THR:CA	1.87	1.03
1:D:91:VAL:HG22	1:D:96:ALA:HB2	1.38	1.03
1:D:224:LEU:HD21	4:E:297:VAL:HG11	1.36	1.03
3:C:149:THR:HG21	3:C:214:ASP:HB3	1.38	1.02
4:E:47:GLU:HB3	4:E:129:ILE:HG12	1.39	1.02
4:E:91:LEU:HD13	4:E:145:PHE:HB3	1.04	1.02
4:E:279:VAL:CB	4:E:280:PRO:HD2	1.89	1.02
1:D:129:GLU:OE1	1:D:129:GLU:HA	1.20	1.02
2:B:75:ILE:CD1	2:B:78:LEU:HD13	1.90	1.02
3:C:12:LEU:HB2	3:C:16:LYS:HG2	1.38	1.02
2:B:243:PRO:HB3	2:B:435:ALA:HB1	1.04	1.02
1:D:57:ARG:O	1:D:57:ARG:HG2	1.53	1.02
1:D:302:SER:HB3	1:D:400:LYS:HG2	1.02	1.02
4:E:34:LEU:HD12	4:E:210:PHE:CE2	1.95	1.02
4:E:185:ILE:HG12	4:E:214:ILE:CG2	1.89	1.02
1:A:67:TRP:CD1	1:A:112:TYR:HA	1.93	1.02
2:B:263:LEU:HD22	2:B:291:VAL:HG22	1.36	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:60:HIS:HB3	3:C:62:TRP:HZ3	1.25	1.02
1:D:305:THR:CG2	1:D:400:LYS:HB3	1.90	1.02
2:B:185:GLN:HB3	2:B:219:PHE:HE2	1.20	1.01
3:C:309:VAL:O	3:C:313:HIS:HB3	1.60	1.01
1:D:56:LEU:HG	1:D:120:PRO:HG2	1.38	1.01
4:E:90:VAL:CG2	4:E:95:VAL:HG11	1.90	1.01
1:A:171:MET:HE3	1:A:176:TRP:CH2	1.95	1.01
4:E:305:ASN:HA	4:E:308:LEU:HD12	1.42	1.01
1:A:133:THR:O	1:A:133:THR:HG22	1.56	1.01
3:C:113:ARG:HD2	3:C:117:TYR:HB3	1.41	1.01
3:C:159:SER:HA	3:C:213:GLN:HG3	1.36	1.01
1:A:17:LYS:HE3	1:A:84:ASP:HA	1.39	1.00
2:B:46:LYS:HB2	2:B:277:VAL:N	1.74	1.00
1:D:43:VAL:HG22	1:D:50:VAL:HA	1.37	1.00
1:D:65:LEU:HD23	1:D:110:LEU:HD13	1.42	1.00
2:B:68:ASP:HB3	2:B:69:PRO:CD	1.89	1.00
2:B:243:PRO:CB	2:B:435:ALA:HB1	1.90	1.00
3:C:243:ALA:CB	3:C:302:VAL:HG12	1.90	1.00
1:A:238:ASP:HB3	2:B:306:HIS:NE2	1.76	1.00
1:A:380:LYS:HD3	2:B:408:ILE:CB	1.91	1.00
2:B:242:PRO:HG2	2:B:243:PRO:HD3	1.41	1.00
1:D:92:LEU:CB	1:D:95:ASN:HB2	1.90	1.00
1:D:129:GLU:OE1	1:D:129:GLU:CA	2.06	1.00
4:E:138:TRP:CZ2	4:E:215:GLN:HB2	1.97	1.00
2:B:176:ASN:CB	2:B:191:LYS:HB3	1.91	1.00
3:C:50:GLU:CA	3:C:132:ILE:HD13	1.92	1.00
2:B:75:ILE:O	2:B:75:ILE:HG13	1.56	1.00
4:E:240:TYR:CD2	4:E:453:ILE:HD13	1.96	1.00
1:D:252:SER:HB2	4:E:259:LEU:HD13	1.39	1.00
4:E:47:GLU:HA	4:E:129:ILE:HD11	1.41	1.00
4:E:91:LEU:HD13	4:E:145:PHE:CB	1.92	1.00
1:D:253:LEU:HD23	1:D:254:THR:N	1.77	0.99
4:E:39:LEU:HD23	4:E:183:TRP:HZ2	1.28	0.99
1:A:41:ILE:HD11	1:A:51:GLU:CD	1.88	0.99
2:B:405:VAL:HG12	2:B:409:LYS:HZ3	1.25	0.99
1:D:377:GLU:HG3	4:E:415:CYS:CB	1.92	0.99
4:E:250:LYS:HB3	4:E:253:LEU:HD23	1.43	0.99
2:B:48:GLU:HB2	2:B:130:ILE:HG12	1.45	0.99
3:C:42:LEU:HD22	3:C:190:TRP:CH2	1.97	0.99
1:D:238:ASP:HB3	4:E:308:LEU:CD2	1.91	0.99
3:C:37:LEU:HB2	3:C:217:PHE:CE2	1.97	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:179:ILE:CD1	3:C:195:LYS:HB3	1.93	0.99
1:D:145:LYS:C	1:D:146:LEU:HD12	1.87	0.99
4:E:138:TRP:HB2	4:E:213:ILE:HG12	1.42	0.99
1:A:238:ASP:HB3	2:B:306:HIS:CE1	1.97	0.99
3:C:115:ASN:O	3:C:115:ASN:ND2	1.94	0.99
4:E:22:LYS:HG3	4:E:23:THR:HB	1.43	0.98
1:A:87:LEU:HD22	1:A:87:LEU:H	1.22	0.98
2:B:311:THR:HB	2:B:430:TYR:CD2	1.98	0.98
3:C:69:TRP:NE1	3:C:114:PRO:HA	1.78	0.98
3:C:122:PRO:HB2	3:C:123:PRO:HD2	1.02	0.98
4:E:79:ILE:HG12	4:E:80:PRO:HD2	1.44	0.98
1:A:57:ARG:HD3	1:A:161:GLU:OE2	1.64	0.98
4:E:436:ASN:HA	4:E:439:TRP:HE1	1.29	0.98
2:B:132:VAL:HG13	2:B:279:ILE:CA	1.93	0.98
1:A:302:SER:HB2	1:A:306:HIS:C	1.87	0.98
2:B:133:MET:CG	2:B:140:GLN:HG3	1.93	0.98
3:C:162:LEU:HD11	3:C:217:PHE:CZ	1.99	0.98
3:C:149:THR:CG2	3:C:214:ASP:HB3	1.94	0.97
1:D:35:LEU:HD23	1:D:164:ARG:NH1	1.79	0.97
1:A:57:ARG:HA	1:A:119:THR:CG2	1.93	0.97
3:C:122:PRO:HB2	3:C:123:PRO:CD	1.92	0.97
1:D:49:ILE:HG21	1:D:125:LYS:NZ	1.78	0.97
4:E:45:LYS:HE2	4:E:278:ASN:C	1.88	0.97
4:E:67:ASN:HD22	4:E:67:ASN:H	1.02	0.97
1:A:166:ASP:HB3	1:A:178:MET:HE2	1.43	0.97
1:A:252:SER:HB3	2:B:257:LEU:HD13	1.46	0.97
3:C:65:HIS:CD2	3:C:65:HIS:H	1.72	0.97
3:C:159:SER:HA	3:C:213:GLN:CG	1.94	0.97
3:C:115:ASN:N	3:C:115:ASN:HD22	1.61	0.97
4:E:59:TRP:C	4:E:60:ASN:HD22	1.71	0.97
3:C:426:THR:HG22	3:C:426:THR:O	1.63	0.97
4:E:146:ARG:NH1	4:E:205:PHE:HB3	1.78	0.97
1:D:203:TYR:N	1:D:203:TYR:CD1	2.27	0.97
2:B:142:CYS:HB3	2:B:211:LEU:HG	1.47	0.96
3:C:145:SER:C	3:C:146:LEU:HD12	1.89	0.96
1:D:187:TRP:HB2	1:D:199:LEU:HD23	1.46	0.96
2:B:56:LEU:CD1	2:B:56:LEU:H	1.63	0.96
1:D:7:LEU:CD2	1:D:70:ALA:HB1	1.95	0.96
4:E:187:HIS:CE1	4:E:189:PRO:HG3	1.99	0.96
1:A:38:ILE:HD11	1:A:55:ARG:HG3	0.97	0.96
1:A:64:ARG:HA	1:A:66:ARG:HH11	1.26	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:TRP:CH2	1:A:189:TYR:HB3	2.00	0.96
1:D:72:TYR:HB2	1:D:112:TYR:HB2	1.44	0.96
1:A:72:TYR:HB2	1:A:112:TYR:CG	2.01	0.96
4:E:62:TYR:O	4:E:62:TYR:HD1	1.48	0.96
1:A:67:TRP:HD1	1:A:112:TYR:HA	1.30	0.96
1:A:167:LEU:CD1	1:A:178:MET:HB2	1.96	0.96
4:E:138:TRP:HB2	4:E:213:ILE:HG13	1.45	0.96
1:D:304:SER:HB3	1:D:397:GLU:HB2	1.45	0.96
1:D:3:HIS:HB3	1:D:7:LEU:HG	1.46	0.95
1:D:64:ARG:HA	1:D:66:ARG:NH1	1.80	0.95
3:C:190:TRP:CD1	3:C:221:ILE:HD12	2.00	0.95
3:C:1:VAL:HG22	3:C:4:GLU:OE2	1.67	0.95
1:D:243:MET:H	1:D:243:MET:HE2	1.29	0.95
1:A:406:ILE:HA	1:A:409:ILE:HD11	1.47	0.95
4:E:183:TRP:HB3	4:E:216:ARG:HG2	1.46	0.95
3:C:93:VAL:HG11	3:C:151:LEU:CD1	1.94	0.95
3:C:316:THR:CG2	3:C:317:PRO:HD2	1.96	0.95
1:D:187:TRP:HB2	1:D:199:LEU:CD2	1.96	0.95
2:B:9:SER:HA	2:B:12:PHE:HE1	1.27	0.95
1:D:107:LYS:CE	4:E:149:THR:HA	1.97	0.95
1:D:408:HIS:O	1:D:412:CYS:HB2	1.67	0.95
4:E:54:TRP:HB3	4:E:118:LEU:HD11	1.45	0.95
4:E:159:LEU:HD12	4:E:192:LYS:CA	1.96	0.95
4:E:236:VAL:HA	4:E:239:VAL:CG2	1.95	0.95
1:D:85:VAL:HG13	1:D:86:TRP:CE3	2.01	0.95
4:E:128:PRO:C	4:E:129:ILE:HG23	1.91	0.95
1:D:160:PRO:HD3	1:D:185:LYS:HB3	1.47	0.94
2:B:238:VAL:CG2	2:B:255:ALA:HB1	1.97	0.94
3:C:278:LEU:C	3:C:278:LEU:CD1	2.33	0.94
1:A:133:THR:CA	1:A:274:ILE:HG22	1.97	0.94
1:D:198:TYR:N	1:D:198:TYR:CD1	2.15	0.94
1:D:305:THR:HB	1:D:401:TYR:CD2	2.01	0.94
1:A:77:LYS:HG3	1:A:77:LYS:O	1.65	0.94
2:B:46:LYS:HE2	2:B:278:PRO:CG	1.97	0.94
1:D:107:LYS:HD3	1:D:107:LYS:N	1.83	0.94
1:D:169:THR:O	1:D:169:THR:HG22	1.65	0.94
4:E:6:LEU:HD12	4:E:69:SER:HB3	1.47	0.94
3:C:37:LEU:HB2	3:C:217:PHE:HE2	1.31	0.94
1:D:107:LYS:HE3	4:E:149:THR:HA	1.48	0.94
4:E:2:GLU:HA	4:E:5:ARG:HG3	1.46	0.94
1:D:136:PRO:HG3	1:D:274:ILE:CD1	1.96	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:255:ILE:CD1	4:E:304:LEU:HD22	1.96	0.94
1:A:155:LYS:HE3	4:E:76:LEU:HD13	1.49	0.94
2:B:104:LEU:HD12	2:B:118:TRP:HH2	1.20	0.94
1:A:148:ILE:CG2	1:A:198:TYR:HB2	1.96	0.94
3:C:52:LEU:HD21	3:C:130:CYS:HB2	1.47	0.94
4:E:91:LEU:HB2	4:E:95:VAL:H	1.32	0.94
1:D:134:HIS:NE2	1:D:207:MET:HE3	1.82	0.94
1:A:148:ILE:HD11	1:A:156:VAL:HG13	1.50	0.94
3:C:162:LEU:HD11	3:C:217:PHE:CE1	2.03	0.94
3:C:453:ILE:HG23	3:C:454:ASP:H	1.31	0.94
4:E:271:LYS:C	4:E:273:PRO:HD2	1.91	0.93
2:B:270:VAL:HG11	2:B:284:LEU:HD11	1.48	0.93
2:B:436:ASP:O	2:B:440:LEU:HD12	1.66	0.93
1:D:136:PRO:HG3	1:D:274:ILE:HD11	1.50	0.93
3:C:42:LEU:HG	3:C:54:THR:HG23	1.51	0.93
1:D:40:LEU:HD13	1:D:52:THR:HB	1.49	0.93
1:A:113:THR:O	1:A:113:THR:HG23	1.67	0.93
2:B:34:GLY:C	2:B:35:LEU:HD23	1.94	0.93
3:C:179:ILE:HD12	3:C:195:LYS:HB3	1.48	0.93
1:D:426:PHE:HE1	1:D:430:LEU:HD12	1.32	0.93
4:E:162:GLU:HA	4:E:190:ALA:H	1.31	0.93
1:A:43:VAL:HG13	1:A:50:VAL:HG22	1.51	0.93
1:A:250:LEU:CD2	1:A:292:THR:HG22	1.98	0.93
3:C:279:PRO:HA	3:C:282:ALA:HB3	1.49	0.92
4:E:272:VAL:O	4:E:272:VAL:HG22	1.70	0.92
1:A:380:LYS:HD3	2:B:408:ILE:HB	1.48	0.92
2:B:46:LYS:CA	2:B:278:PRO:HD2	2.00	0.92
2:B:68:ASP:HB3	2:B:69:PRO:HD3	1.48	0.92
2:B:160:HIS:HE2	2:B:209:PHE:HE1	1.16	0.92
3:C:273:LEU:HA	3:C:276:GLN:HG2	1.50	0.92
1:D:171:MET:HG2	1:D:174:GLY:H	1.34	0.92
4:E:27:VAL:HG12	4:E:153:HIS:O	1.70	0.92
1:A:256:PHE:CE1	2:B:261:VAL:HG23	2.04	0.92
4:E:129:ILE:HG22	4:E:133:TYR:HD2	1.31	0.92
1:A:89:ASP:HB2	1:A:149:TRP:CD1	2.04	0.92
1:A:145:LYS:HG3	1:A:202:THR:CG2	2.00	0.92
2:B:31:VAL:HG21	2:B:86:TRP:HZ3	1.20	0.92
1:D:376:ILE:C	1:D:380:LYS:HE2	1.93	0.92
1:A:134:HIS:CD2	1:A:207:MET:HE3	2.04	0.92
2:B:91:VAL:HG11	2:B:149:TYR:CD1	2.05	0.92
3:C:246:ALA:O	3:C:250:PRO:HD3	1.68	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:140:ASN:C	4:E:140:ASN:HD22	1.77	0.92
2:B:297:LEU:O	2:B:297:LEU:HD23	1.69	0.92
3:C:273:LEU:HD23	3:C:276:GLN:CB	1.99	0.92
4:E:94:ASN:HD22	4:E:125:SER:HB2	1.32	0.92
1:A:89:ASP:OD1	1:A:89:ASP:O	1.87	0.91
2:B:287:ILE:C	2:B:287:ILE:HD12	1.95	0.91
3:C:42:LEU:HG	3:C:54:THR:CG2	2.00	0.91
4:E:433:GLY:O	4:E:436:ASN:HB2	1.69	0.91
1:A:247:ILE:O	1:A:247:ILE:HD13	1.71	0.91
2:B:9:SER:HA	2:B:12:PHE:CD1	2.05	0.91
2:B:56:LEU:HD21	2:B:103:THR:HA	1.53	0.91
2:B:131:LYS:HD3	2:B:132:VAL:N	1.85	0.91
2:B:186:TRP:HB3	2:B:215:ARG:CG	2.00	0.91
1:D:145:LYS:O	1:D:146:LEU:HD12	1.69	0.91
4:E:66:TRP:CD1	4:E:111:ASN:HA	2.05	0.91
2:B:31:VAL:HG21	2:B:86:TRP:CH2	2.04	0.91
3:C:31:VAL:O	3:C:31:VAL:CG1	2.16	0.91
2:B:67:TRP:HB2	2:B:72:TYR:HB2	1.53	0.91
2:B:241:LEU:CD2	2:B:251:LEU:HD11	2.00	0.91
2:B:134:TYR:HE1	2:B:213:ILE:HG13	1.32	0.91
2:B:405:VAL:HG12	2:B:409:LYS:NZ	1.86	0.91
3:C:241:PHE:O	3:C:245:LEU:HG	1.70	0.91
4:E:79:ILE:HG12	4:E:80:PRO:CD	1.98	0.91
1:A:134:HIS:NE2	1:A:207:MET:HE3	1.86	0.91
1:A:265:PRO:HA	1:A:268:SER:HB3	1.53	0.91
1:D:302:SER:CB	1:D:400:LYS:HG2	1.98	0.91
2:B:224:THR:C	2:B:227:PRO:HD2	1.95	0.91
2:B:251:LEU:HB2	3:C:261:ILE:HG13	1.51	0.91
2:B:274:SER:HB2	2:B:278:PRO:HB3	1.50	0.91
3:C:279:PRO:HA	3:C:282:ALA:CB	2.00	0.91
4:E:56:GLU:HA	4:E:118:LEU:CB	2.01	0.91
2:B:37:LEU:HA	2:B:54:VAL:HG12	0.92	0.91
1:D:432:GLU:HG2	1:D:435:GLN:NE2	1.86	0.91
1:A:130:ILE:HD13	1:A:131:ILE:N	1.86	0.91
3:C:191:GLU:CG	3:C:222:ARG:HB3	2.01	0.90
3:C:307:GLY:HA2	3:C:310:LEU:HD23	1.50	0.90
1:D:107:LYS:NZ	4:E:149:THR:HA	1.86	0.90
2:B:81:PRO:HD3	3:C:22:ARG:HH22	1.35	0.90
2:B:186:TRP:HB2	2:B:215:ARG:CB	2.01	0.90
1:A:76:LYS:HG2	1:A:77:LYS:H	1.33	0.90
1:A:142:CYS:HB2	1:A:205:PHE:HB2	1.53	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:270:VAL:CG1	2:B:284:LEU:HD11	2.01	0.90
1:D:48:GLN:CB	1:D:130:ILE:HD12	2.00	0.90
4:E:90:VAL:HG13	4:E:95:VAL:HB	1.51	0.90
2:B:406:GLU:HA	2:B:409:LYS:HD2	1.51	0.90
1:D:28:PHE:CD2	1:D:157:SER:HB3	2.05	0.90
1:D:426:PHE:CE1	1:D:430:LEU:HD12	2.05	0.90
4:E:6:LEU:HD12	4:E:69:SER:CB	2.00	0.90
3:C:1:VAL:HA	3:C:4:GLU:HG2	1.50	0.90
1:A:36:GLN:HA	1:A:164:ARG:NH2	1.87	0.90
1:A:135:PHE:O	1:A:135:PHE:CD1	2.24	0.90
3:C:106:TYR:O	3:C:106:TYR:HD1	1.54	0.90
3:C:434:LYS:HD3	3:C:435:GLU:HG3	1.50	0.90
1:D:160:PRO:HD3	1:D:185:LYS:CB	2.01	0.90
4:E:31:THR:O	4:E:32:LEU:HD23	1.71	0.90
1:D:305:THR:CB	1:D:401:TYR:HD2	1.84	0.90
4:E:216:ARG:O	4:E:217:LYS:HG3	1.72	0.90
1:D:287:SER:HA	1:D:290:ILE:CD1	2.02	0.90
4:E:45:LYS:HD2	4:E:46:GLU:HG2	1.51	0.90
4:E:94:ASN:HB3	4:E:125:SER:CB	2.01	0.90
2:B:46:LYS:CE	2:B:278:PRO:HG3	2.02	0.89
1:D:41:ILE:HD12	1:D:51:GLU:O	1.72	0.89
2:B:131:LYS:CD	2:B:132:VAL:H	1.85	0.89
4:E:32:LEU:O	4:E:33:LYS:HG3	1.71	0.89
2:B:263:LEU:HD22	2:B:291:VAL:CG2	2.03	0.89
3:C:42:LEU:HA	3:C:54:THR:HG22	1.51	0.89
3:C:452:THR:O	3:C:455:ARG:HG2	1.73	0.89
1:D:377:GLU:HB2	4:E:415:CYS:SG	2.13	0.89
2:B:258:ALA:CB	3:C:265:LEU:HD22	2.02	0.89
1:D:46:VAL:HA	1:D:272:PRO:HD3	1.51	0.89
2:B:132:VAL:HG12	2:B:280:ILE:H	1.35	0.89
2:B:142:CYS:HB3	2:B:211:LEU:CG	2.03	0.89
1:D:395:ALA:O	1:D:398:GLU:HG2	1.73	0.89
3:C:138:PRO:HG3	3:C:288:ILE:CD1	2.01	0.89
1:A:102:ILE:O	1:A:102:ILE:HG22	1.72	0.89
1:A:250:LEU:HD11	1:A:296:ILE:HG21	1.55	0.89
3:C:56:VAL:HG13	3:C:126:PHE:HE2	1.35	0.89
4:E:90:VAL:HG22	4:E:95:VAL:HG11	0.94	0.89
2:B:191:LYS:O	2:B:191:LYS:HG3	1.02	0.89
1:D:304:SER:HB3	1:D:397:GLU:CB	2.03	0.89
1:A:382:ILE:O	1:A:386:MET:HG2	1.72	0.89
1:D:238:ASP:HB3	4:E:308:LEU:HD22	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:75:ILE:HD11	2:B:78:LEU:HD13	1.55	0.89
3:C:69:TRP:HE1	3:C:114:PRO:HA	1.35	0.89
1:D:259:VAL:HA	1:D:262:GLU:CD	1.98	0.88
4:E:135:PRO:HG2	4:E:137:ASP:O	1.73	0.88
4:E:172:ILE:CD1	4:E:188:ARG:HB3	2.02	0.88
4:E:183:TRP:HB3	4:E:216:ARG:CG	2.02	0.88
3:C:77:ILE:HD12	3:C:80:LEU:HD13	1.53	0.88
1:D:278:MET:O	1:D:278:MET:HE3	1.73	0.88
4:E:39:LEU:HD23	4:E:183:TRP:CZ2	2.07	0.88
4:E:67:ASN:HD22	4:E:67:ASN:N	1.71	0.88
4:E:172:ILE:HD11	4:E:187:HIS:C	1.98	0.88
1:A:79:ARG:HD2	1:A:107:LYS:HD2	1.55	0.88
1:A:107:LYS:HG2	2:B:150:THR:HG21	1.53	0.88
1:A:166:ASP:CB	1:A:178:MET:HE2	2.02	0.88
1:D:160:PRO:HG3	1:D:185:LYS:HB3	1.53	0.88
1:A:107:LYS:C	1:A:108:LEU:HD23	1.99	0.88
1:A:145:LYS:C	1:A:146:LEU:HD12	1.98	0.88
1:A:406:ILE:HG23	1:A:409:ILE:HD11	1.54	0.88
2:B:81:PRO:HD3	3:C:22:ARG:NH2	1.88	0.88
1:A:38:ILE:HG22	1:A:38:ILE:O	1.71	0.88
1:D:56:LEU:HD21	1:D:122:ALA:HB3	1.54	0.88
4:E:71:TYR:HA	4:E:111:ASN:CB	2.04	0.88
4:E:109:VAL:HG12	4:E:110:TYR:O	1.73	0.88
4:E:183:TRP:HB3	4:E:216:ARG:CD	2.04	0.88
4:E:284:LYS:O	4:E:287:ILE:HG23	1.73	0.88
1:A:242:LYS:HB2	1:A:245:LEU:HB2	1.56	0.88
4:E:172:ILE:HD12	4:E:188:ARG:CB	2.02	0.88
3:C:4:GLU:HG3	3:C:5:GLU:H	1.37	0.88
3:C:144:CYS:SG	3:C:146:LEU:HD11	2.13	0.88
2:B:48:GLU:HA	2:B:130:ILE:CD1	2.04	0.87
3:C:16:LYS:HA	3:C:16:LYS:HE3	1.56	0.87
3:C:159:SER:CA	3:C:213:GLN:HG3	2.04	0.87
1:D:72:TYR:C	1:D:72:TYR:HD1	1.79	0.87
4:E:144:VAL:HA	4:E:208:ILE:O	1.74	0.87
1:D:303:PRO:HD2	1:D:400:LYS:HD2	1.56	0.87
2:B:241:LEU:CG	2:B:248:LYS:HE2	2.05	0.87
4:E:62:TYR:O	4:E:62:TYR:CD1	2.28	0.87
4:E:136:PHE:CE1	4:E:217:LYS:HG2	2.09	0.87
1:D:49:ILE:HD12	1:D:125:LYS:HE3	1.54	0.87
1:D:131:ILE:HG13	1:D:133:THR:N	1.89	0.87
1:D:160:PRO:CD	1:D:185:LYS:HB3	2.04	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:THR:O	1:A:247:ILE:HG22	1.74	0.87
2:B:10:VAL:HG13	2:B:11:LEU:HD22	1.54	0.87
2:B:56:LEU:CD2	2:B:120:PRO:HG2	2.04	0.87
1:D:30:ASP:OD1	1:D:30:ASP:N	2.04	0.87
4:E:31:THR:HB	4:E:58:GLN:HB2	1.57	0.87
4:E:267:LEU:O	4:E:270:GLN:HG3	1.73	0.87
3:C:220:ILE:HG13	3:C:220:ILE:O	1.72	0.87
4:E:132:THR:O	4:E:282:ILE:HD12	1.75	0.87
2:B:185:GLN:HB3	2:B:219:PHE:CE2	2.08	0.87
1:D:106:THR:HG23	1:D:107:LYS:CE	2.03	0.87
4:E:279:VAL:HB	4:E:280:PRO:CD	2.04	0.87
2:B:186:TRP:CB	2:B:215:ARG:HG3	2.03	0.87
1:D:37:LEU:HD12	1:D:53:ASN:O	1.74	0.87
1:D:167:LEU:CD1	1:D:178:MET:HB2	2.04	0.87
3:C:38:THR:CG2	3:C:57:TRP:CE3	2.58	0.87
3:C:316:THR:HG23	3:C:317:PRO:HD2	1.56	0.87
1:A:41:ILE:HD11	1:A:51:GLU:OE1	1.74	0.86
2:B:104:LEU:HA	2:B:118:TRP:CH2	2.09	0.86
3:C:50:GLU:HB3	3:C:130:CYS:O	1.75	0.86
1:D:87:LEU:HD12	1:D:88:PRO:HD2	1.53	0.86
4:E:6:LEU:CD1	4:E:69:SER:HB3	2.05	0.86
4:E:94:ASN:ND2	4:E:143:LEU:HD23	1.90	0.86
1:A:274:ILE:HG12	1:A:277:TYR:HD1	1.40	0.86
2:B:35:LEU:HD23	2:B:35:LEU:N	1.89	0.86
2:B:132:VAL:O	2:B:279:ILE:HG23	1.73	0.86
3:C:18:ASN:CB	3:C:21:VAL:HB	2.05	0.86
1:D:144:MET:HE3	1:D:205:PHE:CE1	2.10	0.86
1:D:187:TRP:CZ2	1:D:189:TYR:HB3	2.10	0.86
1:A:160:PRO:HG3	1:A:185:LYS:HB3	1.55	0.86
4:E:247:GLY:H	4:E:250:LYS:HZ2	1.19	0.86
1:A:420:ILE:HG13	1:A:421:GLY:N	1.90	0.86
4:E:44:GLU:HG3	4:E:129:ILE:HG13	1.56	0.86
4:E:45:LYS:HG2	4:E:279:VAL:C	1.99	0.86
4:E:62:TYR:HD1	4:E:62:TYR:C	1.81	0.86
4:E:69:SER:O	4:E:69:SER:OG	1.84	0.86
2:B:185:GLN:CB	2:B:219:PHE:HE2	1.87	0.86
3:C:65:HIS:CD2	3:C:65:HIS:N	2.43	0.86
4:E:91:LEU:H	4:E:95:VAL:CB	1.89	0.86
4:E:271:LYS:HZ3	4:E:271:LYS:HB2	1.40	0.86
4:E:313:THR:HG21	4:E:441:LEU:HA	1.57	0.86
3:C:269:VAL:HG13	3:C:270:PHE:CD1	2.10	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:252:SER:HB2	4:E:259:LEU:CD1	2.05	0.86
2:B:46:LYS:HA	2:B:278:PRO:CD	2.03	0.86
3:C:190:TRP:CB	3:C:223:ARG:HB2	2.04	0.86
3:C:1:VAL:HG22	3:C:4:GLU:CD	2.01	0.86
4:E:44:GLU:HG3	4:E:129:ILE:CG1	2.06	0.86
4:E:91:LEU:H	4:E:95:VAL:HB	1.41	0.86
2:B:405:VAL:O	2:B:408:ILE:HG22	1.75	0.86
1:A:379:VAL:CG1	4:E:424:LYS:HE2	2.06	0.85
4:E:66:TRP:HB2	4:E:71:TYR:H	1.41	0.85
4:E:146:ARG:CZ	4:E:205:PHE:HB3	2.06	0.85
3:C:137:PHE:CD1	3:C:288:ILE:HB	2.10	0.85
1:A:245:LEU:HD22	2:B:250:SER:HA	1.58	0.85
1:D:203:TYR:H	1:D:203:TYR:HD1	0.85	0.85
2:B:236:ILE:HB	2:B:446:MET:CE	2.06	0.85
3:C:18:ASN:HB3	3:C:21:VAL:HB	1.58	0.85
3:C:83:ARG:O	3:C:87:ILE:HG13	1.74	0.85
4:E:122:ILE:H	4:E:122:ILE:HD13	1.42	0.85
1:A:41:ILE:CG1	1:A:51:GLU:HB3	2.05	0.85
4:E:89:VAL:CG2	4:E:99:PHE:CZ	2.59	0.85
4:E:233:SER:O	4:E:237:VAL:HG23	1.77	0.85
1:A:72:TYR:HB2	1:A:112:TYR:CB	2.06	0.85
2:B:230:LEU:HA	2:B:233:ILE:HG13	1.57	0.85
2:B:279:ILE:CG2	2:B:280:ILE:HD13	2.07	0.85
2:B:407:ALA:O	2:B:411:ILE:HG13	1.76	0.85
1:D:46:VAL:HA	1:D:272:PRO:CD	2.06	0.85
4:E:222:ILE:HG23	4:E:223:ILE:H	1.42	0.85
4:E:250:LYS:HA	4:E:253:LEU:HB3	1.57	0.85
2:B:132:VAL:C	2:B:279:ILE:HG23	2.02	0.85
2:B:175:ILE:HG12	2:B:176:ASN:H	1.39	0.85
3:C:148:PHE:HB2	3:C:215:VAL:HG22	1.58	0.85
1:A:128:CYS:SG	1:A:144:MET:HE2	2.17	0.85
2:B:128:CYS:SG	2:B:144:MET:HG2	2.17	0.85
1:D:75:ILE:HD13	4:E:24:LEU:HD12	1.59	0.85
1:A:242:LYS:HB2	1:A:245:LEU:CB	2.07	0.84
1:D:245:LEU:HD21	4:E:255:ILE:HG13	1.57	0.84
1:A:107:LYS:CE	2:B:150:THR:HB	2.07	0.84
2:B:248:LYS:HD3	2:B:252:SER:CB	2.03	0.84
3:C:110:VAL:HG13	3:C:120:TRP:HB2	1.58	0.84
1:D:398:GLU:HA	1:D:401:TYR:CZ	2.12	0.84
1:A:166:ASP:OD1	1:A:166:ASP:O	1.95	0.84
2:B:92:LEU:N	2:B:96:ASN:HB2	1.93	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:142:CYS:CB	2:B:211:LEU:HB2	2.08	0.84
3:C:242:LEU:CD2	3:C:267:GLN:HB3	2.04	0.84
1:D:86:TRP:O	1:D:86:TRP:CE3	2.30	0.84
4:E:292:VAL:O	4:E:296:ILE:HG23	1.77	0.84
4:E:92:GLU:HB3	4:E:144:VAL:HG23	1.60	0.84
1:A:107:LYS:HE2	2:B:150:THR:HB	1.58	0.84
1:A:433:LEU:O	1:A:433:LEU:HD12	1.77	0.84
1:D:118:TRP:HE1	1:D:120:PRO:HB3	1.39	0.84
3:C:50:GLU:HG2	3:C:132:ILE:HB	1.57	0.84
3:C:138:PRO:CG	3:C:288:ILE:HD11	2.07	0.84
1:D:203:TYR:N	1:D:203:TYR:HD1	1.67	0.84
4:E:132:THR:C	4:E:135:PRO:HD3	2.03	0.84
4:E:159:LEU:HD12	4:E:192:LYS:HB2	1.59	0.84
1:D:37:LEU:HD11	1:D:52:THR:OG1	1.78	0.84
4:E:240:TYR:HD2	4:E:453:ILE:HD13	1.39	0.84
1:A:43:VAL:CG1	1:A:50:VAL:HG22	2.08	0.84
1:A:46:VAL:HG23	1:A:271:VAL:N	1.92	0.84
2:B:265:LEU:O	2:B:268:ASP:HB2	1.77	0.84
1:D:106:THR:HG22	1:D:107:LYS:N	1.93	0.84
1:D:176:TRP:CB	1:D:209:ARG:HD2	2.08	0.84
1:D:379:VAL:HA	1:D:382:ILE:HD12	1.60	0.84
1:A:110:LEU:CD1	1:A:114:GLY:HA2	2.08	0.83
1:A:258:LEU:HD13	4:E:267:LEU:CD2	2.06	0.83
1:A:419:ILE:HG23	1:A:420:ILE:H	1.42	0.83
2:B:176:ASN:HB2	2:B:191:LYS:CB	2.07	0.83
1:D:85:VAL:HG13	1:D:86:TRP:HE3	1.41	0.83
1:D:298:THR:O	1:D:301:ARG:HB3	1.76	0.83
2:B:142:CYS:HB3	2:B:211:LEU:HB2	1.60	0.83
1:A:139:GLN:HB2	1:A:207:MET:C	2.04	0.83
2:B:104:LEU:HD12	2:B:118:TRP:CZ3	2.13	0.83
3:C:462:THR:HB	3:C:463:PRO:CD	2.08	0.83
1:A:255:VAL:HG23	1:A:258:LEU:HD12	1.61	0.83
2:B:31:VAL:CG2	2:B:86:TRP:HZ3	1.90	0.83
2:B:297:LEU:HD13	2:B:445:THR:HG21	1.58	0.83
4:E:182:GLU:HG2	4:E:221:TYR:OH	1.77	0.83
1:A:171:MET:HE3	1:A:176:TRP:CZ2	2.13	0.83
2:B:223:TYR:O	2:B:226:VAL:HG22	1.78	0.83
1:D:49:ILE:HG21	1:D:125:LYS:HZ1	1.44	0.83
1:D:111:ASP:OD2	1:D:115:LYS:HD3	1.77	0.83
1:D:282:MET:HG3	1:D:286:ILE:HD11	1.58	0.83
4:E:227:ALA:N	4:E:228:PRO:HD2	1.93	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:LEU:CD2	2:B:250:SER:HA	2.08	0.83
2:B:47:ASN:HB2	2:B:49:GLU:OE1	1.78	0.83
2:B:160:HIS:NE2	2:B:209:PHE:HE1	1.77	0.83
3:C:81:ARG:CZ	3:C:111:LEU:HD13	2.08	0.83
1:D:166:ASP:OD1	1:D:178:MET:HE2	1.78	0.83
4:E:446:ILE:HG22	4:E:447:ASP:N	1.92	0.83
1:A:33:VAL:CG2	1:A:158:ILE:HG12	2.07	0.83
2:B:38:THR:HG22	2:B:55:PHE:HE1	1.43	0.83
2:B:93:MET:HG3	2:B:206:ASP:CB	2.09	0.83
2:B:242:PRO:CG	2:B:243:PRO:HD3	2.09	0.83
3:C:35:LEU:HD22	3:C:215:VAL:HG11	1.61	0.83
1:D:384:GLU:HG2	4:E:422:ILE:HD12	1.61	0.83
3:C:45:LEU:HD12	3:C:190:TRP:CE3	2.14	0.83
3:C:319:THR:O	3:C:319:THR:CG2	2.27	0.83
1:D:220:ILE:CG2	4:E:294:LEU:HD11	2.09	0.83
4:E:148:GLN:CA	4:E:148:GLN:HE21	1.89	0.83
4:E:283:GLY:O	4:E:287:ILE:HG22	1.78	0.83
1:A:79:ARG:CD	1:A:107:LYS:HD2	2.07	0.83
1:A:171:MET:CE	1:A:176:TRP:CH2	2.62	0.83
1:A:47:ASN:O	1:A:49:ILE:HG13	1.78	0.82
1:D:260:ILE:HG22	1:D:264:ILE:HD11	1.59	0.82
2:B:27:ASP:C	2:B:28:LYS:HG3	2.02	0.82
3:C:60:HIS:CD2	3:C:92:ILE:HD13	2.14	0.82
4:E:132:THR:O	4:E:135:PRO:HD3	1.77	0.82
1:A:160:PRO:HG2	1:A:185:LYS:NZ	1.94	0.82
1:A:423:VAL:O	1:A:426:PHE:HB3	1.79	0.82
1:D:91:VAL:HG22	1:D:96:ALA:CB	2.09	0.82
1:D:109:LEU:O	1:D:116:ILE:HG22	1.80	0.82
4:E:136:PHE:HZ	4:E:217:LYS:HD2	1.40	0.82
4:E:162:GLU:HA	4:E:190:ALA:N	1.94	0.82
1:A:59:GLN:HE22	1:A:117:MET:CG	1.93	0.82
4:E:47:GLU:HB3	4:E:129:ILE:CG1	2.09	0.82
1:A:35:LEU:HD21	1:A:37:LEU:HD23	1.61	0.82
4:E:28:ILE:HD11	4:E:60:ASN:O	1.79	0.82
4:E:159:LEU:HD12	4:E:192:LYS:CB	2.09	0.82
1:A:176:TRP:HB3	1:A:209:ARG:HD2	1.62	0.82
2:B:132:VAL:CG1	2:B:279:ILE:HA	2.07	0.82
3:C:33:ILE:O	3:C:160:MET:HA	1.80	0.82
3:C:56:VAL:HG13	3:C:126:PHE:CE2	2.14	0.82
3:C:77:ILE:CD1	3:C:80:LEU:HD13	2.09	0.82
3:C:190:TRP:HB3	3:C:223:ARG:HB2	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:TRP:HB3	1:D:209:ARG:HD2	1.59	0.82
4:E:62:TYR:CD1	4:E:62:TYR:C	2.54	0.82
2:B:218:LEU:HA	2:B:221:ILE:HD11	1.62	0.82
3:C:38:THR:CG2	3:C:57:TRP:HE3	1.92	0.82
4:E:222:ILE:O	4:E:226:ILE:HG13	1.80	0.82
2:B:3:MET:CE	2:B:69:PRO:HG3	2.08	0.82
1:D:176:TRP:CE3	1:D:209:ARG:CZ	2.63	0.82
1:D:296:ILE:HA	1:D:299:HIS:CB	2.10	0.82
4:E:225:ILE:O	4:E:228:PRO:HG2	1.79	0.82
1:A:376:ILE:HG23	1:A:380:LYS:NZ	1.95	0.82
3:C:42:LEU:HD22	3:C:190:TRP:CZ2	2.15	0.82
4:E:47:GLU:O	4:E:126:THR:HG23	1.80	0.82
4:E:183:TRP:HB2	4:E:216:ARG:HG2	1.62	0.82
1:A:60:TRP:HE1	1:A:116:ILE:HD12	1.45	0.81
1:A:65:LEU:HB3	1:A:110:LEU:CD1	2.09	0.81
1:A:148:ILE:CG2	1:A:198:TYR:HD2	1.92	0.81
1:A:216:VAL:HG13	1:A:220:ILE:HD11	1.61	0.81
3:C:263:VAL:HA	1:D:251:LEU:HD11	1.61	0.81
1:D:398:GLU:HA	1:D:401:TYR:CE2	2.15	0.81
4:E:236:VAL:CA	4:E:239:VAL:HG23	2.09	0.81
1:A:16:ASN:CB	1:A:19:ILE:HD12	2.10	0.81
3:C:216:THR:C	3:C:217:PHE:HD1	1.88	0.81
1:D:189:TYR:HA	1:D:197:PRO:HD2	1.62	0.81
4:E:26:HIS:CG	4:E:26:HIS:O	2.34	0.81
2:B:26:GLY:O	2:B:28:LYS:HE2	1.80	0.81
2:B:247:GLU:O	2:B:249:MET:HG3	1.80	0.81
3:C:113:ARG:HE	3:C:119:THR:HG23	1.46	0.81
3:C:443:VAL:HA	3:C:446:TRP:CD1	2.15	0.81
2:B:45:GLU:HG2	2:B:277:VAL:HB	1.61	0.81
1:D:216:VAL:O	1:D:220:ILE:HG13	1.81	0.81
4:E:44:GLU:C	4:E:280:PRO:HB3	2.06	0.81
2:B:409:LYS:HE2	3:C:423:ILE:HG23	1.63	0.81
1:D:160:PRO:CG	1:D:185:LYS:HB3	2.08	0.81
1:D:166:ASP:OD2	1:D:181:TYR:HB2	1.81	0.81
1:D:286:ILE:O	1:D:290:ILE:HG23	1.80	0.81
2:B:216:LYS:HD2	2:B:216:LYS:O	1.80	0.81
2:B:243:PRO:HB3	2:B:435:ALA:CB	2.00	0.81
3:C:3:GLU:OE1	3:C:7:LEU:HD12	1.80	0.81
1:D:10:ASN:OD1	1:D:11:LEU:HD23	1.81	0.81
2:B:90:ILE:HG23	2:B:147:LYS:H	1.45	0.81
2:B:142:CYS:O	2:B:210:TYR:HA	1.80	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:93:VAL:CG1	3:C:151:LEU:HD13	2.01	0.81
3:C:110:VAL:CG1	3:C:120:TRP:HB2	2.11	0.81
4:E:91:LEU:H	4:E:95:VAL:CG2	1.94	0.81
4:E:219:LEU:HB3	4:E:222:ILE:CB	2.10	0.81
1:A:236:PRO:HB3	1:A:299:HIS:NE2	1.96	0.80
2:B:186:TRP:CB	2:B:215:ARG:CG	2.59	0.80
3:C:241:PHE:C	3:C:241:PHE:CD1	2.58	0.80
1:D:135:PHE:HZ	1:D:273:LEU:HD12	1.45	0.80
1:A:189:TYR:HA	1:A:197:PRO:HD2	1.64	0.80
3:C:135:LEU:O	3:C:138:PRO:HD2	1.82	0.80
3:C:192:ILE:HD12	3:C:219:LEU:HD11	1.63	0.80
3:C:252:GLU:OE2	1:D:301:ARG:HA	1.80	0.80
4:E:63:ARG:HB2	4:E:63:ARG:HH11	1.44	0.80
1:A:110:LEU:HD11	1:A:114:GLY:HA2	1.62	0.80
3:C:42:LEU:HD22	3:C:190:TRP:HH2	1.44	0.80
3:C:463:PRO:HA	3:C:466:VAL:CG2	2.07	0.80
1:A:167:LEU:HD12	1:A:178:MET:CB	2.09	0.80
2:B:218:LEU:HD13	2:B:221:ILE:CG1	2.11	0.80
2:B:269:LYS:HE3	2:B:270:VAL:HG22	1.63	0.80
4:E:44:GLU:HA	4:E:129:ILE:CD1	2.12	0.80
1:A:101:ALA:HB3	1:A:123:ILE:O	1.81	0.80
2:B:281:ILE:HG22	2:B:285:MET:N	1.96	0.80
1:D:255:VAL:O	1:D:259:VAL:HG23	1.80	0.80
1:D:427:ALA:O	1:D:431:ILE:HG13	1.82	0.80
4:E:172:ILE:HG23	4:E:174:PRO:HD2	1.64	0.80
4:E:262:THR:OG1	4:E:265:LEU:HD12	1.81	0.80
4:E:469:GLY:O	4:E:473:GLN:HB2	1.80	0.80
1:A:2:GLU:CG	1:A:74:GLY:HA2	2.11	0.80
1:A:380:LYS:HD3	2:B:408:ILE:CG2	2.11	0.80
3:C:298:LEU:HD11	3:C:471:PHE:HB2	1.64	0.80
1:A:20:ARG:HG2	1:A:20:ARG:NH1	1.85	0.80
1:A:57:ARG:HD3	1:A:161:GLU:CD	2.07	0.80
2:B:91:VAL:HA	2:B:96:ASN:ND2	1.97	0.80
2:B:226:VAL:CG2	2:B:227:PRO:HD3	2.11	0.80
1:D:29:VAL:HG23	1:D:60:TRP:HD1	1.46	0.80
1:D:201:ILE:HG22	1:D:203:TYR:CE1	2.16	0.80
4:E:148:GLN:HA	4:E:148:GLN:NE2	1.97	0.80
1:A:108:LEU:HD13	1:A:118:TRP:HB2	1.62	0.80
3:C:47:GLU:HG2	3:C:286:PRO:HD2	1.62	0.80
3:C:279:PRO:O	3:C:282:ALA:HB3	1.81	0.80
1:D:38:ILE:CA	1:D:169:THR:HG21	2.09	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:233:PHE:HZ	1:D:417:ILE:CD1	1.95	0.80
1:D:379:VAL:HA	1:D:382:ILE:CD1	2.12	0.80
4:E:27:VAL:HG12	4:E:153:HIS:C	2.07	0.80
4:E:436:ASN:HA	4:E:439:TRP:NE1	1.95	0.80
4:E:55:ILE:HG13	4:E:57:ILE:HG13	1.62	0.80
4:E:141:CYS:SG	4:E:143:LEU:HD11	2.22	0.80
4:E:228:PRO:O	4:E:231:LEU:HD23	1.82	0.80
3:C:50:GLU:HA	3:C:132:ILE:CD1	2.08	0.80
3:C:466:VAL:O	3:C:470:ILE:HG12	1.82	0.80
3:C:471:PHE:HD1	3:C:471:PHE:C	1.90	0.80
1:D:72:TYR:HD1	1:D:72:TYR:O	1.64	0.80
1:A:54:VAL:CG2	1:A:122:ALA:HB3	2.12	0.79
1:A:258:LEU:HD13	4:E:267:LEU:HD23	1.62	0.79
2:B:160:HIS:CE1	2:B:207:VAL:HG11	2.17	0.79
4:E:44:GLU:CB	4:E:280:PRO:HG3	2.12	0.79
4:E:76:LEU:HD23	4:E:77:VAL:H	1.47	0.79
2:B:287:ILE:HA	2:B:290:LEU:HD12	1.63	0.79
3:C:275:SER:O	3:C:279:PRO:HD3	1.82	0.79
1:A:36:GLN:C	1:A:36:GLN:OE1	2.25	0.79
1:A:72:TYR:HB2	1:A:112:TYR:HD2	1.44	0.79
3:C:247:PHE:C	3:C:250:PRO:HD2	2.07	0.79
1:D:61:ILE:HA	1:D:116:ILE:CD1	2.10	0.79
1:A:3:HIS:HB2	1:A:7:LEU:CD2	2.12	0.79
2:B:133:MET:SD	2:B:140:GLN:HB2	2.22	0.79
3:C:137:PHE:CD1	3:C:137:PHE:C	2.59	0.79
3:C:249:LEU:N	3:C:250:PRO:HD2	1.96	0.79
1:D:75:ILE:CD1	1:D:78:ILE:CG2	2.60	0.79
4:E:66:TRP:HB2	4:E:71:TYR:N	1.96	0.79
4:E:463:LEU:HD12	4:E:463:LEU:O	1.82	0.79
1:A:37:LEU:CD2	1:A:54:VAL:HG12	2.12	0.79
1:D:167:LEU:HD11	1:D:178:MET:CB	2.11	0.79
4:E:223:ILE:HA	4:E:226:ILE:HB	1.64	0.79
1:A:62:ASP:HB3	1:A:65:LEU:HD12	1.63	0.79
1:A:133:THR:O	1:A:133:THR:CG2	2.30	0.79
2:B:147:LYS:HB2	2:B:206:ASP:HA	1.65	0.79
1:D:107:LYS:HE3	4:E:149:THR:O	1.83	0.79
1:A:176:TRP:HB3	1:A:209:ARG:CD	2.12	0.79
2:B:254:SER:C	3:C:265:LEU:HD11	2.08	0.79
3:C:299:VAL:O	3:C:303:VAL:HG23	1.82	0.79
4:E:91:LEU:CB	4:E:95:VAL:H	1.96	0.79
1:A:66:ARG:HA	1:A:113:THR:C	2.08	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:65:HIS:H	3:C:65:HIS:HD2	1.30	0.79
3:C:179:ILE:HG23	3:C:181:PRO:HD2	1.63	0.79
1:D:167:LEU:HD11	1:D:178:MET:HB2	1.65	0.79
2:B:91:VAL:C	2:B:92:LEU:HD23	2.08	0.79
2:B:142:CYS:HB3	2:B:211:LEU:CB	2.13	0.79
3:C:155:ALA:HB2	3:C:211:ASN:HA	1.65	0.79
3:C:179:ILE:HG13	3:C:181:PRO:HD2	1.65	0.79
3:C:247:PHE:CE1	3:C:309:VAL:HG22	2.18	0.79
1:A:277:TYR:HA	1:A:280:PHE:CE1	2.17	0.78
2:B:281:ILE:HG23	2:B:284:LEU:HB3	1.65	0.78
3:C:113:ARG:CD	3:C:117:TYR:HB3	2.13	0.78
1:D:7:LEU:HD13	1:D:70:ALA:O	1.82	0.78
1:D:72:TYR:CD1	1:D:72:TYR:O	2.37	0.78
1:D:377:GLU:CG	4:E:415:CYS:HB2	2.05	0.78
2:B:129:THR:HG22	2:B:142:CYS:HA	1.64	0.78
2:B:175:ILE:HG12	2:B:176:ASN:N	1.98	0.78
3:C:457:SER:O	3:C:461:ILE:HG13	1.84	0.78
1:D:32:THR:CB	1:D:59:GLN:HB3	2.11	0.78
1:D:198:TYR:HD1	1:D:198:TYR:H	0.84	0.78
1:A:406:ILE:HA	1:A:409:ILE:CD1	2.14	0.78
2:B:23:GLN:N	2:B:23:GLN:NE2	2.18	0.78
2:B:90:ILE:HG23	2:B:147:LYS:N	1.98	0.78
2:B:226:VAL:O	2:B:230:LEU:HG	1.82	0.78
2:B:439:PHE:HA	2:B:442:ILE:HB	1.63	0.78
3:C:107:PHE:CG	3:C:107:PHE:O	2.37	0.78
3:C:137:PHE:CE1	3:C:288:ILE:HG22	2.18	0.78
1:D:57:ARG:HB2	1:D:119:THR:HG22	1.65	0.78
1:D:78:ILE:HD12	1:D:78:ILE:O	1.83	0.78
1:D:187:TRP:CZ3	1:D:189:TYR:CD1	2.71	0.78
3:C:482:PRO:HG2	3:C:483:ALA:H	1.49	0.78
1:D:29:VAL:HG23	1:D:60:TRP:NE1	1.98	0.78
1:D:31:ILE:HG22	1:D:158:ILE:HG23	1.64	0.78
3:C:148:PHE:HB2	3:C:215:VAL:HG21	1.63	0.78
1:A:420:ILE:HG13	1:A:421:GLY:H	1.48	0.78
1:D:75:ILE:HG13	1:D:78:ILE:HG23	1.66	0.78
4:E:27:VAL:HB	4:E:154:GLU:C	2.08	0.78
1:A:218:VAL:HG13	1:A:219:ILE:N	1.99	0.78
1:A:233:PHE:O	1:A:236:PRO:HG2	1.83	0.78
2:B:297:LEU:HD13	2:B:445:THR:CG2	2.13	0.78
2:B:408:ILE:HG23	2:B:409:LYS:N	1.96	0.78
3:C:266:ALA:HB1	3:C:270:PHE:CZ	2.18	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:273:LEU:O	3:C:276:GLN:HB2	1.84	0.78
3:C:278:LEU:HD12	3:C:278:LEU:O	1.82	0.78
1:D:48:GLN:OE1	1:D:130:ILE:HD13	1.83	0.78
1:D:296:ILE:HA	1:D:299:HIS:HB2	1.66	0.78
4:E:142:SER:OG	4:E:209:ILE:HD11	1.84	0.78
1:A:66:ARG:HD3	1:A:66:ARG:N	1.97	0.78
2:B:227:PRO:O	2:B:231:ILE:HG12	1.84	0.78
1:D:152:ASP:HB3	1:D:197:PRO:HA	1.64	0.78
1:D:305:THR:HG22	1:D:400:LYS:CB	2.12	0.78
1:A:43:VAL:HG22	1:A:50:VAL:HG13	1.66	0.78
1:A:166:ASP:OD1	1:A:166:ASP:C	2.27	0.78
2:B:218:LEU:HD11	2:B:222:VAL:HG22	1.66	0.78
1:D:384:GLU:HG2	4:E:422:ILE:CD1	2.14	0.78
1:A:3:HIS:HB2	1:A:7:LEU:HD21	1.64	0.78
1:A:380:LYS:CD	2:B:408:ILE:HB	2.14	0.78
2:B:46:LYS:HB2	2:B:276:SER:C	2.09	0.78
1:D:62:ASP:HB3	1:D:65:LEU:CD1	2.08	0.78
4:E:183:TRP:HA	4:E:216:ARG:HA	1.64	0.78
4:E:225:ILE:HD13	4:E:225:ILE:N	1.99	0.78
4:E:249:GLN:NE2	4:E:250:LYS:HE3	1.98	0.78
1:A:66:ARG:HD3	1:A:66:ARG:H	1.46	0.77
2:B:68:ASP:O	2:B:72:TYR:HB3	1.85	0.77
1:D:106:THR:C	1:D:107:LYS:HD3	2.09	0.77
4:E:100:GLU:HB2	4:E:122:ILE:CD1	2.13	0.77
4:E:229:CYS:HA	4:E:232:ILE:HB	1.65	0.77
3:C:138:PRO:HB3	3:C:290:LYS:HZ2	1.48	0.77
3:C:275:SER:O	3:C:278:LEU:HB3	1.84	0.77
3:C:471:PHE:C	3:C:471:PHE:CD1	2.62	0.77
4:E:144:VAL:HG12	4:E:209:ILE:HA	1.65	0.77
1:A:413:VAL:HG12	1:A:417:ILE:HD11	1.66	0.77
3:C:93:VAL:CG2	3:C:151:LEU:HD22	2.15	0.77
1:D:292:THR:HA	1:D:295:VAL:HG22	1.67	0.77
4:E:129:ILE:HG22	4:E:133:TYR:CE2	2.18	0.77
4:E:141:CYS:HB3	4:E:212:LEU:HB2	1.66	0.77
1:A:72:TYR:CB	1:A:112:TYR:CD2	2.66	0.77
2:B:238:VAL:HG21	2:B:255:ALA:HB1	1.64	0.77
2:B:270:VAL:HG11	2:B:284:LEU:CD1	2.14	0.77
2:B:287:ILE:HD12	2:B:288:MET:N	1.99	0.77
1:D:72:TYR:HB2	1:D:112:TYR:CB	2.15	0.77
1:D:78:ILE:CD1	1:D:110:LEU:HB3	2.15	0.77
1:D:170:PHE:HE2	1:D:176:TRP:CD1	2.02	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:LEU:HD23	1:A:57:ARG:N	2.00	0.77
1:A:176:TRP:CE3	1:A:209:ARG:CZ	2.67	0.77
2:B:269:LYS:C	2:B:271:PRO:HD2	2.10	0.77
2:B:297:LEU:CD1	2:B:445:THR:HG21	2.14	0.77
2:B:425:LYS:HA	2:B:428:TRP:CD1	2.20	0.77
3:C:6:ARG:O	3:C:9:ASN:HB3	1.84	0.77
1:D:141:ASN:HA	1:D:205:PHE:O	1.85	0.77
1:D:263:LEU:O	1:D:267:THR:HG22	1.85	0.77
2:B:9:SER:CA	2:B:12:PHE:CE1	2.67	0.77
2:B:56:LEU:CD2	2:B:103:THR:HA	2.15	0.77
2:B:141:ASN:HA	2:B:211:LEU:O	1.84	0.77
3:C:38:THR:HG22	3:C:57:TRP:CE3	2.18	0.77
3:C:43:ILE:H	3:C:43:ILE:HD12	1.47	0.77
3:C:316:THR:HG22	3:C:317:PRO:HD2	1.66	0.77
3:C:472:ILE:HB	3:C:475:MET:SD	2.25	0.77
1:D:43:VAL:HG13	1:D:49:ILE:O	1.85	0.77
1:A:224:LEU:HG	1:A:225:PHE:N	1.99	0.77
3:C:68:THR:HA	3:C:115:ASN:CA	2.08	0.77
3:C:472:ILE:HA	3:C:475:MET:HB3	1.66	0.77
3:C:1:VAL:HA	3:C:4:GLU:CG	2.14	0.77
3:C:453:ILE:HG23	3:C:454:ASP:N	1.98	0.77
1:D:55:ARG:HA	1:D:120:PRO:O	1.84	0.77
4:E:313:THR:CB	4:E:441:LEU:HB3	2.15	0.77
1:A:262:GLU:C	1:A:265:PRO:HD2	2.10	0.77
2:B:31:VAL:HG12	2:B:158:LEU:HD21	1.67	0.77
2:B:101:GLU:C	2:B:102:ILE:HG13	2.08	0.77
2:B:238:VAL:HG22	2:B:255:ALA:HB1	1.66	0.77
3:C:247:PHE:CD2	3:C:460:ILE:HD11	2.19	0.77
1:D:291:VAL:HG11	1:D:413:VAL:HG11	1.66	0.77
4:E:128:PRO:O	4:E:129:ILE:HG12	1.85	0.77
1:A:20:ARG:HH11	1:A:20:ARG:CG	1.96	0.76
2:B:35:LEU:HD21	2:B:56:LEU:HA	1.65	0.76
3:C:59:ASP:HA	3:C:121:LEU:CB	2.14	0.76
2:B:20:ARG:HD3	2:B:20:ARG:H	1.48	0.76
3:C:232:PHE:C	3:C:235:PRO:HD2	2.10	0.76
3:C:247:PHE:CE2	3:C:460:ILE:HD11	2.20	0.76
1:D:228:LEU:O	1:D:232:VAL:HG23	1.85	0.76
1:D:271:VAL:HG13	1:D:271:VAL:O	1.84	0.76
3:C:90:PRO:HD2	3:C:120:TRP:HZ3	1.50	0.76
3:C:452:THR:O	3:C:456:LEU:HG	1.86	0.76
1:D:135:PHE:C	1:D:135:PHE:CD1	2.60	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:243:MET:H	1:D:243:MET:CE	1.98	0.76
4:E:284:LYS:N	4:E:284:LYS:CE	2.44	0.76
3:C:453:ILE:CG2	3:C:454:ASP:H	1.99	0.76
4:E:35:THR:HB	4:E:54:TRP:HE3	1.51	0.76
1:A:90:LEU:CD1	1:A:100:PHE:HE2	1.99	0.76
1:A:413:VAL:O	1:A:417:ILE:HG13	1.84	0.76
2:B:45:GLU:OE1	2:B:277:VAL:HB	1.84	0.76
3:C:7:LEU:HD23	3:C:10:ASP:HB2	1.68	0.76
3:C:113:ARG:HD2	3:C:117:TYR:CB	2.12	0.76
1:D:405:VAL:O	1:D:409:ILE:HG23	1.86	0.76
1:A:52:THR:O	1:A:123:ILE:HG13	1.86	0.76
2:B:31:VAL:CG2	2:B:86:TRP:CZ3	2.64	0.76
3:C:51:THR:HA	3:C:128:SER:O	1.84	0.76
1:D:233:PHE:HZ	1:D:417:ILE:HD12	1.42	0.76
4:E:45:LYS:CA	4:E:280:PRO:CA	2.60	0.76
4:E:45:LYS:HG2	4:E:279:VAL:CA	2.15	0.76
4:E:197:GLN:HG2	4:E:198:LEU:N	2.00	0.76
4:E:219:LEU:CB	4:E:222:ILE:HB	2.14	0.76
2:B:9:SER:CA	2:B:12:PHE:HE1	1.99	0.76
2:B:93:MET:CG	2:B:206:ASP:HB3	2.14	0.76
2:B:104:LEU:HA	2:B:118:TRP:HH2	1.48	0.76
3:C:122:PRO:HB3	1:D:149:TRP:HZ2	1.49	0.76
1:D:60:TRP:CH2	1:D:86:TRP:CZ3	2.74	0.76
1:A:198:TYR:O	1:A:198:TYR:CD1	2.38	0.76
3:C:271:LEU:HD21	3:C:299:VAL:CG1	2.16	0.76
3:C:431:LYS:HE2	1:D:379:VAL:HG22	1.68	0.76
1:D:36:GLN:HB3	1:D:55:ARG:HG3	1.67	0.76
4:E:209:ILE:HG12	4:E:211:PHE:HE1	1.51	0.76
1:A:290:ILE:O	1:A:293:VAL:HG12	1.86	0.76
2:B:301:VAL:O	2:B:304:LEU:HB3	1.86	0.76
3:C:2:ASN:HD22	3:C:72:SER:HB3	1.50	0.76
4:E:39:LEU:HD12	4:E:49:LEU:HD13	1.66	0.76
4:E:56:GLU:HB2	4:E:118:LEU:HD22	1.65	0.76
1:A:43:VAL:HG13	1:A:50:VAL:CG2	2.16	0.76
2:B:40:LEU:HD23	2:B:52:THR:OG1	1.86	0.76
3:C:138:PRO:N	3:C:288:ILE:HD12	2.01	0.76
3:C:476:GLY:HA2	3:C:479:ASN:HB3	1.66	0.76
1:D:263:LEU:HD11	4:E:266:PHE:CZ	2.21	0.76
1:D:302:SER:HB2	1:D:305:THR:HG23	1.68	0.76
1:A:72:TYR:CD1	1:A:72:TYR:C	2.63	0.75
1:A:102:ILE:O	1:A:102:ILE:CG2	2.34	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:ILE:HG22	1:A:198:TYR:HD2	1.51	0.75
2:B:258:ALA:HB2	3:C:265:LEU:HD13	1.67	0.75
1:D:214:PHE:O	1:D:218:VAL:HG23	1.85	0.75
1:D:261:VAL:O	1:D:265:PRO:HD2	1.87	0.75
4:E:172:ILE:HD11	4:E:187:HIS:CA	2.16	0.75
1:A:391:GLU:HA	1:A:394:ASN:ND2	2.01	0.75
1:D:301:ARG:HH12	1:D:406:ILE:HD11	1.49	0.75
1:D:412:CYS:O	1:D:416:LEU:HD23	1.87	0.75
4:E:456:LEU:O	4:E:456:LEU:HD22	1.86	0.75
1:A:135:PHE:N	1:A:136:PRO:HD2	2.02	0.75
4:E:449:ALA:HA	4:E:452:TRP:CD1	2.21	0.75
1:A:89:ASP:OD2	1:A:150:THR:HG22	1.84	0.75
2:B:242:PRO:HG2	2:B:243:PRO:CD	2.16	0.75
3:C:280:GLU:HG3	3:C:281:THR:N	2.00	0.75
1:D:287:SER:O	1:D:290:ILE:HG12	1.86	0.75
1:D:383:ALA:HA	1:D:386:MET:HG2	1.68	0.75
1:A:95:ASN:N	1:A:95:ASN:ND2	2.34	0.75
3:C:84:PRO:HG3	3:C:107:PHE:C	2.12	0.75
3:C:479:ASN:ND2	3:C:479:ASN:C	2.44	0.75
1:D:157:SER:HA	1:D:199:LEU:HD12	1.66	0.75
1:D:379:VAL:HG22	1:D:382:ILE:HD12	1.67	0.75
4:E:91:LEU:HB3	4:E:94:ASN:H	1.50	0.75
1:A:117:MET:HE3	1:A:119:THR:OG1	1.86	0.75
1:A:148:ILE:HG21	1:A:198:TYR:CB	2.15	0.75
3:C:37:LEU:HD12	3:C:217:PHE:CD2	2.22	0.75
3:C:206:PHE:C	3:C:206:PHE:CD1	2.64	0.75
3:C:319:THR:HB	3:C:447:ASN:HB3	1.68	0.75
1:D:86:TRP:CD2	1:D:86:TRP:C	2.64	0.75
4:E:235:LEU:C	4:E:235:LEU:CD1	2.53	0.75
1:A:35:LEU:HD21	1:A:37:LEU:CD2	2.17	0.75
1:A:63:VAL:O	1:A:66:ARG:HD2	1.86	0.75
1:A:156:VAL:HG22	1:A:157:SER:N	2.02	0.75
1:D:35:LEU:HD11	1:D:54:VAL:CG1	2.15	0.75
1:D:253:LEU:HD23	1:D:254:THR:H	1.52	0.75
4:E:55:ILE:N	4:E:118:LEU:HD13	2.02	0.75
4:E:79:ILE:O	4:E:79:ILE:CG2	2.35	0.75
4:E:91:LEU:N	4:E:95:VAL:HB	2.01	0.75
2:B:278:PRO:O	2:B:278:PRO:HG2	1.87	0.75
3:C:299:VAL:O	3:C:302:VAL:HG23	1.87	0.75
3:C:449:VAL:HG12	3:C:452:THR:CB	2.17	0.75
1:A:46:VAL:HB	1:A:270:ALA:O	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:LYS:HZ2	1:A:202:THR:HG23	1.52	0.75
2:B:31:VAL:HG12	2:B:158:LEU:CD2	2.17	0.75
3:C:227:PHE:O	3:C:230:ILE:HG12	1.87	0.74
1:A:151:TYR:O	1:A:198:TYR:HB3	1.86	0.74
1:A:376:ILE:HG23	1:A:380:LYS:HZ3	1.48	0.74
2:B:58:LEU:HD11	2:B:118:TRP:HE3	1.51	0.74
2:B:92:LEU:H	2:B:96:ASN:CB	1.97	0.74
1:D:244:THR:HG23	1:D:245:LEU:N	2.00	0.74
4:E:75:ASP:HA	4:E:111:ASN:ND2	1.95	0.74
2:B:52:THR:HG22	2:B:53:SER:H	1.51	0.74
2:B:70:ALA:O	2:B:74:GLY:HA3	1.87	0.74
2:B:144:MET:HE2	2:B:211:LEU:HD21	1.69	0.74
3:C:248:TYR:C	3:C:250:PRO:HD2	2.12	0.74
1:D:178:MET:HA	1:D:207:MET:CB	2.17	0.74
1:D:271:VAL:O	1:D:271:VAL:CG1	2.35	0.74
4:E:20:PRO:HB3	4:E:61:ASP:OD1	1.88	0.74
4:E:249:GLN:HE22	4:E:250:LYS:HE3	1.52	0.74
1:A:62:ASP:HB3	1:A:65:LEU:CD1	2.17	0.74
1:A:295:VAL:O	1:A:299:HIS:HB2	1.87	0.74
2:B:129:THR:CG2	2:B:142:CYS:HA	2.17	0.74
3:C:194:HIS:CG	3:C:195:LYS:H	2.05	0.74
1:D:130:ILE:HG12	1:D:131:ILE:N	2.01	0.74
2:B:9:SER:O	2:B:13:GLU:HG3	1.87	0.74
1:D:129:GLU:C	1:D:130:ILE:HG23	2.12	0.74
1:D:132:VAL:C	1:D:274:ILE:HG23	2.12	0.74
1:D:276:LYS:CD	1:D:276:LYS:H	2.00	0.74
1:A:35:LEU:HD23	1:A:35:LEU:C	2.12	0.74
1:A:43:VAL:HG22	1:A:50:VAL:HG22	1.67	0.74
1:A:247:ILE:HG13	4:E:253:LEU:HD12	1.68	0.74
2:B:220:TYR:CB	2:B:223:TYR:CE2	2.71	0.74
3:C:29:GLU:O	3:C:156:ASN:HA	1.88	0.74
3:C:160:MET:H	3:C:213:GLN:HB2	1.52	0.74
3:C:161:ASP:HA	3:C:199:LYS:HG2	1.69	0.74
3:C:216:THR:O	3:C:217:PHE:HD1	1.70	0.74
1:D:153:GLY:HA3	1:D:196:THR:HG22	1.69	0.74
4:E:270:GLN:C	4:E:273:PRO:HD2	2.12	0.74
1:A:67:TRP:HB2	1:A:112:TYR:HB2	1.69	0.74
1:A:239:SER:CB	2:B:312:HIS:HB3	2.17	0.74
1:A:304:SER:HA	1:A:400:LYS:HD3	1.70	0.74
2:B:7:LEU:O	2:B:11:LEU:HD23	1.87	0.74
2:B:46:LYS:HB2	2:B:277:VAL:H	1.50	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:141:ASN:ND2	2:B:212:ILE:HG12	2.02	0.74
3:C:179:ILE:HD12	3:C:195:LYS:CB	2.16	0.74
1:A:106:THR:HG22	1:A:107:LYS:H	1.52	0.74
1:A:388:SER:O	1:A:391:GLU:HB3	1.86	0.74
2:B:20:ARG:HG3	2:B:155:GLU:OE1	1.88	0.74
2:B:147:LYS:HG3	2:B:148:SER:N	2.03	0.74
3:C:132:ILE:O	3:C:136:TYR:HB2	1.88	0.74
1:D:239:SER:HB2	1:D:242:LYS:HE2	1.69	0.74
4:E:184:THR:CG2	4:E:215:GLN:HG2	2.18	0.74
1:A:92:LEU:HB2	1:A:96:ALA:N	2.03	0.74
1:A:107:LYS:HE3	2:B:150:THR:CG2	2.18	0.74
4:E:140:ASN:HD21	4:E:211:PHE:HA	1.53	0.74
1:D:106:THR:HG23	1:D:107:LYS:HE2	1.69	0.73
1:D:118:TRP:NE1	1:D:120:PRO:HB3	2.03	0.73
1:A:65:LEU:CB	1:A:110:LEU:HD11	2.13	0.73
3:C:52:LEU:HD23	3:C:128:SER:OG	1.88	0.73
3:C:106:TYR:C	3:C:107:PHE:HD1	1.95	0.73
3:C:278:LEU:CD1	3:C:278:LEU:O	2.37	0.73
3:C:311:ASN:O	3:C:315:ARG:HB3	1.88	0.73
3:C:427:ASN:HA	3:C:430:VAL:HG23	1.69	0.73
1:D:92:LEU:HD22	1:D:92:LEU:N	2.03	0.73
1:A:141:ASN:HA	1:A:205:PHE:O	1.88	0.73
3:C:137:PHE:CE1	3:C:288:ILE:CG2	2.72	0.73
1:D:56:LEU:HG	1:D:120:PRO:CG	2.15	0.73
1:D:243:MET:HE2	1:D:243:MET:N	2.03	0.73
4:E:449:ALA:O	4:E:452:TRP:HB2	1.87	0.73
3:C:243:ALA:HB3	3:C:302:VAL:HG12	1.70	0.73
1:D:149:TRP:CE2	1:D:150:THR:HB	2.23	0.73
1:A:43:VAL:CG2	1:A:50:VAL:HG22	2.18	0.73
1:A:187:TRP:CZ2	1:A:189:TYR:HB3	2.24	0.73
1:A:406:ILE:CG2	1:A:409:ILE:HD11	2.18	0.73
2:B:109:LEU:HB3	2:B:117:SER:HB2	1.68	0.73
2:B:175:ILE:CD1	2:B:190:HIS:HD2	2.02	0.73
3:C:179:ILE:HD11	3:C:195:LYS:HB3	1.69	0.73
1:D:35:LEU:CD1	1:D:54:VAL:HG11	2.16	0.73
4:E:14:TYR:HE2	4:E:16:LYS:HE3	1.53	0.73
1:A:136:PRO:HB3	1:A:277:TYR:OH	1.88	0.73
1:A:278:MET:O	1:A:281:THR:HG22	1.89	0.73
1:A:291:VAL:O	1:A:295:VAL:HG23	1.89	0.73
1:A:397:GLU:O	1:A:400:LYS:HB2	1.88	0.73
2:B:241:LEU:HG	2:B:248:LYS:HB2	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3:HIS:HB3	1:D:7:LEU:CG	2.18	0.73
1:D:56:LEU:N	1:D:56:LEU:HD23	2.02	0.73
1:A:218:VAL:O	1:A:221:PRO:HD2	1.88	0.73
1:A:221:PRO:C	1:A:224:LEU:HB3	2.13	0.73
3:C:60:HIS:NE2	3:C:92:ILE:HD13	2.02	0.73
4:E:66:TRP:CD1	4:E:111:ASN:CA	2.70	0.73
4:E:127:CYS:SG	4:E:128:PRO:HD2	2.29	0.73
1:A:41:ILE:HD11	1:A:51:GLU:HB3	1.71	0.73
2:B:236:ILE:CB	2:B:446:MET:HE1	2.15	0.73
2:B:435:ALA:O	2:B:439:PHE:HB3	1.89	0.73
1:D:247:ILE:HG22	1:D:248:SER:N	2.04	0.73
1:D:419:ILE:HD12	1:D:420:ILE:N	2.04	0.73
4:E:33:LYS:CE	4:E:160:SER:HB2	2.19	0.73
4:E:148:GLN:CA	4:E:148:GLN:NE2	2.50	0.73
3:C:25:LYS:HG3	3:C:25:LYS:O	1.87	0.73
1:D:291:VAL:O	1:D:295:VAL:HG13	1.88	0.73
1:D:379:VAL:HA	1:D:382:ILE:CG1	2.19	0.73
4:E:27:VAL:HB	4:E:154:GLU:O	1.88	0.73
4:E:45:LYS:HE2	4:E:278:ASN:O	1.88	0.73
4:E:65:SER:HA	4:E:112:ASP:HA	1.70	0.73
4:E:448:LYS:N	4:E:448:LYS:HD2	2.02	0.73
1:A:67:TRP:HB2	1:A:112:TYR:O	1.89	0.73
3:C:271:LEU:HD23	3:C:271:LEU:C	2.13	0.73
1:D:145:LYS:HG3	1:D:202:THR:HG23	0.85	0.73
4:E:247:GLY:N	4:E:250:LYS:HZ2	1.86	0.73
1:A:233:PHE:CE1	1:A:413:VAL:HG11	2.23	0.72
1:A:416:LEU:O	1:A:419:ILE:HG22	1.87	0.72
2:B:93:MET:HB2	2:B:145:VAL:CG2	2.19	0.72
3:C:148:PHE:CB	3:C:215:VAL:CG2	2.63	0.72
3:C:196:PRO:HG2	3:C:218:TYR:HB2	1.69	0.72
4:E:273:PRO:HG2	4:E:274:GLU:H	1.53	0.72
4:E:431:ASP:O	4:E:435:GLU:HG3	1.88	0.72
2:B:55:PHE:N	2:B:55:PHE:HD1	1.85	0.72
3:C:438:ALA:HA	3:C:441:GLU:CD	2.15	0.72
1:D:181:TYR:HE1	1:D:203:TYR:HB3	1.53	0.72
1:D:201:ILE:O	1:D:203:TYR:HE1	1.72	0.72
4:E:42:LEU:HD22	4:E:183:TRP:CZ2	2.23	0.72
4:E:211:PHE:O	4:E:212:LEU:HD12	1.87	0.72
1:A:124:PHE:CD1	1:A:124:PHE:C	2.67	0.72
1:A:141:ASN:HB3	1:A:206:ILE:HG13	1.71	0.72
1:A:148:ILE:HD11	1:A:156:VAL:CG1	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:32:THR:HB	1:D:59:GLN:CB	2.15	0.72
1:D:92:LEU:HD13	1:D:146:LEU:HG	1.71	0.72
1:A:104:HIS:HB2	1:A:105:MET:SD	2.29	0.72
2:B:232:SER:O	2:B:236:ILE:HG22	1.89	0.72
1:D:142:CYS:SG	1:D:144:MET:HG3	2.29	0.72
1:A:77:LYS:O	1:A:77:LYS:CG	2.38	0.72
1:A:245:LEU:HD21	2:B:253:ILE:HB	1.70	0.72
1:A:251:LEU:HD22	4:E:260:ALA:HA	1.70	0.72
2:B:75:ILE:CG2	3:C:27:ASN:HB2	2.19	0.72
4:E:159:LEU:HD12	4:E:192:LYS:N	2.03	0.72
4:E:187:HIS:ND1	4:E:189:PRO:HG3	2.05	0.72
2:B:226:VAL:HG22	2:B:227:PRO:HD3	1.71	0.72
3:C:8:ILE:HG23	3:C:8:ILE:O	1.86	0.72
3:C:111:LEU:HB3	3:C:119:THR:OG1	1.89	0.72
1:D:282:MET:HE2	1:D:286:ILE:HD11	1.71	0.72
4:E:26:HIS:O	4:E:27:VAL:HG22	1.89	0.72
1:A:110:LEU:HD12	1:A:111:ASP:H	1.55	0.72
1:A:274:ILE:O	1:A:277:TYR:HB2	1.89	0.72
1:A:401:TYR:CD1	1:A:401:TYR:O	2.43	0.72
3:C:191:GLU:HG2	3:C:222:ARG:C	2.13	0.72
3:C:201:ILE:HD12	3:C:213:GLN:OE1	1.90	0.72
3:C:257:MET:O	3:C:261:ILE:HG12	1.88	0.72
3:C:306:CYS:O	3:C:309:VAL:HB	1.88	0.72
1:D:64:ARG:HA	1:D:66:ARG:HH11	1.54	0.72
1:A:25:HIS:O	1:A:25:HIS:CG	2.42	0.72
1:A:38:ILE:O	1:A:38:ILE:CG2	2.37	0.72
1:A:56:LEU:O	1:A:119:THR:HA	1.90	0.72
2:B:160:HIS:H	2:B:195:LYS:HZ1	1.37	0.72
3:C:106:TYR:HD1	3:C:106:TYR:C	1.96	0.72
2:B:40:LEU:HD13	2:B:40:LEU:C	2.15	0.72
2:B:220:TYR:HB3	2:B:223:TYR:CZ	2.23	0.72
1:D:43:VAL:HG22	1:D:50:VAL:CA	2.19	0.72
4:E:44:GLU:CG	4:E:129:ILE:HB	2.19	0.72
4:E:172:ILE:HD11	4:E:187:HIS:HA	1.71	0.72
2:B:258:ALA:HB2	3:C:265:LEU:HD22	1.71	0.72
1:D:250:LEU:HD22	1:D:292:THR:OG1	1.89	0.72
4:E:52:ASN:HD21	4:E:120:PRO:HB2	1.55	0.72
4:E:94:ASN:ND2	4:E:125:SER:HB2	2.03	0.72
4:E:214:ILE:C	4:E:214:ILE:HD12	2.13	0.72
2:B:92:LEU:HA	2:B:145:VAL:O	1.90	0.71
3:C:195:LYS:HG3	3:C:195:LYS:O	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:462:THR:HB	3:C:463:PRO:HD3	1.72	0.71
1:D:250:LEU:HD22	1:D:292:THR:CB	2.19	0.71
4:E:44:GLU:CD	4:E:129:ILE:CB	2.60	0.71
4:E:184:THR:O	4:E:214:ILE:HB	1.90	0.71
4:E:240:TYR:HB3	4:E:453:ILE:CD1	2.19	0.71
1:A:39:GLN:O	1:A:53:ASN:HB2	1.89	0.71
1:A:54:VAL:HG23	1:A:122:ALA:HB3	1.71	0.71
1:A:136:PRO:HD3	1:A:274:ILE:HG23	1.70	0.71
2:B:75:ILE:HG22	3:C:27:ASN:HB2	1.71	0.71
2:B:434:VAL:HG13	2:B:438:LEU:HD12	1.71	0.71
3:C:30:VAL:HG13	3:C:31:VAL:C	2.16	0.71
3:C:80:LEU:HD11	1:D:20:ARG:HH22	1.54	0.71
3:C:179:ILE:HG13	3:C:181:PRO:CD	2.21	0.71
1:D:7:LEU:O	1:D:11:LEU:HG	1.90	0.71
1:D:276:LYS:H	1:D:276:LYS:HD2	1.54	0.71
4:E:107:VAL:HG13	4:E:117:TRP:HB2	1.70	0.71
1:A:256:PHE:CZ	2:B:261:VAL:HG23	2.25	0.71
2:B:2:VAL:HG12	2:B:3:MET:HE3	1.72	0.71
3:C:60:HIS:HB3	3:C:62:TRP:CZ3	2.16	0.71
3:C:293:MET:O	3:C:297:SER:HB3	1.89	0.71
1:D:43:VAL:CG1	1:D:50:VAL:HG22	2.19	0.71
4:E:44:GLU:HB3	4:E:280:PRO:CB	2.20	0.71
1:A:265:PRO:HG2	1:A:266:SER:H	1.55	0.71
2:B:183:ASN:HB2	3:C:50:GLU:OE2	1.90	0.71
2:B:311:THR:CB	2:B:430:TYR:CD2	2.74	0.71
3:C:36:SER:HB3	3:C:59:ASP:CB	2.20	0.71
4:E:48:ALA:HA	4:E:125:SER:O	1.90	0.71
1:A:139:GLN:NE2	1:A:206:ILE:HG23	2.05	0.71
1:A:292:THR:HA	1:A:296:ILE:HD11	1.73	0.71
3:C:35:LEU:HD22	3:C:215:VAL:HG21	1.73	0.71
3:C:143:ASN:OD1	3:C:220:ILE:HB	1.91	0.71
1:D:178:MET:SD	1:D:207:MET:HB3	2.30	0.71
4:E:191:LYS:HB2	4:E:209:ILE:CG2	2.20	0.71
2:B:160:HIS:NE2	2:B:207:VAL:HG11	2.05	0.71
3:C:271:LEU:HD21	3:C:299:VAL:HG11	1.71	0.71
4:E:65:SER:CB	4:E:112:ASP:HA	2.21	0.71
4:E:437:GLU:O	4:E:441:LEU:HG	1.90	0.71
2:B:93:MET:HG3	2:B:206:ASP:CG	2.15	0.71
2:B:133:MET:HE2	2:B:140:GLN:HB3	1.72	0.71
3:C:38:THR:HG21	3:C:57:TRP:CE3	2.25	0.71
3:C:458:MET:HA	3:C:461:ILE:HD12	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:262:THR:HA	4:E:265:LEU:HB2	1.72	0.71
4:E:265:LEU:O	4:E:268:ILE:HG23	1.91	0.71
1:A:95:ASN:HA	1:A:127:TYR:HB3	1.73	0.71
1:A:250:LEU:HD22	1:A:292:THR:HG22	1.72	0.71
2:B:4:GLU:OE1	2:B:8:LEU:HG	1.91	0.71
3:C:80:LEU:O	3:C:112:VAL:HB	1.91	0.71
3:C:316:THR:HG22	3:C:317:PRO:CD	2.20	0.71
1:D:287:SER:HA	1:D:290:ILE:HD13	1.72	0.71
1:A:251:LEU:HD13	4:E:260:ALA:HB3	1.72	0.71
3:C:190:TRP:HD1	3:C:221:ILE:HD12	1.52	0.71
3:C:307:GLY:O	3:C:310:LEU:HB2	1.91	0.71
2:B:21:PRO:HG2	2:B:85:VAL:CG1	2.21	0.71
3:C:64:ASP:O	3:C:116:GLY:HA3	1.91	0.71
4:E:100:GLU:HB2	4:E:122:ILE:HD11	1.71	0.71
2:B:35:LEU:CD2	2:B:56:LEU:HA	2.20	0.70
2:B:281:ILE:CG2	2:B:284:LEU:HB3	2.19	0.70
4:E:149:THR:HG23	4:E:150:TYR:H	1.55	0.70
2:B:175:ILE:CG1	2:B:176:ASN:H	2.02	0.70
3:C:55:ASN:HA	3:C:124:ALA:O	1.90	0.70
3:C:199:LYS:HZ2	3:C:199:LYS:C	1.99	0.70
3:C:204:ASP:OD1	3:C:205:LYS:HD3	1.91	0.70
3:C:262:CYS:SG	1:D:251:LEU:CD1	2.78	0.70
1:D:257:LEU:C	1:D:257:LEU:HD12	2.15	0.70
4:E:138:TRP:CZ3	4:E:215:GLN:HA	2.26	0.70
4:E:239:VAL:HA	4:E:242:LEU:HD23	1.73	0.70
1:A:279:LEU:HA	1:A:282:MET:HB2	1.71	0.70
1:A:384:GLU:CD	2:B:411:ILE:HG21	2.16	0.70
2:B:284:LEU:HD23	2:B:287:ILE:HD11	1.74	0.70
2:B:304:LEU:O	2:B:307:ARG:HB3	1.91	0.70
1:A:110:LEU:HD12	1:A:111:ASP:N	2.06	0.70
1:A:227:PHE:HA	1:A:230:VAL:HB	1.71	0.70
3:C:7:LEU:HD23	3:C:10:ASP:CB	2.22	0.70
4:E:44:GLU:OE1	4:E:129:ILE:HD12	1.91	0.70
1:A:158:ILE:O	1:A:199:LEU:HB2	1.91	0.70
2:B:35:LEU:C	2:B:174:MET:HE1	2.17	0.70
3:C:115:ASN:ND2	3:C:115:ASN:N	2.36	0.70
3:C:470:ILE:O	3:C:474:VAL:HG23	1.91	0.70
4:E:45:LYS:CB	4:E:280:PRO:HA	2.20	0.70
3:C:98:ASN:C	3:C:100:GLY:H	2.00	0.70
3:C:247:PHE:CD1	3:C:309:VAL:HG22	2.27	0.70
1:D:169:THR:O	1:D:169:THR:CG2	2.36	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:6:LEU:HD12	4:E:69:SER:OG	1.91	0.70
4:E:436:ASN:CA	4:E:439:TRP:HE1	2.02	0.70
1:A:267:THR:O	1:A:271:VAL:HG22	1.90	0.70
1:A:384:GLU:HA	1:A:387:LYS:CG	2.22	0.70
2:B:85:VAL:HG12	2:B:86:TRP:N	2.05	0.70
1:D:60:TRP:CE2	1:D:86:TRP:CH2	2.80	0.70
1:D:229:THR:HA	1:D:232:VAL:HG23	1.73	0.70
1:D:419:ILE:HD12	1:D:420:ILE:CG2	2.22	0.70
4:E:22:LYS:HG3	4:E:23:THR:CB	2.21	0.70
4:E:291:PHE:O	4:E:295:VAL:HG23	1.91	0.70
1:A:66:ARG:CA	1:A:113:THR:HA	2.14	0.70
1:A:76:LYS:HG2	1:A:77:LYS:N	2.06	0.70
2:B:40:LEU:HD13	2:B:41:LEU:N	2.06	0.70
2:B:272:GLU:HG2	2:B:272:GLU:O	1.92	0.70
3:C:69:TRP:CD1	3:C:114:PRO:C	2.69	0.70
3:C:245:LEU:O	3:C:249:LEU:HD13	1.92	0.70
3:C:305:ASN:O	3:C:309:VAL:HG23	1.92	0.70
2:B:266:LEU:O	2:B:269:LYS:HG3	1.92	0.70
1:D:72:TYR:CD1	1:D:73:GLY:N	2.60	0.70
4:E:2:GLU:HA	4:E:5:ARG:CG	2.21	0.70
1:A:175:GLU:HB3	1:A:211:PRO:HD3	1.72	0.70
2:B:55:PHE:N	2:B:55:PHE:CD1	2.55	0.70
2:B:108:VAL:HG13	2:B:118:TRP:HB2	1.73	0.70
3:C:162:LEU:CD1	3:C:217:PHE:CE1	2.75	0.70
3:C:180:ASP:CB	3:C:181:PRO:HD3	2.11	0.70
1:D:171:MET:HG2	1:D:171:MET:O	1.92	0.70
1:D:261:VAL:HA	1:D:264:ILE:HD12	1.73	0.70
4:E:197:GLN:HG2	4:E:198:LEU:H	1.56	0.70
4:E:226:ILE:O	4:E:230:VAL:HG23	1.92	0.70
3:C:35:LEU:HD12	3:C:60:HIS:NE2	2.07	0.69
3:C:102:TYR:HE1	3:C:106:TYR:HB3	1.55	0.69
3:C:194:HIS:CG	3:C:195:LYS:N	2.57	0.69
1:D:146:LEU:HD22	1:D:203:TYR:CZ	2.27	0.69
1:D:167:LEU:CG	1:D:178:MET:HB2	2.21	0.69
1:D:252:SER:O	1:D:255:VAL:HG12	1.92	0.69
1:A:148:ILE:CG2	1:A:198:TYR:CD2	2.74	0.69
2:B:295:VAL:O	2:B:299:VAL:HG23	1.93	0.69
3:C:262:CYS:SG	1:D:251:LEU:HD12	2.32	0.69
3:C:445:ASN:CA	3:C:448:LEU:HG	2.19	0.69
1:D:135:PHE:CZ	1:D:273:LEU:HD12	2.27	0.69
1:D:233:PHE:CZ	1:D:417:ILE:CD1	2.68	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:TYR:CB	1:A:112:TYR:CB	2.70	0.69
1:A:148:ILE:HG22	1:A:198:TYR:CD2	2.26	0.69
2:B:218:LEU:HD13	2:B:221:ILE:HG13	1.73	0.69
3:C:60:HIS:NE2	3:C:92:ILE:HG21	2.06	0.69
3:C:138:PRO:CD	3:C:288:ILE:HD12	2.22	0.69
1:D:49:ILE:CD1	1:D:125:LYS:HE3	2.22	0.69
1:D:137:PHE:CD2	1:D:431:ILE:HB	2.26	0.69
1:D:167:LEU:N	1:D:167:LEU:HD12	2.06	0.69
1:D:245:LEU:HD11	4:E:252:THR:HA	1.74	0.69
4:E:279:VAL:CB	4:E:280:PRO:CD	2.65	0.69
1:A:17:LYS:HB3	1:A:84:ASP:HA	1.73	0.69
1:A:36:GLN:OE1	1:A:36:GLN:O	2.10	0.69
1:A:68:ASN:CG	1:A:69:PRO:HD2	2.18	0.69
3:C:106:TYR:C	3:C:106:TYR:CD1	2.69	0.69
1:D:7:LEU:HD22	1:D:70:ALA:O	1.91	0.69
4:E:138:TRP:CE3	4:E:215:GLN:HA	2.28	0.69
1:A:76:LYS:HG3	1:A:112:TYR:CE2	2.27	0.69
3:C:137:PHE:HZ	3:C:291:TYR:CD2	2.10	0.69
1:D:20:ARG:HH11	1:D:20:ARG:CG	2.03	0.69
1:D:392:SER:O	1:D:395:ALA:HB3	1.91	0.69
4:E:266:PHE:CD1	4:E:266:PHE:O	2.45	0.69
4:E:444:LYS:O	4:E:448:LYS:HG2	1.91	0.69
2:B:267:ALA:O	2:B:271:PRO:HD3	1.92	0.69
3:C:19:LYS:O	3:C:19:LYS:CD	2.41	0.69
3:C:42:LEU:HD13	3:C:190:TRP:HZ2	1.56	0.69
4:E:162:GLU:O	4:E:189:PRO:HA	1.91	0.69
1:A:207:MET:HE2	1:A:207:MET:O	1.92	0.69
1:D:102:ILE:HG23	4:E:98:GLN:HE21	1.57	0.69
1:D:152:ASP:HA	1:D:197:PRO:HA	1.74	0.69
1:D:178:MET:HA	1:D:207:MET:HB2	1.73	0.69
4:E:44:GLU:HA	4:E:129:ILE:HD11	1.74	0.69
1:A:67:TRP:HA	1:A:67:TRP:CE3	2.27	0.69
1:A:87:LEU:H	1:A:87:LEU:CD2	2.01	0.69
1:A:176:TRP:HA	1:A:209:ARG:HG3	1.74	0.69
1:A:179:LYS:HE2	1:A:208:GLN:CD	2.17	0.69
1:A:426:PHE:HD1	1:A:427:ALA:N	1.90	0.69
2:B:129:THR:HG23	2:B:129:THR:O	1.93	0.69
2:B:449:ILE:HA	2:B:452:PHE:CD2	2.27	0.69
1:D:195:ASP:O	1:D:197:PRO:HD3	1.93	0.69
1:A:56:LEU:HD22	1:A:58:GLN:HG3	1.75	0.69
2:B:33:VAL:HG21	2:B:158:LEU:HD13	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:409:LYS:CE	3:C:423:ILE:HG23	2.23	0.69
3:C:230:ILE:HG13	3:C:231:ASN:ND2	2.07	0.69
1:D:86:TRP:O	1:D:86:TRP:CE2	2.44	0.69
4:E:138:TRP:CB	4:E:213:ILE:HG12	2.21	0.69
2:B:38:THR:HG22	2:B:55:PHE:CE1	2.27	0.69
3:C:30:VAL:HG22	3:C:157:GLU:C	2.18	0.69
3:C:137:PHE:CD1	3:C:137:PHE:O	2.46	0.69
3:C:279:PRO:CA	3:C:282:ALA:HB3	2.22	0.69
1:D:60:TRP:CZ2	1:D:86:TRP:CH2	2.80	0.69
1:A:155:LYS:CE	4:E:76:LEU:HD13	2.22	0.68
2:B:241:LEU:HD21	2:B:251:LEU:CD1	2.08	0.68
3:C:102:TYR:CE1	3:C:106:TYR:HB3	2.29	0.68
3:C:179:ILE:CG2	3:C:181:PRO:HD2	2.22	0.68
3:C:296:MET:HA	3:C:296:MET:HE2	1.74	0.68
1:D:239:SER:O	1:D:242:LYS:HG2	1.92	0.68
4:E:217:LYS:N	4:E:218:PRO:HD2	2.08	0.68
2:B:11:LEU:HD22	2:B:11:LEU:N	2.08	0.68
1:D:134:HIS:C	1:D:134:HIS:ND1	2.50	0.68
1:D:245:LEU:HD21	4:E:255:ILE:CG1	2.23	0.68
1:D:257:LEU:HD12	1:D:258:LEU:N	2.09	0.68
4:E:82:GLU:C	4:E:83:LEU:HD22	2.18	0.68
4:E:253:LEU:HG	4:E:254:SER:N	2.08	0.68
1:A:41:ILE:CD1	1:A:51:GLU:HB3	2.22	0.68
1:A:261:VAL:O	1:A:261:VAL:CG1	2.42	0.68
1:A:286:ILE:HG22	1:A:286:ILE:O	1.93	0.68
2:B:212:ILE:HG22	2:B:212:ILE:O	1.92	0.68
3:C:269:VAL:HG13	3:C:270:PHE:CE1	2.27	0.68
1:D:215:VAL:O	1:D:219:ILE:HG23	1.93	0.68
4:E:89:VAL:O	4:E:90:VAL:HG23	1.92	0.68
2:B:263:LEU:CD2	2:B:291:VAL:CG2	2.71	0.68
3:C:191:GLU:HG3	3:C:222:ARG:HB3	1.76	0.68
1:D:53:ASN:HB2	1:D:123:ILE:HG12	1.74	0.68
1:D:112:TYR:HD1	1:D:113:THR:H	1.41	0.68
4:E:34:LEU:HD12	4:E:210:PHE:HE2	1.55	0.68
1:A:41:ILE:HG13	1:A:42:ASN:N	2.08	0.68
2:B:56:LEU:O	2:B:120:PRO:HD2	1.93	0.68
2:B:89:ASP:OD1	2:B:148:SER:HB2	1.93	0.68
1:D:135:PHE:C	1:D:135:PHE:HD1	2.01	0.68
1:D:135:PHE:HE1	1:D:277:TYR:CE2	2.10	0.68
4:E:146:ARG:HD2	4:E:205:PHE:CD2	2.29	0.68
4:E:182:GLU:HA	4:E:218:PRO:CG	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:313:THR:HB	4:E:441:LEU:HB3	1.73	0.68
2:B:35:LEU:N	2:B:35:LEU:CD2	2.55	0.68
2:B:415:LEU:HD13	2:B:415:LEU:C	2.18	0.68
1:D:140:GLN:HG3	1:D:141:ASN:H	1.58	0.68
1:D:227:PHE:O	1:D:230:VAL:HG12	1.93	0.68
1:A:24:HIS:CD2	1:A:24:HIS:N	2.62	0.68
1:A:247:ILE:O	1:A:247:ILE:CD1	2.42	0.68
3:C:7:LEU:HA	3:C:10:ASP:OD2	1.94	0.68
1:D:78:ILE:O	1:D:78:ILE:CD1	2.40	0.68
1:D:106:THR:CG2	1:D:107:LYS:H	1.98	0.68
1:D:420:ILE:HA	1:D:423:VAL:CG2	2.24	0.68
4:E:42:LEU:HD22	4:E:183:TRP:CE2	2.28	0.68
4:E:45:LYS:HA	4:E:280:PRO:CA	2.16	0.68
4:E:54:TRP:C	4:E:118:LEU:CD1	2.67	0.68
4:E:138:TRP:HH2	4:E:215:GLN:NE2	1.91	0.68
4:E:236:VAL:O	4:E:239:VAL:HG23	1.93	0.68
4:E:284:LYS:HE3	4:E:284:LYS:H	1.56	0.68
1:A:29:VAL:HB	1:A:31:ILE:HD12	1.76	0.68
3:C:12:LEU:HB2	3:C:16:LYS:CG	2.20	0.68
1:D:141:ASN:HB3	1:D:206:ILE:CD1	2.24	0.68
1:D:252:SER:OG	4:E:259:LEU:HD22	1.93	0.68
4:E:102:ALA:HB2	4:E:121:ALA:HB2	1.75	0.68
1:A:274:ILE:HG12	1:A:277:TYR:CD1	2.26	0.68
2:B:55:PHE:HA	2:B:120:PRO:O	1.94	0.68
2:B:145:VAL:HA	2:B:207:VAL:O	1.93	0.68
2:B:406:GLU:HG2	2:B:409:LYS:HD2	1.76	0.68
3:C:199:LYS:NZ	3:C:199:LYS:O	2.27	0.68
3:C:270:PHE:CD1	3:C:270:PHE:N	2.60	0.68
1:D:187:TRP:CH2	1:D:189:TYR:HB3	2.29	0.68
4:E:126:THR:O	4:E:126:THR:HG22	1.92	0.68
1:A:422:THR:O	1:A:425:VAL:HG12	1.93	0.68
2:B:421:PHE:HA	2:B:424:LEU:HB2	1.75	0.68
3:C:242:LEU:HD22	3:C:267:GLN:CB	2.12	0.68
3:C:316:THR:CG2	3:C:317:PRO:CD	2.72	0.68
1:D:92:LEU:CD2	1:D:92:LEU:H	2.06	0.68
1:D:166:ASP:HB3	1:D:167:LEU:HD12	1.75	0.68
1:A:220:ILE:N	1:A:221:PRO:HD2	2.10	0.67
1:D:129:GLU:O	1:D:142:CYS:HB2	1.94	0.67
1:D:167:LEU:CD1	1:D:178:MET:CB	2.70	0.67
1:D:260:ILE:O	1:D:264:ILE:HG13	1.94	0.67
4:E:172:ILE:CD1	4:E:188:ARG:N	2.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:453:ILE:HD12	4:E:454:ALA:N	2.09	0.67
1:A:89:ASP:HB2	1:A:149:TRP:HD1	1.54	0.67
1:A:90:LEU:HD13	1:A:100:PHE:HE2	1.58	0.67
1:A:175:GLU:HB3	1:A:211:PRO:CD	2.23	0.67
1:A:406:ILE:HG23	1:A:409:ILE:CD1	2.24	0.67
3:C:36:SER:HB3	3:C:59:ASP:HB3	1.75	0.67
3:C:138:PRO:CG	3:C:288:ILE:CD1	2.71	0.67
3:C:180:ASP:HB3	3:C:181:PRO:CD	2.21	0.67
1:D:80:LEU:O	1:D:108:LEU:HB3	1.95	0.67
1:D:260:ILE:HG22	1:D:264:ILE:CD1	2.24	0.67
1:A:139:GLN:OE1	1:A:179:LYS:HG3	1.95	0.67
2:B:58:LEU:HD11	2:B:118:TRP:CE3	2.28	0.67
2:B:439:PHE:O	2:B:442:ILE:HG22	1.95	0.67
3:C:59:ASP:CG	3:C:121:LEU:HD22	2.19	0.67
3:C:77:ILE:O	3:C:77:ILE:HG13	1.93	0.67
3:C:122:PRO:CB	3:C:123:PRO:CD	2.61	0.67
3:C:462:THR:N	3:C:463:PRO:HD2	2.09	0.67
1:D:76:LYS:HG2	1:D:112:TYR:CD2	2.29	0.67
1:D:145:LYS:C	1:D:146:LEU:CD1	2.66	0.67
1:D:287:SER:O	1:D:291:VAL:HG23	1.95	0.67
1:D:395:ALA:HB1	1:D:399:TRP:CZ2	2.29	0.67
4:E:2:GLU:CA	4:E:5:ARG:HG3	2.24	0.67
4:E:20:PRO:HG2	4:E:28:ILE:HD12	1.74	0.67
4:E:47:GLU:CA	4:E:129:ILE:HD11	2.20	0.67
4:E:67:ASN:H	4:E:67:ASN:ND2	1.82	0.67
3:C:220:ILE:O	3:C:220:ILE:CG1	2.42	0.67
3:C:264:LEU:HA	3:C:267:GLN:HG3	1.75	0.67
1:D:296:ILE:HA	1:D:299:HIS:HB3	1.76	0.67
1:D:305:THR:OG1	1:D:305:THR:O	2.12	0.67
1:A:2:GLU:O	1:A:2:GLU:CG	2.34	0.67
1:A:107:LYS:HE3	2:B:150:THR:CB	2.25	0.67
1:A:118:TRP:CD1	1:A:120:PRO:HD3	2.29	0.67
2:B:143:THR:HG23	2:B:208:THR:HG23	1.77	0.67
2:B:279:ILE:HG22	2:B:280:ILE:N	2.08	0.67
3:C:69:TRP:HE3	3:C:73:GLU:HB3	1.59	0.67
3:C:269:VAL:HG13	3:C:270:PHE:HD1	1.55	0.67
1:D:28:PHE:HA	1:D:155:LYS:O	1.93	0.67
1:D:166:ASP:N	1:D:181:TYR:HB3	2.10	0.67
4:E:188:ARG:O	4:E:188:ARG:HG3	1.94	0.67
1:A:209:ARG:CG	1:A:210:ILE:H	2.07	0.67
1:A:384:GLU:OE2	1:A:387:LYS:HE2	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:137:PHE:CD1	3:C:288:ILE:CG2	2.77	0.67
3:C:273:LEU:HD23	3:C:276:GLN:HB2	1.75	0.67
1:D:426:PHE:CE1	1:D:430:LEU:CD1	2.78	0.67
4:E:172:ILE:CG2	4:E:174:PRO:HD2	2.24	0.67
4:E:182:GLU:CD	4:E:220:PHE:HE2	2.02	0.67
4:E:224:ASN:OD1	4:E:224:ASN:O	2.11	0.67
1:A:139:GLN:HB2	1:A:207:MET:O	1.95	0.67
1:A:216:VAL:CG1	1:A:220:ILE:HD11	2.25	0.67
2:B:56:LEU:N	2:B:56:LEU:HD12	2.08	0.67
2:B:101:GLU:O	2:B:102:ILE:HG13	1.94	0.67
2:B:218:LEU:CD1	2:B:221:ILE:CG1	2.72	0.67
1:D:187:TRP:HB2	1:D:199:LEU:HD21	1.77	0.67
1:D:382:ILE:O	1:D:386:MET:HG2	1.94	0.67
4:E:56:GLU:CA	4:E:118:LEU:HB2	2.21	0.67
4:E:83:LEU:HD22	4:E:83:LEU:N	2.10	0.67
4:E:172:ILE:HG23	4:E:174:PRO:CD	2.24	0.67
1:A:79:ARG:HH11	1:A:107:LYS:NZ	1.93	0.67
1:A:148:ILE:CG2	1:A:198:TYR:CB	2.72	0.67
1:A:207:MET:HE2	1:A:207:MET:H	1.58	0.67
2:B:236:ILE:O	2:B:240:TYR:HB2	1.95	0.67
3:C:226:LEU:H	3:C:227:PHE:HD1	1.40	0.67
1:D:107:LYS:HZ1	4:E:149:THR:HA	1.57	0.67
1:D:259:VAL:HG13	1:D:262:GLU:OE1	1.95	0.67
4:E:77:VAL:CG1	4:E:78:ARG:H	2.07	0.67
4:E:146:ARG:HB3	4:E:207:GLU:HA	1.77	0.67
1:A:238:ASP:CB	2:B:306:HIS:CE1	2.75	0.67
2:B:40:LEU:HD22	2:B:51:THR:O	1.94	0.67
2:B:112:HIS:CG	2:B:113:THR:H	2.12	0.67
3:C:191:GLU:CD	3:C:222:ARG:HB3	2.19	0.67
3:C:199:LYS:HD2	3:C:200:ASN:N	2.10	0.67
1:D:62:ASP:CB	1:D:65:LEU:HD13	2.11	0.67
1:A:34:GLY:CA	1:A:57:ARG:HG2	2.25	0.67
1:A:34:GLY:HA3	1:A:57:ARG:HG2	1.77	0.67
1:A:76:LYS:HA	1:A:112:TYR:CD2	2.29	0.67
1:A:176:TRP:CE3	1:A:209:ARG:NH2	2.63	0.67
2:B:259:LEU:HD23	2:B:259:LEU:O	1.95	0.67
2:B:289:ILE:HG22	2:B:293:PHE:CZ	2.29	0.67
1:D:60:TRP:CZ2	1:D:86:TRP:CZ3	2.83	0.67
1:A:168:SER:OG	1:A:169:THR:HG23	1.95	0.66
2:B:47:ASN:HB2	2:B:49:GLU:CD	2.19	0.66
2:B:48:GLU:HB2	2:B:130:ILE:CG1	2.22	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:35:LEU:CD2	1:D:164:ARG:NH1	2.56	0.66
1:D:287:SER:HA	1:D:290:ILE:HG12	1.77	0.66
4:E:54:TRP:CB	4:E:118:LEU:HD11	2.21	0.66
1:A:108:LEU:CD1	1:A:118:TRP:HB2	2.24	0.66
1:A:136:PRO:HA	1:A:277:TYR:OH	1.95	0.66
1:A:216:VAL:HG12	1:A:220:ILE:HD12	1.75	0.66
2:B:270:VAL:HG11	2:B:284:LEU:CG	2.25	0.66
3:C:478:PHE:C	3:C:478:PHE:HD1	2.03	0.66
1:D:7:LEU:HA	1:D:10:ASN:ND2	2.10	0.66
4:E:33:LYS:HE3	4:E:160:SER:HB2	1.78	0.66
4:E:44:GLU:HB3	4:E:280:PRO:CD	2.26	0.66
4:E:75:ASP:HB3	4:E:110:TYR:CZ	2.31	0.66
1:A:34:GLY:HA3	1:A:161:GLU:CD	2.21	0.66
1:A:156:VAL:CG2	1:A:157:SER:N	2.57	0.66
1:A:209:ARG:HG2	1:A:210:ILE:H	1.59	0.66
2:B:160:HIS:H	2:B:195:LYS:NZ	1.93	0.66
2:B:297:LEU:CD1	2:B:445:THR:CG2	2.72	0.66
2:B:304:LEU:O	2:B:304:LEU:HD23	1.96	0.66
1:D:109:LEU:HD12	1:D:117:MET:HB3	1.77	0.66
1:D:129:GLU:O	1:D:130:ILE:HG23	1.95	0.66
1:D:229:THR:HA	1:D:232:VAL:CG2	2.25	0.66
1:D:254:THR:HG23	1:D:255:VAL:N	2.09	0.66
1:D:292:THR:HA	1:D:295:VAL:CG2	2.25	0.66
4:E:131:VAL:HG12	4:E:131:VAL:O	1.94	0.66
4:E:159:LEU:CD1	4:E:191:LYS:C	2.69	0.66
4:E:238:LEU:C	4:E:242:LEU:HD23	2.21	0.66
1:A:145:LYS:NZ	1:A:202:THR:CG2	2.58	0.66
2:B:296:ILE:O	2:B:296:ILE:HG22	1.96	0.66
3:C:11:LEU:C	3:C:16:LYS:HG3	2.20	0.66
3:C:270:PHE:N	3:C:270:PHE:HD1	1.92	0.66
1:D:104:HIS:HB2	1:D:105:MET:SD	2.35	0.66
1:D:241:GLU:O	1:D:243:MET:HE1	1.95	0.66
1:A:29:VAL:HG21	1:A:86:TRP:CZ3	2.31	0.66
1:A:41:ILE:CD1	1:A:51:GLU:CD	2.66	0.66
1:A:155:LYS:HG3	4:E:78:ARG:HE	1.60	0.66
1:A:216:VAL:CG1	1:A:220:ILE:CD1	2.74	0.66
1:A:389:ASP:O	1:A:392:SER:HB3	1.94	0.66
1:D:110:LEU:HD12	1:D:111:ASP:H	1.60	0.66
2:B:92:LEU:HD22	2:B:146:PHE:CD1	2.30	0.66
2:B:111:GLN:CD	2:B:115:ALA:HB3	2.21	0.66
2:B:261:VAL:HG12	2:B:262:PHE:HD1	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:269:LYS:HE3	2:B:270:VAL:CG2	2.25	0.66
2:B:279:ILE:CG2	2:B:280:ILE:N	2.58	0.66
3:C:138:PRO:HB3	3:C:290:LYS:NZ	2.11	0.66
1:D:177:VAL:HG12	1:D:208:GLN:HG2	1.77	0.66
4:E:71:TYR:HD1	4:E:111:ASN:ND2	1.92	0.66
1:A:35:LEU:HD23	1:A:36:GLN:N	2.09	0.66
1:A:201:ILE:HG21	1:A:203:TYR:HE1	1.60	0.66
1:A:218:VAL:CG1	1:A:219:ILE:N	2.59	0.66
1:A:239:SER:HB2	2:B:312:HIS:HB3	1.76	0.66
1:A:265:PRO:CA	1:A:268:SER:HB3	2.25	0.66
2:B:429:GLN:HA	2:B:429:GLN:HE21	1.60	0.66
3:C:233:ILE:HD13	3:C:233:ILE:N	2.10	0.66
1:D:137:PHE:O	1:D:435:GLN:HA	1.96	0.66
4:E:20:PRO:HG3	4:E:61:ASP:CG	2.21	0.66
4:E:255:ILE:HG22	4:E:256:SER:N	2.06	0.66
1:A:107:LYS:O	1:A:108:LEU:HD23	1.96	0.66
2:B:82:SER:O	2:B:83:ASP:HB3	1.94	0.66
2:B:176:ASN:HD22	2:B:188:ILE:HG21	1.61	0.66
3:C:138:PRO:HB2	3:C:140:ASP:OD1	1.96	0.66
3:C:195:LYS:HE3	3:C:217:PHE:HB3	1.78	0.66
3:C:243:ALA:CB	3:C:302:VAL:CG1	2.72	0.66
1:D:249:VAL:O	1:D:253:LEU:HB3	1.95	0.66
1:A:46:VAL:CG2	1:A:270:ALA:C	2.69	0.66
1:A:134:HIS:CD2	1:A:207:MET:CE	2.79	0.66
1:D:107:LYS:HB3	4:E:150:TYR:HE1	1.61	0.66
1:D:220:ILE:HG21	4:E:294:LEU:CD1	2.19	0.66
1:A:187:TRP:CH2	1:A:189:TYR:CB	2.78	0.66
2:B:56:LEU:HD23	2:B:103:THR:HG23	1.78	0.66
2:B:244:ASP:CG	3:C:314:PHE:HE1	2.04	0.66
2:B:290:LEU:HD21	2:B:453:SER:CB	2.26	0.66
1:D:289:ILE:HG22	1:D:290:ILE:N	2.11	0.66
4:E:159:LEU:HD12	4:E:191:LYS:C	2.21	0.66
4:E:309:ARG:HD2	4:E:310:THR:OG1	1.96	0.66
1:A:380:LYS:HD3	2:B:408:ILE:HG21	1.76	0.65
2:B:440:LEU:O	2:B:443:PHE:HB3	1.96	0.65
3:C:482:PRO:HG2	3:C:483:ALA:N	2.10	0.65
1:D:132:VAL:HB	1:D:274:ILE:HA	1.76	0.65
4:E:77:VAL:CG1	4:E:78:ARG:N	2.59	0.65
1:A:139:GLN:NE2	1:A:206:ILE:CG2	2.59	0.65
3:C:42:LEU:CD2	3:C:190:TRP:CH2	2.77	0.65
3:C:274:THR:HG22	3:C:275:SER:N	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:455:ARG:O	3:C:459:PHE:HD1	1.80	0.65
1:D:177:VAL:O	1:D:207:MET:HB2	1.96	0.65
4:E:56:GLU:N	4:E:118:LEU:HD13	2.12	0.65
4:E:237:VAL:CG2	4:E:457:LEU:HD21	2.26	0.65
1:A:27:HIS:C	1:A:28:PHE:CG	2.74	0.65
3:C:18:ASN:HB2	3:C:21:VAL:HB	1.78	0.65
3:C:67:LEU:C	3:C:116:GLY:H	2.05	0.65
3:C:80:LEU:CD1	1:D:20:ARG:HH22	2.08	0.65
3:C:153:TYR:O	3:C:212:TYR:HB3	1.96	0.65
1:D:40:LEU:CD1	1:D:52:THR:HB	2.24	0.65
1:D:176:TRP:HB3	1:D:209:ARG:CD	2.24	0.65
1:D:287:SER:HA	1:D:290:ILE:CG1	2.25	0.65
1:D:393:SER:O	1:D:396:ALA:HB3	1.97	0.65
4:E:144:VAL:HG12	4:E:209:ILE:CA	2.26	0.65
4:E:221:TYR:N	4:E:221:TYR:CD1	2.63	0.65
4:E:252:THR:O	4:E:255:ILE:HB	1.96	0.65
4:E:39:LEU:CD1	4:E:49:LEU:HD13	2.25	0.65
3:C:223:ARG:HG2	3:C:224:LYS:N	2.12	0.65
3:C:230:ILE:HG13	3:C:231:ASN:N	2.11	0.65
1:D:37:LEU:CD1	1:D:54:VAL:HG13	2.25	0.65
4:E:183:TRP:HB3	4:E:216:ARG:NE	2.11	0.65
4:E:262:THR:O	4:E:262:THR:HG22	1.95	0.65
1:A:34:GLY:HA3	1:A:57:ARG:HD3	1.79	0.65
3:C:19:LYS:O	3:C:19:LYS:HD2	1.96	0.65
3:C:38:THR:OG1	3:C:178:ILE:HD13	1.97	0.65
3:C:447:ASN:O	3:C:449:VAL:HG23	1.96	0.65
1:D:92:LEU:N	1:D:92:LEU:CD2	2.58	0.65
1:D:178:MET:SD	1:D:207:MET:CB	2.85	0.65
4:E:235:LEU:HA	4:E:238:LEU:HG	1.77	0.65
1:A:190:TYR:HB2	1:A:192:CYS:SG	2.36	0.65
3:C:78:SER:C	3:C:114:PRO:HB3	2.21	0.65
1:D:75:ILE:HG13	1:D:78:ILE:CG2	2.27	0.65
1:D:379:VAL:O	1:D:379:VAL:HG12	1.96	0.65
4:E:9:LYS:HG3	4:E:10:LEU:N	2.11	0.65
4:E:138:TRP:CH2	4:E:215:GLN:CD	2.75	0.65
4:E:152:ALA:HB3	4:E:204:ASP:O	1.96	0.65
4:E:182:GLU:HG3	4:E:218:PRO:O	1.96	0.65
1:A:224:LEU:CG	1:A:225:PHE:N	2.58	0.65
1:A:235:LEU:HB3	1:A:236:PRO:CD	2.27	0.65
3:C:11:LEU:O	3:C:16:LYS:HB2	1.97	0.65
3:C:60:HIS:CD2	3:C:92:ILE:CD1	2.80	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:434:LYS:HD3	3:C:435:GLU:CG	2.25	0.65
1:D:107:LYS:HB3	4:E:150:TYR:CE1	2.31	0.65
1:D:152:ASP:CA	1:D:197:PRO:HA	2.26	0.65
1:A:17:LYS:HE3	1:A:84:ASP:CA	2.22	0.65
1:A:160:PRO:HG3	1:A:185:LYS:HE2	1.77	0.65
1:A:397:GLU:HA	1:A:400:LYS:HD2	1.78	0.65
2:B:32:ARG:HE	2:B:59:ALA:C	2.04	0.65
2:B:34:GLY:C	2:B:35:LEU:CD2	2.69	0.65
2:B:46:LYS:HB2	2:B:278:PRO:HD3	1.79	0.65
2:B:187:SER:C	2:B:188:ILE:HG12	2.20	0.65
3:C:247:PHE:CE1	3:C:309:VAL:CG2	2.80	0.65
3:C:319:THR:O	3:C:319:THR:HG22	1.97	0.65
3:C:443:VAL:HA	3:C:446:TRP:HD1	1.61	0.65
1:D:21:PRO:HB3	1:D:62:ASP:OD2	1.96	0.65
4:E:159:LEU:CD1	4:E:192:LYS:HB2	2.27	0.65
4:E:284:LYS:HE3	4:E:284:LYS:CA	2.27	0.65
1:A:41:ILE:HD11	1:A:51:GLU:CB	2.26	0.65
1:A:160:PRO:HG2	1:A:185:LYS:HZ1	1.59	0.65
2:B:111:GLN:HB2	2:B:115:ALA:HB3	1.78	0.65
2:B:438:LEU:HA	2:B:441:TYR:HB3	1.78	0.65
3:C:33:ILE:HG22	3:C:160:MET:SD	2.37	0.65
3:C:60:HIS:CE1	3:C:160:MET:HE1	2.32	0.65
3:C:205:LYS:HD3	3:C:205:LYS:H	1.61	0.65
1:D:302:SER:CB	1:D:305:THR:HG23	2.26	0.65
4:E:76:LEU:HD23	4:E:77:VAL:N	2.12	0.65
4:E:148:GLN:HE21	4:E:148:GLN:N	1.94	0.65
1:A:45:GLU:OE1	1:A:271:VAL:HB	1.97	0.64
2:B:82:SER:C	2:B:84:ASP:H	2.05	0.64
2:B:198:ARG:HH11	2:B:198:ARG:HG3	1.62	0.64
3:C:63:TYR:CE1	3:C:116:GLY:HA3	2.32	0.64
3:C:69:TRP:HB2	3:C:74:TYR:N	2.12	0.64
3:C:102:TYR:HD1	3:C:102:TYR:O	1.79	0.64
1:D:219:ILE:HD12	1:D:219:ILE:O	1.97	0.64
4:E:293:SER:O	4:E:296:ILE:HG12	1.97	0.64
1:A:137:PHE:CE1	1:A:210:ILE:HD12	2.33	0.64
1:A:301:ARG:HH11	1:A:301:ARG:HG2	1.61	0.64
1:A:394:ASN:O	1:A:398:GLU:HG3	1.97	0.64
3:C:137:PHE:CZ	3:C:291:TYR:CE2	2.86	0.64
3:C:276:GLN:C	3:C:279:PRO:HD2	2.22	0.64
1:D:167:LEU:CD1	1:D:167:LEU:N	2.60	0.64
4:E:103:TYR:CG	4:E:104:TYR:N	2.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:191:LYS:O	4:E:209:ILE:HG22	1.96	0.64
4:E:272:VAL:O	4:E:272:VAL:CG2	2.42	0.64
1:A:52:THR:O	1:A:123:ILE:HA	1.96	0.64
2:B:132:VAL:HG12	2:B:280:ILE:N	2.10	0.64
2:B:252:SER:O	2:B:255:ALA:HB3	1.98	0.64
3:C:4:GLU:HG3	3:C:5:GLU:N	2.09	0.64
3:C:135:LEU:C	3:C:137:PHE:H	2.06	0.64
3:C:247:PHE:C	3:C:250:PRO:CD	2.70	0.64
1:D:213:TYR:O	1:D:216:VAL:HG23	1.97	0.64
2:B:276:SER:OG	2:B:277:VAL:HG13	1.98	0.64
1:D:379:VAL:HA	1:D:382:ILE:HG13	1.79	0.64
4:E:131:VAL:HA	4:E:281:LEU:O	1.97	0.64
4:E:184:THR:HG23	4:E:215:GLN:HG2	1.78	0.64
4:E:189:PRO:HD2	4:E:211:PHE:CB	2.12	0.64
4:E:267:LEU:HD12	4:E:270:GLN:OE1	1.96	0.64
4:E:276:SER:HB3	4:E:281:LEU:HD13	1.78	0.64
1:A:31:ILE:CG1	1:A:60:TRP:HB3	2.27	0.64
1:A:92:LEU:HB2	1:A:96:ALA:H	1.60	0.64
1:A:108:LEU:HB3	1:A:117:MET:O	1.97	0.64
2:B:138:ASP:HB3	2:B:464:PRO:O	1.98	0.64
1:D:20:ARG:HG2	1:D:20:ARG:NH1	1.92	0.64
4:E:172:ILE:CD1	4:E:187:HIS:HA	2.28	0.64
1:A:245:LEU:HD13	2:B:250:SER:HB2	1.79	0.64
3:C:68:THR:N	3:C:116:GLY:H	1.95	0.64
3:C:465:MET:HE2	3:C:466:VAL:HA	1.79	0.64
1:D:58:GLN:NE2	1:D:88:PRO:HG3	2.13	0.64
4:E:227:ALA:N	4:E:228:PRO:CD	2.61	0.64
4:E:237:VAL:HG21	4:E:457:LEU:HD21	1.80	0.64
2:B:142:CYS:O	2:B:210:TYR:HD1	1.80	0.64
3:C:42:LEU:HA	3:C:54:THR:CG2	2.26	0.64
3:C:58:MET:SD	3:C:92:ILE:CD1	2.86	0.64
3:C:76:ASP:C	3:C:77:ILE:HG23	2.21	0.64
1:D:78:ILE:HD11	1:D:110:LEU:HG	1.80	0.64
1:D:92:LEU:HB2	1:D:95:ASN:HB2	1.80	0.64
4:E:38:ASN:O	4:E:51:THR:HA	1.96	0.64
4:E:215:GLN:HG3	4:E:216:ARG:N	2.13	0.64
1:A:15:TYR:CE2	1:A:84:ASP:HB3	2.32	0.64
1:A:20:ARG:HB3	1:A:86:TRP:CD2	2.33	0.64
1:A:106:THR:HG22	1:A:107:LYS:N	2.12	0.64
2:B:3:MET:O	2:B:7:LEU:HG	1.98	0.64
2:B:278:PRO:CG	2:B:278:PRO:O	2.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:429:ILE:O	3:C:433:ILE:HG13	1.98	0.64
1:A:212:LEU:HA	1:A:215:VAL:HG23	1.79	0.64
3:C:58:MET:HE1	3:C:105:ALA:O	1.97	0.64
3:C:137:PHE:CZ	3:C:291:TYR:CD2	2.86	0.64
3:C:273:LEU:HD23	3:C:276:GLN:CG	2.28	0.64
1:D:77:LYS:HB2	1:D:111:ASP:OD1	1.98	0.64
2:B:92:LEU:HD13	2:B:146:PHE:CE1	2.32	0.64
3:C:110:VAL:HG13	3:C:120:TRP:CB	2.27	0.64
1:D:92:LEU:HD13	1:D:146:LEU:CG	2.28	0.64
1:D:134:HIS:C	1:D:134:HIS:HD1	2.06	0.64
1:D:164:ARG:HH11	1:D:181:TYR:HE2	1.45	0.64
1:D:211:PRO:HB3	1:D:213:TYR:HD2	1.62	0.64
4:E:52:ASN:HA	4:E:121:ALA:O	1.97	0.64
1:A:20:ARG:NH1	1:A:20:ARG:CG	2.58	0.63
1:A:108:LEU:HD13	1:A:118:TRP:CB	2.28	0.63
1:A:239:SER:HB2	2:B:312:HIS:CB	2.29	0.63
2:B:150:THR:O	2:B:150:THR:HG22	1.97	0.63
2:B:175:ILE:HG12	2:B:177:GLN:H	1.63	0.63
2:B:254:SER:O	3:C:265:LEU:HD11	1.98	0.63
3:C:435:GLU:O	3:C:438:ALA:HB3	1.98	0.63
1:D:263:LEU:HD11	4:E:266:PHE:CE2	2.33	0.63
4:E:89:VAL:HG23	4:E:99:PHE:CE1	2.33	0.63
1:A:139:GLN:HE21	1:A:206:ILE:HG23	1.62	0.63
1:A:414:PHE:HA	1:A:417:ILE:HD12	1.80	0.63
2:B:56:LEU:HD13	2:B:120:PRO:O	1.98	0.63
2:B:138:ASP:HA	2:B:464:PRO:O	1.98	0.63
1:D:152:ASP:CB	1:D:197:PRO:HA	2.27	0.63
4:E:269:ALA:O	4:E:273:PRO:HD3	1.98	0.63
1:A:146:LEU:HD12	1:A:146:LEU:N	2.13	0.63
2:B:128:CYS:SG	2:B:144:MET:CG	2.86	0.63
2:B:296:ILE:O	2:B:296:ILE:CG2	2.46	0.63
3:C:155:ALA:CB	3:C:211:ASN:HA	2.28	0.63
3:C:199:LYS:HZ3	3:C:200:ASN:HA	1.63	0.63
3:C:234:THR:N	3:C:235:PRO:HD2	2.13	0.63
1:D:167:LEU:HG	1:D:178:MET:HB2	1.79	0.63
1:A:34:GLY:HA3	1:A:57:ARG:CG	2.29	0.63
1:D:282:MET:HG3	1:D:286:ILE:CD1	2.27	0.63
4:E:71:TYR:HD1	4:E:111:ASN:CG	2.05	0.63
2:B:141:ASN:HD21	2:B:212:ILE:HG12	1.64	0.63
2:B:155:GLU:O	2:B:156:VAL:HB	1.99	0.63
2:B:218:LEU:HD13	2:B:221:ILE:HD11	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:TRP:CE3	1:D:209:ARG:NE	2.66	0.63
1:D:391:GLU:HA	1:D:394:ASN:OD1	1.98	0.63
1:A:54:VAL:HG22	1:A:122:ALA:HB3	1.81	0.63
1:A:89:ASP:OD1	1:A:89:ASP:C	2.40	0.63
1:A:136:PRO:HG3	1:A:274:ILE:CG2	2.28	0.63
1:A:305:THR:O	1:A:306:HIS:HB3	1.97	0.63
2:B:278:PRO:C	2:B:279:ILE:HG13	2.24	0.63
3:C:113:ARG:HG3	3:C:117:TYR:O	1.97	0.63
3:C:158:ILE:HG23	3:C:159:SER:N	2.14	0.63
3:C:426:THR:O	3:C:426:THR:CG2	2.33	0.63
1:D:253:LEU:HD23	1:D:254:THR:CA	2.27	0.63
4:E:34:LEU:HB2	4:E:210:PHE:HZ	1.64	0.63
1:A:72:TYR:CB	1:A:112:TYR:HB2	2.28	0.63
1:A:144:MET:HB2	1:A:203:TYR:HB2	1.78	0.63
1:A:419:ILE:CG2	1:A:420:ILE:H	2.12	0.63
2:B:184:GLY:C	2:B:186:TRP:H	2.06	0.63
1:D:231:LEU:O	1:D:235:LEU:HG	1.98	0.63
4:E:103:TYR:C	4:E:104:TYR:CD1	2.77	0.63
1:A:52:THR:C	1:A:123:ILE:HG13	2.23	0.63
1:A:176:TRP:CA	1:A:209:ARG:HG3	2.28	0.63
1:A:212:LEU:HA	1:A:215:VAL:CG2	2.29	0.63
1:A:243:MET:HG2	1:A:244:THR:H	1.63	0.63
2:B:185:GLN:CD	2:B:219:PHE:CE2	2.77	0.63
2:B:186:TRP:CB	2:B:215:ARG:HB2	2.12	0.63
3:C:266:ALA:CB	1:D:251:LEU:HD13	2.28	0.63
1:D:176:TRP:CZ3	1:D:209:ARG:CZ	2.82	0.63
1:D:223:LEU:HD23	1:D:223:LEU:C	2.23	0.63
1:D:253:LEU:HD23	1:D:254:THR:HB	1.79	0.63
2:B:112:HIS:CG	2:B:113:THR:N	2.66	0.63
2:B:242:PRO:HB3	2:B:305:HIS:HE1	1.63	0.63
3:C:179:ILE:CD1	3:C:195:LYS:CB	2.72	0.63
3:C:259:THR:O	3:C:263:VAL:HG23	1.98	0.63
1:D:387:LYS:O	1:D:391:GLU:HG3	1.99	0.63
4:E:27:VAL:CG1	4:E:153:HIS:C	2.71	0.63
4:E:55:ILE:N	4:E:118:LEU:CD1	2.61	0.63
4:E:136:PHE:HA	4:E:138:TRP:CZ3	2.33	0.63
4:E:212:LEU:O	4:E:214:ILE:HG23	1.98	0.63
4:E:242:LEU:C	4:E:242:LEU:HD12	2.24	0.63
1:A:306:HIS:O	1:A:306:HIS:CD2	2.51	0.62
2:B:91:VAL:HA	2:B:96:ASN:CG	2.24	0.62
2:B:134:TYR:HE1	2:B:213:ILE:CG1	2.09	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:218:LEU:HD13	2:B:221:ILE:CD1	2.28	0.62
1:D:75:ILE:HD12	1:D:78:ILE:HG22	1.81	0.62
1:D:171:MET:SD	1:D:176:TRP:CH2	2.92	0.62
4:E:77:VAL:HG13	4:E:78:ARG:H	1.63	0.62
1:A:60:TRP:NE1	1:A:116:ILE:HD12	2.13	0.62
1:A:171:MET:CE	1:A:176:TRP:HH2	2.10	0.62
1:A:265:PRO:HG2	1:A:266:SER:N	2.14	0.62
2:B:93:MET:HG3	2:B:206:ASP:HB3	1.77	0.62
2:B:175:ILE:HD12	2:B:190:HIS:HD2	1.64	0.62
3:C:137:PHE:CD1	3:C:288:ILE:CB	2.83	0.62
3:C:206:PHE:CD1	3:C:206:PHE:O	2.52	0.62
1:D:296:ILE:HG22	1:D:299:HIS:ND1	2.14	0.62
1:D:398:GLU:HG3	1:D:399:TRP:CE3	2.34	0.62
4:E:19:LYS:HZ1	4:E:154:GLU:HB3	1.64	0.62
4:E:33:LYS:NZ	4:E:160:SER:HB2	2.14	0.62
4:E:453:ILE:O	4:E:457:LEU:HB2	1.99	0.62
1:A:34:GLY:HA3	1:A:57:ARG:CD	2.30	0.62
1:A:133:THR:C	1:A:136:PRO:HG2	2.24	0.62
1:A:139:GLN:CB	1:A:207:MET:C	2.72	0.62
2:B:11:LEU:HD22	2:B:11:LEU:H	1.64	0.62
2:B:242:PRO:CB	2:B:243:PRO:HD3	2.29	0.62
3:C:431:LYS:HE2	1:D:379:VAL:CG2	2.29	0.62
1:D:292:THR:O	1:D:296:ILE:HG12	1.99	0.62
1:D:384:GLU:OE1	1:D:384:GLU:HA	1.99	0.62
1:A:37:LEU:HA	1:A:53:ASN:O	1.99	0.62
1:A:133:THR:O	1:A:136:PRO:HG2	2.00	0.62
1:A:156:VAL:CG2	1:A:157:SER:H	2.12	0.62
2:B:85:VAL:O	2:B:87:GLN:HG3	1.99	0.62
1:D:75:ILE:CD1	1:D:78:ILE:HG22	2.28	0.62
1:D:280:PHE:N	1:D:280:PHE:CD1	2.63	0.62
1:A:247:ILE:CD1	1:A:247:ILE:C	2.72	0.62
2:B:45:GLU:CG	2:B:277:VAL:HB	2.27	0.62
1:D:36:GLN:HE21	1:D:38:ILE:HG13	1.64	0.62
2:B:270:VAL:N	2:B:271:PRO:HD2	2.15	0.62
2:B:408:ILE:CG2	2:B:409:LYS:N	2.61	0.62
3:C:33:ILE:HG12	3:C:62:TRP:HB3	1.81	0.62
3:C:113:ARG:HB3	3:C:114:PRO:HD2	1.81	0.62
3:C:150:ALA:H	3:C:160:MET:HE2	1.65	0.62
3:C:160:MET:H	3:C:213:GLN:CB	2.12	0.62
4:E:246:ALA:HB1	4:E:250:LYS:CG	2.16	0.62
1:A:46:VAL:HA	1:A:272:PRO:HD2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:SER:OG	2:B:257:LEU:HD22	1.99	0.62
1:A:286:ILE:O	1:A:286:ILE:CG2	2.47	0.62
1:D:92:LEU:HD21	1:D:124:PHE:CZ	2.35	0.62
1:D:111:ASP:OD2	1:D:115:LYS:HB3	1.98	0.62
4:E:32:LEU:HD12	4:E:208:ILE:HD11	1.81	0.62
1:A:291:VAL:O	1:A:294:VAL:HG12	2.00	0.62
1:D:28:PHE:HB3	1:D:156:VAL:C	2.23	0.62
4:E:32:LEU:HD12	4:E:157:LEU:HD13	1.81	0.62
4:E:33:LYS:HE3	4:E:160:SER:CB	2.29	0.62
4:E:79:ILE:O	4:E:79:ILE:HG22	1.99	0.62
4:E:140:ASN:OD1	4:E:211:PHE:HB3	2.00	0.62
1:A:75:ILE:HG13	1:A:78:ILE:CG2	2.29	0.62
1:A:235:LEU:HB3	1:A:236:PRO:HD3	1.80	0.62
1:A:282:MET:O	1:A:285:VAL:HG12	2.00	0.62
2:B:283:TYR:HA	2:B:286:PHE:CZ	2.35	0.62
2:B:287:ILE:C	2:B:287:ILE:CD1	2.68	0.62
3:C:58:MET:O	3:C:58:MET:HG2	2.00	0.62
3:C:106:TYR:C	3:C:107:PHE:CD1	2.76	0.62
3:C:147:LYS:HE2	3:C:216:THR:HG23	1.81	0.62
3:C:319:THR:O	3:C:319:THR:HG23	1.98	0.62
3:C:478:PHE:C	3:C:478:PHE:CD1	2.78	0.62
1:D:45:GLU:CD	1:D:271:VAL:HG22	2.23	0.62
1:D:282:MET:CE	1:D:286:ILE:HD11	2.30	0.62
4:E:61:ASP:OD1	4:E:63:ARG:HB3	1.99	0.62
1:A:67:TRP:CG	1:A:71:ASP:HB3	2.34	0.62
1:A:121:PRO:HB2	2:B:149:TYR:CZ	2.34	0.62
1:A:245:LEU:HD13	2:B:250:SER:CB	2.30	0.62
2:B:408:ILE:HG13	2:B:408:ILE:O	1.97	0.62
3:C:279:PRO:HA	3:C:282:ALA:HB2	1.80	0.62
3:C:422:GLY:O	3:C:425:SER:HB2	2.00	0.62
4:E:213:ILE:HG23	4:E:213:ILE:O	2.00	0.62
4:E:219:LEU:HB3	4:E:222:ILE:CG2	2.30	0.62
1:A:105:MET:O	1:A:105:MET:HG2	1.99	0.61
1:A:132:VAL:O	1:A:274:ILE:HG22	2.00	0.61
2:B:195:LYS:HA	2:B:207:VAL:HG13	1.82	0.61
2:B:261:VAL:HG12	2:B:262:PHE:CD1	2.34	0.61
2:B:283:TYR:HD1	2:B:283:TYR:H	1.48	0.61
2:B:287:ILE:HA	2:B:290:LEU:CD1	2.29	0.61
2:B:438:LEU:O	2:B:442:ILE:HB	2.00	0.61
3:C:52:LEU:HD22	3:C:52:LEU:N	2.14	0.61
3:C:81:ARG:NH1	3:C:111:LEU:HB2	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:102:ILE:O	1:D:102:ILE:HG22	2.00	0.61
1:A:274:ILE:HD13	1:A:277:TYR:HE1	1.64	0.61
2:B:11:LEU:H	2:B:11:LEU:CD2	2.13	0.61
2:B:58:LEU:CD1	2:B:118:TRP:HB3	2.29	0.61
3:C:63:TYR:HD1	3:C:64:ASP:N	1.98	0.61
3:C:263:VAL:CA	1:D:251:LEU:HD11	2.31	0.61
1:A:198:TYR:CD1	1:A:198:TYR:C	2.76	0.61
1:A:379:VAL:HA	1:A:382:ILE:HD11	1.81	0.61
2:B:274:SER:HB2	2:B:278:PRO:CB	2.29	0.61
3:C:12:LEU:C	3:C:13:ILE:HG13	2.24	0.61
3:C:146:LEU:HD12	3:C:146:LEU:N	2.15	0.61
3:C:180:ASP:OD2	3:C:192:ILE:HG21	1.99	0.61
3:C:193:ILE:HD11	3:C:222:ARG:HB2	1.82	0.61
1:D:48:GLN:CB	1:D:130:ILE:CD1	2.65	0.61
1:D:138:ASP:OD1	1:D:138:ASP:N	2.33	0.61
4:E:32:LEU:HA	4:E:56:GLU:O	2.01	0.61
4:E:44:GLU:HA	4:E:129:ILE:HD12	1.81	0.61
4:E:284:LYS:CE	4:E:284:LYS:H	2.12	0.61
1:A:148:ILE:CG2	1:A:148:ILE:O	2.49	0.61
1:A:416:LEU:O	1:A:420:ILE:HG23	2.01	0.61
2:B:35:LEU:HD22	2:B:55:PHE:O	2.01	0.61
2:B:270:VAL:N	2:B:271:PRO:CD	2.64	0.61
3:C:69:TRP:HZ2	3:C:112:VAL:HG12	1.66	0.61
3:C:243:ALA:HB3	3:C:302:VAL:CG1	2.31	0.61
3:C:475:MET:HA	3:C:478:PHE:CZ	2.35	0.61
1:D:106:THR:CG2	1:D:107:LYS:HE2	2.30	0.61
4:E:14:TYR:CE1	4:E:84:LEU:CD1	2.83	0.61
4:E:55:ILE:HG23	4:E:119:PRO:CD	2.29	0.61
4:E:55:ILE:O	4:E:118:LEU:HB2	2.01	0.61
1:A:62:ASP:HB3	1:A:65:LEU:HG	1.81	0.61
1:A:108:LEU:HD22	1:A:118:TRP:HA	1.82	0.61
2:B:160:HIS:NE2	2:B:209:PHE:CE1	2.58	0.61
3:C:160:MET:H	3:C:213:GLN:CG	2.13	0.61
3:C:228:TYR:CD1	3:C:229:VAL:N	2.68	0.61
4:E:59:TRP:CD2	4:E:115:MET:HB2	2.36	0.61
1:A:201:ILE:CG2	1:A:203:TYR:HE1	2.14	0.61
2:B:285:MET:O	2:B:289:ILE:HG12	1.99	0.61
3:C:50:GLU:CG	3:C:132:ILE:HB	2.27	0.61
3:C:106:TYR:CE1	3:C:107:PHE:HE1	2.19	0.61
3:C:241:PHE:C	3:C:241:PHE:HD1	2.09	0.61
1:D:260:ILE:CG2	1:D:264:ILE:HD11	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:419:ILE:HD12	1:D:420:ILE:HG22	1.83	0.61
4:E:14:TYR:HE1	4:E:84:LEU:CD1	2.12	0.61
4:E:22:LYS:HG3	4:E:23:THR:N	2.16	0.61
4:E:185:ILE:HG12	4:E:214:ILE:HG21	1.82	0.61
4:E:414:SER:N	4:E:416:VAL:HG13	2.15	0.61
1:A:17:LYS:CE	1:A:84:ASP:HA	2.25	0.61
1:A:233:PHE:HE1	1:A:413:VAL:HG11	1.63	0.61
2:B:3:MET:O	2:B:6:THR:HB	2.01	0.61
2:B:108:VAL:HG22	2:B:118:TRP:CG	2.36	0.61
2:B:108:VAL:HG22	2:B:118:TRP:HB2	1.83	0.61
2:B:270:VAL:CG1	2:B:284:LEU:CD1	2.74	0.61
3:C:90:PRO:HD2	3:C:120:TRP:CZ3	2.34	0.61
3:C:316:THR:HG22	3:C:317:PRO:N	2.14	0.61
1:D:381:TYR:CE1	4:E:419:CYS:SG	2.93	0.61
1:A:37:LEU:HD23	1:A:54:VAL:HG12	1.82	0.61
2:B:40:LEU:HA	2:B:52:THR:HG23	1.81	0.61
2:B:187:SER:OG	2:B:216:LYS:HE2	2.01	0.61
2:B:226:VAL:HG23	2:B:227:PRO:HD3	1.82	0.61
3:C:66:ARG:HG2	3:C:66:ARG:HH11	1.65	0.61
3:C:93:VAL:CB	3:C:151:LEU:HD22	2.31	0.61
3:C:147:LYS:HE2	3:C:216:THR:CG2	2.31	0.61
3:C:241:PHE:HA	3:C:244:ALA:HB3	1.83	0.61
1:D:102:ILE:HG12	4:E:98:GLN:HE21	1.66	0.61
1:D:106:THR:CG2	1:D:107:LYS:HD3	2.31	0.61
4:E:56:GLU:CB	4:E:118:LEU:HD22	2.29	0.61
4:E:305:ASN:HA	4:E:308:LEU:CD1	2.25	0.61
1:A:306:HIS:C	1:A:306:HIS:CD2	2.79	0.61
1:A:426:PHE:CD1	1:A:426:PHE:C	2.79	0.61
2:B:56:LEU:CD2	2:B:103:THR:HG23	2.31	0.61
2:B:84:ASP:C	2:B:85:VAL:CG2	2.73	0.61
2:B:176:ASN:ND2	2:B:188:ILE:HD12	2.15	0.61
2:B:248:LYS:HZ3	2:B:252:SER:CB	2.14	0.61
2:B:439:PHE:O	2:B:439:PHE:CD1	2.54	0.61
3:C:93:VAL:HG21	3:C:151:LEU:HD22	1.82	0.61
3:C:271:LEU:C	3:C:271:LEU:CD2	2.73	0.61
1:D:60:TRP:CZ3	1:D:116:ILE:HG13	2.36	0.61
1:D:257:LEU:HA	1:D:260:ILE:CG1	2.31	0.61
4:E:61:ASP:O	4:E:113:GLY:HA2	2.00	0.61
4:E:91:LEU:HB2	4:E:95:VAL:HG23	1.83	0.61
4:E:138:TRP:CH2	4:E:215:GLN:CG	2.84	0.61
2:B:134:TYR:CE1	2:B:213:ILE:CG1	2.77	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:189:GLU:HG3	2:B:468:PHE:CB	2.30	0.61
2:B:442:ILE:O	2:B:446:MET:HG2	2.01	0.61
3:C:69:TRP:CE3	3:C:73:GLU:HB3	2.36	0.61
3:C:190:TRP:HB2	3:C:223:ARG:HB2	1.82	0.61
3:C:200:ASN:ND2	3:C:201:ILE:H	1.98	0.61
3:C:247:PHE:HA	3:C:250:PRO:HG3	1.81	0.61
3:C:319:THR:CB	3:C:447:ASN:HB3	2.31	0.61
4:E:31:THR:HA	4:E:158:GLN:HG3	1.83	0.61
4:E:74:ILE:HG12	4:E:76:LEU:O	2.01	0.61
4:E:195:ASN:OD1	4:E:204:ASP:HA	2.01	0.61
1:A:135:PHE:CD1	1:A:135:PHE:C	2.78	0.60
2:B:35:LEU:HD13	2:B:55:PHE:O	2.01	0.60
2:B:87:GLN:CB	2:B:104:LEU:HD11	2.13	0.60
3:C:7:LEU:HD13	3:C:73:GLU:CD	2.26	0.60
3:C:269:VAL:HA	3:C:272:LEU:HD11	1.81	0.60
1:D:222:CYS:SG	1:D:225:PHE:CZ	2.92	0.60
4:E:209:ILE:HG12	4:E:211:PHE:CE1	2.35	0.60
1:A:58:GLN:HB3	1:A:60:TRP:CZ3	2.36	0.60
1:A:100:PHE:HB3	1:A:103:VAL:HG21	1.82	0.60
1:A:175:GLU:OE1	1:A:175:GLU:HA	2.01	0.60
2:B:58:LEU:HD11	2:B:118:TRP:HB3	1.83	0.60
3:C:81:ARG:NH1	3:C:111:LEU:HD13	2.14	0.60
3:C:216:THR:C	3:C:217:PHE:CD1	2.77	0.60
4:E:50:THR:HA	4:E:123:TYR:O	2.00	0.60
4:E:250:LYS:HD2	4:E:253:LEU:HD22	1.83	0.60
1:A:145:LYS:HZ2	1:A:202:THR:CG2	2.13	0.60
2:B:37:LEU:HD23	2:B:179:ALA:HB3	1.83	0.60
2:B:197:TRP:CD1	2:B:204:TYR:HB3	2.36	0.60
1:D:44:ASP:OD2	1:D:46:VAL:HG23	2.01	0.60
1:D:175:GLU:HB3	1:D:211:PRO:HG3	1.81	0.60
4:E:173:ASP:OD1	4:E:173:ASP:O	2.19	0.60
1:A:174:GLY:HA2	1:A:176:TRP:CZ3	2.36	0.60
2:B:69:PRO:O	2:B:73:GLU:HB2	2.01	0.60
3:C:238:LEU:HA	3:C:241:PHE:CE2	2.36	0.60
1:D:36:GLN:HE21	1:D:38:ILE:CG1	2.15	0.60
1:D:107:LYS:HE3	4:E:149:THR:CA	2.29	0.60
1:D:381:TYR:O	1:D:385:HIS:HB2	2.00	0.60
2:B:145:VAL:CG1	2:B:206:ASP:HB2	2.32	0.60
2:B:153:THR:HG23	2:B:156:VAL:O	2.01	0.60
1:D:187:TRP:CZ3	1:D:189:TYR:HD1	2.16	0.60
1:D:379:VAL:CA	1:D:382:ILE:HD12	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:182:GLU:HA	4:E:218:PRO:HG3	1.83	0.60
4:E:214:ILE:HD12	4:E:215:GLN:N	2.16	0.60
4:E:222:ILE:HG23	4:E:223:ILE:N	2.15	0.60
4:E:283:GLY:C	4:E:284:LYS:HE3	2.23	0.60
1:A:58:GLN:NE2	1:A:90:LEU:HD11	2.16	0.60
1:A:100:PHE:HB3	1:A:103:VAL:CG2	2.30	0.60
1:A:207:MET:O	1:A:207:MET:CE	2.49	0.60
1:A:93:TYR:CD2	1:A:145:LYS:HB3	2.37	0.60
1:A:135:PHE:N	1:A:136:PRO:CD	2.63	0.60
1:A:166:ASP:CG	1:A:178:MET:HE2	2.26	0.60
1:A:250:LEU:CD2	1:A:292:THR:CG2	2.78	0.60
1:A:305:THR:HB	1:A:400:LYS:HB2	1.83	0.60
2:B:75:ILE:HG22	3:C:27:ASN:CB	2.32	0.60
3:C:19:LYS:HZ3	3:C:88:TRP:CD1	2.19	0.60
3:C:43:ILE:HD12	3:C:43:ILE:N	2.17	0.60
3:C:247:PHE:CE1	3:C:309:VAL:HA	2.37	0.60
1:D:56:LEU:N	1:D:120:PRO:HD2	2.17	0.60
1:D:91:VAL:CG2	1:D:96:ALA:CB	2.80	0.60
1:D:137:PHE:HD2	1:D:431:ILE:HB	1.67	0.60
1:D:192:CYS:SG	1:D:193:CYS:N	2.75	0.60
1:D:259:VAL:HA	1:D:262:GLU:OE2	2.01	0.60
1:D:301:ARG:HH12	1:D:406:ILE:CD1	2.15	0.60
1:D:432:GLU:HG2	1:D:435:GLN:HE21	1.65	0.60
4:E:14:TYR:HE2	4:E:16:LYS:CE	2.12	0.60
4:E:36:LEU:CD2	4:E:51:THR:CG2	2.74	0.60
4:E:101:VAL:CG2	4:E:101:VAL:O	2.50	0.60
1:A:74:GLY:O	1:A:75:ILE:HG23	2.01	0.60
1:A:76:LYS:HG3	1:A:112:TYR:CZ	2.37	0.60
2:B:239:PHE:HB3	2:B:442:ILE:HG12	1.83	0.60
3:C:460:ILE:HG22	3:C:461:ILE:N	2.15	0.60
4:E:182:GLU:OE1	4:E:220:PHE:HE2	1.84	0.60
1:A:75:ILE:HG13	1:A:78:ILE:HG21	1.83	0.60
1:A:247:ILE:HD13	1:A:247:ILE:C	2.20	0.60
3:C:129:SER:O	3:C:129:SER:OG	2.20	0.60
1:D:43:VAL:HG11	1:D:50:VAL:HG22	1.83	0.60
1:D:75:ILE:HD11	1:D:78:ILE:CG2	2.32	0.60
1:D:103:VAL:HG13	1:D:118:TRP:CZ2	2.37	0.60
1:D:141:ASN:HB3	1:D:206:ILE:HD11	1.83	0.60
4:E:49:LEU:O	4:E:124:ARG:HD2	2.02	0.60
4:E:75:ASP:HB3	4:E:110:TYR:CE1	2.37	0.60
4:E:146:ARG:NH1	4:E:205:PHE:CB	2.60	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:PHE:C	1:A:124:PHE:HD1	2.09	0.60
1:A:242:LYS:HB2	1:A:245:LEU:HB3	1.83	0.60
1:A:426:PHE:HD1	1:A:426:PHE:C	2.09	0.60
2:B:46:LYS:HB3	2:B:276:SER:O	2.02	0.60
2:B:104:LEU:CD1	2:B:118:TRP:HH2	2.06	0.60
3:C:58:MET:SD	3:C:92:ILE:HD11	2.42	0.60
3:C:463:PRO:O	3:C:467:LEU:HD23	2.02	0.60
1:D:107:LYS:HE3	4:E:149:THR:C	2.27	0.60
1:D:379:VAL:HG22	1:D:382:ILE:CD1	2.32	0.60
1:D:409:ILE:HG13	1:D:410:LEU:N	2.16	0.60
1:A:72:TYR:CB	1:A:112:TYR:HD2	2.09	0.59
1:A:157:SER:HB2	1:A:199:LEU:CD1	2.32	0.59
4:E:31:THR:CB	4:E:58:GLN:HB2	2.31	0.59
4:E:86:LEU:HD13	4:E:103:TYR:CE1	2.37	0.59
4:E:441:LEU:C	4:E:441:LEU:HD12	2.27	0.59
1:A:66:ARG:O	1:A:66:ARG:CD	2.50	0.59
1:A:107:LYS:HE3	2:B:150:THR:HG22	1.82	0.59
1:A:132:VAL:C	1:A:274:ILE:HG22	2.25	0.59
2:B:56:LEU:HD22	2:B:120:PRO:HG3	1.82	0.59
3:C:247:PHE:CD2	3:C:460:ILE:CD1	2.84	0.59
1:D:49:ILE:HG21	1:D:125:LYS:HZ2	1.65	0.59
4:E:47:GLU:HB3	4:E:129:ILE:CD1	2.31	0.59
2:B:46:LYS:CB	2:B:278:PRO:HD3	2.32	0.59
2:B:238:VAL:HG22	2:B:255:ALA:CB	2.31	0.59
2:B:450:GLY:O	2:B:454:ILE:HG13	2.01	0.59
3:C:234:THR:O	3:C:238:LEU:HD13	2.02	0.59
1:D:409:ILE:O	1:D:412:CYS:HB3	2.02	0.59
4:E:54:TRP:C	4:E:118:LEU:HD13	2.27	0.59
4:E:289:VAL:HG12	4:E:290:MET:N	2.18	0.59
2:B:188:ILE:CG2	2:B:190:HIS:H	2.14	0.59
2:B:248:LYS:HZ3	2:B:252:SER:HA	1.67	0.59
1:D:65:LEU:HD23	1:D:110:LEU:CD1	2.25	0.59
1:D:419:ILE:CD1	1:D:420:ILE:CG2	2.80	0.59
1:D:420:ILE:HA	1:D:423:VAL:HG23	1.84	0.59
1:A:80:LEU:CD2	1:A:110:LEU:HB2	2.32	0.59
1:A:148:ILE:O	1:A:148:ILE:HG23	2.00	0.59
2:B:153:THR:CB	2:B:204:TYR:HB2	2.20	0.59
3:C:67:LEU:HD11	3:C:112:VAL:HG13	1.84	0.59
1:D:79:ARG:NH1	4:E:154:GLU:CD	2.61	0.59
1:D:187:TRP:CB	1:D:199:LEU:HD23	2.27	0.59
4:E:55:ILE:CG2	4:E:119:PRO:HG2	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:83:LEU:N	4:E:83:LEU:CD2	2.64	0.59
4:E:271:LYS:HB2	4:E:271:LYS:NZ	2.14	0.59
1:A:32:THR:HG23	1:A:159:SER:O	2.02	0.59
1:A:245:LEU:CD2	2:B:253:ILE:HB	2.32	0.59
3:C:67:LEU:HD11	3:C:112:VAL:CG1	2.32	0.59
4:E:468:THR:HG22	4:E:468:THR:O	2.03	0.59
1:A:1:SER:N	1:A:4:GLU:HB2	2.18	0.59
1:A:243:MET:HG2	1:A:244:THR:N	2.16	0.59
1:A:296:ILE:HD13	1:A:296:ILE:N	2.17	0.59
1:D:45:GLU:OE2	1:D:271:VAL:HG22	2.03	0.59
1:D:171:MET:HG2	1:D:174:GLY:N	2.13	0.59
1:D:409:ILE:HA	1:D:412:CYS:HB2	1.85	0.59
4:E:41:SER:O	4:E:49:LEU:HA	2.03	0.59
4:E:250:LYS:HB3	4:E:253:LEU:CD2	2.27	0.59
1:A:3:HIS:O	1:A:7:LEU:HG	2.02	0.59
1:A:41:ILE:HD11	1:A:51:GLU:CG	2.32	0.59
1:A:93:TYR:N	1:A:93:TYR:CD1	2.63	0.59
1:A:104:HIS:C	1:A:105:MET:SD	2.85	0.59
2:B:28:LYS:HD3	2:B:154:SER:O	2.03	0.59
2:B:84:ASP:C	2:B:85:VAL:HG23	2.28	0.59
3:C:84:PRO:HG3	3:C:107:PHE:O	2.03	0.59
3:C:219:LEU:HD11	3:C:221:ILE:HG22	1.83	0.59
3:C:249:LEU:N	3:C:250:PRO:CD	2.64	0.59
1:D:135:PHE:N	1:D:136:PRO:CD	2.66	0.59
4:E:14:TYR:CE1	4:E:84:LEU:HD12	2.38	0.59
4:E:80:PRO:HB2	4:E:83:LEU:HD23	1.85	0.59
4:E:138:TRP:CB	4:E:213:ILE:CG1	2.68	0.59
1:A:7:LEU:HD22	1:A:70:ALA:O	2.02	0.59
2:B:33:VAL:HG11	2:B:158:LEU:HD11	1.85	0.59
2:B:135:PHE:HD2	2:B:283:TYR:CE1	2.20	0.59
2:B:265:LEU:HA	2:B:268:ASP:OD2	2.02	0.59
3:C:84:PRO:HD2	3:C:85:GLU:OE1	2.02	0.59
3:C:225:PRO:O	3:C:226:LEU:HD23	2.03	0.59
3:C:461:ILE:O	3:C:464:VAL:HG12	2.03	0.59
4:E:432:SER:O	4:E:435:GLU:HB2	2.03	0.59
1:A:59:GLN:HE22	1:A:117:MET:HG3	1.66	0.59
1:A:90:LEU:O	1:A:91:VAL:HG23	2.03	0.59
1:A:108:LEU:HD21	1:A:118:TRP:CD1	2.38	0.59
2:B:258:ALA:HB2	3:C:265:LEU:CD1	2.33	0.59
2:B:308:SER:HB2	2:B:311:THR:CG2	2.04	0.59
1:D:390:GLU:O	1:D:393:SER:HB2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:138:TRP:CD1	4:E:213:ILE:HG12	2.38	0.59
4:E:182:GLU:HA	4:E:218:PRO:HG2	1.84	0.59
4:E:416:VAL:HG22	4:E:417:GLU:H	1.68	0.59
1:A:145:LYS:NZ	1:A:202:THR:HG23	2.17	0.58
2:B:153:THR:O	2:B:204:TYR:HD2	1.84	0.58
2:B:248:LYS:NZ	2:B:252:SER:CB	2.66	0.58
3:C:270:PHE:CE1	1:D:255:VAL:CG2	2.86	0.58
1:D:261:VAL:O	1:D:261:VAL:CG1	2.51	0.58
4:E:45:LYS:N	4:E:280:PRO:CA	2.66	0.58
4:E:135:PRO:HB2	4:E:137:ASP:OD1	2.03	0.58
4:E:313:THR:HG21	4:E:441:LEU:CA	2.32	0.58
1:A:35:LEU:HD13	1:A:203:TYR:OH	2.03	0.58
2:B:285:MET:O	2:B:288:MET:HB3	2.03	0.58
3:C:60:HIS:HE1	3:C:160:MET:HE1	1.67	0.58
3:C:93:VAL:HG21	3:C:151:LEU:CD2	2.33	0.58
3:C:104:VAL:O	3:C:123:PRO:HG2	2.03	0.58
1:D:33:VAL:HA	1:D:57:ARG:O	2.04	0.58
1:D:240:GLY:C	1:D:242:LYS:H	2.12	0.58
4:E:35:THR:HB	4:E:54:TRP:CE3	2.37	0.58
4:E:77:VAL:HB	4:E:109:VAL:O	2.02	0.58
1:A:187:TRP:HD1	1:A:199:LEU:HD23	1.67	0.58
3:C:35:LEU:HD21	3:C:37:LEU:CD2	2.33	0.58
4:E:287:ILE:HG13	4:E:291:PHE:CD2	2.38	0.58
1:A:90:LEU:HD12	1:A:100:PHE:HE2	1.68	0.58
1:A:148:ILE:CD1	1:A:156:VAL:HG13	2.29	0.58
1:A:236:PRO:HG3	1:A:299:HIS:NE2	2.18	0.58
2:B:49:GLU:HA	2:B:127:SER:HA	1.86	0.58
2:B:95:ASN:HB3	2:B:127:SER:H	1.67	0.58
2:B:290:LEU:HD21	2:B:453:SER:HB3	1.83	0.58
3:C:33:ILE:CG2	3:C:160:MET:SD	2.90	0.58
3:C:204:ASP:H	3:C:207:PRO:HG2	1.68	0.58
4:E:36:LEU:HD23	4:E:51:THR:CG2	2.26	0.58
4:E:45:LYS:HG2	4:E:279:VAL:HA	1.85	0.58
4:E:212:LEU:HD12	4:E:212:LEU:N	2.18	0.58
1:A:216:VAL:HG13	1:A:220:ILE:CD1	2.34	0.58
2:B:10:VAL:CG1	2:B:11:LEU:HD22	2.30	0.58
2:B:251:LEU:C	2:B:251:LEU:HD12	2.29	0.58
2:B:291:VAL:HG12	2:B:292:ALA:N	2.18	0.58
3:C:482:PRO:CG	3:C:483:ALA:H	2.15	0.58
1:D:166:ASP:CB	1:D:181:TYR:HB2	2.33	0.58
1:D:187:TRP:CH2	1:D:189:TYR:CD1	2.91	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:291:VAL:O	1:D:295:VAL:HG22	2.04	0.58
4:E:9:LYS:O	4:E:9:LYS:HD2	2.03	0.58
4:E:44:GLU:OE2	4:E:129:ILE:HB	2.00	0.58
1:A:43:VAL:HG22	1:A:50:VAL:CG1	2.33	0.58
1:A:50:VAL:HG12	1:A:51:GLU:N	2.17	0.58
1:A:107:LYS:HG2	2:B:150:THR:CG2	2.31	0.58
2:B:186:TRP:CE3	2:B:215:ARG:CZ	2.87	0.58
1:D:30:ASP:O	1:D:60:TRP:HB2	2.02	0.58
1:D:62:ASP:O	1:D:65:LEU:HB2	2.04	0.58
1:A:148:ILE:HG23	1:A:198:TYR:HD2	1.68	0.58
1:A:419:ILE:HG23	1:A:420:ILE:N	2.16	0.58
2:B:35:LEU:HD13	2:B:55:PHE:C	2.28	0.58
2:B:226:VAL:C	2:B:230:LEU:HG	2.29	0.58
2:B:241:LEU:N	2:B:242:PRO:HD2	2.19	0.58
3:C:42:LEU:CA	3:C:54:THR:HG22	2.30	0.58
3:C:252:GLU:HG3	1:D:300:HIS:C	2.29	0.58
3:C:452:THR:O	3:C:452:THR:HG23	2.03	0.58
4:E:34:LEU:HB2	4:E:210:PHE:CZ	2.38	0.58
2:B:230:LEU:CA	2:B:233:ILE:HG13	2.29	0.58
2:B:279:ILE:HG22	2:B:280:ILE:HD13	1.84	0.58
3:C:3:GLU:O	3:C:7:LEU:HB2	2.04	0.58
3:C:228:TYR:HD1	3:C:229:VAL:H	1.52	0.58
3:C:426:THR:HA	3:C:429:ILE:HG23	1.85	0.58
1:D:76:LYS:HD2	1:D:112:TYR:HE2	1.68	0.58
1:D:106:THR:HG23	1:D:107:LYS:CD	2.32	0.58
1:D:228:LEU:HD11	4:E:258:LEU:HD21	1.84	0.58
4:E:416:VAL:CG2	4:E:417:GLU:N	2.65	0.58
1:A:6:ARG:HB3	1:A:6:ARG:HH11	1.67	0.58
1:A:64:ARG:CA	1:A:66:ARG:HH11	2.11	0.58
1:A:107:LYS:HE3	2:B:150:THR:HB	1.80	0.58
1:A:131:ILE:HD11	1:A:140:GLN:CD	2.28	0.58
1:A:255:VAL:CG2	1:A:258:LEU:HD12	2.30	0.58
2:B:130:ILE:O	2:B:134:TYR:HB2	2.04	0.58
2:B:185:GLN:CG	2:B:219:PHE:HE2	2.16	0.58
3:C:59:ASP:OD1	3:C:121:LEU:HD13	2.03	0.58
3:C:142:GLN:HG3	3:C:143:ASN:H	1.69	0.58
3:C:262:CYS:SG	1:D:251:LEU:HD11	2.44	0.58
1:D:101:ALA:C	1:D:102:ILE:HD12	2.28	0.58
1:D:244:THR:HG23	1:D:245:LEU:H	1.69	0.58
4:E:140:ASN:HD22	4:E:141:CYS:N	2.02	0.58
1:A:59:GLN:NE2	1:A:117:MET:SD	2.77	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:132:VAL:CG1	2:B:280:ILE:H	2.11	0.58
2:B:279:ILE:HG21	2:B:280:ILE:HD13	1.85	0.58
3:C:115:ASN:ND2	3:C:115:ASN:C	2.52	0.58
1:D:35:LEU:CD1	1:D:54:VAL:CG1	2.79	0.58
1:D:54:VAL:O	1:D:56:LEU:HD23	2.04	0.58
1:D:105:MET:HG2	1:D:105:MET:O	2.03	0.58
1:D:133:THR:HG22	1:D:136:PRO:HG2	1.85	0.58
4:E:89:VAL:CG2	4:E:99:PHE:CE2	2.87	0.58
4:E:117:TRP:CD1	4:E:119:PRO:HD3	2.39	0.58
4:E:297:VAL:O	4:E:301:VAL:HG22	2.03	0.58
4:E:304:LEU:HG	4:E:304:LEU:O	2.04	0.58
4:E:416:VAL:HG22	4:E:417:GLU:N	2.19	0.58
1:A:29:VAL:HB	1:A:31:ILE:CD1	2.32	0.57
1:A:207:MET:H	1:A:207:MET:CE	2.16	0.57
2:B:33:VAL:HG22	2:B:158:LEU:HD22	1.85	0.57
3:C:429:ILE:HG13	3:C:430:VAL:N	2.19	0.57
1:D:76:LYS:HE3	1:D:112:TYR:CE2	2.39	0.57
1:D:407:ASP:OD1	1:D:408:HIS:HD2	1.87	0.57
4:E:273:PRO:HG2	4:E:274:GLU:N	2.19	0.57
1:A:107:LYS:CE	2:B:150:THR:CB	2.81	0.57
1:A:176:TRP:CE3	1:A:209:ARG:NH1	2.72	0.57
2:B:2:VAL:HG12	2:B:69:PRO:HG3	1.86	0.57
3:C:154:ASN:HB3	3:C:211:ASN:HB3	1.86	0.57
1:D:280:PHE:HB3	1:D:284:PHE:CZ	2.40	0.57
1:A:46:VAL:HG21	1:A:269:SER:O	2.04	0.57
2:B:56:LEU:HD21	2:B:103:THR:CA	2.31	0.57
2:B:270:VAL:HG12	2:B:284:LEU:HD11	1.87	0.57
3:C:319:THR:HG22	3:C:320:HIS:N	2.18	0.57
4:E:159:LEU:CG	4:E:192:LYS:HB2	2.34	0.57
1:A:378:GLY:O	1:A:382:ILE:HG12	2.04	0.57
2:B:59:ALA:HA	2:B:116:VAL:O	2.05	0.57
3:C:70:ASN:O	3:C:74:TYR:HB3	2.04	0.57
1:D:167:LEU:HD11	1:D:178:MET:HB3	1.84	0.57
1:D:281:THR:O	1:D:285:VAL:HB	2.04	0.57
4:E:14:TYR:CZ	4:E:84:LEU:HD12	2.40	0.57
3:C:104:VAL:HA	3:C:106:TYR:CE1	2.40	0.57
3:C:271:LEU:HD21	3:C:299:VAL:HG12	1.87	0.57
3:C:449:VAL:O	3:C:452:THR:HG22	2.03	0.57
3:C:469:THR:O	3:C:473:PHE:HB2	2.04	0.57
4:E:34:LEU:HD12	4:E:210:PHE:CZ	2.40	0.57
4:E:34:LEU:CD2	4:E:55:ILE:HA	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:436:ASN:CA	4:E:439:TRP:NE1	2.63	0.57
1:A:35:LEU:C	1:A:35:LEU:CD2	2.77	0.57
1:A:134:HIS:C	1:A:136:PRO:HD2	2.29	0.57
2:B:28:LYS:HB3	2:B:155:GLU:HA	1.87	0.57
2:B:68:ASP:CB	2:B:69:PRO:CD	2.73	0.57
2:B:274:SER:CB	2:B:278:PRO:HB3	2.29	0.57
3:C:193:ILE:CD1	3:C:222:ARG:HB2	2.33	0.57
4:E:30:VAL:O	4:E:158:GLN:HG3	2.05	0.57
4:E:172:ILE:HD11	4:E:188:ARG:N	2.19	0.57
1:A:92:LEU:HB3	1:A:95:ASN:HB2	1.86	0.57
1:A:263:LEU:N	1:A:263:LEU:HD23	2.19	0.57
2:B:35:LEU:O	2:B:174:MET:HE1	2.04	0.57
3:C:243:ALA:HB2	3:C:302:VAL:HG12	1.81	0.57
1:D:110:LEU:HD12	1:D:111:ASP:N	2.20	0.57
1:D:136:PRO:CG	1:D:274:ILE:HD11	2.32	0.57
1:D:149:TRP:CG	1:D:150:THR:H	2.23	0.57
1:D:419:ILE:CD1	1:D:420:ILE:HG22	2.35	0.57
4:E:67:ASN:N	4:E:67:ASN:ND2	2.42	0.57
4:E:94:ASN:CG	4:E:143:LEU:HD23	2.29	0.57
1:A:41:ILE:HG12	1:A:51:GLU:HB3	1.84	0.57
1:A:286:ILE:O	1:A:290:ILE:HG12	2.04	0.57
2:B:10:VAL:O	2:B:13:GLU:HB2	2.05	0.57
2:B:145:VAL:HG12	2:B:206:ASP:HB2	1.86	0.57
2:B:281:ILE:HG22	2:B:285:MET:H	1.66	0.57
3:C:16:LYS:HA	3:C:16:LYS:CE	2.33	0.57
3:C:291:TYR:N	3:C:291:TYR:CD1	2.71	0.57
3:C:452:THR:C	3:C:455:ARG:HG2	2.28	0.57
1:D:88:PRO:HG2	1:D:88:PRO:O	2.05	0.57
4:E:235:LEU:O	4:E:235:LEU:CD1	2.43	0.57
1:A:31:ILE:HG13	1:A:60:TRP:HB3	1.87	0.57
1:A:56:LEU:CD2	1:A:57:ARG:N	2.68	0.57
1:A:66:ARG:CA	1:A:113:THR:C	2.78	0.57
1:A:80:LEU:HD23	1:A:110:LEU:HB2	1.87	0.57
1:A:147:GLY:HA2	1:A:158:ILE:HG21	1.87	0.57
1:A:160:PRO:CG	1:A:185:LYS:NZ	2.68	0.57
2:B:144:MET:CE	2:B:211:LEU:HD21	2.34	0.57
2:B:222:VAL:O	2:B:225:ILE:HB	2.05	0.57
2:B:280:ILE:C	2:B:282:SER:H	2.11	0.57
3:C:47:GLU:CD	3:C:285:VAL:HB	2.29	0.57
3:C:63:TYR:HB2	3:C:117:TYR:CE1	2.39	0.57
3:C:190:TRP:CD1	3:C:221:ILE:CD1	2.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:88:ASP:O	4:E:88:ASP:CG	2.47	0.57
4:E:134:PHE:N	4:E:135:PRO:CD	2.68	0.57
4:E:184:THR:HG21	4:E:215:GLN:HG2	1.85	0.57
4:E:224:ASN:O	4:E:228:PRO:HG3	2.04	0.57
1:A:2:GLU:O	1:A:7:LEU:HD21	2.05	0.57
1:A:107:LYS:NZ	2:B:151:TYR:CD2	2.73	0.57
1:A:406:ILE:HA	1:A:409:ILE:CG1	2.34	0.57
2:B:281:ILE:H	2:B:281:ILE:HD12	1.70	0.57
3:C:36:SER:HB3	3:C:59:ASP:HB2	1.86	0.57
3:C:135:LEU:C	3:C:138:PRO:HD2	2.30	0.57
3:C:247:PHE:HE1	3:C:309:VAL:CG2	2.18	0.57
1:D:274:ILE:HB	1:D:276:LYS:HD3	1.87	0.57
4:E:32:LEU:CD1	4:E:157:LEU:HD13	2.33	0.57
4:E:138:TRP:CZ2	4:E:215:GLN:CB	2.82	0.57
2:B:36:THR:O	2:B:54:VAL:HB	2.05	0.56
2:B:91:VAL:HG12	2:B:147:LYS:O	2.05	0.56
2:B:147:LYS:CG	2:B:148:SER:N	2.68	0.56
3:C:42:LEU:CD2	3:C:190:TRP:CZ2	2.86	0.56
3:C:472:ILE:CA	3:C:475:MET:HB3	2.34	0.56
1:D:201:ILE:O	1:D:203:TYR:CE1	2.56	0.56
1:A:175:GLU:OE1	1:A:211:PRO:HG3	2.04	0.56
1:A:209:ARG:CG	1:A:210:ILE:N	2.68	0.56
1:A:220:ILE:N	1:A:221:PRO:CD	2.68	0.56
1:A:227:PHE:CD2	2:B:299:VAL:HG11	2.41	0.56
1:A:258:LEU:HD13	4:E:267:LEU:HD22	1.86	0.56
2:B:223:TYR:O	2:B:227:PRO:HD3	2.05	0.56
2:B:232:SER:O	2:B:235:ALA:HB3	2.05	0.56
2:B:287:ILE:CA	2:B:290:LEU:HD12	2.35	0.56
2:B:444:ILE:HG23	2:B:445:THR:N	2.20	0.56
3:C:35:LEU:HD22	3:C:215:VAL:CG1	2.33	0.56
3:C:93:VAL:HB	3:C:151:LEU:HD22	1.85	0.56
3:C:139:PHE:O	3:C:222:ARG:HG2	2.05	0.56
1:D:15:TYR:CE2	1:D:84:ASP:HB3	2.40	0.56
1:A:231:LEU:C	1:A:233:PHE:N	2.64	0.56
1:A:256:PHE:N	1:A:256:PHE:CD1	2.70	0.56
1:A:385:HIS:HD1	1:A:385:HIS:C	2.13	0.56
2:B:40:LEU:HB2	2:B:52:THR:HG23	1.87	0.56
2:B:72:TYR:O	2:B:76:LYS:HG2	2.05	0.56
2:B:227:PRO:C	2:B:231:ILE:HG12	2.30	0.56
2:B:230:LEU:HA	2:B:233:ILE:CG1	2.34	0.56
3:C:137:PHE:H	3:C:138:PRO:CD	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:475:MET:O	3:C:478:PHE:CE1	2.59	0.56
1:D:37:LEU:CA	1:D:54:VAL:HG13	2.35	0.56
2:B:108:VAL:CG1	2:B:118:TRP:HB2	2.35	0.56
3:C:25:LYS:O	3:C:25:LYS:CG	2.52	0.56
3:C:222:ARG:NH2	3:C:223:ARG:C	2.64	0.56
3:C:434:LYS:CE	3:C:435:GLU:HG2	2.35	0.56
4:E:79:ILE:CG1	4:E:80:PRO:CD	2.79	0.56
4:E:140:ASN:C	4:E:140:ASN:ND2	2.53	0.56
4:E:273:PRO:CG	4:E:274:GLU:H	2.18	0.56
1:A:45:GLU:CD	1:A:271:VAL:HB	2.30	0.56
2:B:425:LYS:HA	2:B:428:TRP:HD1	1.67	0.56
3:C:59:ASP:OD1	3:C:121:LEU:HB2	2.06	0.56
4:E:55:ILE:CA	4:E:118:LEU:HD13	2.35	0.56
4:E:76:LEU:CD2	4:E:77:VAL:N	2.68	0.56
4:E:103:TYR:CD2	4:E:104:TYR:HD1	2.22	0.56
4:E:133:TYR:C	4:E:135:PRO:HD2	2.30	0.56
4:E:257:VAL:O	4:E:257:VAL:HG12	2.06	0.56
1:A:36:GLN:O	1:A:38:ILE:HD12	2.03	0.56
1:A:43:VAL:HG22	1:A:50:VAL:CG2	2.35	0.56
1:A:260:ILE:CG2	1:A:261:VAL:N	2.67	0.56
1:A:384:GLU:HA	1:A:387:LYS:HG3	1.87	0.56
2:B:431:VAL:O	2:B:432:ALA:HB3	2.05	0.56
2:B:431:VAL:HG23	2:B:433:MET:H	1.71	0.56
1:D:253:LEU:CD2	1:D:254:THR:N	2.59	0.56
4:E:182:GLU:CD	4:E:220:PHE:CE2	2.82	0.56
4:E:453:ILE:HD12	4:E:453:ILE:C	2.31	0.56
1:A:133:THR:C	1:A:136:PRO:HD2	2.30	0.56
1:A:294:VAL:HG13	1:A:295:VAL:N	2.19	0.56
2:B:93:MET:HG2	2:B:206:ASP:HB3	1.88	0.56
3:C:33:ILE:HG12	3:C:62:TRP:CB	2.36	0.56
1:D:239:SER:CB	1:D:242:LYS:HE2	2.34	0.56
4:E:158:GLN:O	4:E:159:LEU:HD23	2.05	0.56
1:A:67:TRP:HA	1:A:67:TRP:HE3	1.66	0.56
1:A:213:TYR:CG	1:A:214:PHE:N	2.73	0.56
1:A:236:PRO:CB	1:A:299:HIS:NE2	2.68	0.56
2:B:46:LYS:HE2	2:B:278:PRO:CD	2.36	0.56
2:B:248:LYS:CD	2:B:252:SER:CB	2.69	0.56
3:C:30:VAL:HG21	3:C:158:ILE:O	2.05	0.56
3:C:120:TRP:CD1	3:C:122:PRO:HD3	2.41	0.56
3:C:437:ASN:O	3:C:441:GLU:HG3	2.06	0.56
1:D:75:ILE:HD11	1:D:78:ILE:HG21	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:92:GLU:OE1	4:E:144:VAL:HG21	2.05	0.56
4:E:173:ASP:CG	4:E:185:ILE:HD13	2.31	0.56
2:B:46:LYS:CB	2:B:276:SER:C	2.77	0.56
3:C:3:GLU:OE1	3:C:3:GLU:O	2.23	0.56
1:D:11:LEU:O	1:D:15:TYR:HB2	2.06	0.56
4:E:27:VAL:HG12	4:E:154:GLU:HA	1.88	0.56
4:E:59:TRP:CZ2	4:E:115:MET:HB3	2.41	0.56
4:E:452:TRP:CE3	4:E:452:TRP:HA	2.40	0.56
1:A:177:VAL:O	1:A:207:MET:HB2	2.06	0.56
2:B:32:ARG:HH21	2:B:60:TRP:C	2.13	0.56
2:B:54:VAL:O	2:B:121:SER:HA	2.06	0.56
2:B:205:GLU:HB3	2:B:206:ASP:OD1	2.05	0.56
2:B:283:TYR:O	2:B:287:ILE:HG23	2.06	0.56
3:C:215:VAL:HG23	3:C:215:VAL:O	2.06	0.56
3:C:256:LYS:HB2	3:C:259:THR:HG22	1.87	0.56
1:D:106:THR:CG2	1:D:107:LYS:N	2.60	0.56
1:D:260:ILE:HA	1:D:263:LEU:HD12	1.88	0.56
4:E:138:TRP:CH2	4:E:215:GLN:CB	2.89	0.56
4:E:146:ARG:HD2	4:E:206:GLN:O	2.06	0.56
1:A:293:VAL:HG23	4:E:238:LEU:HD11	1.88	0.55
1:A:380:LYS:CG	2:B:408:ILE:HD13	2.35	0.55
1:A:385:HIS:C	1:A:385:HIS:ND1	2.64	0.55
1:A:390:GLU:HA	1:A:393:SER:OG	2.06	0.55
3:C:30:VAL:HG22	3:C:158:ILE:CA	2.36	0.55
3:C:475:MET:HA	3:C:478:PHE:CE2	2.41	0.55
4:E:44:GLU:HG3	4:E:129:ILE:CB	2.35	0.55
1:A:20:ARG:HG3	1:A:22:VAL:HG22	1.87	0.55
1:A:384:GLU:CD	2:B:411:ILE:CG2	2.79	0.55
2:B:54:VAL:C	2:B:55:PHE:HD1	2.14	0.55
2:B:136:PRO:HD3	2:B:280:ILE:HD11	1.87	0.55
2:B:239:PHE:N	2:B:239:PHE:CD1	2.73	0.55
3:C:37:LEU:HD12	3:C:217:PHE:CE2	2.41	0.55
3:C:74:TYR:O	3:C:78:SER:HA	2.06	0.55
3:C:431:LYS:CE	1:D:379:VAL:HG22	2.34	0.55
1:D:37:LEU:HD13	1:D:54:VAL:HG13	1.87	0.55
1:D:78:ILE:HD13	1:D:110:LEU:HB3	1.89	0.55
4:E:270:GLN:C	4:E:273:PRO:CD	2.80	0.55
1:A:111:ASP:C	1:A:113:THR:N	2.64	0.55
1:A:118:TRP:NE1	1:A:120:PRO:HG3	2.22	0.55
1:A:284:PHE:CD1	1:A:284:PHE:N	2.73	0.55
2:B:284:LEU:O	2:B:288:MET:HB2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:69:TRP:HB2	3:C:74:TYR:H	1.71	0.55
3:C:229:VAL:O	3:C:233:ILE:HG12	2.06	0.55
1:D:141:ASN:HB3	1:D:206:ILE:HG12	1.89	0.55
1:D:166:ASP:HB2	1:D:181:TYR:HB2	1.87	0.55
4:E:448:LYS:N	4:E:448:LYS:CD	2.63	0.55
1:A:2:GLU:O	1:A:7:LEU:HD11	2.06	0.55
1:A:20:ARG:HG3	1:A:20:ARG:O	2.05	0.55
1:A:171:MET:HE1	1:A:176:TRP:HH2	1.71	0.55
2:B:37:LEU:CB	2:B:54:VAL:HG12	2.35	0.55
2:B:67:TRP:HB2	2:B:72:TYR:CB	2.33	0.55
2:B:266:LEU:O	2:B:270:VAL:HG23	2.05	0.55
3:C:237:VAL:HG23	3:C:238:LEU:HD12	1.87	0.55
1:D:16:ASN:C	1:D:17:LYS:HG3	2.31	0.55
4:E:91:LEU:HB2	4:E:95:VAL:N	2.12	0.55
1:A:43:VAL:CB	1:A:50:VAL:HG22	2.36	0.55
1:A:292:THR:O	1:A:296:ILE:HG12	2.05	0.55
2:B:21:PRO:CG	2:B:85:VAL:CG1	2.84	0.55
2:B:185:GLN:CG	2:B:219:PHE:CE2	2.89	0.55
2:B:210:TYR:C	2:B:211:LEU:HD23	2.31	0.55
2:B:220:TYR:CG	2:B:223:TYR:HE2	2.25	0.55
3:C:35:LEU:HD12	3:C:92:ILE:HG21	1.87	0.55
3:C:443:VAL:O	3:C:443:VAL:HG12	2.05	0.55
1:D:43:VAL:CG2	1:D:50:VAL:HG13	2.36	0.55
1:D:76:LYS:CD	1:D:112:TYR:CE2	2.90	0.55
1:D:429:ARG:N	1:D:429:ARG:HE	2.04	0.55
4:E:44:GLU:HB3	4:E:280:PRO:HB3	1.87	0.55
4:E:268:ILE:HG13	4:E:269:ALA:N	2.22	0.55
1:A:31:ILE:HG12	1:A:60:TRP:HB3	1.88	0.55
1:A:46:VAL:HG23	1:A:270:ALA:C	2.30	0.55
1:A:301:ARG:HA	4:E:245:GLN:HB3	1.89	0.55
1:A:410:LEU:HD13	1:A:414:PHE:HD2	1.72	0.55
2:B:130:ILE:HD12	2:B:134:TYR:HE2	1.71	0.55
2:B:248:LYS:CE	2:B:252:SER:HB3	2.35	0.55
3:C:63:TYR:HA	3:C:117:TYR:HA	1.88	0.55
3:C:77:ILE:HD11	3:C:80:LEU:HD22	1.89	0.55
3:C:107:PHE:O	3:C:107:PHE:CD2	2.59	0.55
3:C:460:ILE:O	3:C:463:PRO:HG2	2.07	0.55
4:E:227:ALA:H	4:E:228:PRO:HD2	1.72	0.55
1:A:15:TYR:HE2	1:A:84:ASP:HB3	1.71	0.55
1:A:285:VAL:O	1:A:288:SER:HB3	2.07	0.55
2:B:15:TYR:O	2:B:15:TYR:CD1	2.60	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:21:PRO:HG2	2:B:85:VAL:HG11	1.89	0.55
2:B:95:ASN:HB3	2:B:126:SER:HB2	1.88	0.55
2:B:197:TRP:HB3	2:B:204:TYR:HD1	1.72	0.55
3:C:38:THR:HG21	3:C:57:TRP:CZ3	2.41	0.55
3:C:42:LEU:CD1	3:C:190:TRP:HZ2	2.18	0.55
3:C:252:GLU:CG	1:D:300:HIS:C	2.80	0.55
1:D:253:LEU:HD23	1:D:254:THR:CB	2.36	0.55
1:D:401:TYR:O	1:D:401:TYR:CD1	2.60	0.55
4:E:144:VAL:HG23	4:E:144:VAL:O	2.07	0.55
4:E:191:LYS:HB2	4:E:209:ILE:HG21	1.87	0.55
1:A:15:TYR:HE2	1:A:84:ASP:OD2	1.89	0.55
1:A:207:MET:O	1:A:207:MET:HG2	2.06	0.55
2:B:28:LYS:HD3	2:B:154:SER:C	2.31	0.55
2:B:67:TRP:CB	2:B:72:TYR:HB2	2.34	0.55
3:C:38:THR:CG2	3:C:57:TRP:CZ3	2.90	0.55
3:C:270:PHE:CE1	1:D:255:VAL:HG21	2.42	0.55
4:E:239:VAL:O	4:E:243:PRO:HD3	2.07	0.55
1:A:200:ASP:OD1	1:A:200:ASP:N	2.40	0.55
1:A:280:PHE:HB3	1:A:284:PHE:CE2	2.41	0.55
3:C:225:PRO:HG2	3:C:228:TYR:CD1	2.42	0.55
3:C:249:LEU:HB3	3:C:256:LYS:NZ	2.22	0.55
1:D:7:LEU:HD22	1:D:70:ALA:HB1	1.86	0.55
1:D:78:ILE:HD11	1:D:110:LEU:CG	2.37	0.55
1:D:149:TRP:CG	1:D:150:THR:N	2.74	0.55
1:D:191:THR:O	1:D:191:THR:HG22	2.06	0.55
4:E:63:ARG:O	4:E:64:LEU:HG	2.07	0.55
4:E:255:ILE:HD11	4:E:304:LEU:HD21	1.80	0.55
4:E:289:VAL:HG12	4:E:290:MET:CG	2.36	0.55
1:A:9:ALA:O	1:A:13:GLU:HG3	2.06	0.55
1:A:238:ASP:O	1:A:239:SER:HB2	2.07	0.55
1:A:252:SER:O	1:A:256:PHE:CD1	2.60	0.55
3:C:184:PHE:CD1	3:C:185:THR:N	2.75	0.55
4:E:58:GLN:C	4:E:59:TRP:HE3	2.14	0.55
4:E:147:SER:O	4:E:205:PHE:CE2	2.60	0.55
4:E:240:TYR:HB3	4:E:453:ILE:HD11	1.88	0.55
2:B:135:PHE:N	2:B:136:PRO:CD	2.70	0.54
3:C:83:ARG:HB3	3:C:84:PRO:HD2	1.89	0.54
3:C:291:TYR:N	3:C:291:TYR:HD1	2.06	0.54
3:C:438:ALA:HA	3:C:441:GLU:OE1	2.07	0.54
1:D:21:PRO:HD2	1:D:86:TRP:CG	2.42	0.54
1:D:106:THR:HG23	1:D:107:LYS:HD3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:120:PRO:HG2	1:D:120:PRO:O	2.07	0.54
1:D:152:ASP:HB3	1:D:197:PRO:CA	2.37	0.54
1:D:250:LEU:HA	1:D:253:LEU:HD22	1.87	0.54
4:E:40:ILE:HB	4:E:50:THR:HB	1.88	0.54
4:E:138:TRP:CH2	4:E:215:GLN:NE2	2.73	0.54
4:E:172:ILE:CD1	4:E:187:HIS:C	2.78	0.54
4:E:242:LEU:N	4:E:243:PRO:HD2	2.21	0.54
1:A:79:ARG:HH11	1:A:107:LYS:HZ2	1.55	0.54
1:A:85:VAL:CG1	1:A:86:TRP:N	2.69	0.54
2:B:291:VAL:HG12	2:B:292:ALA:H	1.71	0.54
2:B:441:TYR:O	2:B:444:ILE:HG22	2.07	0.54
3:C:9:ASN:O	3:C:12:LEU:HG	2.07	0.54
3:C:26:HIS:ND1	3:C:26:HIS:N	2.51	0.54
1:D:103:VAL:HG13	1:D:118:TRP:HZ2	1.71	0.54
1:D:395:ALA:HB1	1:D:399:TRP:CE2	2.41	0.54
4:E:34:LEU:HD23	4:E:55:ILE:HA	1.89	0.54
4:E:44:GLU:HG3	4:E:129:ILE:HB	1.89	0.54
4:E:45:LYS:HB3	4:E:280:PRO:HA	1.87	0.54
1:A:258:LEU:O	1:A:261:VAL:HB	2.07	0.54
1:A:417:ILE:HA	1:A:420:ILE:HG12	1.89	0.54
3:C:12:LEU:HB3	3:C:15:ASN:HB3	1.90	0.54
1:D:75:ILE:HD13	4:E:24:LEU:CD1	2.34	0.54
1:D:75:ILE:CG1	1:D:78:ILE:CG2	2.85	0.54
1:D:102:ILE:HG12	4:E:98:GLN:NE2	2.21	0.54
1:D:414:PHE:HE1	1:D:418:CYS:HG	1.56	0.54
4:E:34:LEU:HA	4:E:54:TRP:O	2.07	0.54
4:E:49:LEU:HD12	4:E:50:THR:N	2.21	0.54
4:E:100:GLU:HB2	4:E:122:ILE:CG1	2.38	0.54
2:B:216:LYS:HE3	2:B:216:LYS:H	1.72	0.54
2:B:258:ALA:O	2:B:262:PHE:CD1	2.60	0.54
2:B:258:ALA:HB1	3:C:265:LEU:HD22	1.89	0.54
2:B:409:LYS:O	2:B:412:ALA:HB3	2.07	0.54
1:D:92:LEU:HD13	1:D:146:LEU:CD1	2.37	0.54
1:D:92:LEU:HB2	1:D:96:ALA:N	2.22	0.54
1:A:37:LEU:HD22	1:A:54:VAL:HG12	1.88	0.54
2:B:304:LEU:HD23	2:B:304:LEU:C	2.32	0.54
3:C:65:HIS:N	3:C:65:HIS:HD2	1.96	0.54
3:C:266:ALA:HB3	1:D:251:LEU:HD13	1.89	0.54
1:D:414:PHE:O	1:D:414:PHE:HD1	1.90	0.54
4:E:289:VAL:HG12	4:E:290:MET:HG3	1.90	0.54
1:A:36:GLN:HG2	1:A:164:ARG:HH21	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:ARG:C	1:A:210:ILE:CG1	2.79	0.54
1:A:214:PHE:CD1	1:A:214:PHE:C	2.83	0.54
2:B:46:LYS:CB	2:B:278:PRO:CD	2.85	0.54
2:B:133:MET:SD	2:B:140:GLN:CB	2.94	0.54
2:B:147:LYS:HG3	2:B:148:SER:H	1.73	0.54
1:D:37:LEU:CB	1:D:54:VAL:HG13	2.37	0.54
1:D:76:LYS:HD2	1:D:112:TYR:CE2	2.43	0.54
1:D:85:VAL:HG13	1:D:86:TRP:N	2.22	0.54
4:E:133:TYR:C	4:E:135:PRO:CD	2.81	0.54
1:A:87:LEU:HD22	1:A:87:LEU:N	2.04	0.54
2:B:142:CYS:SG	2:B:143:THR:N	2.81	0.54
2:B:258:ALA:HB2	3:C:265:LEU:CD2	2.35	0.54
3:C:22:ARG:O	3:C:24:VAL:HG23	2.07	0.54
3:C:63:TYR:HE1	3:C:116:GLY:HA3	1.70	0.54
3:C:201:ILE:O	3:C:202:TYR:CG	2.60	0.54
1:D:53:ASN:HD21	1:D:121:PRO:C	2.14	0.54
4:E:136:PHE:CZ	4:E:217:LYS:CD	2.79	0.54
4:E:233:SER:O	4:E:236:VAL:HG23	2.07	0.54
1:A:217:ASN:O	1:A:221:PRO:HD3	2.08	0.54
2:B:132:VAL:HG13	2:B:279:ILE:C	2.32	0.54
3:C:51:THR:C	3:C:52:LEU:HD13	2.32	0.54
4:E:37:THR:OG1	4:E:54:TRP:CZ3	2.60	0.54
1:A:239:SER:CB	2:B:312:HIS:CB	2.84	0.54
1:A:406:ILE:CG2	1:A:409:ILE:CD1	2.84	0.54
2:B:104:LEU:HA	2:B:118:TRP:CZ2	2.42	0.54
2:B:159:GLN:HA	2:B:195:LYS:HZ3	1.73	0.54
2:B:220:TYR:HD2	2:B:223:TYR:HH	1.55	0.54
3:C:160:MET:N	3:C:213:GLN:HG3	2.23	0.54
3:C:272:LEU:O	3:C:276:GLN:HG2	2.07	0.54
1:D:38:ILE:O	1:D:39:GLN:HG3	2.08	0.54
4:E:138:TRP:CH2	4:E:215:GLN:HB2	2.42	0.54
1:A:93:TYR:H	1:A:93:TYR:HD1	1.52	0.54
1:A:147:GLY:HA2	1:A:158:ILE:HD13	1.90	0.54
1:A:236:PRO:CG	1:A:299:HIS:NE2	2.71	0.54
1:A:293:VAL:CG2	4:E:238:LEU:HD11	2.38	0.54
1:A:435:GLN:HG2	1:A:435:GLN:O	2.08	0.54
2:B:132:VAL:CG1	2:B:280:ILE:N	2.71	0.54
2:B:290:LEU:HD21	2:B:453:SER:OG	2.08	0.54
2:B:404:ALA:O	2:B:407:ALA:HB3	2.08	0.54
3:C:190:TRP:HB2	3:C:222:ARG:O	2.07	0.54
3:C:436:LYS:O	3:C:439:TYR:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:VAL:HG13	1:D:50:VAL:HG22	1.89	0.54
4:E:45:LYS:CE	4:E:278:ASN:C	2.72	0.54
4:E:59:TRP:HH2	4:E:107:VAL:CG1	2.21	0.54
4:E:140:ASN:CG	4:E:211:PHE:HB3	2.34	0.54
4:E:259:LEU:N	4:E:259:LEU:HD23	2.23	0.54
1:A:175:GLU:C	1:A:211:PRO:HD3	2.33	0.53
1:A:255:VAL:O	1:A:259:VAL:HG23	2.08	0.53
2:B:141:ASN:HA	2:B:211:LEU:C	2.33	0.53
3:C:263:VAL:HA	1:D:251:LEU:CD1	2.35	0.53
1:D:26:THR:C	1:D:28:PHE:H	2.15	0.53
1:D:102:ILE:CG2	4:E:98:GLN:HE21	2.21	0.53
1:D:135:PHE:CE1	1:D:277:TYR:CE2	2.95	0.53
1:D:166:ASP:CG	1:D:181:TYR:HB2	2.32	0.53
1:D:376:ILE:HG22	1:D:380:LYS:NZ	2.22	0.53
4:E:68:THR:HB	4:E:72:GLU:OE1	2.08	0.53
1:A:46:VAL:CG2	1:A:271:VAL:N	2.68	0.53
1:A:66:ARG:H	1:A:66:ARG:CD	2.18	0.53
3:C:35:LEU:CD2	3:C:215:VAL:HG11	2.35	0.53
3:C:92:ILE:HA	3:C:149:THR:O	2.08	0.53
3:C:230:ILE:HG13	3:C:231:ASN:HD22	1.74	0.53
3:C:252:GLU:CD	1:D:301:ARG:HA	2.33	0.53
1:D:27:HIS:O	1:D:28:PHE:HB2	2.08	0.53
1:D:49:ILE:CG2	1:D:125:LYS:HE3	2.38	0.53
1:D:170:PHE:CE2	1:D:176:TRP:CD1	2.91	0.53
1:A:38:ILE:HD12	1:A:38:ILE:N	2.23	0.53
2:B:270:VAL:HG11	2:B:284:LEU:HD21	1.90	0.53
3:C:69:TRP:CD1	3:C:114:PRO:HA	2.43	0.53
3:C:72:SER:HA	3:C:76:ASP:HB2	1.90	0.53
3:C:137:PHE:CE1	3:C:291:TYR:CE2	2.96	0.53
3:C:182:GLU:O	3:C:183:ALA:HB2	2.08	0.53
3:C:305:ASN:O	3:C:308:ILE:HG22	2.08	0.53
1:D:239:SER:HB3	1:D:242:LYS:HD3	1.90	0.53
4:E:129:ILE:CG2	4:E:133:TYR:HD2	2.11	0.53
4:E:143:LEU:HD12	4:E:210:PHE:O	2.07	0.53
4:E:159:LEU:HB2	4:E:192:LYS:HB2	1.89	0.53
4:E:239:VAL:HA	4:E:242:LEU:CD2	2.38	0.53
1:A:201:ILE:CG2	1:A:203:TYR:CE1	2.91	0.53
2:B:201:ASP:OD1	2:B:202:PRO:HD2	2.09	0.53
2:B:304:LEU:O	2:B:307:ARG:HD3	2.08	0.53
3:C:148:PHE:HB2	3:C:215:VAL:HG23	1.83	0.53
1:D:233:PHE:CE2	1:D:413:VAL:HG11	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:298:THR:C	1:D:301:ARG:HB3	2.34	0.53
4:E:313:THR:HB	4:E:440:VAL:HG12	1.90	0.53
1:A:160:PRO:HG3	1:A:185:LYS:CE	2.37	0.53
2:B:46:LYS:CB	2:B:276:SER:O	2.56	0.53
3:C:82:LEU:HG	3:C:86:LEU:HB2	1.91	0.53
3:C:228:TYR:CD1	3:C:229:VAL:HG22	2.44	0.53
3:C:475:MET:O	3:C:478:PHE:CD1	2.62	0.53
1:D:86:TRP:CE3	1:D:86:TRP:C	2.87	0.53
4:E:91:LEU:HA	4:E:145:PHE:CB	2.37	0.53
4:E:283:GLY:O	4:E:286:LEU:HB2	2.08	0.53
1:A:391:GLU:HA	1:A:394:ASN:HD21	1.73	0.53
1:A:419:ILE:O	1:A:423:VAL:HG23	2.08	0.53
2:B:28:LYS:HB3	2:B:155:GLU:CA	2.39	0.53
2:B:186:TRP:CB	2:B:215:ARG:CB	2.78	0.53
2:B:218:LEU:HD11	2:B:222:VAL:CG2	2.36	0.53
3:C:228:TYR:CE1	3:C:229:VAL:HG22	2.43	0.53
3:C:273:LEU:HD23	3:C:276:GLN:HB3	1.88	0.53
3:C:429:ILE:C	3:C:429:ILE:HD12	2.34	0.53
1:D:29:VAL:CG2	1:D:60:TRP:NE1	2.70	0.53
1:D:179:LYS:HB2	1:D:206:ILE:HG22	1.90	0.53
1:D:376:ILE:O	1:D:380:LYS:HG3	2.08	0.53
4:E:38:ASN:O	4:E:51:THR:HG23	2.09	0.53
4:E:65:SER:CA	4:E:112:ASP:HA	2.38	0.53
4:E:83:LEU:O	4:E:84:LEU:HB2	2.07	0.53
4:E:109:VAL:HG13	4:E:115:MET:HE1	1.91	0.53
4:E:237:VAL:HG22	4:E:457:LEU:CD2	2.39	0.53
4:E:296:ILE:CG1	4:E:297:VAL:N	2.72	0.53
1:A:33:VAL:HG22	1:A:158:ILE:HG12	1.87	0.53
1:A:178:MET:SD	1:A:207:MET:HB3	2.48	0.53
1:A:241:GLU:O	1:A:243:MET:HE1	2.09	0.53
1:A:257:LEU:O	1:A:260:ILE:HG22	2.07	0.53
1:A:294:VAL:CG1	1:A:295:VAL:N	2.72	0.53
1:A:397:GLU:HA	1:A:400:LYS:CD	2.38	0.53
2:B:459:SER:HA	2:B:463:PRO:HD2	1.89	0.53
3:C:247:PHE:O	3:C:250:PRO:CG	2.57	0.53
3:C:300:THR:O	3:C:300:THR:HG22	2.09	0.53
1:D:235:LEU:HD23	1:D:235:LEU:N	2.23	0.53
1:D:254:THR:CG2	1:D:255:VAL:N	2.71	0.53
4:E:9:LYS:HD2	4:E:9:LYS:C	2.32	0.53
4:E:100:GLU:HB2	4:E:122:ILE:HG12	1.91	0.53
4:E:152:ALA:HA	4:E:155:VAL:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:HIS:HB2	1:A:7:LEU:HD23	1.87	0.53
1:A:195:ASP:OD1	1:A:197:PRO:HG3	2.09	0.53
2:B:45:GLU:HG2	2:B:277:VAL:HA	1.91	0.53
2:B:46:LYS:HD2	2:B:275:LEU:C	2.33	0.53
1:D:222:CYS:O	1:D:225:PHE:CD1	2.61	0.53
1:D:412:CYS:HB3	1:D:413:VAL:HG23	1.90	0.53
4:E:2:GLU:HB3	4:E:6:LEU:HG	1.91	0.53
4:E:123:TYR:N	4:E:123:TYR:CD1	2.77	0.53
4:E:223:ILE:HG12	4:E:226:ILE:HD12	1.91	0.53
4:E:302:ILE:O	4:E:305:ASN:HB3	2.09	0.53
4:E:313:THR:OG1	4:E:441:LEU:HB3	2.09	0.53
2:B:449:ILE:HA	2:B:452:PHE:HD2	1.73	0.53
3:C:30:VAL:HG21	3:C:158:ILE:C	2.34	0.53
3:C:56:VAL:CG2	3:C:124:ALA:HB3	2.39	0.53
3:C:113:ARG:HB2	3:C:117:TYR:O	2.07	0.53
1:D:130:ILE:O	1:D:134:HIS:HB2	2.07	0.53
1:A:171:MET:HG2	1:A:174:GLY:N	2.24	0.53
2:B:11:LEU:N	2:B:11:LEU:CD2	2.71	0.53
2:B:135:PHE:H	2:B:136:PRO:CD	2.22	0.53
2:B:280:ILE:C	2:B:282:SER:N	2.67	0.53
3:C:289:GLY:O	3:C:293:MET:HE2	2.09	0.53
3:C:465:MET:O	3:C:465:MET:HG2	2.07	0.53
1:D:63:VAL:O	1:D:63:VAL:HG22	2.08	0.53
1:D:250:LEU:O	1:D:254:THR:HG22	2.09	0.53
1:A:251:LEU:HD22	4:E:260:ALA:CA	2.39	0.52
1:A:261:VAL:O	1:A:265:PRO:HD3	2.09	0.52
1:A:410:LEU:O	1:A:414:PHE:HB2	2.09	0.52
2:B:97:ASP:HB3	2:B:125:ARG:HG3	1.91	0.52
2:B:247:GLU:O	2:B:249:MET:CG	2.56	0.52
3:C:69:TRP:HD1	3:C:114:PRO:C	2.15	0.52
3:C:159:SER:HA	3:C:213:GLN:HG2	1.88	0.52
1:D:426:PHE:CG	1:D:427:ALA:N	2.77	0.52
4:E:44:GLU:CA	4:E:129:ILE:HD12	2.38	0.52
4:E:153:HIS:C	4:E:154:GLU:HG3	2.33	0.52
1:A:247:ILE:CG1	4:E:253:LEU:HD12	2.38	0.52
1:A:380:LYS:O	1:A:384:GLU:HB2	2.09	0.52
2:B:53:SER:HA	2:B:122:ALA:O	2.09	0.52
2:B:438:LEU:HD23	2:B:441:TYR:CB	2.38	0.52
3:C:114:PRO:O	3:C:115:ASN:HB3	2.09	0.52
3:C:201:ILE:HB	3:C:213:GLN:OE1	2.09	0.52
1:D:85:VAL:CG1	1:D:86:TRP:N	2.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:301:ARG:HH22	1:D:406:ILE:CD1	2.21	0.52
4:E:178:THR:HG22	4:E:180:ASN:H	1.74	0.52
1:A:49:ILE:HG12	1:A:97:ASP:OD2	2.09	0.52
1:A:66:ARG:HD3	1:A:66:ARG:O	2.09	0.52
2:B:37:LEU:HD12	2:B:54:VAL:HG11	1.91	0.52
2:B:108:VAL:CG2	2:B:118:TRP:HB2	2.40	0.52
2:B:409:LYS:HE2	3:C:423:ILE:CG2	2.37	0.52
3:C:180:ASP:CB	3:C:181:PRO:CD	2.84	0.52
3:C:266:ALA:HB2	1:D:251:LEU:HD13	1.91	0.52
1:D:20:ARG:CG	1:D:20:ARG:NH1	2.66	0.52
1:D:181:TYR:CE1	1:D:203:TYR:HB3	2.40	0.52
1:D:186:HIS:CE1	1:D:187:TRP:O	2.63	0.52
4:E:215:GLN:HG3	4:E:216:ARG:H	1.74	0.52
4:E:455:LEU:HD12	4:E:455:LEU:O	2.09	0.52
1:A:261:VAL:O	1:A:261:VAL:HG12	2.08	0.52
2:B:144:MET:HE2	2:B:211:LEU:CD2	2.38	0.52
2:B:247:GLU:CA	2:B:249:MET:HG3	2.37	0.52
3:C:106:TYR:CD1	3:C:107:PHE:CD1	2.96	0.52
3:C:190:TRP:HA	3:C:223:ARG:HA	1.92	0.52
1:D:167:LEU:CD1	1:D:167:LEU:H	2.23	0.52
4:E:44:GLU:CB	4:E:280:PRO:HB3	2.39	0.52
4:E:264:PHE:O	4:E:267:LEU:HB3	2.09	0.52
1:A:89:ASP:O	1:A:149:TRP:HB3	2.10	0.52
1:A:93:TYR:N	1:A:93:TYR:HD1	2.06	0.52
2:B:93:MET:HB2	2:B:145:VAL:CB	2.40	0.52
2:B:175:ILE:HD12	2:B:190:HIS:CD2	2.43	0.52
3:C:426:THR:CA	3:C:429:ILE:HG23	2.39	0.52
4:E:463:LEU:HD12	4:E:463:LEU:C	2.30	0.52
1:A:79:ARG:HD3	1:A:107:LYS:HD2	1.90	0.52
1:A:251:LEU:HD11	4:E:256:SER:O	2.08	0.52
2:B:223:TYR:C	2:B:223:TYR:CD1	2.88	0.52
3:C:81:ARG:HA	3:C:112:VAL:HG23	1.92	0.52
3:C:234:THR:N	3:C:235:PRO:CD	2.72	0.52
3:C:464:VAL:O	3:C:464:VAL:HG22	2.09	0.52
1:D:233:PHE:CE1	1:D:417:ILE:HD12	2.43	0.52
4:E:116:TYR:CD1	4:E:116:TYR:C	2.88	0.52
4:E:454:ALA:O	4:E:457:LEU:HB3	2.09	0.52
1:A:117:MET:CG	1:A:119:THR:HG23	2.40	0.52
1:A:133:THR:C	1:A:136:PRO:CG	2.82	0.52
2:B:184:GLY:C	2:B:186:TRP:N	2.68	0.52
2:B:186:TRP:HB3	2:B:215:ARG:CD	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:444:ILE:O	2:B:448:SER:HB2	2.08	0.52
3:C:295:ILE:HG22	3:C:296:MET:HE3	1.90	0.52
3:C:314:PHE:CD1	3:C:314:PHE:O	2.62	0.52
1:D:93:TYR:CE2	1:D:198:TYR:CE2	2.98	0.52
1:D:224:LEU:O	1:D:228:LEU:HD23	2.10	0.52
1:D:302:SER:CB	1:D:400:LYS:CG	2.75	0.52
4:E:83:LEU:O	4:E:84:LEU:HD13	2.09	0.52
4:E:444:LYS:HA	4:E:444:LYS:HE3	1.91	0.52
1:A:95:ASN:HA	1:A:127:TYR:O	2.08	0.52
1:A:136:PRO:HG3	1:A:274:ILE:HG23	1.91	0.52
1:A:196:THR:HG22	1:A:196:THR:O	2.10	0.52
1:A:251:LEU:HD11	4:E:256:SER:C	2.35	0.52
1:A:287:SER:HA	1:A:290:ILE:HG13	1.92	0.52
1:A:293:VAL:O	1:A:297:ASN:HB3	2.10	0.52
2:B:56:LEU:C	2:B:120:PRO:HD2	2.34	0.52
2:B:103:THR:OG1	2:B:122:ALA:CB	2.57	0.52
2:B:290:LEU:HD11	2:B:453:SER:HB2	1.92	0.52
3:C:132:ILE:HG22	3:C:133:ASN:N	2.25	0.52
3:C:162:LEU:CD1	3:C:217:PHE:CZ	2.84	0.52
1:D:226:SER:O	1:D:230:VAL:HB	2.10	0.52
1:D:305:THR:CB	1:D:401:TYR:CD2	2.76	0.52
4:E:58:GLN:HA	4:E:59:TRP:HE3	1.75	0.52
1:A:72:TYR:HB2	1:A:112:TYR:HB2	1.86	0.52
1:A:176:TRP:CZ3	1:A:209:ARG:NH2	2.78	0.52
2:B:45:GLU:CD	2:B:277:VAL:HB	2.34	0.52
3:C:63:TYR:CD1	3:C:64:ASP:N	2.77	0.52
1:D:28:PHE:CZ	1:D:153:GLY:O	2.63	0.52
1:D:289:ILE:O	1:D:293:VAL:HG23	2.09	0.52
4:E:62:TYR:C	4:E:64:LEU:H	2.18	0.52
4:E:182:GLU:CA	4:E:218:PRO:CG	2.88	0.52
1:A:108:LEU:CD2	1:A:118:TRP:CD1	2.93	0.52
1:A:379:VAL:CG1	4:E:424:LYS:CE	2.86	0.52
2:B:196:ASN:C	2:B:196:ASN:OD1	2.53	0.52
2:B:284:LEU:HA	2:B:287:ILE:HG13	1.90	0.52
3:C:42:LEU:CD2	3:C:190:TRP:HH2	2.17	0.52
3:C:42:LEU:CG	3:C:54:THR:CG2	2.83	0.52
3:C:67:LEU:HB3	3:C:116:GLY:HA2	0.78	0.52
3:C:482:PRO:CG	3:C:483:ALA:N	2.73	0.52
4:E:452:TRP:HA	4:E:452:TRP:HE3	1.75	0.52
1:A:237:THR:HB	1:A:406:ILE:CG2	2.40	0.51
3:C:93:VAL:CG1	3:C:151:LEU:HB2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:223:ARG:CG	3:C:224:LYS:N	2.73	0.51
3:C:308:ILE:CG2	3:C:309:VAL:N	2.73	0.51
1:D:34:GLY:C	1:D:57:ARG:HD2	2.34	0.51
1:D:242:LYS:HB2	1:D:245:LEU:CD1	2.40	0.51
1:D:298:THR:O	1:D:301:ARG:HD3	2.09	0.51
4:E:55:ILE:HG13	4:E:57:ILE:CG1	2.35	0.51
4:E:216:ARG:C	4:E:218:PRO:HD2	2.35	0.51
1:A:151:TYR:HB2	1:A:156:VAL:HG13	1.92	0.51
1:A:270:ALA:C	1:A:271:VAL:HG13	2.36	0.51
2:B:145:VAL:HG13	2:B:208:THR:HA	1.93	0.51
2:B:409:LYS:CE	3:C:423:ILE:CG2	2.88	0.51
3:C:438:ALA:O	3:C:442:GLU:HB2	2.10	0.51
4:E:173:ASP:OD2	4:E:185:ILE:HD13	2.10	0.51
1:A:47:ASN:O	1:A:48:GLN:HG2	2.09	0.51
1:A:142:CYS:CB	1:A:205:PHE:HB2	2.35	0.51
1:A:227:PHE:CD1	1:A:227:PHE:O	2.63	0.51
2:B:85:VAL:HG12	2:B:86:TRP:CA	2.39	0.51
2:B:135:PHE:CD2	2:B:283:TYR:CE1	2.98	0.51
2:B:248:LYS:HZ3	2:B:252:SER:CA	2.23	0.51
1:D:36:GLN:NE2	1:D:38:ILE:CG1	2.73	0.51
1:D:49:ILE:CG1	1:D:125:LYS:HE3	2.40	0.51
1:D:92:LEU:HG	1:D:124:PHE:CE1	2.46	0.51
1:D:129:GLU:C	1:D:130:ILE:CG2	2.80	0.51
4:E:143:LEU:O	4:E:210:PHE:HB2	2.10	0.51
4:E:217:LYS:N	4:E:218:PRO:CD	2.72	0.51
4:E:283:GLY:HA3	4:E:284:LYS:NZ	2.25	0.51
4:E:296:ILE:HG13	4:E:297:VAL:N	2.24	0.51
1:A:41:ILE:CG2	1:A:123:ILE:HD11	2.41	0.51
1:A:106:THR:HG21	1:A:120:PRO:HB3	1.92	0.51
1:A:254:THR:O	1:A:258:LEU:HG	2.10	0.51
1:D:76:LYS:HG2	1:D:112:TYR:HD2	1.75	0.51
1:D:78:ILE:HD12	1:D:78:ILE:H	1.76	0.51
1:D:97:ASP:OD1	1:D:97:ASP:O	2.27	0.51
4:E:145:PHE:O	4:E:208:ILE:HD12	2.10	0.51
4:E:159:LEU:HD12	4:E:192:LYS:HA	1.91	0.51
4:E:173:ASP:CB	4:E:185:ILE:HG21	2.40	0.51
4:E:231:LEU:HG	4:E:232:ILE:N	2.17	0.51
4:E:463:LEU:O	4:E:463:LEU:CD1	2.57	0.51
1:A:50:VAL:HG12	1:A:52:THR:HG23	1.90	0.51
1:A:54:VAL:HG22	1:A:122:ALA:CB	2.41	0.51
2:B:10:VAL:CG1	2:B:11:LEU:CD2	2.88	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:189:GLU:O	2:B:190:HIS:CG	2.63	0.51
2:B:218:LEU:CD1	2:B:221:ILE:HD11	2.40	0.51
2:B:291:VAL:CG1	2:B:292:ALA:N	2.72	0.51
3:C:80:LEU:HG	3:C:81:ARG:N	2.26	0.51
3:C:106:TYR:CD1	3:C:107:PHE:CE1	2.98	0.51
1:D:244:THR:CG2	1:D:245:LEU:N	2.70	0.51
1:D:250:LEU:HD23	1:D:253:LEU:HD22	1.91	0.51
1:A:107:LYS:O	1:A:108:LEU:CD2	2.59	0.51
1:A:218:VAL:CG1	1:A:219:ILE:H	2.23	0.51
1:A:243:MET:HE2	1:A:244:THR:HG22	1.92	0.51
1:A:390:GLU:C	1:A:390:GLU:CD	2.78	0.51
1:A:413:VAL:O	1:A:416:LEU:HB3	2.09	0.51
2:B:258:ALA:CB	3:C:265:LEU:CD2	2.85	0.51
3:C:94:LEU:N	3:C:94:LEU:HD23	2.26	0.51
1:D:38:ILE:O	1:D:38:ILE:HG22	2.11	0.51
1:D:56:LEU:CG	1:D:120:PRO:CG	2.88	0.51
1:D:225:PHE:HD1	1:D:226:SER:N	2.08	0.51
1:D:249:VAL:HA	1:D:252:SER:HB3	1.92	0.51
1:D:305:THR:CG2	1:D:400:LYS:CB	2.78	0.51
1:A:56:LEU:CD2	1:A:56:LEU:C	2.83	0.51
1:A:131:ILE:CD1	1:A:133:THR:HB	2.41	0.51
2:B:112:HIS:NE2	2:B:113:THR:HG23	2.26	0.51
2:B:269:LYS:HD2	2:B:270:VAL:N	2.25	0.51
2:B:306:HIS:ND1	2:B:306:HIS:C	2.30	0.51
3:C:69:TRP:HB2	3:C:74:TYR:HB2	1.92	0.51
3:C:110:VAL:HG13	3:C:120:TRP:CA	2.41	0.51
3:C:289:GLY:O	3:C:293:MET:CE	2.59	0.51
1:D:280:PHE:O	1:D:284:PHE:CD1	2.64	0.51
1:D:283:ILE:N	1:D:286:ILE:HD12	2.25	0.51
4:E:58:GLN:HA	4:E:59:TRP:CE3	2.45	0.51
4:E:93:ASN:O	4:E:93:ASN:CG	2.54	0.51
1:A:15:TYR:OH	1:A:84:ASP:HB3	2.10	0.51
1:A:94:ASN:ND2	1:A:94:ASN:C	2.69	0.51
1:A:129:GLU:HG2	1:A:130:ILE:N	2.24	0.51
2:B:132:VAL:HA	2:B:279:ILE:HG12	1.92	0.51
2:B:307:ARG:NH1	2:B:434:VAL:HG21	2.25	0.51
3:C:201:ILE:O	3:C:202:TYR:CD1	2.64	0.51
1:D:107:LYS:NZ	4:E:149:THR:CA	2.68	0.51
4:E:58:GLN:CA	4:E:59:TRP:HE3	2.24	0.51
4:E:143:LEU:HD12	4:E:143:LEU:H	1.75	0.51
4:E:242:LEU:HD12	4:E:242:LEU:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:PRO:CB	1:A:138:ASP:OD1	2.59	0.51
1:A:139:GLN:HG3	1:A:207:MET:N	2.26	0.51
1:A:278:MET:HE1	1:A:282:MET:HE1	1.92	0.51
1:A:431:ILE:HG22	1:A:431:ILE:O	2.10	0.51
2:B:40:LEU:CA	2:B:52:THR:HG23	2.40	0.51
2:B:185:GLN:CB	2:B:219:PHE:CE2	2.78	0.51
3:C:192:ILE:HD13	3:C:221:ILE:CG2	2.40	0.51
3:C:318:SER:HB2	3:C:447:ASN:ND2	2.26	0.51
1:D:57:ARG:CB	1:D:119:THR:HG22	2.37	0.51
4:E:77:VAL:HG12	4:E:78:ARG:N	2.26	0.51
4:E:258:LEU:O	4:E:258:LEU:HG	2.10	0.51
1:A:50:VAL:HG12	1:A:52:THR:CG2	2.41	0.51
1:A:137:PHE:O	1:A:208:GLN:HB2	2.11	0.51
1:A:250:LEU:HD21	1:A:292:THR:HG22	1.88	0.51
2:B:248:LYS:NZ	2:B:252:SER:HB3	2.25	0.51
3:C:30:VAL:HG22	3:C:158:ILE:N	2.26	0.51
3:C:221:ILE:HG13	3:C:222:ARG:N	2.25	0.51
3:C:279:PRO:C	3:C:282:ALA:HB3	2.35	0.51
3:C:298:LEU:CD1	3:C:471:PHE:HD2	2.24	0.51
1:D:212:LEU:O	1:D:215:VAL:HB	2.11	0.51
1:D:377:GLU:CB	4:E:415:CYS:SG	2.95	0.51
1:D:398:GLU:CA	1:D:401:TYR:CZ	2.92	0.51
1:D:419:ILE:CD1	1:D:420:ILE:HG23	2.41	0.51
4:E:14:TYR:CE2	4:E:16:LYS:CE	2.93	0.51
4:E:37:THR:OG1	4:E:54:TRP:CE3	2.63	0.51
4:E:59:TRP:CE3	4:E:59:TRP:N	2.79	0.51
4:E:262:THR:CA	4:E:265:LEU:HB2	2.40	0.51
1:A:187:TRP:HD1	1:A:199:LEU:CD2	2.24	0.50
2:B:40:LEU:CB	2:B:52:THR:HG23	2.40	0.50
2:B:69:PRO:O	2:B:73:GLU:CB	2.59	0.50
2:B:138:ASP:CA	2:B:464:PRO:O	2.59	0.50
2:B:263:LEU:CD2	2:B:291:VAL:HG23	2.39	0.50
2:B:406:GLU:HG2	2:B:409:LYS:CD	2.41	0.50
3:C:260:ALA:HB1	3:C:313:HIS:NE2	2.26	0.50
1:D:38:ILE:C	1:D:39:GLN:HG3	2.36	0.50
1:D:58:GLN:NE2	1:D:88:PRO:CG	2.74	0.50
1:D:100:PHE:N	1:D:100:PHE:CD1	2.78	0.50
1:D:261:VAL:O	1:D:261:VAL:HG12	2.11	0.50
1:D:295:VAL:O	1:D:299:HIS:HB2	2.10	0.50
1:D:410:LEU:O	1:D:414:PHE:HB2	2.11	0.50
4:E:75:ASP:HB3	4:E:110:TYR:OH	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:76:LEU:C	4:E:77:VAL:HG23	2.36	0.50
1:A:20:ARG:CG	1:A:20:ARG:O	2.59	0.50
1:A:41:ILE:HG12	1:A:51:GLU:O	2.11	0.50
1:A:57:ARG:HD3	1:A:161:GLU:OE1	2.10	0.50
2:B:223:TYR:O	2:B:223:TYR:HD1	1.93	0.50
3:C:30:VAL:HG23	3:C:157:GLU:H	1.76	0.50
3:C:74:TYR:HD1	3:C:114:PRO:HB2	1.75	0.50
3:C:179:ILE:CG1	3:C:181:PRO:HD2	2.38	0.50
1:D:56:LEU:HD12	1:D:120:PRO:HG3	1.93	0.50
1:D:95:ASN:ND2	1:D:127:TYR:C	2.69	0.50
1:D:257:LEU:HA	1:D:260:ILE:HG13	1.92	0.50
1:D:282:MET:C	1:D:286:ILE:HD12	2.37	0.50
4:E:116:TYR:C	4:E:116:TYR:HD1	2.19	0.50
4:E:138:TRP:HD1	4:E:213:ILE:CD1	2.24	0.50
4:E:173:ASP:HB2	4:E:185:ILE:HG21	1.93	0.50
4:E:240:TYR:O	4:E:243:PRO:CG	2.60	0.50
4:E:425:SER:O	4:E:429:GLN:HB3	2.12	0.50
1:A:2:GLU:HG3	1:A:74:GLY:HA2	1.93	0.50
1:A:34:GLY:CA	1:A:161:GLU:CD	2.85	0.50
1:A:39:GLN:C	1:A:40:LEU:HD23	2.35	0.50
2:B:58:LEU:HD21	2:B:118:TRP:CE3	2.46	0.50
2:B:218:LEU:C	2:B:219:PHE:CD1	2.89	0.50
2:B:220:TYR:CG	2:B:223:TYR:CE2	2.99	0.50
2:B:277:VAL:H	2:B:278:PRO:HD3	1.75	0.50
3:C:63:TYR:CE1	3:C:65:HIS:HA	2.46	0.50
3:C:80:LEU:CD1	1:D:20:ARG:NH2	2.73	0.50
1:D:50:VAL:HB	1:D:126:SER:OG	2.11	0.50
4:E:48:ALA:HA	4:E:126:THR:HA	1.94	0.50
4:E:54:TRP:C	4:E:118:LEU:HD11	2.36	0.50
4:E:79:ILE:O	4:E:79:ILE:HG23	2.09	0.50
4:E:90:VAL:HA	4:E:99:PHE:HE1	1.77	0.50
4:E:138:TRP:CE2	4:E:215:GLN:HB2	2.44	0.50
4:E:152:ALA:H	4:E:205:PHE:HD1	1.59	0.50
4:E:309:ARG:HD2	4:E:310:THR:HG23	1.91	0.50
1:A:401:TYR:O	1:A:401:TYR:CG	2.65	0.50
3:C:7:LEU:CD2	3:C:10:ASP:HB2	2.39	0.50
3:C:30:VAL:HG22	3:C:158:ILE:HA	1.93	0.50
3:C:35:LEU:CD2	3:C:37:LEU:HG	2.42	0.50
3:C:69:TRP:HD1	3:C:114:PRO:O	1.94	0.50
3:C:426:THR:HA	3:C:429:ILE:CG2	2.41	0.50
1:D:37:LEU:HA	1:D:54:VAL:HG13	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:107:LYS:HZ2	4:E:149:THR:CB	2.24	0.50
1:D:398:GLU:OE2	1:D:399:TRP:CZ3	2.64	0.50
1:D:432:GLU:O	1:D:436:GLU:HG3	2.11	0.50
4:E:239:VAL:CA	4:E:242:LEU:HD23	2.41	0.50
4:E:473:GLN:HA	4:E:476:GLU:HB2	1.92	0.50
1:A:56:LEU:HD23	1:A:57:ARG:H	1.77	0.50
2:B:175:ILE:CD1	2:B:190:HIS:CD2	2.90	0.50
3:C:54:THR:O	3:C:126:PHE:CD2	2.65	0.50
3:C:219:LEU:HG	3:C:221:ILE:HG23	1.94	0.50
1:D:11:LEU:HD11	1:D:71:ASP:OD2	2.11	0.50
1:D:63:VAL:O	1:D:66:ARG:HD3	2.12	0.50
1:D:63:VAL:C	1:D:65:LEU:H	2.20	0.50
1:D:176:TRP:HB3	1:D:209:ARG:HG3	1.94	0.50
1:D:407:ASP:OD1	1:D:408:HIS:CD2	2.64	0.50
4:E:104:TYR:N	4:E:104:TYR:CD1	2.79	0.50
4:E:240:TYR:C	4:E:243:PRO:HD2	2.36	0.50
1:A:287:SER:O	1:A:291:VAL:HG23	2.11	0.50
1:A:380:LYS:CA	2:B:408:ILE:HD13	2.38	0.50
2:B:4:GLU:O	2:B:8:LEU:HG	2.11	0.50
2:B:185:GLN:O	2:B:217:PRO:HB3	2.11	0.50
3:C:102:TYR:O	3:C:102:TYR:CD1	2.62	0.50
3:C:161:ASP:OD1	3:C:199:LYS:HD3	2.11	0.50
3:C:258:SER:O	3:C:261:ILE:HB	2.12	0.50
3:C:426:THR:C	3:C:429:ILE:HG23	2.37	0.50
1:D:54:VAL:O	1:D:56:LEU:CD2	2.60	0.50
4:E:122:ILE:HG12	4:E:122:ILE:O	2.10	0.50
4:E:147:SER:O	4:E:205:PHE:HE2	1.94	0.50
1:A:20:ARG:HB2	1:A:86:TRP:CE3	2.46	0.50
1:A:151:TYR:HB2	1:A:156:VAL:CG1	2.41	0.50
1:A:160:PRO:HG2	1:A:185:LYS:HZ3	1.72	0.50
1:A:161:GLU:HG3	1:A:162:SER:N	2.27	0.50
1:A:227:PHE:CE2	2:B:299:VAL:CG1	2.94	0.50
2:B:2:VAL:HG12	2:B:3:MET:CE	2.41	0.50
2:B:85:VAL:CG1	2:B:86:TRP:N	2.74	0.50
2:B:199:SER:C	2:B:201:ASP:N	2.69	0.50
3:C:68:THR:CA	3:C:115:ASN:HA	2.16	0.50
3:C:132:ILE:CG2	3:C:133:ASN:N	2.75	0.50
3:C:160:MET:N	3:C:213:GLN:HB2	2.25	0.50
1:D:18:VAL:O	1:D:18:VAL:HG12	2.12	0.50
1:D:58:GLN:HE21	1:D:88:PRO:HG3	1.75	0.50
1:D:176:TRP:HE3	1:D:209:ARG:NE	2.08	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:398:GLU:HA	1:D:401:TYR:CD2	2.47	0.50
4:E:103:TYR:CD2	4:E:104:TYR:CD1	3.00	0.50
4:E:128:PRO:HD2	4:E:141:CYS:HA	1.93	0.50
4:E:207:GLU:C	4:E:208:ILE:HG13	2.33	0.50
4:E:282:ILE:HG23	4:E:282:ILE:O	2.11	0.50
1:A:36:GLN:HA	1:A:164:ARG:CZ	2.41	0.50
1:A:50:VAL:CG1	1:A:51:GLU:N	2.75	0.50
1:A:249:VAL:HG12	1:A:250:LEU:N	2.27	0.50
2:B:112:HIS:CD2	2:B:113:THR:HG23	2.47	0.50
2:B:284:LEU:HA	2:B:287:ILE:CG1	2.42	0.50
1:D:259:VAL:HG22	1:D:262:GLU:OE2	2.11	0.50
1:D:289:ILE:O	1:D:292:THR:HG22	2.12	0.50
1:D:298:THR:O	1:D:301:ARG:CB	2.56	0.50
1:D:415:MET:O	1:D:419:ILE:HG23	2.12	0.50
4:E:86:LEU:CD1	4:E:103:TYR:OH	2.60	0.50
4:E:174:PRO:HA	4:E:177:PHE:CB	2.42	0.50
1:A:3:HIS:CB	1:A:7:LEU:HD23	2.42	0.50
1:A:58:GLN:HE21	1:A:90:LEU:HD21	1.76	0.50
1:A:92:LEU:CB	1:A:95:ASN:HB2	2.42	0.50
1:A:178:MET:HA	1:A:207:MET:CB	2.42	0.50
1:A:179:LYS:HB2	1:A:206:ILE:HG22	1.93	0.50
1:A:251:LEU:HD22	4:E:260:ALA:CB	2.42	0.50
1:A:379:VAL:CG2	4:E:424:LYS:HE3	2.40	0.50
1:A:410:LEU:HD13	1:A:410:LEU:C	2.37	0.50
2:B:130:ILE:HB	2:B:134:TYR:CE2	2.43	0.50
2:B:133:MET:HE2	2:B:140:GLN:CB	2.40	0.50
2:B:439:PHE:CA	2:B:442:ILE:HB	2.37	0.50
3:C:122:PRO:CB	1:D:149:TRP:HZ2	2.20	0.50
3:C:122:PRO:HB3	1:D:149:TRP:CZ2	2.38	0.50
3:C:233:ILE:C	3:C:235:PRO:HD2	2.37	0.50
3:C:263:VAL:O	3:C:267:GLN:HG2	2.12	0.50
1:D:7:LEU:HD13	1:D:70:ALA:C	2.37	0.50
1:D:66:ARG:O	1:D:67:TRP:CE3	2.65	0.50
1:D:76:LYS:HG2	1:D:112:TYR:CE2	2.47	0.50
4:E:14:TYR:OH	4:E:84:LEU:HD12	2.11	0.50
4:E:123:TYR:HD1	4:E:123:TYR:H	1.60	0.50
1:A:46:VAL:HG12	1:A:47:ASN:CG	2.36	0.49
1:A:90:LEU:HD12	1:A:100:PHE:CE2	2.47	0.49
2:B:229:ILE:O	2:B:233:ILE:HG12	2.11	0.49
3:C:63:TYR:O	3:C:65:HIS:CD2	2.65	0.49
1:D:229:THR:O	1:D:232:VAL:HB	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:414:PHE:O	1:D:414:PHE:CD1	2.64	0.49
4:E:33:LYS:HG2	4:E:160:SER:HB3	1.94	0.49
4:E:123:TYR:N	4:E:123:TYR:HD1	2.10	0.49
4:E:271:LYS:C	4:E:273:PRO:CD	2.77	0.49
4:E:313:THR:OG1	4:E:313:THR:O	2.24	0.49
1:A:56:LEU:HD12	1:A:90:LEU:HD13	1.93	0.49
1:A:95:ASN:OD1	1:A:144:MET:CG	2.59	0.49
1:A:274:ILE:HD13	1:A:277:TYR:CE1	2.47	0.49
2:B:286:PHE:CE1	2:B:287:ILE:HG23	2.46	0.49
3:C:141:TRP:CH2	3:C:223:ARG:HD3	2.48	0.49
3:C:148:PHE:C	3:C:149:THR:HG22	2.36	0.49
3:C:462:THR:N	3:C:463:PRO:CD	2.73	0.49
1:D:32:THR:HG21	1:D:59:GLN:HE21	1.76	0.49
1:D:137:PHE:CE2	1:D:277:TYR:HE1	2.30	0.49
4:E:27:VAL:HB	4:E:154:GLU:CA	2.42	0.49
1:A:111:ASP:C	1:A:113:THR:H	2.19	0.49
1:A:175:GLU:CD	1:A:211:PRO:HG3	2.37	0.49
1:A:233:PHE:CE1	1:A:413:VAL:CG1	2.94	0.49
1:A:304:SER:HB2	1:A:397:GLU:HG2	1.94	0.49
1:A:385:HIS:ND1	1:A:385:HIS:O	2.46	0.49
2:B:75:ILE:HG21	3:C:27:ASN:HB2	1.93	0.49
2:B:147:LYS:CG	2:B:148:SER:H	2.25	0.49
2:B:223:TYR:O	2:B:223:TYR:CD1	2.66	0.49
3:C:110:VAL:CG2	3:C:120:TRP:HB2	2.42	0.49
3:C:308:ILE:HG22	3:C:309:VAL:N	2.27	0.49
1:D:106:THR:CG2	1:D:107:LYS:CD	2.90	0.49
1:D:140:GLN:HG3	1:D:141:ASN:N	2.25	0.49
1:D:152:ASP:CB	1:D:196:THR:O	2.60	0.49
4:E:140:ASN:HD21	4:E:211:PHE:CA	2.22	0.49
1:A:136:PRO:CD	1:A:274:ILE:HG23	2.38	0.49
1:A:136:PRO:CA	1:A:277:TYR:OH	2.60	0.49
1:A:276:LYS:N	1:A:276:LYS:HD2	2.27	0.49
1:A:284:PHE:N	1:A:284:PHE:HD1	2.10	0.49
2:B:137:PHE:CD1	2:B:137:PHE:N	2.79	0.49
2:B:146:PHE:O	2:B:147:LYS:HB2	2.11	0.49
3:C:192:ILE:CD1	3:C:221:ILE:CG2	2.90	0.49
3:C:427:ASN:HA	3:C:430:VAL:CG2	2.40	0.49
1:D:93:TYR:OH	1:D:198:TYR:CD2	2.66	0.49
1:D:157:SER:CA	1:D:199:LEU:HD12	2.40	0.49
1:D:291:VAL:HG12	1:D:295:VAL:HG11	1.94	0.49
1:D:394:ASN:C	1:D:396:ALA:N	2.66	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:192:LYS:NZ	4:E:206:GLN:HE22	2.10	0.49
4:E:250:LYS:CA	4:E:253:LEU:HB3	2.34	0.49
1:A:207:MET:N	1:A:207:MET:SD	2.86	0.49
1:A:379:VAL:HG22	4:E:424:LYS:HE3	1.94	0.49
2:B:185:GLN:O	2:B:217:PRO:CA	2.60	0.49
2:B:302:LEU:O	2:B:305:HIS:HB2	2.12	0.49
3:C:249:LEU:N	3:C:249:LEU:CD1	2.75	0.49
3:C:464:VAL:CG1	3:C:465:MET:N	2.76	0.49
1:D:32:THR:O	1:D:58:GLN:HA	2.12	0.49
1:D:49:ILE:HG21	1:D:125:LYS:CE	2.42	0.49
1:D:432:GLU:HG2	1:D:435:GLN:HE22	1.74	0.49
4:E:35:THR:CB	4:E:54:TRP:HE3	2.22	0.49
4:E:44:GLU:CG	4:E:129:ILE:HD12	2.42	0.49
4:E:107:VAL:CG1	4:E:117:TRP:HB2	2.39	0.49
4:E:258:LEU:HD13	4:E:301:VAL:HG13	1.93	0.49
4:E:289:VAL:O	4:E:293:SER:HB3	2.12	0.49
1:A:170:PHE:HZ	1:A:176:TRP:O	1.94	0.49
1:A:225:PHE:CD1	1:A:225:PHE:C	2.89	0.49
2:B:35:LEU:CD1	2:B:56:LEU:HD12	2.41	0.49
2:B:50:MET:HB3	2:B:126:SER:OG	2.12	0.49
2:B:92:LEU:N	2:B:92:LEU:HD23	2.20	0.49
2:B:92:LEU:HD12	2:B:95:ASN:HB2	1.95	0.49
2:B:103:THR:OG1	2:B:122:ALA:HB1	2.12	0.49
2:B:269:LYS:O	2:B:273:THR:HG23	2.13	0.49
3:C:76:ASP:C	3:C:77:ILE:CG2	2.86	0.49
1:D:135:PHE:CZ	1:D:273:LEU:CD1	2.96	0.49
1:D:191:THR:O	1:D:191:THR:CG2	2.61	0.49
1:D:419:ILE:HD12	1:D:420:ILE:HG23	1.95	0.49
4:E:135:PRO:C	4:E:136:PHE:HD1	2.20	0.49
2:B:133:MET:CB	2:B:140:GLN:HG3	2.43	0.49
3:C:63:TYR:CD1	3:C:116:GLY:HA3	2.48	0.49
3:C:148:PHE:CB	3:C:215:VAL:HG22	2.39	0.49
3:C:185:THR:O	3:C:185:THR:HG22	2.11	0.49
3:C:222:ARG:NH2	3:C:224:LYS:N	2.61	0.49
3:C:298:LEU:CD1	3:C:471:PHE:CD2	2.95	0.49
3:C:434:LYS:HE2	3:C:435:GLU:HG2	1.94	0.49
1:D:289:ILE:CG2	1:D:290:ILE:N	2.76	0.49
4:E:138:TRP:CD1	4:E:213:ILE:CD1	2.96	0.49
4:E:192:LYS:HZ2	4:E:206:GLN:HE22	1.60	0.49
4:E:284:LYS:H	4:E:284:LYS:CD	2.26	0.49
1:A:7:LEU:O	1:A:11:LEU:HG	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:MET:HG2	1:A:174:GLY:H	1.77	0.49
1:A:419:ILE:CG2	1:A:420:ILE:N	2.74	0.49
2:B:185:GLN:NE2	2:B:219:PHE:CD2	2.81	0.49
2:B:192:PRO:HD2	2:B:210:TYR:O	2.13	0.49
2:B:279:ILE:HG22	2:B:280:ILE:CA	2.42	0.49
3:C:252:GLU:HG3	1:D:300:HIS:CB	2.43	0.49
1:D:28:PHE:HB3	1:D:156:VAL:CA	2.43	0.49
1:D:29:VAL:CG2	1:D:60:TRP:CD1	2.73	0.49
4:E:183:TRP:HB2	4:E:215:GLN:O	2.13	0.49
1:A:209:ARG:C	1:A:210:ILE:HG12	2.37	0.49
2:B:28:LYS:HB3	2:B:155:GLU:C	2.38	0.49
2:B:92:LEU:HD22	2:B:146:PHE:CG	2.48	0.49
2:B:93:MET:HB2	2:B:145:VAL:HB	1.95	0.49
2:B:444:ILE:CG2	2:B:445:THR:N	2.76	0.49
2:B:468:PHE:O	2:B:469:ALA:HB2	2.13	0.49
3:C:21:VAL:O	3:C:23:PRO:HD3	2.13	0.49
1:D:405:VAL:O	1:D:405:VAL:HG12	2.11	0.49
1:D:420:ILE:HA	1:D:423:VAL:HB	1.95	0.49
4:E:14:TYR:HE1	4:E:84:LEU:HD11	1.77	0.49
4:E:161:ALA:O	4:E:190:ALA:HB3	2.12	0.49
2:B:101:GLU:CD	2:B:123:ILE:HG22	2.38	0.49
2:B:238:VAL:CG2	2:B:255:ALA:CB	2.82	0.49
3:C:141:TRP:HB2	3:C:222:ARG:HA	1.95	0.49
3:C:235:PRO:HG2	3:C:236:CYS:H	1.78	0.49
1:D:35:LEU:HD23	1:D:164:ARG:HH11	1.70	0.49
1:D:72:TYR:CG	1:D:73:GLY:N	2.78	0.49
4:E:1:ASN:C	4:E:3:GLU:N	2.71	0.49
4:E:66:TRP:NE1	4:E:111:ASN:CA	2.56	0.49
4:E:86:LEU:HD13	4:E:103:TYR:OH	2.12	0.49
1:A:62:ASP:CB	1:A:65:LEU:HD12	2.37	0.48
1:A:171:MET:CE	1:A:176:TRP:CZ2	2.87	0.48
1:A:227:PHE:CE2	2:B:299:VAL:HG12	2.48	0.48
4:E:215:GLN:CG	4:E:216:ARG:N	2.76	0.48
4:E:240:TYR:CD2	4:E:453:ILE:CD1	2.83	0.48
1:A:256:PHE:N	1:A:256:PHE:HD1	2.10	0.48
2:B:422:ASP:C	2:B:422:ASP:OD1	2.55	0.48
3:C:136:TYR:CD1	3:C:142:GLN:HB3	2.48	0.48
3:C:314:PHE:O	3:C:314:PHE:HD1	1.96	0.48
3:C:315:ARG:H	3:C:315:ARG:CD	2.25	0.48
3:C:431:LYS:HA	3:C:434:LYS:HB3	1.94	0.48
1:D:244:THR:O	1:D:247:ILE:HB	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:283:ILE:HA	1:D:286:ILE:HD12	1.94	0.48
4:E:44:GLU:CG	4:E:129:ILE:CG1	2.86	0.48
4:E:59:TRP:CE2	4:E:115:MET:HB2	2.48	0.48
4:E:187:HIS:ND1	4:E:189:PRO:CG	2.74	0.48
4:E:262:THR:CB	4:E:265:LEU:HD12	2.42	0.48
4:E:302:ILE:O	4:E:306:VAL:HG23	2.13	0.48
1:A:67:TRP:HB2	1:A:112:TYR:CB	2.41	0.48
2:B:55:PHE:C	2:B:56:LEU:HD13	2.33	0.48
2:B:188:ILE:CG2	2:B:189:GLU:N	2.74	0.48
1:D:63:VAL:O	1:D:63:VAL:CG2	2.61	0.48
1:D:228:LEU:CD1	4:E:258:LEU:HD21	2.43	0.48
4:E:182:GLU:CA	4:E:218:PRO:HG2	2.42	0.48
4:E:303:VAL:O	4:E:306:VAL:HB	2.13	0.48
1:A:136:PRO:CB	1:A:277:TYR:OH	2.58	0.48
2:B:139:TRP:CZ2	2:B:215:ARG:O	2.66	0.48
3:C:12:LEU:HD12	3:C:16:LYS:HD2	1.96	0.48
3:C:30:VAL:HG13	3:C:31:VAL:O	2.12	0.48
3:C:59:ASP:OD2	3:C:121:LEU:HD22	2.13	0.48
3:C:80:LEU:O	3:C:112:VAL:CB	2.60	0.48
3:C:113:ARG:CG	3:C:117:TYR:O	2.62	0.48
3:C:179:ILE:HG23	3:C:181:PRO:CD	2.41	0.48
3:C:264:LEU:HA	3:C:267:GLN:CG	2.40	0.48
1:D:48:GLN:HB3	1:D:130:ILE:HD13	1.83	0.48
4:E:13:ASP:C	4:E:13:ASP:OD1	2.57	0.48
4:E:38:ASN:O	4:E:51:THR:CA	2.61	0.48
4:E:79:ILE:CG1	4:E:80:PRO:HD3	2.44	0.48
4:E:138:TRP:O	4:E:213:ILE:HG13	2.13	0.48
1:A:181:TYR:HB2	1:A:204:HIS:O	2.13	0.48
1:A:249:VAL:HG13	1:A:253:LEU:HD23	1.94	0.48
2:B:82:SER:C	2:B:84:ASP:N	2.71	0.48
2:B:101:GLU:CD	2:B:123:ILE:CG2	2.87	0.48
2:B:138:ASP:CB	2:B:464:PRO:O	2.61	0.48
2:B:221:ILE:HA	2:B:224:THR:HB	1.94	0.48
2:B:241:LEU:HD12	2:B:241:LEU:O	2.14	0.48
3:C:39:LEU:HD12	3:C:39:LEU:N	2.28	0.48
3:C:247:PHE:C	3:C:250:PRO:CG	2.86	0.48
1:D:112:TYR:HD1	1:D:113:THR:N	2.07	0.48
4:E:95:VAL:HG22	4:E:123:TYR:CD2	2.49	0.48
4:E:184:THR:HG23	4:E:215:GLN:CG	2.44	0.48
4:E:232:ILE:HG22	4:E:233:SER:N	2.29	0.48
4:E:237:VAL:HG22	4:E:457:LEU:HD21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:239:VAL:N	4:E:242:LEU:HD23	2.28	0.48
4:E:264:PHE:N	4:E:264:PHE:HD1	2.12	0.48
1:A:51:GLU:HA	1:A:124:PHE:O	2.14	0.48
3:C:25:LYS:HA	3:C:25:LYS:NZ	2.29	0.48
3:C:290:LYS:O	3:C:294:PHE:CE2	2.66	0.48
1:D:47:ASN:O	1:D:49:ILE:HG12	2.14	0.48
1:D:201:ILE:CG2	1:D:203:TYR:CE1	2.94	0.48
1:D:225:PHE:CD1	1:D:225:PHE:C	2.91	0.48
1:D:245:LEU:CD1	4:E:252:THR:HA	2.42	0.48
4:E:56:GLU:HA	4:E:118:LEU:CG	2.43	0.48
4:E:100:GLU:CD	4:E:122:ILE:HG12	2.39	0.48
4:E:143:LEU:HD12	4:E:143:LEU:N	2.29	0.48
4:E:266:PHE:HD1	4:E:269:ALA:HB3	1.79	0.48
1:A:17:LYS:HB3	1:A:84:ASP:O	2.13	0.48
1:A:133:THR:O	1:A:140:GLN:HB2	2.13	0.48
1:A:136:PRO:HB3	1:A:138:ASP:OD1	2.14	0.48
2:B:129:THR:HG22	2:B:142:CYS:CA	2.39	0.48
2:B:130:ILE:HD12	2:B:134:TYR:CE2	2.48	0.48
3:C:69:TRP:HE1	3:C:114:PRO:CA	2.15	0.48
1:D:141:ASN:HB3	1:D:206:ILE:CG1	2.43	0.48
1:D:241:GLU:C	1:D:243:MET:HE1	2.38	0.48
4:E:240:TYR:HB3	4:E:453:ILE:HG12	1.95	0.48
4:E:261:GLN:HG3	4:E:262:THR:N	2.29	0.48
1:A:27:HIS:C	1:A:28:PHE:CD2	2.92	0.48
1:A:276:LYS:HD2	1:A:276:LYS:H	1.78	0.48
2:B:32:ARG:HG3	2:B:59:ALA:O	2.13	0.48
2:B:101:GLU:OE1	2:B:123:ILE:HG21	2.14	0.48
2:B:186:TRP:CZ3	2:B:215:ARG:CZ	2.96	0.48
2:B:187:SER:O	2:B:188:ILE:HG12	2.14	0.48
2:B:218:LEU:CD1	2:B:221:ILE:HG12	2.44	0.48
3:C:184:PHE:CE1	3:C:185:THR:O	2.66	0.48
1:D:93:TYR:CZ	1:D:198:TYR:CE2	3.01	0.48
1:D:112:TYR:HE1	1:D:113:THR:HG1	1.57	0.48
1:D:146:LEU:HD22	1:D:203:TYR:OH	2.14	0.48
1:D:291:VAL:HG12	1:D:295:VAL:CG1	2.43	0.48
1:D:305:THR:C	1:D:306:HIS:CG	2.91	0.48
4:E:44:GLU:OE1	4:E:129:ILE:CD1	2.61	0.48
4:E:236:VAL:C	4:E:239:VAL:HG23	2.38	0.48
4:E:293:SER:O	4:E:297:VAL:HG23	2.14	0.48
1:A:33:VAL:O	1:A:161:GLU:HG2	2.14	0.48
1:A:41:ILE:O	1:A:42:ASN:CG	2.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:TYR:N	1:A:112:TYR:CD1	2.79	0.48
1:A:247:ILE:CG2	1:A:248:SER:N	2.77	0.48
1:A:393:SER:O	1:A:396:ALA:HB3	2.13	0.48
2:B:185:GLN:HB3	2:B:217:PRO:HB3	1.94	0.48
2:B:438:LEU:O	2:B:442:ILE:CD1	2.61	0.48
3:C:56:VAL:HG22	3:C:124:ALA:HB3	1.96	0.48
3:C:60:HIS:HE1	3:C:160:MET:CE	2.26	0.48
3:C:194:HIS:ND1	3:C:195:LYS:N	2.62	0.48
4:E:29:ASP:N	4:E:29:ASP:OD1	2.46	0.48
4:E:79:ILE:HG12	4:E:80:PRO:HD3	1.88	0.48
4:E:299:ASN:ND2	4:E:456:LEU:HG	2.28	0.48
3:C:160:MET:H	3:C:213:GLN:HG3	1.78	0.48
3:C:271:LEU:HD23	3:C:271:LEU:O	2.13	0.48
3:C:275:SER:O	3:C:279:PRO:CD	2.58	0.48
1:D:36:GLN:NE2	1:D:38:ILE:HG12	2.29	0.48
1:D:100:PHE:N	1:D:100:PHE:HD1	2.11	0.48
4:E:91:LEU:HB3	4:E:94:ASN:N	2.22	0.48
4:E:294:LEU:HA	4:E:297:VAL:HG23	1.96	0.48
1:A:62:ASP:OD1	1:A:64:ARG:HB2	2.13	0.47
1:A:145:LYS:CG	1:A:202:THR:HG22	2.19	0.47
1:A:163:ASP:C	1:A:164:ARG:HG3	2.39	0.47
2:B:186:TRP:CG	2:B:215:ARG:HD2	2.48	0.47
3:C:204:ASP:H	3:C:207:PRO:CG	2.26	0.47
1:D:60:TRP:O	1:D:61:ILE:HG23	2.14	0.47
1:D:376:ILE:O	1:D:380:LYS:HE2	2.13	0.47
4:E:94:ASN:ND2	4:E:143:LEU:CD2	2.72	0.47
4:E:304:LEU:O	4:E:308:LEU:HB2	2.13	0.47
1:A:252:SER:O	1:A:256:PHE:CE1	2.67	0.47
1:A:422:THR:HA	1:A:425:VAL:HG12	1.96	0.47
2:B:20:ARG:H	2:B:20:ARG:CD	2.23	0.47
2:B:92:LEU:HD22	2:B:146:PHE:HA	1.96	0.47
2:B:135:PHE:N	2:B:136:PRO:HD2	2.29	0.47
2:B:199:SER:C	2:B:201:ASP:H	2.21	0.47
3:C:137:PHE:O	3:C:137:PHE:CG	2.66	0.47
3:C:233:ILE:N	3:C:233:ILE:CD1	2.77	0.47
1:D:106:THR:HG23	1:D:107:LYS:NZ	2.28	0.47
1:D:390:GLU:O	1:D:393:SER:CB	2.61	0.47
1:D:419:ILE:O	1:D:422:THR:HG22	2.13	0.47
4:E:113:GLY:C	4:E:115:MET:SD	2.97	0.47
4:E:262:THR:HG23	4:E:265:LEU:HB2	1.96	0.47
1:A:15:TYR:CD1	1:A:15:TYR:C	2.85	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:75:ILE:HD11	2:B:78:LEU:CD1	2.36	0.47
2:B:176:ASN:HB3	2:B:191:LYS:HB3	1.87	0.47
2:B:192:PRO:HB2	2:B:210:TYR:HB2	1.95	0.47
3:C:3:GLU:OE1	3:C:7:LEU:CD1	2.58	0.47
3:C:185:THR:HG22	3:C:188:GLY:H	1.79	0.47
1:D:35:LEU:HB3	1:D:164:ARG:CZ	2.44	0.47
1:D:44:ASP:CG	1:D:46:VAL:HG23	2.39	0.47
1:D:60:TRP:O	1:D:116:ILE:HG12	2.14	0.47
1:D:130:ILE:CA	1:D:134:HIS:HB2	2.44	0.47
4:E:22:LYS:HZ1	4:E:26:HIS:HB3	1.79	0.47
4:E:81:SER:O	4:E:86:LEU:HD11	2.15	0.47
4:E:177:PHE:CE1	4:E:178:THR:O	2.67	0.47
4:E:456:LEU:C	4:E:456:LEU:HD13	2.39	0.47
1:A:416:LEU:C	1:A:419:ILE:HG22	2.40	0.47
2:B:236:ILE:CD1	2:B:446:MET:HE1	2.44	0.47
2:B:239:PHE:HB3	2:B:442:ILE:CG1	2.42	0.47
2:B:299:VAL:O	2:B:302:LEU:HB3	2.13	0.47
3:C:16:LYS:HE3	3:C:16:LYS:CA	2.35	0.47
3:C:98:ASN:CG	3:C:98:ASN:O	2.55	0.47
3:C:150:ALA:HB3	3:C:158:ILE:CD1	2.44	0.47
3:C:185:THR:HG22	3:C:188:GLY:N	2.29	0.47
3:C:270:PHE:CZ	1:D:255:VAL:HB	2.49	0.47
3:C:471:PHE:CD1	3:C:472:ILE:N	2.82	0.47
1:D:37:LEU:CD1	1:D:54:VAL:HG22	2.44	0.47
1:D:199:LEU:C	1:D:200:ASP:OD1	2.56	0.47
1:D:233:PHE:O	1:D:236:PRO:HG2	2.13	0.47
1:D:250:LEU:CD2	1:D:292:THR:CB	2.91	0.47
1:D:419:ILE:HD12	1:D:419:ILE:C	2.39	0.47
4:E:94:ASN:CG	4:E:126:THR:H	2.22	0.47
4:E:117:TRP:O	4:E:118:LEU:CB	2.59	0.47
4:E:209:ILE:CG1	4:E:211:PHE:CE1	2.97	0.47
4:E:240:TYR:CB	4:E:453:ILE:CD1	2.91	0.47
1:A:29:VAL:HG21	1:A:86:TRP:HZ3	1.78	0.47
1:A:43:VAL:CG1	1:A:50:VAL:CG2	2.85	0.47
1:A:108:LEU:HD13	1:A:118:TRP:CA	2.44	0.47
2:B:91:VAL:HG22	2:B:92:LEU:N	2.29	0.47
3:C:42:LEU:HD23	3:C:42:LEU:C	2.40	0.47
3:C:113:ARG:NE	3:C:119:THR:HG23	2.24	0.47
3:C:156:ASN:O	3:C:157:GLU:HG3	2.15	0.47
3:C:158:ILE:CG2	3:C:159:SER:N	2.75	0.47
1:D:379:VAL:CG2	1:D:382:ILE:HD12	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:VAL:HG23	1:A:158:ILE:HG12	1.91	0.47
1:A:92:LEU:C	1:A:95:ASN:HD22	2.23	0.47
1:A:176:TRP:HB3	1:A:209:ARG:CG	2.44	0.47
1:A:201:ILE:HG22	1:A:203:TYR:CE1	2.50	0.47
2:B:21:PRO:CG	2:B:85:VAL:HG13	2.44	0.47
2:B:234:LEU:HD11	2:B:262:PHE:CE2	2.50	0.47
3:C:312:PHE:O	3:C:315:ARG:HD2	2.15	0.47
3:C:429:ILE:CG1	3:C:430:VAL:N	2.77	0.47
3:C:464:VAL:HG13	3:C:465:MET:N	2.30	0.47
1:D:176:TRP:CZ3	1:D:209:ARG:NH2	2.82	0.47
1:D:236:PRO:HB3	1:D:299:HIS:NE2	2.29	0.47
4:E:157:LEU:CD1	4:E:208:ILE:HD11	2.44	0.47
4:E:185:ILE:CG1	4:E:214:ILE:CG2	2.79	0.47
4:E:238:LEU:O	4:E:242:LEU:HB3	2.15	0.47
4:E:262:THR:HG23	4:E:265:LEU:HD12	1.96	0.47
1:A:41:ILE:HG13	1:A:51:GLU:HB3	1.94	0.47
1:A:130:ILE:O	1:A:134:HIS:HB2	2.14	0.47
1:A:192:CYS:SG	1:A:193:CYS:N	2.87	0.47
1:A:224:LEU:C	1:A:224:LEU:HD12	2.38	0.47
1:A:259:VAL:HG13	1:A:262:GLU:OE1	2.15	0.47
2:B:81:PRO:HA	2:B:107:ASN:HA	1.96	0.47
2:B:415:LEU:C	2:B:415:LEU:CD1	2.87	0.47
3:C:35:LEU:HD21	3:C:37:LEU:HD21	1.97	0.47
3:C:110:VAL:HG12	3:C:111:LEU:N	2.29	0.47
3:C:211:ASN:ND2	3:C:212:TYR:CE1	2.82	0.47
3:C:253:SER:HB2	1:D:306:HIS:HB3	1.96	0.47
3:C:439:TYR:O	3:C:443:VAL:HG23	2.14	0.47
3:C:449:VAL:CG1	3:C:452:THR:HB	2.25	0.47
1:D:49:ILE:CG2	1:D:125:LYS:CE	2.93	0.47
1:D:92:LEU:HD13	1:D:146:LEU:HD11	1.95	0.47
1:D:137:PHE:HB3	1:D:431:ILE:O	2.14	0.47
1:D:420:ILE:HA	1:D:423:VAL:CB	2.44	0.47
4:E:20:PRO:CB	4:E:61:ASP:OD1	2.60	0.47
4:E:45:LYS:CG	4:E:279:VAL:C	2.81	0.47
4:E:66:TRP:C	4:E:71:TYR:HB3	2.39	0.47
4:E:116:TYR:HD1	4:E:117:TRP:N	2.13	0.47
4:E:131:VAL:HA	4:E:282:ILE:HA	1.96	0.47
4:E:174:PRO:HA	4:E:177:PHE:HB3	1.96	0.47
4:E:219:LEU:HD13	4:E:222:ILE:HB	1.95	0.47
4:E:232:ILE:O	4:E:236:VAL:HG22	2.14	0.47
4:E:262:THR:O	4:E:262:THR:CG2	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:VAL:O	1:A:218:VAL:HG12	2.15	0.47
1:A:281:THR:O	1:A:285:VAL:HG12	2.14	0.47
2:B:152:ASP:OD1	2:B:203:SER:CB	2.63	0.47
3:C:122:PRO:HA	1:D:149:TRP:CH2	2.50	0.47
3:C:179:ILE:HD12	3:C:179:ILE:HA	1.79	0.47
3:C:252:GLU:HG3	1:D:300:HIS:HB3	1.96	0.47
3:C:452:THR:HG23	3:C:456:LEU:HG	1.97	0.47
1:D:43:VAL:HG21	1:D:50:VAL:HG13	1.95	0.47
1:D:112:TYR:CD1	1:D:112:TYR:N	2.83	0.47
1:D:117:MET:HE3	1:D:119:THR:HG23	1.96	0.47
1:D:135:PHE:CD2	1:D:210:ILE:HG12	2.50	0.47
4:E:264:PHE:N	4:E:264:PHE:CD1	2.82	0.47
1:A:76:LYS:O	1:A:112:TYR:CD2	2.68	0.47
2:B:15:TYR:O	2:B:15:TYR:HD1	1.97	0.47
2:B:69:PRO:HG2	2:B:70:ALA:H	1.80	0.47
2:B:92:LEU:HB2	2:B:95:ASN:HB2	1.97	0.47
2:B:233:ILE:O	2:B:237:LEU:HD22	2.15	0.47
3:C:19:LYS:O	3:C:19:LYS:CE	2.63	0.47
3:C:143:ASN:OD1	3:C:220:ILE:CB	2.62	0.47
1:D:384:GLU:HG2	4:E:422:ILE:HD11	1.93	0.47
4:E:90:VAL:HG13	4:E:95:VAL:CB	2.36	0.47
4:E:100:GLU:HG3	4:E:122:ILE:O	2.14	0.47
4:E:417:GLU:O	4:E:421:PHE:CG	2.68	0.47
1:A:216:VAL:O	1:A:217:ASN:C	2.58	0.47
1:A:236:PRO:CB	1:A:299:HIS:CE1	2.65	0.47
1:A:405:VAL:HG23	1:A:405:VAL:O	2.15	0.47
2:B:78:LEU:HD23	2:B:80:ILE:HD11	1.96	0.47
2:B:223:TYR:C	2:B:226:VAL:HG22	2.37	0.47
2:B:240:TYR:O	2:B:244:ASP:HB2	2.15	0.47
3:C:41:ASN:HD22	3:C:41:ASN:HA	1.23	0.47
3:C:66:ARG:HH11	3:C:66:ARG:CG	2.27	0.47
3:C:113:ARG:NE	3:C:117:TYR:HB3	2.30	0.47
3:C:137:PHE:N	3:C:138:PRO:CD	2.76	0.47
3:C:138:PRO:CD	3:C:288:ILE:CD1	2.91	0.47
3:C:148:PHE:CD1	3:C:148:PHE:N	2.83	0.47
3:C:179:ILE:HD12	3:C:195:LYS:CG	2.44	0.47
3:C:251:ALA:C	3:C:253:SER:H	2.23	0.47
3:C:427:ASN:O	3:C:431:LYS:HG3	2.14	0.47
1:D:47:ASN:C	1:D:48:GLN:HG2	2.40	0.47
1:D:66:ARG:HA	1:D:113:THR:O	2.15	0.47
4:E:45:LYS:HZ1	4:E:278:ASN:HA	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:71:TYR:CG	4:E:72:GLU:N	2.83	0.47
4:E:107:VAL:HG13	4:E:117:TRP:CB	2.43	0.47
4:E:146:ARG:CD	4:E:205:PHE:CD2	2.97	0.47
4:E:172:ILE:HD12	4:E:188:ARG:CA	2.44	0.47
4:E:183:TRP:C	4:E:184:THR:HG22	2.40	0.47
4:E:206:GLN:HE21	4:E:206:GLN:HB3	1.36	0.47
1:A:223:LEU:HA	1:A:226:SER:OG	2.15	0.46
2:B:182:GLU:C	2:B:184:GLY:H	2.23	0.46
2:B:460:HIS:C	2:B:464:PRO:HD2	2.40	0.46
3:C:125:ILE:O	3:C:125:ILE:HG22	2.13	0.46
1:D:157:SER:HB2	1:D:199:LEU:CD1	2.44	0.46
4:E:110:TYR:HB3	4:E:112:ASP:OD1	2.15	0.46
4:E:263:ILE:HG21	4:E:263:ILE:HD13	1.55	0.46
1:A:129:GLU:O	1:A:142:CYS:SG	2.74	0.46
1:A:187:TRP:CD1	1:A:199:LEU:CD2	2.98	0.46
1:A:233:PHE:CZ	1:A:413:VAL:HG11	2.49	0.46
2:B:10:VAL:HG13	2:B:11:LEU:CD2	2.33	0.46
3:C:38:THR:OG1	3:C:178:ILE:HG21	2.14	0.46
3:C:232:PHE:O	3:C:235:PRO:CG	2.63	0.46
3:C:289:GLY:O	3:C:293:MET:SD	2.73	0.46
1:D:78:ILE:CD1	1:D:78:ILE:C	2.88	0.46
1:D:85:VAL:HG13	1:D:86:TRP:C	2.40	0.46
4:E:30:VAL:O	4:E:157:LEU:HA	2.15	0.46
4:E:138:TRP:CG	4:E:213:ILE:HG12	2.50	0.46
1:A:72:TYR:HB3	1:A:112:TYR:HB2	1.97	0.46
1:A:227:PHE:O	1:A:230:VAL:HB	2.15	0.46
2:B:196:ASN:O	2:B:197:TRP:CD1	2.68	0.46
2:B:245:ALA:O	2:B:248:LYS:HB3	2.16	0.46
2:B:268:ASP:O	2:B:271:PRO:HD2	2.15	0.46
3:C:63:TYR:HD1	3:C:64:ASP:H	1.61	0.46
3:C:63:TYR:HB2	3:C:117:TYR:CZ	2.51	0.46
4:E:216:ARG:C	4:E:217:LYS:HG3	2.38	0.46
1:A:176:TRP:CB	1:A:209:ARG:HG3	2.46	0.46
1:A:280:PHE:O	1:A:284:PHE:CG	2.68	0.46
2:B:7:LEU:HD11	2:B:69:PRO:HD2	1.97	0.46
2:B:188:ILE:HG22	2:B:190:HIS:N	2.29	0.46
3:C:77:ILE:HD12	3:C:80:LEU:CD1	2.36	0.46
3:C:84:PRO:CG	3:C:107:PHE:O	2.63	0.46
3:C:111:LEU:O	3:C:118:VAL:HG13	2.16	0.46
3:C:113:ARG:CB	3:C:117:TYR:O	2.64	0.46
3:C:266:ALA:HB3	1:D:251:LEU:HD22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:447:ASN:O	3:C:448:LEU:C	2.58	0.46
1:D:44:ASP:O	1:D:48:GLN:HA	2.15	0.46
1:D:111:ASP:OD2	1:D:115:LYS:CD	2.58	0.46
1:D:151:TYR:O	1:D:198:TYR:HB3	2.16	0.46
1:D:177:VAL:HG12	1:D:208:GLN:CG	2.43	0.46
1:D:305:THR:C	1:D:306:HIS:ND1	2.74	0.46
1:D:377:GLU:HA	1:D:380:LYS:CE	2.46	0.46
1:D:398:GLU:C	1:D:400:LYS:N	2.73	0.46
4:E:55:ILE:HG23	4:E:119:PRO:HD2	1.97	0.46
4:E:59:TRP:HH2	4:E:107:VAL:HG12	1.81	0.46
4:E:267:LEU:HD12	4:E:270:GLN:CD	2.40	0.46
4:E:270:GLN:O	4:E:273:PRO:CG	2.64	0.46
1:A:285:VAL:HG13	1:A:286:ILE:HG13	1.98	0.46
1:A:379:VAL:HG13	4:E:424:LYS:CE	2.28	0.46
1:A:415:MET:HA	1:A:415:MET:HE3	1.96	0.46
2:B:252:SER:O	2:B:255:ALA:CB	2.63	0.46
3:C:80:LEU:HG	3:C:81:ARG:H	1.81	0.46
3:C:115:ASN:HD22	3:C:115:ASN:H	1.51	0.46
3:C:122:PRO:CB	1:D:149:TRP:CZ2	2.98	0.46
1:D:176:TRP:CB	1:D:209:ARG:HG3	2.46	0.46
4:E:172:ILE:HG13	4:E:173:ASP:HA	1.98	0.46
4:E:232:ILE:HA	4:E:232:ILE:HD13	1.51	0.46
4:E:256:SER:O	4:E:259:LEU:HB2	2.16	0.46
2:B:109:LEU:HB3	2:B:117:SER:CB	2.40	0.46
3:C:35:LEU:HD22	3:C:215:VAL:CG2	2.43	0.46
3:C:283:LEU:C	3:C:285:VAL:H	2.22	0.46
3:C:462:THR:O	3:C:466:VAL:HG22	2.16	0.46
1:D:78:ILE:CD1	1:D:110:LEU:CB	2.91	0.46
1:D:170:PHE:CZ	1:D:171:MET:O	2.68	0.46
1:D:264:ILE:HG13	1:D:264:ILE:H	1.39	0.46
4:E:266:PHE:CD1	4:E:266:PHE:C	2.91	0.46
4:E:444:LYS:HA	4:E:444:LYS:CE	2.45	0.46
4:E:470:HIS:CE1	4:E:474:VAL:HG23	2.50	0.46
1:A:75:ILE:O	1:A:78:ILE:HG23	2.16	0.46
1:A:262:GLU:O	1:A:265:PRO:HD2	2.15	0.46
1:A:415:MET:HA	1:A:415:MET:CE	2.46	0.46
2:B:427:ASP:OD1	2:B:427:ASP:C	2.59	0.46
3:C:206:PHE:O	3:C:206:PHE:HD1	1.98	0.46
3:C:269:VAL:HA	3:C:272:LEU:CD1	2.45	0.46
3:C:310:LEU:O	3:C:314:PHE:CD2	2.69	0.46
1:D:35:LEU:HD12	1:D:36:GLN:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:51:GLU:HA	1:D:124:PHE:O	2.16	0.46
1:D:68:ASN:HB2	1:D:69:PRO:CD	2.44	0.46
1:D:128:CYS:SG	1:D:144:MET:HE2	2.56	0.46
1:D:195:ASP:C	1:D:197:PRO:HD3	2.41	0.46
4:E:214:ILE:C	4:E:214:ILE:CD1	2.79	0.46
4:E:287:ILE:HG13	4:E:291:PHE:CE2	2.51	0.46
1:A:28:PHE:HD1	1:A:154:THR:O	1.99	0.46
1:A:409:ILE:H	1:A:409:ILE:HG13	1.46	0.46
2:B:35:LEU:HD22	2:B:35:LEU:HA	1.55	0.46
2:B:162:LEU:C	2:B:174:MET:N	2.74	0.46
2:B:239:PHE:CB	2:B:442:ILE:HG12	2.45	0.46
2:B:242:PRO:CG	2:B:243:PRO:CD	2.88	0.46
2:B:284:LEU:O	2:B:288:MET:CB	2.64	0.46
3:C:52:LEU:HD22	3:C:52:LEU:H	1.80	0.46
3:C:189:GLU:C	3:C:223:ARG:HG3	2.40	0.46
3:C:216:THR:O	3:C:217:PHE:CD1	2.60	0.46
3:C:245:LEU:HA	3:C:248:TYR:HD2	1.80	0.46
3:C:294:PHE:CE1	3:C:474:VAL:HG11	2.50	0.46
1:D:21:PRO:CB	1:D:62:ASP:OD2	2.63	0.46
1:D:28:PHE:CE1	1:D:153:GLY:O	2.69	0.46
1:D:412:CYS:O	1:D:415:MET:HE2	2.16	0.46
4:E:182:GLU:CG	4:E:221:TYR:OH	2.59	0.46
4:E:217:LYS:NZ	4:E:219:LEU:HD12	2.30	0.46
1:A:26:THR:O	1:A:28:PHE:CD1	2.69	0.46
1:A:31:ILE:HG23	1:A:60:TRP:HE3	1.81	0.46
1:A:48:GLN:HB2	1:A:128:CYS:O	2.15	0.46
1:A:128:CYS:HB3	1:A:144:MET:HE2	1.98	0.46
1:A:137:PHE:CE1	1:A:210:ILE:CD1	2.98	0.46
1:A:218:VAL:C	1:A:221:PRO:HD2	2.41	0.46
1:A:246:SER:C	1:A:248:SER:N	2.67	0.46
1:A:258:LEU:HB3	4:E:267:LEU:HD21	1.98	0.46
2:B:56:LEU:CG	2:B:120:PRO:HG2	2.45	0.46
2:B:136:PRO:O	2:B:136:PRO:HG2	2.16	0.46
2:B:283:TYR:CD1	2:B:283:TYR:N	2.82	0.46
2:B:431:VAL:O	2:B:432:ALA:CB	2.63	0.46
3:C:22:ARG:CD	3:C:22:ARG:H	2.29	0.46
3:C:276:GLN:O	3:C:279:PRO:HD2	2.16	0.46
3:C:479:ASN:C	3:C:479:ASN:HD22	2.20	0.46
1:D:287:SER:CA	1:D:290:ILE:HG12	2.46	0.46
1:D:379:VAL:O	1:D:379:VAL:CG1	2.61	0.46
4:E:272:VAL:N	4:E:273:PRO:HD2	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:ARG:HH11	1:A:107:LYS:HZ1	1.63	0.46
1:A:152:ASP:HA	1:A:198:TYR:H	1.81	0.46
1:A:255:VAL:CG1	1:A:256:PHE:N	2.78	0.46
1:A:377:GLU:N	1:A:380:LYS:HE2	2.31	0.46
2:B:27:ASP:C	2:B:28:LYS:CG	2.79	0.46
2:B:160:HIS:HE2	2:B:207:VAL:HG11	1.80	0.46
3:C:230:ILE:CD1	3:C:231:ASN:ND2	2.79	0.46
1:D:33:VAL:HG13	1:D:201:ILE:HD11	1.98	0.46
1:D:53:ASN:HD22	1:D:123:ILE:HG13	1.81	0.46
1:D:252:SER:CB	4:E:259:LEU:HD22	2.46	0.46
4:E:86:LEU:HD13	4:E:103:TYR:HE1	1.78	0.46
4:E:93:ASN:HB3	4:E:143:LEU:HA	1.98	0.46
4:E:133:TYR:CZ	4:E:139:GLN:O	2.69	0.46
4:E:255:ILE:C	4:E:257:VAL:N	2.73	0.46
4:E:283:GLY:C	4:E:287:ILE:HG22	2.40	0.46
1:A:76:LYS:C	1:A:112:TYR:CD2	2.94	0.45
1:A:107:LYS:NZ	2:B:151:TYR:CG	2.80	0.45
1:A:145:LYS:HZ3	1:A:202:THR:HG21	1.81	0.45
1:A:160:PRO:CG	1:A:185:LYS:CE	2.94	0.45
1:A:256:PHE:CE1	2:B:261:VAL:CG2	2.89	0.45
2:B:10:VAL:HG13	2:B:11:LEU:N	2.31	0.45
2:B:90:ILE:HA	2:B:148:SER:HA	1.97	0.45
2:B:281:ILE:O	2:B:282:SER:C	2.59	0.45
3:C:47:GLU:O	3:C:132:ILE:HG21	2.16	0.45
3:C:271:LEU:CD2	3:C:299:VAL:CG1	2.92	0.45
3:C:298:LEU:CD1	3:C:471:PHE:HB2	2.39	0.45
3:C:443:VAL:O	3:C:443:VAL:CG1	2.64	0.45
1:D:25:HIS:CD2	1:D:155:LYS:NZ	2.84	0.45
1:D:38:ILE:C	1:D:169:THR:HG21	2.40	0.45
1:D:57:ARG:HA	1:D:119:THR:HG22	1.97	0.45
4:E:101:VAL:O	4:E:101:VAL:HG23	2.15	0.45
4:E:232:ILE:O	4:E:235:LEU:HB3	2.16	0.45
4:E:245:GLN:H	4:E:245:GLN:HG3	1.44	0.45
1:A:260:ILE:HG23	1:A:261:VAL:N	2.31	0.45
2:B:142:CYS:CB	2:B:211:LEU:CB	2.81	0.45
2:B:270:VAL:HG11	2:B:284:LEU:CD2	2.45	0.45
3:C:199:LYS:C	3:C:199:LYS:NZ	2.72	0.45
3:C:234:THR:HB	3:C:235:PRO:HD3	1.99	0.45
3:C:431:LYS:O	3:C:434:LYS:HB3	2.15	0.45
1:D:225:PHE:HD1	1:D:225:PHE:C	2.24	0.45
1:D:246:SER:O	1:D:250:LEU:HD12	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:30:VAL:HG22	4:E:59:TRP:HB3	1.97	0.45
4:E:159:LEU:CB	4:E:192:LYS:HB2	2.46	0.45
4:E:184:THR:HG23	4:E:215:GLN:CB	2.46	0.45
4:E:209:ILE:CG1	4:E:211:PHE:HE1	2.24	0.45
4:E:240:TYR:CD2	4:E:453:ILE:HB	2.51	0.45
1:A:65:LEU:HD13	1:A:110:LEU:HD13	1.98	0.45
1:A:163:ASP:O	1:A:164:ARG:HG3	2.17	0.45
1:A:176:TRP:HB3	1:A:209:ARG:HG3	1.98	0.45
2:B:37:LEU:CA	2:B:54:VAL:CG1	2.66	0.45
2:B:108:VAL:HG22	2:B:118:TRP:CB	2.46	0.45
2:B:130:ILE:CB	2:B:134:TYR:CD2	2.82	0.45
2:B:147:LYS:CB	2:B:206:ASP:HA	2.41	0.45
2:B:422:ASP:O	2:B:425:LYS:HB3	2.17	0.45
2:B:424:LEU:O	2:B:427:ASP:HB3	2.16	0.45
1:D:300:HIS:O	1:D:306:HIS:HA	2.16	0.45
1:D:413:VAL:HA	1:D:416:LEU:HB2	1.99	0.45
4:E:250:LYS:CB	4:E:253:LEU:HD23	2.32	0.45
1:A:6:ARG:NH1	1:A:6:ARG:CB	2.80	0.45
1:A:67:TRP:CD1	1:A:71:ASP:HB3	2.51	0.45
1:A:140:GLN:O	1:A:207:MET:HE1	2.16	0.45
1:A:305:THR:HB	1:A:400:LYS:CB	2.46	0.45
2:B:185:GLN:CD	2:B:219:PHE:CD2	2.94	0.45
2:B:248:LYS:O	2:B:249:MET:C	2.59	0.45
3:C:25:LYS:HB3	3:C:28:ASN:HD21	1.80	0.45
3:C:50:GLU:CB	3:C:132:ILE:HD13	2.43	0.45
3:C:478:PHE:O	3:C:482:PRO:HD3	2.16	0.45
1:D:280:PHE:N	1:D:280:PHE:HD1	2.13	0.45
4:E:20:PRO:HG3	4:E:61:ASP:CB	2.46	0.45
4:E:140:ASN:OD1	4:E:211:PHE:CD2	2.70	0.45
4:E:294:LEU:C	4:E:297:VAL:HG23	2.41	0.45
4:E:453:ILE:HD12	4:E:454:ALA:CA	2.47	0.45
1:A:3:HIS:C	1:A:7:LEU:HG	2.42	0.45
1:A:46:VAL:HG23	1:A:271:VAL:CA	2.47	0.45
1:A:65:LEU:CB	1:A:114:GLY:HA2	2.47	0.45
1:A:176:TRP:CD2	1:A:209:ARG:NH1	2.85	0.45
1:A:292:THR:CA	1:A:296:ILE:HD11	2.44	0.45
2:B:101:GLU:HB2	2:B:123:ILE:HG22	1.98	0.45
2:B:186:TRP:HB2	2:B:215:ARG:CG	2.32	0.45
2:B:289:ILE:HG22	2:B:293:PHE:CE2	2.51	0.45
2:B:442:ILE:HG22	2:B:443:PHE:N	2.29	0.45
3:C:3:GLU:CD	3:C:7:LEU:HG	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:37:LEU:HD21	3:C:148:PHE:CD2	2.51	0.45
3:C:84:PRO:CG	3:C:107:PHE:C	2.85	0.45
3:C:247:PHE:HE1	3:C:309:VAL:HA	1.81	0.45
3:C:278:LEU:O	3:C:278:LEU:HD13	2.13	0.45
1:D:187:TRP:HZ2	1:D:196:THR:HA	1.81	0.45
1:D:382:ILE:O	1:D:385:HIS:HB3	2.16	0.45
1:D:419:ILE:O	1:D:423:VAL:HG23	2.17	0.45
4:E:71:TYR:CD1	4:E:111:ASN:ND2	2.81	0.45
4:E:91:LEU:HD13	4:E:145:PHE:CA	2.45	0.45
4:E:93:ASN:HB3	4:E:144:VAL:H	1.82	0.45
4:E:222:ILE:CG2	4:E:223:ILE:H	2.22	0.45
4:E:222:ILE:HG12	4:E:226:ILE:CD1	2.45	0.45
4:E:235:LEU:O	4:E:238:LEU:HB2	2.17	0.45
1:A:20:ARG:CB	1:A:86:TRP:CD2	3.00	0.45
1:A:110:LEU:HG	1:A:111:ASP:O	2.16	0.45
1:A:174:GLY:HA2	1:A:176:TRP:CE3	2.52	0.45
2:B:137:PHE:H	2:B:137:PHE:HD1	1.61	0.45
2:B:233:ILE:HG12	2:B:233:ILE:H	1.63	0.45
3:C:46:LYS:HG3	3:C:49:ASP:OD1	2.17	0.45
3:C:431:LYS:CE	1:D:379:VAL:CG2	2.95	0.45
1:D:43:VAL:HG13	1:D:49:ILE:C	2.39	0.45
1:D:178:MET:HA	1:D:207:MET:HB3	1.96	0.45
1:D:286:ILE:HG22	1:D:290:ILE:HG23	1.98	0.45
1:D:398:GLU:HA	1:D:401:TYR:CE1	2.52	0.45
4:E:221:TYR:O	4:E:224:ASN:HB3	2.16	0.45
4:E:240:TYR:CG	4:E:453:ILE:HD13	2.49	0.45
4:E:262:THR:HA	4:E:265:LEU:CB	2.45	0.45
4:E:284:LYS:C	4:E:287:ILE:HG23	2.41	0.45
4:E:472:ASN:ND2	4:E:472:ASN:O	2.50	0.45
1:A:170:PHE:HE1	1:A:176:TRP:CD1	2.35	0.45
1:A:241:GLU:O	1:A:241:GLU:HG2	2.15	0.45
2:B:92:LEU:HB2	2:B:96:ASN:H	1.82	0.45
3:C:30:VAL:HG13	3:C:31:VAL:N	2.31	0.45
3:C:137:PHE:CE1	3:C:288:ILE:HG21	2.50	0.45
3:C:149:THR:HG22	3:C:214:ASP:HB3	1.92	0.45
3:C:179:ILE:HG13	3:C:181:PRO:HD3	1.96	0.45
3:C:288:ILE:HG21	3:C:288:ILE:HD13	1.77	0.45
1:D:38:ILE:O	1:D:39:GLN:CG	2.65	0.45
1:D:128:CYS:O	1:D:129:GLU:C	2.60	0.45
1:D:130:ILE:O	1:D:131:ILE:HG12	2.15	0.45
1:D:283:ILE:O	1:D:287:SER:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:127:CYS:SG	4:E:128:PRO:CD	3.04	0.45
4:E:140:ASN:OD1	4:E:211:PHE:CG	2.70	0.45
4:E:240:TYR:HB3	4:E:453:ILE:CG1	2.47	0.45
4:E:431:ASP:C	4:E:435:GLU:HG3	2.42	0.45
1:A:3:HIS:CB	1:A:7:LEU:CD2	2.89	0.45
1:A:37:LEU:O	1:A:169:THR:HG21	2.16	0.45
1:A:251:LEU:CD2	4:E:260:ALA:HA	2.42	0.45
2:B:45:GLU:OE1	2:B:277:VAL:CB	2.60	0.45
2:B:75:ILE:HD11	2:B:78:LEU:HB2	1.98	0.45
2:B:132:VAL:CG1	2:B:279:ILE:CA	2.81	0.45
2:B:296:ILE:HD13	2:B:296:ILE:HA	1.82	0.45
3:C:48:THR:H	3:C:285:VAL:HA	1.82	0.45
3:C:106:TYR:O	3:C:106:TYR:CD1	2.46	0.45
3:C:150:ALA:HB3	3:C:158:ILE:HD13	1.98	0.45
3:C:200:ASN:OD1	3:C:202:TYR:CE2	2.70	0.45
1:D:43:VAL:HA	1:D:49:ILE:O	2.16	0.45
1:D:176:TRP:CG	1:D:209:ARG:HD2	2.52	0.45
1:D:265:PRO:O	1:D:269:SER:HB2	2.16	0.45
4:E:44:GLU:CB	4:E:129:ILE:HD12	2.46	0.45
4:E:55:ILE:HG21	4:E:119:PRO:HG2	1.97	0.45
4:E:138:TRP:HB3	4:E:214:ILE:O	2.17	0.45
4:E:159:LEU:HD23	4:E:159:LEU:HA	1.59	0.45
4:E:270:GLN:O	4:E:273:PRO:HD2	2.16	0.45
1:A:28:PHE:CD1	1:A:154:THR:O	2.70	0.45
1:A:227:PHE:O	1:A:227:PHE:HD1	2.00	0.45
1:A:396:ALA:O	1:A:400:LYS:HG3	2.16	0.45
2:B:35:LEU:HA	2:B:55:PHE:O	2.16	0.45
2:B:45:GLU:HG2	2:B:277:VAL:CB	2.40	0.45
2:B:141:ASN:CA	2:B:211:LEU:O	2.62	0.45
1:D:61:ILE:HG22	1:D:116:ILE:HD13	1.98	0.45
1:D:130:ILE:HG22	1:D:134:HIS:HD2	1.82	0.45
4:E:44:GLU:O	4:E:129:ILE:HG13	2.16	0.45
4:E:135:PRO:CG	4:E:137:ASP:OD1	2.65	0.45
1:A:35:LEU:CD1	1:A:203:TYR:OH	2.65	0.45
1:A:106:THR:CG2	1:A:107:LYS:N	2.79	0.45
1:A:134:HIS:C	1:A:134:HIS:ND1	2.75	0.45
1:A:148:ILE:O	1:A:198:TYR:HD2	1.98	0.45
1:A:293:VAL:HG22	4:E:238:LEU:HD21	1.98	0.45
1:A:293:VAL:CG1	1:A:294:VAL:N	2.76	0.45
2:B:101:GLU:OE1	2:B:123:ILE:CG2	2.65	0.45
2:B:439:PHE:HA	2:B:442:ILE:CB	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:23:PRO:HB3	3:C:66:ARG:NH1	2.32	0.45
3:C:219:LEU:HG	3:C:221:ILE:CG2	2.46	0.45
3:C:298:LEU:HD13	3:C:471:PHE:HD2	1.82	0.45
1:D:56:LEU:CG	1:D:120:PRO:HG2	2.27	0.45
1:D:105:MET:O	1:D:105:MET:CG	2.63	0.45
4:E:202:ASP:C	4:E:203:ILE:HG13	2.42	0.45
1:A:221:PRO:O	1:A:224:LEU:HB3	2.16	0.44
1:D:218:VAL:O	1:D:221:PRO:HG2	2.17	0.44
1:D:409:ILE:CA	1:D:412:CYS:HB2	2.47	0.44
4:E:30:VAL:HG12	4:E:157:LEU:HD22	1.99	0.44
4:E:172:ILE:HD12	4:E:188:ARG:N	2.30	0.44
4:E:242:LEU:HG	4:E:243:PRO:CD	2.48	0.44
1:A:72:TYR:HA	1:A:112:TYR:HB3	1.98	0.44
1:A:222:CYS:HA	1:A:225:PHE:HD2	1.82	0.44
2:B:118:TRP:CD1	2:B:120:PRO:HD3	2.52	0.44
2:B:189:GLU:HG3	2:B:468:PHE:HB2	1.98	0.44
3:C:109:ASN:OD1	1:D:150:THR:HG21	2.18	0.44
3:C:159:SER:C	3:C:213:GLN:HG3	2.42	0.44
1:D:60:TRP:HZ3	1:D:116:ILE:HG13	1.81	0.44
1:D:88:PRO:O	1:D:88:PRO:CG	2.65	0.44
4:E:146:ARG:CD	4:E:206:GLN:O	2.65	0.44
4:E:146:ARG:HG3	4:E:147:SER:O	2.16	0.44
1:A:6:ARG:HH11	1:A:6:ARG:CB	2.29	0.44
1:A:64:ARG:HH11	1:A:64:ARG:HD2	1.47	0.44
1:A:111:ASP:N	1:A:111:ASP:OD1	2.51	0.44
1:A:133:THR:C	1:A:136:PRO:CD	2.90	0.44
1:A:276:LYS:H	1:A:276:LYS:CD	2.30	0.44
2:B:297:LEU:HD11	2:B:445:THR:CG2	2.48	0.44
3:C:56:VAL:CG1	3:C:126:PHE:HE2	2.19	0.44
3:C:191:GLU:OE2	3:C:222:ARG:HB3	2.18	0.44
3:C:480:ARG:HB2	3:C:481:PRO:HD3	1.99	0.44
1:D:3:HIS:O	1:D:4:GLU:C	2.60	0.44
1:D:90:LEU:HA	1:D:90:LEU:HD23	1.74	0.44
4:E:175:GLU:HG2	4:E:176:ASP:N	2.33	0.44
4:E:269:ALA:O	4:E:273:PRO:CD	2.64	0.44
1:A:57:ARG:CG	1:A:57:ARG:O	2.65	0.44
1:A:92:LEU:HB3	1:A:95:ASN:ND2	2.33	0.44
1:A:306:HIS:O	1:A:306:HIS:CG	2.70	0.44
2:B:34:GLY:O	2:B:35:LEU:CD2	2.65	0.44
2:B:53:SER:O	2:B:54:VAL:HG13	2.17	0.44
2:B:75:ILE:CD1	2:B:78:LEU:CD1	2.79	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:112:HIS:N	2:B:112:HIS:ND1	2.65	0.44
2:B:132:VAL:CG1	2:B:279:ILE:C	2.91	0.44
2:B:250:SER:C	2:B:252:SER:N	2.74	0.44
2:B:251:LEU:HD12	2:B:251:LEU:O	2.16	0.44
2:B:259:LEU:HD23	2:B:259:LEU:C	2.43	0.44
3:C:17:TYR:OH	3:C:19:LYS:HD2	2.17	0.44
3:C:85:GLU:C	3:C:87:ILE:H	2.25	0.44
3:C:106:TYR:CD1	3:C:107:PHE:HD1	2.36	0.44
3:C:118:VAL:HG12	3:C:119:THR:N	2.33	0.44
3:C:231:ASN:O	3:C:235:PRO:HD3	2.17	0.44
3:C:266:ALA:O	3:C:270:PHE:CD1	2.70	0.44
1:D:46:VAL:HG22	1:D:270:ALA:O	2.17	0.44
1:D:134:HIS:NE2	1:D:207:MET:CE	2.69	0.44
1:D:426:PHE:HE1	1:D:430:LEU:CD1	2.13	0.44
4:E:59:TRP:CZ2	4:E:115:MET:CB	3.01	0.44
4:E:281:LEU:HA	4:E:281:LEU:HD12	1.61	0.44
1:A:168:SER:C	1:A:169:THR:HG23	2.43	0.44
1:A:301:ARG:C	4:E:245:GLN:HB3	2.42	0.44
2:B:247:GLU:C	2:B:249:MET:N	2.76	0.44
3:C:112:VAL:C	3:C:113:ARG:O	2.61	0.44
3:C:247:PHE:O	3:C:250:PRO:HG2	2.18	0.44
1:D:63:VAL:C	1:D:65:LEU:N	2.76	0.44
1:D:77:LYS:HA	1:D:111:ASP:HA	2.00	0.44
1:D:245:LEU:HD21	4:E:255:ILE:HG21	2.00	0.44
1:D:277:TYR:HA	1:D:280:PHE:CZ	2.52	0.44
1:D:377:GLU:N	1:D:380:LYS:HE2	2.29	0.44
4:E:47:GLU:CB	4:E:129:ILE:HG12	2.29	0.44
4:E:173:ASP:HA	4:E:174:PRO:HD2	1.84	0.44
4:E:304:LEU:O	4:E:304:LEU:CG	2.65	0.44
1:A:27:HIS:O	1:A:28:PHE:CD2	2.71	0.44
1:A:95:ASN:HB3	1:A:144:MET:SD	2.58	0.44
1:A:110:LEU:HD12	1:A:114:GLY:HA2	1.96	0.44
1:A:271:VAL:HG23	1:A:271:VAL:O	2.18	0.44
2:B:40:LEU:C	2:B:40:LEU:CD1	2.85	0.44
2:B:46:LYS:CA	2:B:278:PRO:CD	2.78	0.44
2:B:46:LYS:HG2	2:B:47:ASN:CG	2.42	0.44
2:B:146:PHE:O	2:B:206:ASP:HA	2.17	0.44
2:B:212:ILE:O	2:B:212:ILE:CG2	2.64	0.44
3:C:53:THR:HA	3:C:126:PHE:O	2.17	0.44
3:C:230:ILE:CG1	3:C:231:ASN:ND2	2.77	0.44
3:C:288:ILE:HD13	3:C:290:LYS:HD2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:315:ARG:H	3:C:315:ARG:HD3	1.82	0.44
1:D:149:TRP:CD2	1:D:150:THR:N	2.85	0.44
1:D:176:TRP:HB3	1:D:209:ARG:CG	2.48	0.44
1:D:381:TYR:CD1	4:E:419:CYS:SG	3.06	0.44
4:E:75:ASP:CB	4:E:110:TYR:CZ	3.00	0.44
4:E:131:VAL:O	4:E:131:VAL:CG1	2.63	0.44
4:E:138:TRP:C	4:E:213:ILE:HG13	2.43	0.44
4:E:302:ILE:HG21	4:E:302:ILE:HD13	1.73	0.44
4:E:441:LEU:C	4:E:441:LEU:CD1	2.91	0.44
1:A:41:ILE:HG21	1:A:123:ILE:HD11	1.99	0.44
1:A:152:ASP:N	1:A:152:ASP:OD1	2.50	0.44
1:A:185:LYS:HB3	1:A:185:LYS:HE2	1.82	0.44
1:A:298:THR:O	1:A:299:HIS:C	2.60	0.44
2:B:56:LEU:CD2	2:B:103:THR:CA	2.91	0.44
2:B:85:VAL:HG12	2:B:86:TRP:HB3	2.00	0.44
2:B:189:GLU:HG3	2:B:468:PHE:HB3	2.00	0.44
3:C:20:HIS:O	3:C:20:HIS:CG	2.69	0.44
3:C:130:CYS:HA	3:C:131:PRO:HD2	1.58	0.44
3:C:137:PHE:HD1	3:C:288:ILE:CD1	2.31	0.44
3:C:219:LEU:CD1	3:C:221:ILE:HG22	2.47	0.44
3:C:319:THR:CB	3:C:447:ASN:CB	2.96	0.44
1:D:93:TYR:OH	1:D:198:TYR:HD2	2.00	0.44
1:D:187:TRP:CH2	1:D:189:TYR:CG	3.06	0.44
1:D:210:ILE:HG22	1:D:211:PRO:O	2.18	0.44
4:E:1:ASN:O	4:E:69:SER:HB2	2.18	0.44
4:E:104:TYR:N	4:E:104:TYR:HD1	2.15	0.44
4:E:183:TRP:HB2	4:E:214:ILE:HD13	1.99	0.44
4:E:252:THR:O	4:E:253:LEU:C	2.58	0.44
1:A:89:ASP:OD2	1:A:151:TYR:CE1	2.71	0.44
1:A:95:ASN:ND2	1:A:95:ASN:H	2.12	0.44
1:A:219:ILE:O	1:A:222:CYS:HB2	2.16	0.44
1:A:252:SER:CB	2:B:257:LEU:HD13	2.31	0.44
2:B:59:ALA:CB	2:B:116:VAL:O	2.66	0.44
2:B:129:THR:CG2	2:B:129:THR:O	2.62	0.44
2:B:140:GLN:HB3	2:B:141:ASN:H	1.64	0.44
3:C:48:THR:N	3:C:285:VAL:HA	2.33	0.44
3:C:153:TYR:HB2	3:C:158:ILE:HB	2.00	0.44
3:C:279:PRO:O	3:C:282:ALA:CB	2.59	0.44
1:D:37:LEU:HD13	1:D:54:VAL:HG22	1.99	0.44
1:D:130:ILE:HA	1:D:134:HIS:HB2	1.99	0.44
1:D:167:LEU:HD21	1:D:178:MET:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:HIS:CG	1:D:187:TRP:N	2.85	0.44
1:D:409:ILE:HA	1:D:412:CYS:CB	2.47	0.44
4:E:108:LEU:O	4:E:115:MET:HA	2.18	0.44
1:A:12:LEU:HG	1:A:13:GLU:N	2.32	0.44
1:A:50:VAL:CG1	1:A:52:THR:CG2	2.96	0.44
1:A:104:HIS:CB	1:A:105:MET:SD	3.03	0.44
1:A:130:ILE:O	1:A:134:HIS:CB	2.66	0.44
1:A:235:LEU:N	1:A:236:PRO:HD2	2.32	0.44
2:B:68:ASP:HB3	2:B:69:PRO:HD2	1.88	0.44
2:B:135:PHE:CD2	2:B:283:TYR:CZ	3.06	0.44
2:B:202:PRO:HG2	2:B:203:SER:N	2.33	0.44
2:B:302:LEU:HD12	2:B:302:LEU:HA	1.87	0.44
2:B:429:GLN:HA	2:B:429:GLN:NE2	2.29	0.44
1:D:60:TRP:C	1:D:61:ILE:HG23	2.43	0.44
1:D:106:THR:HG23	1:D:107:LYS:HZ3	1.83	0.44
1:D:107:LYS:NZ	4:E:149:THR:CB	2.81	0.44
1:D:377:GLU:HA	1:D:380:LYS:HD2	2.00	0.44
4:E:49:LEU:HD12	4:E:49:LEU:C	2.43	0.44
4:E:59:TRP:C	4:E:60:ASN:ND2	2.56	0.44
4:E:267:LEU:HA	4:E:270:GLN:CG	2.48	0.44
4:E:447:ASP:O	4:E:450:CYS:HB2	2.18	0.44
1:A:15:TYR:CZ	1:A:84:ASP:HB3	2.53	0.43
1:A:74:GLY:C	1:A:75:ILE:HG23	2.43	0.43
1:A:120:PRO:HA	1:A:121:PRO:HD3	1.68	0.43
2:B:111:GLN:CB	2:B:115:ALA:HB3	2.47	0.43
2:B:281:ILE:HG22	2:B:284:LEU:HB3	1.99	0.43
2:B:408:ILE:CG2	2:B:409:LYS:H	2.29	0.43
1:D:7:LEU:CD1	1:D:70:ALA:O	2.60	0.43
1:D:53:ASN:HD22	1:D:123:ILE:CG1	2.31	0.43
1:D:76:LYS:HE2	1:D:76:LYS:HB3	1.83	0.43
1:D:178:MET:SD	1:D:207:MET:CG	3.06	0.43
1:D:274:ILE:HG13	1:D:277:TYR:CD2	2.53	0.43
1:D:283:ILE:CA	1:D:286:ILE:HD12	2.48	0.43
1:D:429:ARG:CA	1:D:429:ARG:NE	2.81	0.43
4:E:60:ASN:HD22	4:E:60:ASN:N	2.07	0.43
4:E:242:LEU:HA	4:E:245:GLN:OE1	2.18	0.43
4:E:281:LEU:HD11	4:E:286:LEU:HD11	1.98	0.43
1:A:100:PHE:CB	1:A:103:VAL:HG21	2.46	0.43
1:A:224:LEU:HG	1:A:225:PHE:CA	2.49	0.43
2:B:46:LYS:HE2	2:B:278:PRO:HD3	1.99	0.43
2:B:95:ASN:O	2:B:96:ASN:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:142:CYS:N	2:B:211:LEU:HB2	2.32	0.43
2:B:297:LEU:CD1	2:B:445:THR:HG23	2.46	0.43
2:B:406:GLU:CG	2:B:409:LYS:HD2	2.46	0.43
1:D:66:ARG:HD3	1:D:66:ARG:H	1.83	0.43
1:D:245:LEU:O	1:D:249:VAL:HG23	2.19	0.43
4:E:72:GLU:O	4:E:73:GLY:C	2.60	0.43
4:E:173:ASP:CB	4:E:185:ILE:HD13	2.47	0.43
1:A:66:ARG:O	1:A:66:ARG:CG	2.65	0.43
2:B:92:LEU:CA	2:B:145:VAL:O	2.65	0.43
2:B:93:MET:CG	2:B:206:ASP:CB	2.77	0.43
2:B:104:LEU:CD1	2:B:118:TRP:CZ3	2.93	0.43
2:B:108:VAL:HG13	2:B:117:SER:C	2.43	0.43
2:B:448:SER:C	2:B:452:PHE:CE2	2.96	0.43
3:C:69:TRP:HB3	3:C:73:GLU:CB	2.48	0.43
1:D:286:ILE:O	1:D:286:ILE:HG22	2.16	0.43
4:E:22:LYS:CG	4:E:23:THR:N	2.78	0.43
4:E:91:LEU:HA	4:E:145:PHE:HA	1.99	0.43
4:E:187:HIS:ND1	4:E:188:ARG:N	2.67	0.43
4:E:227:ALA:O	4:E:231:LEU:HB3	2.18	0.43
1:A:80:LEU:HD21	1:A:110:LEU:HB2	2.00	0.43
1:A:146:LEU:N	1:A:146:LEU:CD1	2.79	0.43
1:A:189:TYR:HA	1:A:197:PRO:CD	2.42	0.43
1:A:255:VAL:HA	1:A:258:LEU:HD12	1.99	0.43
1:A:431:ILE:O	1:A:431:ILE:CG2	2.66	0.43
2:B:24:THR:HG22	2:B:25:VAL:H	1.84	0.43
2:B:101:GLU:C	2:B:102:ILE:CG1	2.84	0.43
3:C:58:MET:HE1	3:C:120:TRP:CZ2	2.54	0.43
3:C:64:ASP:CB	3:C:116:GLY:O	2.65	0.43
1:D:141:ASN:ND2	1:D:182:ARG:HH22	2.17	0.43
1:D:212:LEU:O	1:D:216:VAL:HG22	2.17	0.43
1:D:257:LEU:HA	1:D:260:ILE:HB	2.00	0.43
4:E:44:GLU:CG	4:E:129:ILE:CB	2.91	0.43
4:E:45:LYS:NZ	4:E:278:ASN:HA	2.33	0.43
4:E:262:THR:O	4:E:263:ILE:C	2.60	0.43
4:E:273:PRO:CG	4:E:274:GLU:N	2.78	0.43
4:E:294:LEU:CA	4:E:297:VAL:HG23	2.48	0.43
1:A:134:HIS:N	1:A:136:PRO:HD2	2.34	0.43
1:A:237:THR:HB	1:A:406:ILE:HG22	2.00	0.43
1:A:243:MET:SD	4:E:249:GLN:OE1	2.77	0.43
1:A:298:THR:HG23	1:A:301:ARG:HD3	1.99	0.43
2:B:93:MET:CG	2:B:145:VAL:HB	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:251:ALA:C	3:C:253:SER:N	2.73	0.43
3:C:252:GLU:HG3	1:D:300:HIS:O	2.18	0.43
3:C:295:ILE:O	3:C:299:VAL:HG23	2.18	0.43
4:E:19:LYS:NZ	4:E:154:GLU:CB	2.62	0.43
4:E:83:LEU:O	4:E:84:LEU:CD1	2.67	0.43
4:E:103:TYR:C	4:E:104:TYR:HD1	2.25	0.43
4:E:191:LYS:HB2	4:E:191:LYS:HE2	1.49	0.43
4:E:210:PHE:O	4:E:212:LEU:CD1	2.67	0.43
4:E:271:LYS:HZ2	4:E:271:LYS:HG3	1.42	0.43
1:A:5:THR:HA	1:A:8:VAL:HG22	2.00	0.43
1:A:92:LEU:CD2	1:A:92:LEU:N	2.82	0.43
1:A:221:PRO:CA	1:A:224:LEU:HB3	2.48	0.43
1:A:228:LEU:HD12	1:A:253:LEU:CD2	2.49	0.43
2:B:11:LEU:HD13	2:B:11:LEU:HA	1.88	0.43
2:B:158:LEU:HD23	2:B:158:LEU:HA	1.59	0.43
2:B:218:LEU:CD1	2:B:222:VAL:CG2	2.96	0.43
2:B:235:ALA:C	2:B:237:LEU:N	2.77	0.43
2:B:284:LEU:O	2:B:287:ILE:HG13	2.18	0.43
2:B:434:VAL:CG1	2:B:438:LEU:HD12	2.42	0.43
3:C:19:LYS:O	3:C:19:LYS:CG	2.67	0.43
3:C:77:ILE:CD1	3:C:80:LEU:HB2	2.49	0.43
3:C:106:TYR:CE1	3:C:107:PHE:CE1	3.03	0.43
1:D:75:ILE:CG1	1:D:78:ILE:HG23	2.43	0.43
1:D:144:MET:HE3	1:D:205:PHE:CD1	2.52	0.43
1:D:416:LEU:HA	1:D:419:ILE:HG13	2.00	0.43
4:E:14:TYR:CE2	4:E:16:LYS:NZ	2.87	0.43
4:E:159:LEU:CD1	4:E:192:LYS:CA	2.83	0.43
1:A:135:PHE:CD1	1:A:273:LEU:HB2	2.53	0.43
1:A:187:TRP:CZ3	1:A:189:TYR:HB3	2.52	0.43
1:A:301:ARG:HG2	1:A:301:ARG:NH1	2.33	0.43
2:B:93:MET:HB2	2:B:145:VAL:HG23	2.00	0.43
3:C:13:ILE:HB	3:C:14:VAL:H	1.64	0.43
3:C:80:LEU:HD12	1:D:20:ARG:NH2	2.33	0.43
3:C:142:GLN:CG	3:C:143:ASN:H	2.29	0.43
3:C:148:PHE:O	3:C:215:VAL:HG22	2.18	0.43
3:C:471:PHE:HD1	3:C:471:PHE:O	1.99	0.43
1:D:34:GLY:CA	1:D:57:ARG:HD2	2.48	0.43
1:D:95:ASN:HD21	1:D:128:CYS:HB3	1.83	0.43
1:D:170:PHE:CG	1:D:171:MET:N	2.87	0.43
4:E:39:LEU:CD2	4:E:183:TRP:CZ2	2.92	0.43
4:E:44:GLU:HB3	4:E:280:PRO:HD3	1.96	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:94:ASN:ND2	4:E:126:THR:H	2.17	0.43
4:E:216:ARG:C	4:E:218:PRO:CD	2.92	0.43
2:B:35:LEU:O	2:B:174:MET:CE	2.66	0.43
3:C:12:LEU:HD23	3:C:12:LEU:HA	1.96	0.43
3:C:82:LEU:HB2	3:C:112:VAL:HG21	2.00	0.43
3:C:137:PHE:HD1	3:C:288:ILE:HD12	1.84	0.43
3:C:269:VAL:CG1	3:C:270:PHE:CE1	3.01	0.43
1:D:80:LEU:CB	1:D:81:PRO:HD2	2.48	0.43
1:D:170:PHE:CD1	1:D:170:PHE:C	2.95	0.43
1:D:189:TYR:HA	1:D:197:PRO:CD	2.39	0.43
1:D:216:VAL:O	1:D:220:ILE:CG1	2.58	0.43
4:E:27:VAL:HG12	4:E:154:GLU:CA	2.49	0.43
4:E:47:GLU:HB3	4:E:128:PRO:O	2.19	0.43
4:E:145:PHE:O	4:E:208:ILE:CG1	2.66	0.43
4:E:262:THR:HG23	4:E:265:LEU:CD1	2.49	0.43
4:E:287:ILE:O	4:E:288:PHE:C	2.61	0.43
4:E:288:PHE:O	4:E:292:VAL:HG23	2.19	0.43
4:E:301:VAL:C	4:E:303:VAL:N	2.75	0.43
1:A:68:ASN:ND2	1:A:69:PRO:HD2	2.33	0.43
2:B:456:LEU:O	2:B:457:ASP:C	2.61	0.43
3:C:11:LEU:C	3:C:16:LYS:CG	2.89	0.43
3:C:60:HIS:NE2	3:C:92:ILE:CG2	2.81	0.43
3:C:98:ASN:C	3:C:100:GLY:N	2.69	0.43
3:C:308:ILE:HG22	3:C:309:VAL:H	1.84	0.43
1:D:37:LEU:HD12	1:D:53:ASN:C	2.42	0.43
1:D:293:VAL:HG12	1:D:294:VAL:N	2.33	0.43
4:E:55:ILE:HG13	4:E:55:ILE:O	2.18	0.43
1:A:65:LEU:HB2	1:A:114:GLY:CA	2.48	0.43
1:A:106:THR:CG2	1:A:107:LYS:H	2.25	0.43
1:A:258:LEU:HB3	4:E:267:LEU:CD2	2.49	0.43
1:A:406:ILE:C	1:A:409:ILE:HG13	2.44	0.43
2:B:428:TRP:O	2:B:431:VAL:HG13	2.19	0.43
3:C:45:LEU:HD23	3:C:52:LEU:HD12	2.01	0.43
3:C:156:ASN:C	3:C:157:GLU:HG3	2.43	0.43
3:C:195:LYS:HA	3:C:196:PRO:HD2	1.82	0.43
1:D:29:VAL:HG13	1:D:156:VAL:HG12	2.00	0.43
1:D:92:LEU:H	1:D:92:LEU:HD23	1.81	0.43
1:D:263:LEU:CD1	4:E:266:PHE:CZ	2.99	0.43
4:E:42:LEU:HD22	4:E:183:TRP:CH2	2.52	0.43
4:E:95:VAL:O	4:E:95:VAL:HG12	2.19	0.43
4:E:242:LEU:C	4:E:242:LEU:CD1	2.89	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:PRO:HB2	1:A:138:ASP:OD1	2.18	0.42
1:A:137:PHE:HE1	1:A:210:ILE:HG13	1.84	0.42
1:A:145:LYS:NZ	1:A:202:THR:HG21	2.32	0.42
1:A:187:TRP:CD1	1:A:197:PRO:O	2.73	0.42
1:A:279:LEU:HD13	1:A:282:MET:HB3	2.01	0.42
1:A:305:THR:OG1	1:A:400:LYS:HB3	2.19	0.42
1:A:419:ILE:HD13	1:A:423:VAL:CG2	2.49	0.42
3:C:191:GLU:HG3	3:C:222:ARG:CB	2.48	0.42
3:C:222:ARG:NH2	3:C:224:LYS:CA	2.82	0.42
1:D:26:THR:C	1:D:28:PHE:N	2.77	0.42
1:D:233:PHE:HE2	1:D:413:VAL:HG11	1.84	0.42
4:E:219:LEU:HD23	4:E:221:TYR:CE2	2.54	0.42
4:E:269:ALA:O	4:E:273:PRO:HG3	2.18	0.42
1:A:66:ARG:O	1:A:67:TRP:CE3	2.72	0.42
1:A:94:ASN:C	1:A:94:ASN:HD22	2.28	0.42
1:A:228:LEU:CD1	1:A:253:LEU:HD23	2.49	0.42
2:B:185:GLN:O	2:B:217:PRO:CB	2.67	0.42
3:C:108:CYS:SG	3:C:109:ASN:N	2.91	0.42
3:C:162:LEU:CD1	3:C:217:PHE:HE1	2.29	0.42
1:D:25:HIS:CD2	1:D:155:LYS:HZ1	2.36	0.42
4:E:159:LEU:HD21	4:E:208:ILE:HG23	2.01	0.42
4:E:463:LEU:C	4:E:463:LEU:CD1	2.81	0.42
1:A:148:ILE:O	1:A:198:TYR:CD2	2.72	0.42
1:A:267:THR:HA	1:A:270:ALA:HB3	2.02	0.42
1:A:298:THR:C	1:A:300:HIS:N	2.76	0.42
1:A:376:ILE:O	1:A:380:LYS:HG3	2.20	0.42
2:B:20:ARG:C	2:B:22:SER:H	2.27	0.42
2:B:233:ILE:O	2:B:237:LEU:HB2	2.19	0.42
1:D:57:ARG:HA	1:D:119:THR:HA	2.02	0.42
1:D:80:LEU:HB2	1:D:108:LEU:CD2	2.49	0.42
1:D:260:ILE:O	1:D:263:LEU:HB2	2.19	0.42
4:E:76:LEU:O	4:E:77:VAL:CG2	2.67	0.42
4:E:219:LEU:C	4:E:222:ILE:HG22	2.44	0.42
1:A:15:TYR:CE2	1:A:84:ASP:OD2	2.71	0.42
1:A:95:ASN:OD1	1:A:144:MET:CB	2.68	0.42
1:A:229:THR:HG21	1:A:291:VAL:HG11	2.02	0.42
1:A:402:VAL:CG1	1:A:404:MET:HG2	2.50	0.42
2:B:187:SER:CB	2:B:216:LYS:HE2	2.50	0.42
1:D:53:ASN:CB	1:D:123:ILE:HG12	2.47	0.42
1:D:242:LYS:HB2	1:D:245:LEU:HD13	2.01	0.42
1:D:411:LEU:HD23	1:D:411:LEU:HA	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:55:ILE:HG23	4:E:119:PRO:N	2.35	0.42
4:E:109:VAL:HG13	4:E:115:MET:CE	2.48	0.42
4:E:147:SER:O	4:E:205:PHE:CD2	2.72	0.42
4:E:242:LEU:HG	4:E:243:PRO:HD3	2.01	0.42
4:E:248:GLY:C	4:E:250:LYS:H	2.28	0.42
1:A:54:VAL:CG2	1:A:122:ALA:CB	2.91	0.42
1:A:76:LYS:CG	1:A:77:LYS:N	2.81	0.42
1:A:244:THR:HG23	1:A:245:LEU:N	2.34	0.42
1:A:261:VAL:O	1:A:265:PRO:HG3	2.19	0.42
1:A:274:ILE:O	1:A:277:TYR:CB	2.64	0.42
1:A:279:LEU:HD13	1:A:282:MET:CB	2.49	0.42
1:A:306:HIS:O	1:A:306:HIS:HD2	1.99	0.42
2:B:142:CYS:CB	2:B:211:LEU:HD12	2.49	0.42
2:B:254:SER:O	3:C:265:LEU:CD1	2.67	0.42
3:C:7:LEU:HD23	3:C:10:ASP:CG	2.43	0.42
3:C:247:PHE:HE1	3:C:309:VAL:HG23	1.84	0.42
3:C:270:PHE:CE1	1:D:255:VAL:HG23	2.53	0.42
3:C:271:LEU:CD2	3:C:299:VAL:HG11	2.44	0.42
3:C:422:GLY:H	3:C:423:ILE:HG13	1.85	0.42
1:D:35:LEU:HD12	1:D:36:GLN:H	1.84	0.42
1:D:93:TYR:OH	1:D:147:GLY:HA3	2.19	0.42
1:D:133:THR:O	1:D:136:PRO:HD2	2.19	0.42
4:E:59:TRP:CE3	4:E:115:MET:HB2	2.54	0.42
4:E:66:TRP:CD1	4:E:111:ASN:HB2	2.54	0.42
1:A:31:ILE:HA	1:A:59:GLN:O	2.20	0.42
1:A:95:ASN:OD1	1:A:144:MET:SD	2.78	0.42
1:A:117:MET:HG3	1:A:119:THR:HG23	2.02	0.42
1:A:184:TRP:CE3	1:A:185:LYS:O	2.73	0.42
1:A:377:GLU:OE2	2:B:404:ALA:HB3	2.20	0.42
1:A:379:VAL:HG22	4:E:424:LYS:CE	2.49	0.42
2:B:69:PRO:HG2	2:B:70:ALA:N	2.34	0.42
2:B:272:GLU:O	2:B:272:GLU:CG	2.58	0.42
3:C:7:LEU:HD13	3:C:73:GLU:CG	2.49	0.42
3:C:303:VAL:O	3:C:306:CYS:HB2	2.19	0.42
1:D:60:TRP:O	1:D:61:ILE:CG2	2.67	0.42
1:D:80:LEU:HD12	1:D:80:LEU:HA	1.72	0.42
1:D:89:ASP:OD1	1:D:89:ASP:O	2.37	0.42
1:D:227:PHE:HE1	1:D:231:LEU:HD21	1.84	0.42
1:D:381:TYR:O	1:D:385:HIS:CB	2.67	0.42
4:E:247:GLY:H	4:E:250:LYS:NZ	2.02	0.42
4:E:453:ILE:O	4:E:457:LEU:CB	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:VAL:O	1:A:122:ALA:HB3	2.20	0.42
1:A:95:ASN:HD22	1:A:95:ASN:H	1.68	0.42
1:A:136:PRO:CG	1:A:274:ILE:HG23	2.50	0.42
1:A:261:VAL:O	1:A:265:PRO:CD	2.67	0.42
1:A:291:VAL:HG12	1:A:292:THR:N	2.35	0.42
1:A:384:GLU:OE1	2:B:411:ILE:CG2	2.68	0.42
2:B:424:LEU:HD22	2:B:428:TRP:CZ2	2.55	0.42
3:C:215:VAL:HB	3:C:217:PHE:CE1	2.55	0.42
3:C:296:MET:HA	3:C:296:MET:CE	2.46	0.42
1:D:92:LEU:HB2	1:D:96:ALA:H	1.85	0.42
1:D:178:MET:HE1	1:D:207:MET:SD	2.59	0.42
4:E:1:ASN:O	4:E:2:GLU:C	2.61	0.42
4:E:74:ILE:CG1	4:E:74:ILE:O	2.68	0.42
4:E:80:PRO:HB2	4:E:83:LEU:CD2	2.50	0.42
4:E:149:THR:HG23	4:E:150:TYR:N	2.30	0.42
4:E:196:TRP:CD1	4:E:196:TRP:C	2.95	0.42
1:A:58:GLN:HB2	1:A:118:TRP:HB3	2.00	0.42
1:A:305:THR:O	1:A:305:THR:HG22	2.19	0.42
2:B:92:LEU:HG	2:B:96:ASN:HD22	1.83	0.42
2:B:175:ILE:CG1	2:B:176:ASN:N	2.62	0.42
2:B:262:PHE:CD1	2:B:262:PHE:N	2.86	0.42
3:C:161:ASP:HA	3:C:199:LYS:CG	2.45	0.42
3:C:233:ILE:O	3:C:234:THR:C	2.63	0.42
3:C:434:LYS:CG	3:C:435:GLU:N	2.81	0.42
1:D:152:ASP:HB2	1:D:196:THR:O	2.20	0.42
1:D:377:GLU:HA	1:D:380:LYS:HE3	2.00	0.42
4:E:200:LYS:O	4:E:200:LYS:HG3	2.19	0.42
4:E:242:LEU:N	4:E:243:PRO:CD	2.83	0.42
4:E:419:CYS:HA	4:E:422:ILE:HG12	2.02	0.42
1:A:146:LEU:HD22	1:A:203:TYR:OH	2.20	0.42
1:A:249:VAL:O	1:A:250:LEU:C	2.58	0.42
1:A:276:LYS:N	1:A:276:LYS:CD	2.83	0.42
1:A:281:THR:HG23	1:A:282:MET:N	2.34	0.42
2:B:45:GLU:HG2	2:B:277:VAL:CA	2.48	0.42
2:B:130:ILE:CB	2:B:134:TYR:CE2	3.03	0.42
2:B:147:LYS:HE2	2:B:148:SER:OG	2.20	0.42
3:C:30:VAL:CG2	3:C:157:GLU:H	2.32	0.42
3:C:149:THR:HB	3:C:214:ASP:HA	2.02	0.42
3:C:199:LYS:NZ	3:C:200:ASN:HA	2.33	0.42
1:D:26:THR:O	1:D:28:PHE:HD1	2.03	0.42
1:D:37:LEU:HD13	1:D:54:VAL:CG1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:238:ASP:HB3	4:E:308:LEU:HD23	1.91	0.42
1:D:240:GLY:C	1:D:242:LYS:N	2.77	0.42
1:D:245:LEU:HD12	4:E:252:THR:HB	2.01	0.42
1:D:264:ILE:HA	1:D:267:THR:HG23	2.02	0.42
1:D:377:GLU:CG	4:E:415:CYS:CB	2.81	0.42
4:E:83:LEU:O	4:E:84:LEU:CB	2.67	0.42
4:E:261:GLN:HE22	4:E:296:ILE:HD11	1.84	0.42
1:A:21:PRO:HB3	1:A:62:ASP:OD2	2.20	0.42
1:A:51:GLU:HG3	1:A:125:LYS:HD2	2.01	0.42
1:A:92:LEU:O	1:A:93:TYR:C	2.63	0.42
1:A:203:TYR:HB3	1:A:205:PHE:HE1	1.84	0.42
1:A:229:THR:O	1:A:232:VAL:N	2.53	0.42
2:B:31:VAL:HG12	2:B:158:LEU:HD23	1.96	0.42
2:B:133:MET:CE	2:B:140:GLN:CB	2.98	0.42
2:B:140:GLN:O	2:B:213:ILE:HD13	2.20	0.42
2:B:180:PHE:CZ	2:B:186:TRP:O	2.72	0.42
2:B:191:LYS:HA	2:B:210:TYR:O	2.20	0.42
2:B:254:SER:OG	3:C:261:ILE:CG2	2.67	0.42
2:B:288:MET:O	2:B:291:VAL:HG12	2.20	0.42
3:C:137:PHE:O	3:C:138:PRO:C	2.62	0.42
4:E:20:PRO:CG	4:E:61:ASP:CG	2.93	0.42
4:E:145:PHE:O	4:E:208:ILE:HG13	2.20	0.42
4:E:212:LEU:N	4:E:212:LEU:CD1	2.83	0.42
1:A:72:TYR:CD1	1:A:72:TYR:O	2.72	0.41
1:A:80:LEU:HD23	1:A:110:LEU:CB	2.49	0.41
1:A:108:LEU:O	1:A:109:LEU:HD23	2.20	0.41
1:A:131:ILE:HD11	1:A:140:GLN:NE2	2.34	0.41
1:A:167:LEU:HA	1:A:170:PHE:HB2	2.02	0.41
1:A:187:TRP:CD1	1:A:199:LEU:HD23	2.51	0.41
1:A:243:MET:CG	4:E:249:GLN:OE1	2.68	0.41
1:A:406:ILE:HD13	1:A:406:ILE:N	2.35	0.41
2:B:7:LEU:O	2:B:8:LEU:C	2.62	0.41
3:C:137:PHE:C	3:C:138:PRO:O	2.62	0.41
3:C:150:ALA:CB	3:C:158:ILE:CD1	2.98	0.41
4:E:70:GLU:O	4:E:74:ILE:HD13	2.20	0.41
1:A:15:TYR:HE2	1:A:84:ASP:CG	2.27	0.41
2:B:203:SER:O	2:B:205:GLU:HG2	2.20	0.41
3:C:130:CYS:SG	3:C:146:LEU:HD11	2.59	0.41
3:C:139:PHE:CE1	3:C:291:TYR:OH	2.61	0.41
1:D:135:PHE:HD1	1:D:136:PRO:N	2.18	0.41
1:D:137:PHE:HD2	1:D:431:ILE:CB	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:212:LEU:O	1:D:216:VAL:CG2	2.68	0.41
1:D:402:VAL:H	1:D:402:VAL:HG23	1.32	0.41
1:D:416:LEU:HA	1:D:419:ILE:CG1	2.50	0.41
4:E:128:PRO:C	4:E:129:ILE:HG12	2.45	0.41
4:E:417:GLU:O	4:E:418:ALA:C	2.63	0.41
1:A:128:CYS:CB	1:A:144:MET:HE2	2.50	0.41
1:A:176:TRP:HE3	1:A:209:ARG:CZ	2.27	0.41
2:B:89:ASP:CG	2:B:148:SER:HB2	2.45	0.41
2:B:186:TRP:C	2:B:216:LYS:HZ1	2.28	0.41
2:B:188:ILE:HG23	2:B:189:GLU:N	2.34	0.41
3:C:29:GLU:O	3:C:156:ASN:CA	2.64	0.41
3:C:67:LEU:CG	3:C:116:GLY:HA2	2.46	0.41
3:C:110:VAL:HG22	3:C:120:TRP:HB2	2.02	0.41
1:D:250:LEU:HD23	1:D:253:LEU:HD13	2.03	0.41
1:D:415:MET:HE2	1:D:415:MET:HB2	1.85	0.41
4:E:54:TRP:CA	4:E:118:LEU:HD11	2.49	0.41
4:E:63:ARG:HB2	4:E:63:ARG:NH1	2.24	0.41
4:E:89:VAL:O	4:E:99:PHE:CE1	2.73	0.41
4:E:133:TYR:CG	4:E:139:GLN:HB3	2.55	0.41
4:E:159:LEU:HB3	4:E:160:SER:H	1.57	0.41
4:E:195:ASN:HB3	4:E:205:PHE:H	1.85	0.41
4:E:451:PHE:HA	4:E:454:ALA:HB3	2.02	0.41
1:A:123:ILE:O	1:A:123:ILE:HG23	2.19	0.41
1:A:130:ILE:CD1	1:A:131:ILE:N	2.71	0.41
1:A:245:LEU:CD1	2:B:250:SER:HB2	2.49	0.41
1:A:387:LYS:H	1:A:387:LYS:HG2	1.54	0.41
2:B:235:ALA:O	2:B:236:ILE:C	2.62	0.41
3:C:102:TYR:CD1	3:C:102:TYR:C	2.99	0.41
3:C:110:VAL:HG22	3:C:120:TRP:CG	2.56	0.41
3:C:134:VAL:HG12	3:C:134:VAL:O	2.20	0.41
3:C:135:LEU:C	3:C:138:PRO:CD	2.92	0.41
1:D:255:VAL:O	1:D:259:VAL:CG2	2.61	0.41
1:D:287:SER:C	1:D:290:ILE:HG12	2.43	0.41
4:E:103:TYR:CD2	4:E:104:TYR:N	2.88	0.41
4:E:261:GLN:HE21	4:E:265:LEU:HD11	1.84	0.41
4:E:276:SER:HB3	4:E:281:LEU:CD1	2.47	0.41
4:E:436:ASN:HA	4:E:439:TRP:CD1	2.52	0.41
1:A:27:HIS:O	1:A:28:PHE:CB	2.69	0.41
1:A:155:LYS:HD3	1:A:155:LYS:HA	1.50	0.41
1:A:198:TYR:O	1:A:198:TYR:HD1	1.99	0.41
2:B:144:MET:O	2:B:209:PHE:CD2	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:159:GLN:O	2:B:159:GLN:HG3	2.19	0.41
2:B:192:PRO:HD2	2:B:210:TYR:CB	2.51	0.41
2:B:221:ILE:O	2:B:224:THR:HB	2.21	0.41
2:B:249:MET:CE	2:B:250:SER:HB3	2.50	0.41
2:B:282:SER:O	2:B:286:PHE:CD2	2.74	0.41
2:B:409:LYS:NZ	3:C:423:ILE:HG23	2.35	0.41
3:C:35:LEU:CD2	3:C:215:VAL:HG21	2.46	0.41
3:C:162:LEU:HD11	3:C:197:ALA:HB1	2.01	0.41
3:C:316:THR:HB	3:C:320:HIS:H	1.85	0.41
1:D:31:ILE:O	1:D:158:ILE:HA	2.21	0.41
1:D:49:ILE:CG2	1:D:125:LYS:NZ	2.66	0.41
4:E:182:GLU:HG3	4:E:218:PRO:HG2	2.02	0.41
4:E:266:PHE:CZ	4:E:270:GLN:HB3	2.55	0.41
1:A:203:TYR:CD1	1:A:203:TYR:N	2.89	0.41
1:A:381:TYR:CD1	1:A:381:TYR:N	2.89	0.41
2:B:53:SER:C	2:B:54:VAL:HG13	2.46	0.41
2:B:57:ASN:HA	2:B:118:TRP:O	2.20	0.41
2:B:136:PRO:HD3	2:B:280:ILE:CD1	2.51	0.41
3:C:262:CYS:C	1:D:251:LEU:CD1	2.93	0.41
4:E:74:ILE:O	4:E:74:ILE:HD13	2.21	0.41
4:E:140:ASN:ND2	4:E:212:LEU:H	2.18	0.41
4:E:213:ILE:O	4:E:213:ILE:CG2	2.68	0.41
1:A:148:ILE:HG23	1:A:198:TYR:CD2	2.51	0.41
1:A:265:PRO:CG	1:A:266:SER:N	2.80	0.41
1:A:273:LEU:O	1:A:274:ILE:C	2.64	0.41
1:A:406:ILE:O	1:A:409:ILE:HG13	2.20	0.41
2:B:46:LYS:HB2	2:B:278:PRO:CD	2.48	0.41
2:B:52:THR:HG22	2:B:53:SER:N	2.28	0.41
2:B:61:THR:CG2	2:B:62:ASP:N	2.81	0.41
2:B:420:GLU:O	2:B:424:LEU:N	2.53	0.41
2:B:456:LEU:N	2:B:456:LEU:CD2	2.84	0.41
3:C:143:ASN:HA	3:C:220:ILE:HA	2.02	0.41
3:C:278:LEU:N	3:C:279:PRO:HD2	2.35	0.41
1:D:227:PHE:CD1	1:D:227:PHE:C	2.99	0.41
1:D:235:LEU:HD13	1:D:242:LYS:HE3	2.01	0.41
1:D:264:ILE:HB	1:D:265:PRO:CD	2.50	0.41
4:E:6:LEU:HD11	4:E:69:SER:HB3	1.96	0.41
4:E:20:PRO:HG3	4:E:61:ASP:HB2	2.01	0.41
4:E:42:LEU:HA	4:E:42:LEU:HD12	1.84	0.41
4:E:47:GLU:CB	4:E:128:PRO:O	2.69	0.41
4:E:92:GLU:HB3	4:E:93:ASN:H	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:435:GLU:HB3	4:E:439:TRP:CZ2	2.55	0.41
1:A:175:GLU:CB	1:A:211:PRO:HG3	2.50	0.41
1:A:303:PRO:HB2	1:A:304:SER:H	1.73	0.41
1:A:306:HIS:C	1:A:306:HIS:HD2	2.27	0.41
1:A:379:VAL:HA	1:A:382:ILE:CG1	2.50	0.41
2:B:46:LYS:CB	2:B:277:VAL:N	2.63	0.41
2:B:248:LYS:HE2	2:B:248:LYS:HB2	1.82	0.41
2:B:261:VAL:O	2:B:265:LEU:HG	2.21	0.41
2:B:282:SER:HB3	2:B:283:TYR:HD1	1.85	0.41
3:C:58:MET:SD	3:C:92:ILE:HD12	2.58	0.41
3:C:245:LEU:O	3:C:246:ALA:C	2.64	0.41
3:C:462:THR:H	3:C:463:PRO:HD2	1.82	0.41
1:D:3:HIS:HB3	1:D:7:LEU:CD2	2.51	0.41
1:D:26:THR:O	1:D:28:PHE:CD1	2.73	0.41
1:D:76:LYS:CE	1:D:112:TYR:CE2	3.03	0.41
1:D:251:LEU:HA	1:D:251:LEU:HD23	1.70	0.41
1:D:423:VAL:C	1:D:426:PHE:HB3	2.46	0.41
4:E:66:TRP:CD1	4:E:66:TRP:N	2.89	0.41
4:E:91:LEU:O	4:E:92:GLU:C	2.64	0.41
4:E:138:TRP:HH2	4:E:215:GLN:HE21	1.64	0.41
4:E:138:TRP:CD1	4:E:213:ILE:HD11	2.56	0.41
4:E:200:LYS:O	4:E:200:LYS:CG	2.67	0.41
4:E:304:LEU:C	4:E:306:VAL:N	2.78	0.41
1:A:46:VAL:HG12	1:A:47:ASN:ND2	2.35	0.41
1:A:146:LEU:HD22	1:A:203:TYR:CZ	2.55	0.41
1:A:195:ASP:OD1	1:A:195:ASP:C	2.64	0.41
1:A:235:LEU:CB	1:A:236:PRO:CD	2.96	0.41
1:A:270:ALA:C	1:A:271:VAL:CG1	2.94	0.41
1:A:277:TYR:O	1:A:280:PHE:CG	2.74	0.41
1:A:410:LEU:C	1:A:410:LEU:CD1	2.94	0.41
2:B:2:VAL:CG1	2:B:69:PRO:HG3	2.50	0.41
2:B:35:LEU:HD11	2:B:56:LEU:HD12	2.01	0.41
2:B:236:ILE:HD12	2:B:446:MET:HE1	2.02	0.41
2:B:250:SER:H	2:B:250:SER:HG	1.45	0.41
2:B:276:SER:C	2:B:277:VAL:HG13	2.45	0.41
2:B:417:SER:O	2:B:421:PHE:CE2	2.74	0.41
3:C:37:LEU:HD11	3:C:148:PHE:CG	2.56	0.41
3:C:43:ILE:H	3:C:43:ILE:CD1	2.22	0.41
3:C:86:LEU:HD23	3:C:86:LEU:HA	1.83	0.41
3:C:89:ILE:HD13	3:C:89:ILE:HG21	1.64	0.41
3:C:137:PHE:CD1	3:C:288:ILE:HG21	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:142:GLN:HG3	3:C:143:ASN:N	2.35	0.41
3:C:154:ASN:HA	3:C:211:ASN:HB2	2.02	0.41
3:C:180:ASP:HB3	3:C:192:ILE:HG21	2.03	0.41
3:C:247:PHE:CD1	3:C:309:VAL:CG2	3.00	0.41
3:C:471:PHE:C	3:C:473:PHE:N	2.78	0.41
1:D:93:TYR:CD1	1:D:93:TYR:N	2.88	0.41
1:D:184:TRP:HE3	1:D:185:LYS:O	2.03	0.41
1:D:247:ILE:O	1:D:248:SER:C	2.63	0.41
1:D:377:GLU:HA	1:D:380:LYS:CD	2.51	0.41
1:D:398:GLU:C	1:D:400:LYS:H	2.29	0.41
1:D:429:ARG:NE	1:D:429:ARG:HA	2.36	0.41
4:E:33:LYS:CE	4:E:160:SER:CB	2.89	0.41
4:E:273:PRO:O	4:E:277:LEU:HG	2.21	0.41
4:E:297:VAL:HB	4:E:298:THR:H	1.56	0.41
1:A:206:ILE:HD12	1:A:206:ILE:N	2.36	0.41
1:A:226:SER:O	1:A:230:VAL:HG23	2.21	0.41
1:A:265:PRO:CG	1:A:266:SER:H	2.28	0.41
2:B:129:THR:O	2:B:133:MET:HE1	2.20	0.41
2:B:180:PHE:HZ	2:B:186:TRP:O	2.04	0.41
3:C:58:MET:CG	3:C:92:ILE:HD12	2.50	0.41
3:C:224:LYS:HZ3	3:C:291:TYR:HE2	1.69	0.41
3:C:280:GLU:HG3	3:C:281:THR:H	1.79	0.41
1:D:133:THR:HG23	1:D:274:ILE:HG21	2.02	0.41
1:D:155:LYS:HA	1:D:155:LYS:HD3	1.88	0.41
1:D:166:ASP:CG	1:D:178:MET:CE	2.72	0.41
1:D:175:GLU:HB3	1:D:211:PRO:CG	2.50	0.41
1:A:259:VAL:O	1:A:263:LEU:HG	2.21	0.40
2:B:96:ASN:C	2:B:98:GLY:H	2.29	0.40
2:B:108:VAL:HG13	2:B:117:SER:O	2.20	0.40
2:B:147:LYS:CD	2:B:148:SER:H	2.34	0.40
2:B:150:THR:CG2	2:B:150:THR:O	2.67	0.40
3:C:148:PHE:N	3:C:148:PHE:HD1	2.19	0.40
3:C:474:VAL:HA	3:C:477:ASN:ND2	2.36	0.40
4:E:1:ASN:HD22	4:E:69:SER:HA	1.86	0.40
4:E:45:LYS:N	4:E:280:PRO:HB3	2.37	0.40
4:E:59:TRP:CE2	4:E:115:MET:CB	3.03	0.40
4:E:136:PHE:HB3	4:E:475:PRO:CB	2.51	0.40
1:A:46:VAL:CB	1:A:270:ALA:O	2.62	0.40
1:A:67:TRP:HB2	1:A:112:TYR:C	2.45	0.40
1:A:95:ASN:OD1	1:A:144:MET:HA	2.21	0.40
1:A:305:THR:CB	1:A:400:LYS:HB2	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:30:VAL:CG1	3:C:31:VAL:C	2.91	0.40
3:C:116:GLY:O	3:C:118:VAL:HG23	2.21	0.40
1:D:56:LEU:CA	1:D:120:PRO:HD2	2.51	0.40
1:D:137:PHE:HB2	1:D:431:ILE:HG22	2.02	0.40
1:D:410:LEU:O	1:D:414:PHE:CB	2.69	0.40
4:E:217:LYS:HE3	4:E:217:LYS:HB2	1.84	0.40
4:E:222:ILE:O	4:E:225:ILE:HB	2.20	0.40
4:E:294:LEU:O	4:E:297:VAL:HG23	2.21	0.40
4:E:470:HIS:C	4:E:472:ASN:H	2.29	0.40
1:A:72:TYR:CG	1:A:73:GLY:N	2.89	0.40
1:A:97:ASP:CB	1:A:126:SER:C	2.95	0.40
1:A:165:PRO:O	1:A:168:SER:HB3	2.21	0.40
1:A:251:LEU:CD1	4:E:256:SER:O	2.70	0.40
1:A:379:VAL:HA	1:A:382:ILE:CD1	2.49	0.40
2:B:10:VAL:CG1	2:B:11:LEU:N	2.84	0.40
2:B:93:MET:CG	2:B:206:ASP:CG	2.91	0.40
2:B:218:LEU:CD1	2:B:221:ILE:HG13	2.43	0.40
2:B:459:SER:O	2:B:463:PRO:HB2	2.22	0.40
3:C:28:ASN:HB2	3:C:29:GLU:H	1.48	0.40
3:C:43:ILE:N	3:C:43:ILE:CD1	2.80	0.40
3:C:230:ILE:CG1	3:C:231:ASN:N	2.82	0.40
1:D:34:GLY:N	1:D:57:ARG:HD2	2.37	0.40
1:D:92:LEU:CD1	1:D:146:LEU:HD11	2.51	0.40
1:D:423:VAL:CA	1:D:426:PHE:HB3	2.51	0.40
4:E:9:LYS:C	4:E:9:LYS:CD	2.88	0.40
4:E:30:VAL:C	4:E:158:GLN:HG3	2.47	0.40
4:E:66:TRP:HB2	4:E:71:TYR:CB	2.51	0.40
4:E:66:TRP:CE3	4:E:70:GLU:CG	3.05	0.40
4:E:91:LEU:HA	4:E:145:PHE:CA	2.52	0.40
4:E:182:GLU:HA	4:E:182:GLU:OE1	2.21	0.40
4:E:187:HIS:HE1	4:E:189:PRO:HG3	1.69	0.40
4:E:195:ASN:HB3	4:E:205:PHE:N	2.36	0.40
4:E:269:ALA:O	4:E:273:PRO:CG	2.69	0.40
4:E:283:GLY:O	4:E:287:ILE:CG2	2.61	0.40
4:E:306:VAL:O	4:E:309:ARG:CG	2.69	0.40
1:A:56:LEU:CD1	1:A:90:LEU:HD13	2.51	0.40
1:A:82:SER:O	1:A:84:ASP:N	2.54	0.40
1:A:148:ILE:N	1:A:158:ILE:HD12	2.36	0.40
1:A:227:PHE:CE2	2:B:299:VAL:HG11	2.56	0.40
1:A:397:GLU:HG2	1:A:400:LYS:HD2	2.04	0.40
1:A:426:PHE:CD1	1:A:427:ALA:N	2.78	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:250:SER:O	2:B:251:LEU:C	2.63	0.40
2:B:262:PHE:HA	2:B:265:LEU:HD12	2.03	0.40
2:B:438:LEU:HD23	2:B:441:TYR:HB3	2.03	0.40
3:C:47:GLU:HG2	3:C:286:PRO:CD	2.43	0.40
3:C:58:MET:HG3	3:C:92:ILE:HD12	2.03	0.40
3:C:200:ASN:CG	3:C:201:ILE:H	2.30	0.40
3:C:227:PHE:C	3:C:230:ILE:HG12	2.47	0.40
3:C:452:THR:CG2	3:C:453:ILE:N	2.77	0.40
1:D:111:ASP:C	1:D:113:THR:N	2.76	0.40
1:D:130:ILE:C	1:D:134:HIS:HB2	2.47	0.40
1:D:253:LEU:CD2	1:D:254:THR:HB	2.50	0.40
4:E:38:ASN:ND2	4:E:40:ILE:HG12	2.37	0.40
4:E:55:ILE:C	4:E:118:LEU:CD1	2.74	0.40
4:E:173:ASP:HB3	4:E:185:ILE:HG21	2.03	0.40
4:E:306:VAL:O	4:E:309:ARG:HG2	2.22	0.40
4:E:448:LYS:HD2	4:E:448:LYS:HA	1.68	0.40
1:A:43:VAL:HG12	1:A:44:ASP:N	2.36	0.40
1:A:52:THR:O	1:A:123:ILE:CG1	2.64	0.40
1:A:91:VAL:HB	1:A:149:TRP:HB2	2.04	0.40
1:A:175:GLU:HB3	1:A:211:PRO:HG3	2.03	0.40
1:A:260:ILE:O	1:A:264:ILE:HG23	2.22	0.40
2:B:46:LYS:CB	2:B:278:PRO:HD2	2.49	0.40
2:B:271:PRO:O	2:B:275:LEU:HD23	2.22	0.40
2:B:437:ARG:HD2	2:B:437:ARG:HA	1.72	0.40
2:B:451:THR:HA	2:B:454:ILE:HD12	2.04	0.40
3:C:48:THR:HB	3:C:284:ALA:C	2.46	0.40
3:C:54:THR:O	3:C:126:PHE:CE2	2.75	0.40
3:C:194:HIS:HB3	3:C:220:ILE:HG12	2.02	0.40
3:C:439:TYR:CD1	3:C:439:TYR:N	2.90	0.40
3:C:450:GLY:O	3:C:453:ILE:HG22	2.22	0.40
3:C:470:ILE:HD13	3:C:470:ILE:HA	1.80	0.40
1:D:41:ILE:HG21	4:E:96:ASP:OD2	2.21	0.40
1:D:44:ASP:O	1:D:48:GLN:CA	2.70	0.40
1:D:178:MET:CE	1:D:207:MET:HB3	2.51	0.40
4:E:63:ARG:C	4:E:64:LEU:HG	2.47	0.40
4:E:188:ARG:N	4:E:189:PRO:HD3	2.33	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%)	260 (71%)	58 (16%)	48 (13%)	0	4
1	D	366/461 (79%)	264 (72%)	56 (15%)	46 (13%)	0	4
2	B	364/493 (74%)	243 (67%)	65 (18%)	56 (15%)	0	3
3	C	364/522 (70%)	252 (69%)	68 (19%)	44 (12%)	0	4
4	E	365/488 (75%)	234 (64%)	80 (22%)	51 (14%)	0	3
All	All	1825/2425 (75%)	1253 (69%)	327 (18%)	245 (13%)	0	4

All (245) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	21	PRO
1	A	24	HIS
1	A	27	HIS
1	A	48	GLN
1	A	76	LYS
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	212	LEU
1	A	215	VAL
1	A	216	VAL
1	A	282	MET
1	A	292	THR
1	A	301	ARG
1	A	303	PRO
1	A	304	SER
1	A	420	ILE
2	B	27	ASP

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Mol	Chain	Res	Type
2	B	48	GLU
2	B	68	ASP
2	B	81	PRO
2	B	90	ILE
2	B	93	MET
2	B	96	ASN
2	B	99	SER
2	B	102	ILE
2	B	107	ASN
2	B	129	THR
2	B	139	TRP
2	B	185	GLN
2	B	206	ASP
2	B	222	VAL
2	B	235	ALA
2	B	249	MET
2	B	251	LEU
2	B	277	VAL
2	B	280	ILE
2	B	283	TYR
2	B	284	LEU
2	B	306	HIS
2	B	307	ARG
2	B	410	TYR
3	C	2	ASN
3	C	5	GLU
3	C	30	VAL
3	C	48	THR
3	C	99	ASP
3	C	115	ASN
3	C	116	GLY
3	C	131	PRO
3	C	180	ASP
3	C	212	TYR
3	C	224	LYS
3	C	253	SER
3	C	310	LEU
3	C	423	ILE
3	C	453	ILE
3	C	484	LYS
1	D	2	GLU
1	D	24	HIS

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Mol	Chain	Res	Type
1	D	30	ASP
1	D	45	GLU
1	D	64	ARG
1	D	74	GLY
1	D	75	ILE
1	D	84	ASP
1	D	102	ILE
1	D	130	ILE
1	D	131	ILE
1	D	136	PRO
1	D	153	GLY
1	D	210	ILE
1	D	239	SER
1	D	241	GLU
1	D	269	SER
1	D	282	MET
1	D	301	ARG
1	D	423	VAL
1	D	426	PHE
1	D	435	GLN
1	D	436	GLU
4	E	16	LYS
4	E	27	VAL
4	E	84	LEU
4	E	93	ASN
4	E	95	VAL
4	E	106	ASN
4	E	111	ASN
4	E	128	PRO
4	E	129	ILE
4	E	152	ALA
4	E	173	ASP
4	E	217	LYS
4	E	253	LEU
4	E	271	LYS
4	E	280	PRO
4	E	298	THR
4	E	309	ARG
4	E	443	GLY
1	A	2	GLU
1	A	7	LEU
1	A	17	LYS

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Mol	Chain	Res	Type
1	A	75	ILE
1	A	232	VAL
1	A	239	SER
1	A	265	PRO
1	A	293	VAL
1	A	392	SER
2	B	2	VAL
2	B	4	GLU
2	B	86	TRP
2	B	156	VAL
2	B	190	HIS
2	B	236	ILE
2	B	246	GLY
2	B	279	ILE
2	B	304	LEU
2	B	415	LEU
3	C	13	ILE
3	C	132	ILE
3	C	136	TYR
3	C	157	GLU
3	C	301	GLY
3	C	434	LYS
3	C	449	VAL
3	C	471	PHE
1	D	73	GLY
1	D	76	LYS
1	D	174	GLY
1	D	220	ILE
1	D	276	LYS
1	D	280	PHE
1	D	428	GLY
4	E	2	GLU
4	E	47	GLU
4	E	63	ARG
4	E	64	LEU
4	E	74	ILE
4	E	92	GLU
4	E	98	GLN
4	E	101	VAL
4	E	112	ASP
4	E	132	THR
4	E	196	TRP

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Mol	Chain	Res	Type
4	E	249	GLN
1	A	28	PHE
1	A	82	SER
1	A	180	ASP
1	A	210	ILE
1	A	419	ILE
1	A	426	PHE
2	B	39	SER
2	B	147	LYS
2	B	198	ARG
2	B	200	ASP
2	B	432	ALA
2	B	458	ALA
3	C	6	ARG
3	C	12	LEU
3	C	205	LYS
3	C	482	PRO
1	D	139	GLN
1	D	192	CYS
1	D	235	LEU
4	E	22	LYS
4	E	135	PRO
4	E	184	THR
4	E	198	LEU
4	E	246	ALA
4	E	297	VAL
1	A	26	THR
1	A	135	PHE
1	A	198	TYR
1	A	248	SER
1	A	396	ALA
2	B	5	ASP
2	B	153	THR
2	B	183	ASN
2	B	291	VAL
2	B	413	GLU
2	B	435	ALA
3	C	225	PRO
3	C	440	ASP
1	D	162	SER
1	D	268	SER
1	D	303	PRO

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Mol	Chain	Res	Type
4	E	149	THR
4	E	161	ALA
4	E	177	PHE
4	E	231	LEU
4	E	272	VAL
1	A	148	ILE
1	A	291	VAL
1	A	430	LEU
2	B	154	SER
2	B	248	LYS
2	B	411	ILE
3	C	19	LYS
3	C	76	ASP
3	C	137	PHE
3	C	138	PRO
3	C	150	ALA
3	C	195	LYS
3	C	235	PRO
1	D	25	HIS
1	D	95	ASN
1	D	97	ASP
1	D	99	ASP
1	D	252	SER
1	D	263	LEU
4	E	85	TRP
4	E	120	PRO
4	E	200	LYS
4	E	222	ILE
1	A	214	PHE
2	B	24	THR
3	C	77	ILE
3	C	142	GLN
3	C	477	ASN
1	D	68	ASN
1	D	236	PRO
4	E	7	ILE
4	E	203	ILE
4	E	256	SER
1	A	160	PRO
2	B	135	PHE
3	C	122	PRO
3	C	239	ILE

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Mol	Chain	Res	Type
1	D	264	ILE
4	E	134	PHE
1	A	264	ILE
2	B	75	ILE
2	B	243	PRO
1	A	249	VAL
2	B	175	ILE
3	C	134	VAL
4	E	119	PRO
2	B	295	VAL
3	C	181	PRO
1	A	247	ILE
1	D	196	THR
4	E	416	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%)	213 (62%)	130 (38%)	0	1
1	D	343/427 (80%)	213 (62%)	130 (38%)	0	1
2	B	340/449 (76%)	237 (70%)	103 (30%)	0	2
3	C	335/475 (70%)	232 (69%)	103 (31%)	0	2
4	E	337/447 (75%)	212 (63%)	125 (37%)	0	1
All	All	1698/2225 (76%)	1107 (65%)	591 (35%)	1	1

All (591) 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

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Mol	Chain	Res	Type
1	A	17	LYS
1	A	18	VAL
1	A	20	ARG
1	A	22	VAL
1	A	23	GLU
1	A	24	HIS
1	A	26	THR
1	A	29	VAL
1	A	30	ASP
1	A	31	ILE
1	A	33	VAL
1	A	35	LEU
1	A	36	GLN
1	A	38	ILE
1	A	39	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
1	A	75	ILE
1	A	87	LEU
1	A	92	LEU
1	A	93	TYR
1	A	94	ASN
1	A	95	ASN
1	A	100	PHE
1	A	103	VAL
1	A	105	MET
1	A	107	LYS
1	A	108	LEU
1	A	111	ASP
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

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Mol	Chain	Res	Type
1	A	129	GLU
1	A	130	ILE
1	A	137	PHE
1	A	141	ASN
1	A	142	CYS
1	A	144	MET
1	A	145	LYS
1	A	149	TRP
1	A	151	TYR
1	A	156	VAL
1	A	158	ILE
1	A	164	ARG
1	A	167	LEU
1	A	168	SER
1	A	180	ASP
1	A	181	TYR
1	A	190	TYR
1	A	193	CYS
1	A	195	ASP
1	A	198	TYR
1	A	200	ASP
1	A	201	ILE
1	A	207	MET
1	A	210	ILE
1	A	216	VAL
1	A	224	LEU
1	A	225	PHE
1	A	228	LEU
1	A	235	LEU
1	A	243	MET
1	A	246	SER
1	A	247	ILE
1	A	249	VAL
1	A	254	THR
1	A	255	VAL
1	A	256	PHE
1	A	257	LEU
1	A	260	ILE
1	A	263	LEU
1	A	264	ILE
1	A	267	THR
1	A	268	SER

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Mol	Chain	Res	Type
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	293	VAL
1	A	296	ILE
1	A	297	ASN
1	A	298	THR
1	A	304	SER
1	A	306	HIS
1	A	381	TYR
1	A	382	ILE
1	A	385	HIS
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	406	ILE
1	A	408	HIS
1	A	409	ILE
1	A	410	LEU
1	A	412	CYS
1	A	414	PHE
1	A	415	MET
1	A	419	ILE
1	A	420	ILE
1	A	424	SER
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	5	ASP

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Mol	Chain	Res	Type
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	27	ASP
2	B	28	LYS
2	B	29	VAL
2	B	31	VAL
2	B	32	ARG
2	B	33	VAL
2	B	35	LEU
2	B	37	LEU
2	B	40	LEU
2	B	41	LEU
2	B	42	ILE
2	B	43	LEU
2	B	46	LYS
2	B	48	GLU
2	B	53	SER
2	B	55	PHE
2	B	56	LEU
2	B	58	LEU
2	B	64	ARG
2	B	65	LEU
2	B	68	ASP
2	B	69	PRO
2	B	73	GLU
2	B	79	SER
2	B	89	ASP
2	B	95	ASN
2	B	97	ASP
2	B	102	ILE
2	B	106	VAL
2	B	107	ASN
2	B	117	SER
2	B	128	CYS
2	B	129	THR
2	B	133	MET
2	B	135	PHE
2	B	136	PRO

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Mol	Chain	Res	Type
2	B	138	ASP
2	B	145	VAL
2	B	158	LEU
2	B	159	GLN
2	B	174	MET
2	B	180	PHE
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	202	PRO
2	B	213	ILE
2	B	216	LYS
2	B	220	TYR
2	B	221	ILE
2	B	222	VAL
2	B	225	ILE
2	B	233	ILE
2	B	234	LEU
2	B	236	ILE
2	B	237	LEU
2	B	239	PHE
2	B	241	LEU
2	B	248	LYS
2	B	251	LEU
2	B	253	ILE
2	B	257	LEU
2	B	260	THR
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	278	PRO
2	B	280	ILE
2	B	281	ILE
2	B	283	TYR
2	B	288	MET
2	B	291	VAL

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Mol	Chain	Res	Type
2	B	297	LEU
2	B	304	LEU
2	B	306	HIS
2	B	307	ARG
2	B	308	SER
2	B	311	THR
2	B	403	GLU
2	B	408	ILE
2	B	426	LYS
2	B	429	GLN
2	B	437	ARG
2	B	439	PHE
2	B	442	ILE
2	B	447	CYS
2	B	462	VAL
2	B	463	PRO
2	B	464	PRO
2	B	468	PHE
3	C	3	GLU
3	C	7	LEU
3	C	13	ILE
3	C	16	LYS
3	C	19	LYS
3	C	22	ARG
3	C	25	LYS
3	C	27	ASN
3	C	28	ASN
3	C	30	VAL
3	C	41	ASN
3	C	43	ILE
3	C	45	LEU
3	C	46	LYS
3	C	48	THR
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	69	TRP
3	C	87	ILE
3	C	91	ASP

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Mol	Chain	Res	Type
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	114	PRO
3	C	115	ASN
3	C	130	CYS
3	C	132	ILE
3	C	135	LEU
3	C	148	PHE
3	C	149	THR
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	205	LYS
3	C	206	PHE
3	C	211	ASN
3	C	220	ILE
3	C	222	ARG
3	C	224	LYS
3	C	225	PRO
3	C	228	TYR
3	C	229	VAL
3	C	233	ILE
3	C	241	PHE
3	C	242	LEU
3	C	249	LEU
3	C	256	LYS
3	C	259	THR
3	C	264	LEU
3	C	267	GLN
3	C	270	PHE
3	C	271	LEU
3	C	272	LEU

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Mol	Chain	Res	Type
3	C	273	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	288	ILE
3	C	291	TYR
3	C	293	MET
3	C	296	MET
3	C	297	SER
3	C	302	VAL
3	C	308	ILE
3	C	309	VAL
3	C	310	LEU
3	C	319	THR
3	C	421	SER
3	C	423	ILE
3	C	429	ILE
3	C	430	VAL
3	C	432	GLN
3	C	442	GLU
3	C	446	TRP
3	C	451	GLN
3	C	452	THR
3	C	455	ARG
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
1	D	1	SER
1	D	3	HIS
1	D	6	ARG
1	D	8	VAL
1	D	16	ASN

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Mol	Chain	Res	Type
1	D	17	LYS
1	D	20	ARG
1	D	22	VAL
1	D	23	GLU
1	D	26	THR
1	D	27	HIS
1	D	29	VAL
1	D	30	ASP
1	D	35	LEU
1	D	36	GLN
1	D	40	LEU
1	D	41	ILE
1	D	46	VAL
1	D	52	THR
1	D	54	VAL
1	D	55	ARG
1	D	57	ARG
1	D	60	TRP
1	D	61	ILE
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	85	VAL
1	D	86	TRP
1	D	92	LEU
1	D	94	ASN
1	D	99	ASP
1	D	102	ILE
1	D	105	MET
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	129	GLU
1	D	130	ILE

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Mol	Chain	Res	Type
1	D	133	THR
1	D	134	HIS
1	D	135	PHE
1	D	138	ASP
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	166	ASP
1	D	167	LEU
1	D	170	PHE
1	D	173	SER
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	206	ILE
1	D	207	MET
1	D	210	ILE
1	D	212	LEU
1	D	216	VAL
1	D	219	ILE
1	D	220	ILE
1	D	222	CYS
1	D	225	PHE
1	D	228	LEU
1	D	230	VAL
1	D	237	THR

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Mol	Chain	Res	Type
1	D	238	ASP
1	D	243	MET
1	D	244	THR
1	D	247	ILE
1	D	250	LEU
1	D	253	LEU
1	D	257	LEU
1	D	265	PRO
1	D	271	VAL
1	D	272	PRO
1	D	274	ILE
1	D	278	MET
1	D	280	PHE
1	D	281	THR
1	D	284	PHE
1	D	285	VAL
1	D	289	ILE
1	D	294	VAL
1	D	295	VAL
1	D	297	ASN
1	D	301	ARG
1	D	303	PRO
1	D	305	THR
1	D	377	GLU
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	415	MET
1	D	420	ILE
1	D	422	THR
1	D	426	PHE
1	D	430	LEU
1	D	431	ILE
1	D	436	GLU
4	E	5	ARG

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Mol	Chain	Res	Type
4	E	8	GLU
4	E	13	ASP
4	E	18	ILE
4	E	19	LYS
4	E	23	THR
4	E	25	ASP
4	E	27	VAL
4	E	29	ASP
4	E	31	THR
4	E	44	GLU
4	E	45	LYS
4	E	47	GLU
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	78	ARG
4	E	79	ILE
4	E	82	GLU
4	E	83	LEU
4	E	86	LEU
4	E	89	VAL
4	E	90	VAL
4	E	93	ASN
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	111	ASN

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Mol	Chain	Res	Type
4	E	116	TYR
4	E	122	ILE
4	E	123	TYR
4	E	124	ARG
4	E	125	SER
4	E	127	CYS
4	E	135	PRO
4	E	138	TRP
4	E	140	ASN
4	E	143	LEU
4	E	147	SER
4	E	148	GLN
4	E	156	ASN
4	E	158	GLN
4	E	160	SER
4	E	172	ILE
4	E	175	GLU
4	E	176	ASP
4	E	179	GLU
4	E	182	GLU
4	E	184	THR
4	E	191	LYS
4	E	195	ASN
4	E	198	LEU
4	E	203	ILE
4	E	206	GLN
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	221	TYR
4	E	225	ILE
4	E	231	LEU
4	E	232	ILE
4	E	235	LEU
4	E	237	VAL
4	E	238	LEU
4	E	239	VAL
4	E	242	LEU
4	E	252	THR

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Mol	Chain	Res	Type
4	E	255	ILE
4	E	258	LEU
4	E	263	ILE
4	E	268	ILE
4	E	270	GLN
4	E	271	LYS
4	E	276	SER
4	E	277	LEU
4	E	279	VAL
4	E	281	LEU
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	295	VAL
4	E	296	ILE
4	E	297	VAL
4	E	301	VAL
4	E	302	ILE
4	E	303	VAL
4	E	308	LEU
4	E	309	ARG
4	E	310	THR
4	E	416	VAL
4	E	419	CYS
4	E	436	ASN
4	E	439	TRP
4	E	440	VAL
4	E	442	ILE
4	E	444	LYS
4	E	446	ILE
4	E	452	TRP
4	E	455	LEU
4	E	456	LEU
4	E	465	ILE
4	E	471	LEU
4	E	473	GLN
4	E	474	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	24	HIS
1	A	47	ASN
1	A	53	ASN
1	A	58	GLN
1	A	59	GLN
1	A	94	ASN
1	A	306	HIS
1	A	435	GLN
2	B	23	GLN
2	B	47	ASN
2	B	96	ASN
2	B	111	GLN
2	B	140	GLN
2	B	141	ASN
2	B	176	ASN
2	B	185	GLN
2	B	190	HIS
2	B	303	ASN
2	B	305	HIS
2	B	310	ASN
2	B	429	GLN
3	C	2	ASN
3	C	9	ASN
3	C	41	ASN
3	C	55	ASN
3	C	65	HIS
3	C	97	ASN
3	C	103	ASN
3	C	115	ASN
3	C	200	ASN
3	C	231	ASN
3	C	267	GLN
3	C	427	ASN
3	C	447	ASN
1	D	16	ASN
1	D	36	GLN
1	D	53	ASN
1	D	58	GLN
1	D	59	GLN
1	D	141	ASN
1	D	408	HIS
1	D	435	GLN

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Mol	Chain	Res	Type
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	148	GLN
4	E	156	ASN
4	E	197	GLN
4	E	206	GLN
4	E	215	GLN
4	E	261	GLN
4	E	278	ASN
4	E	299	ASN
4	E	420	ASN
4	E	430	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	3
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	306:VAL	C	307:SER	N	1.19
1	E	309:ARG	C	310:THR	N	1.19
1	B	129:THR	C	130:ILE	N	1.12

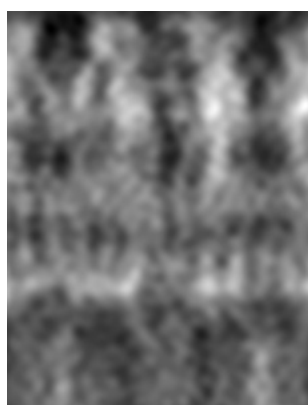
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2071. These allow visual inspection of the internal detail of the map and identification of artifacts.

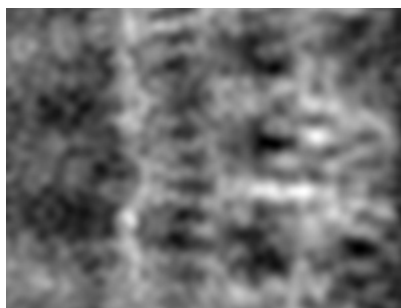
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

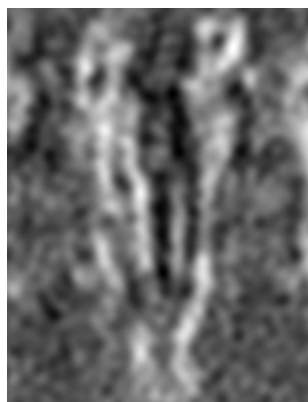


Z

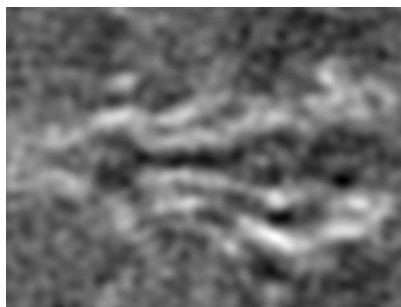
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

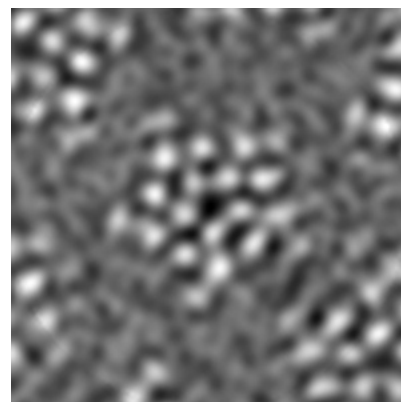
6.2.1 Primary map



X Index: 64



Y Index: 64

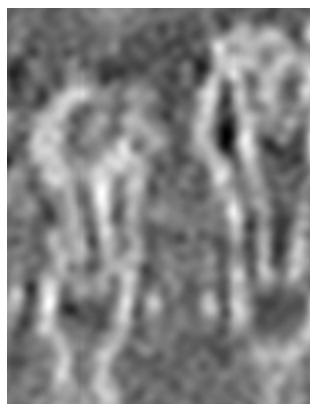


Z Index: 84

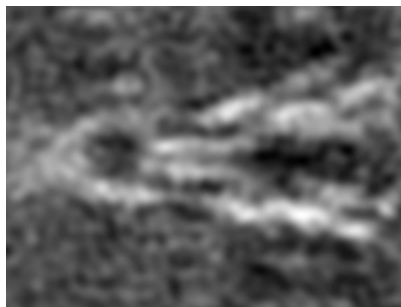
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

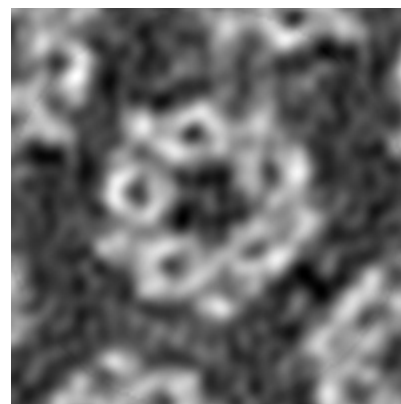
6.3.1 Primary map



X Index: 7



Y Index: 71

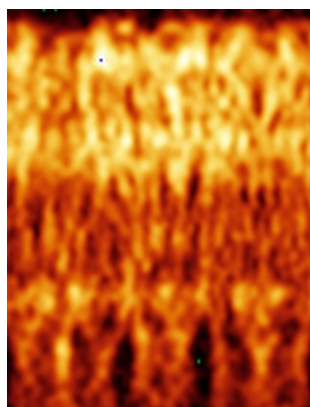


Z Index: 145

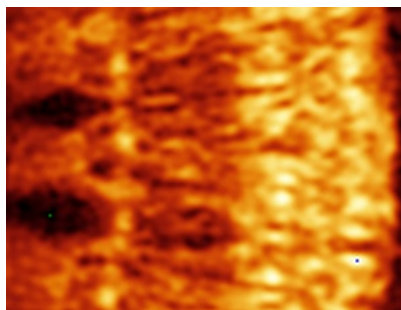
The images above show the largest variance slices of the map in three orthogonal directions.

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

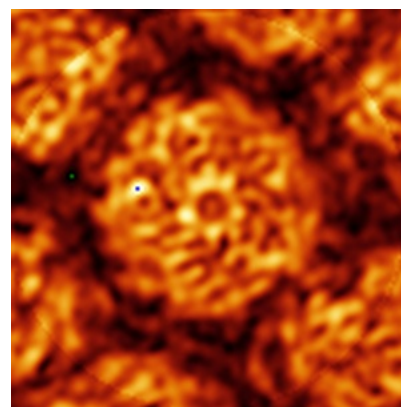
6.4.1 Primary map



X



Y

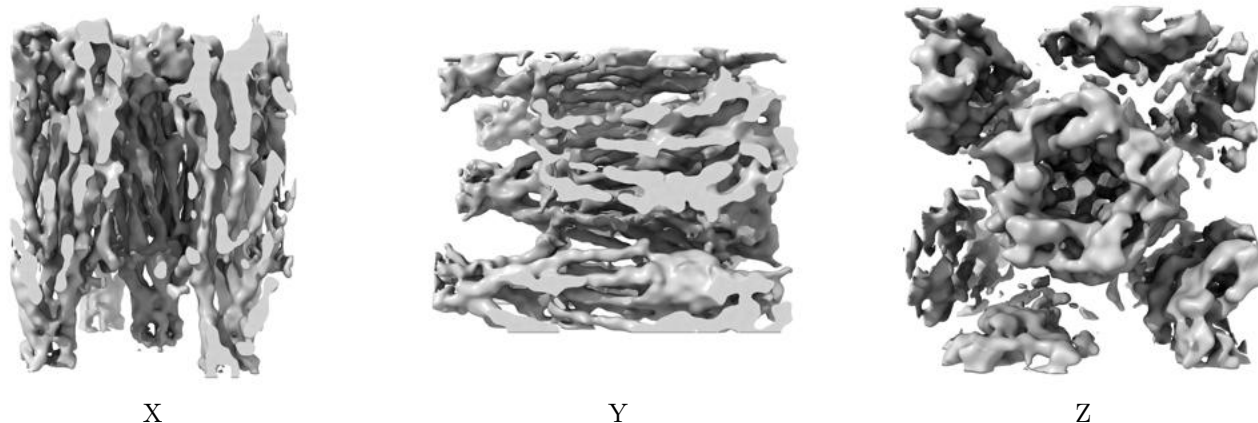


Z

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 1.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

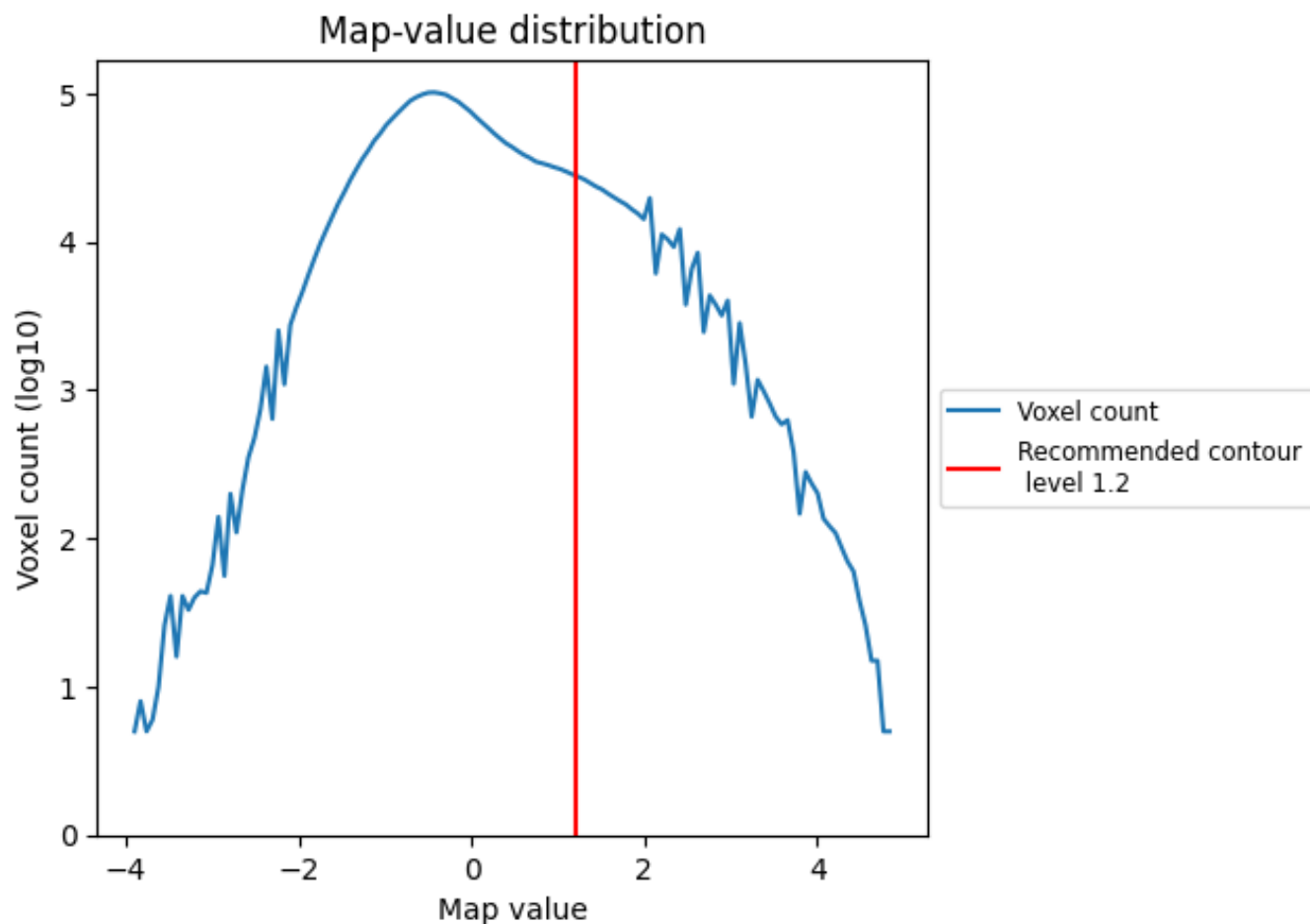
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

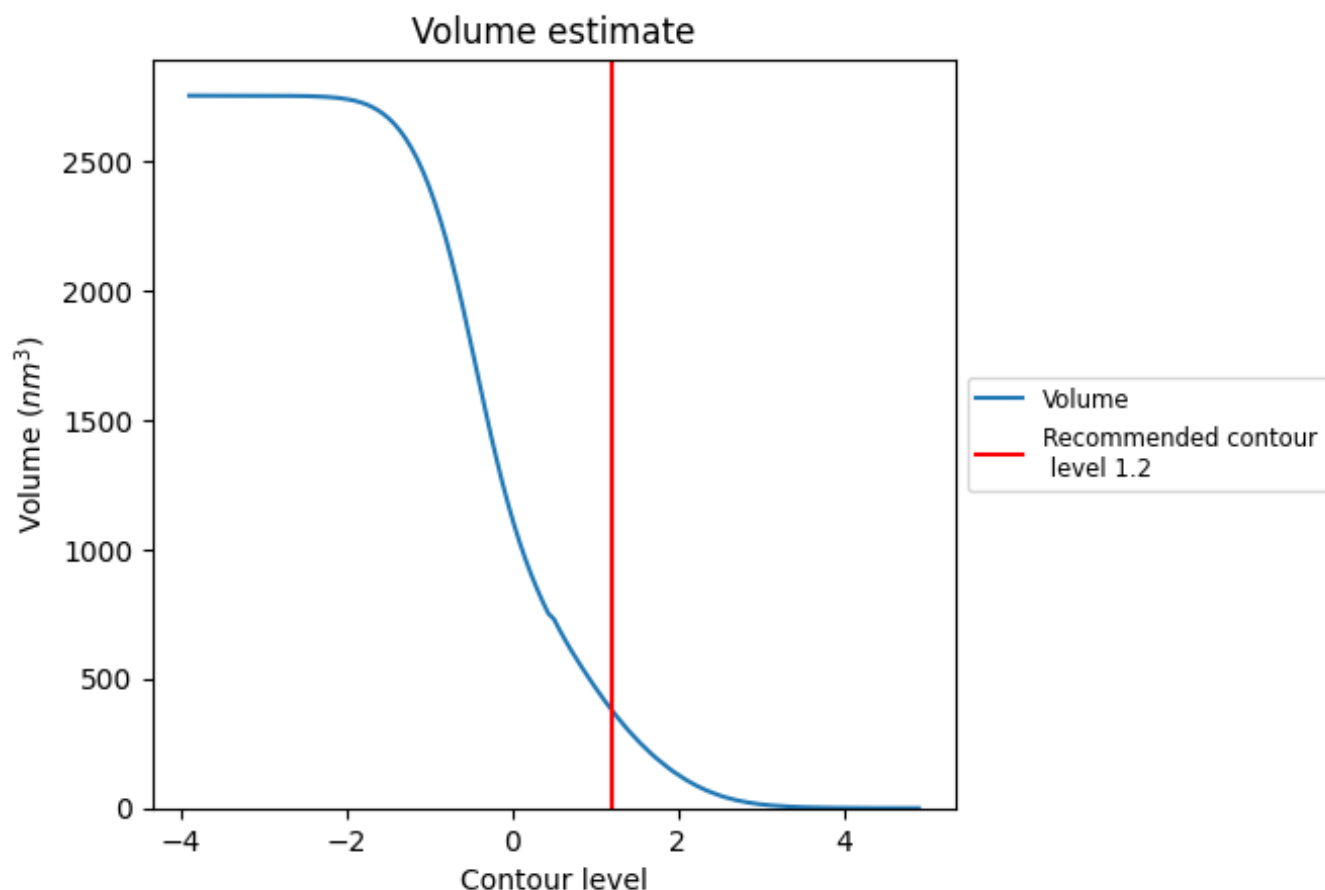
This section contains the results of statistical analysis of the map.

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 379 nm³; this corresponds to an approximate mass of 342 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.

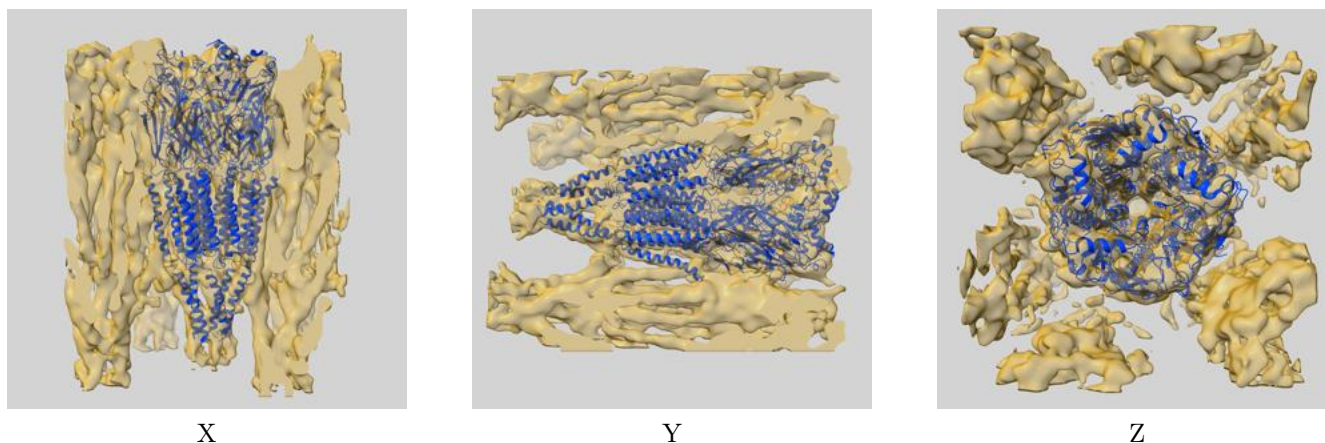
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

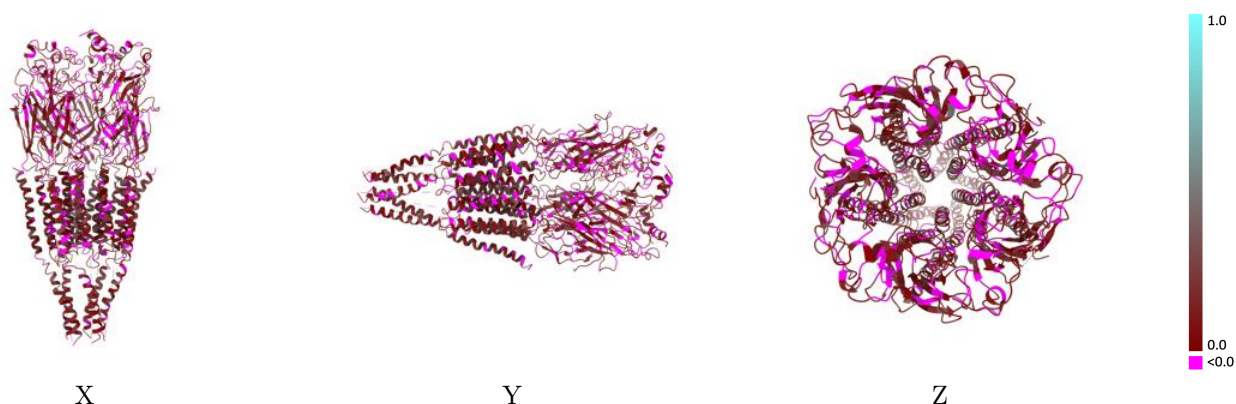
This section contains information regarding the fit between EMDB map EMD-2071 and PDB model 4AQ5. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



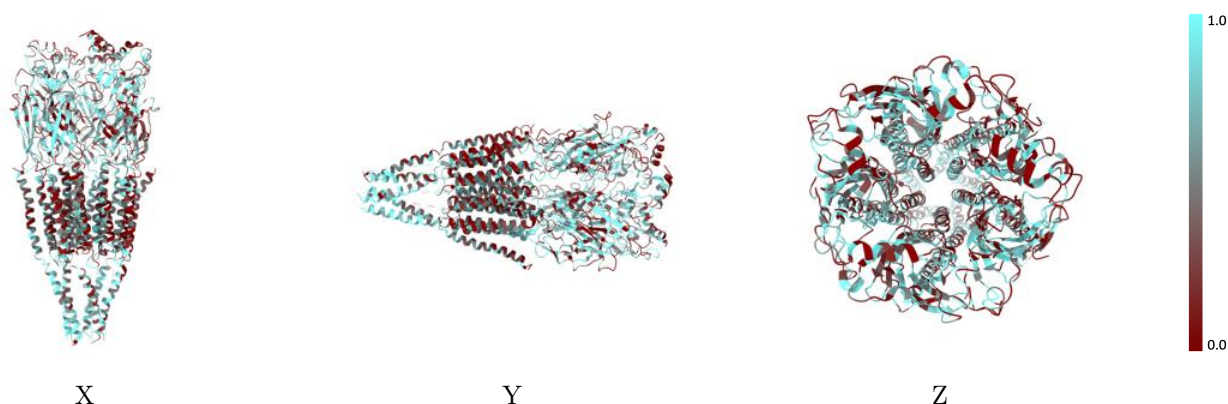
The images above show the 3D surface view of the map at the recommended contour level 1.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



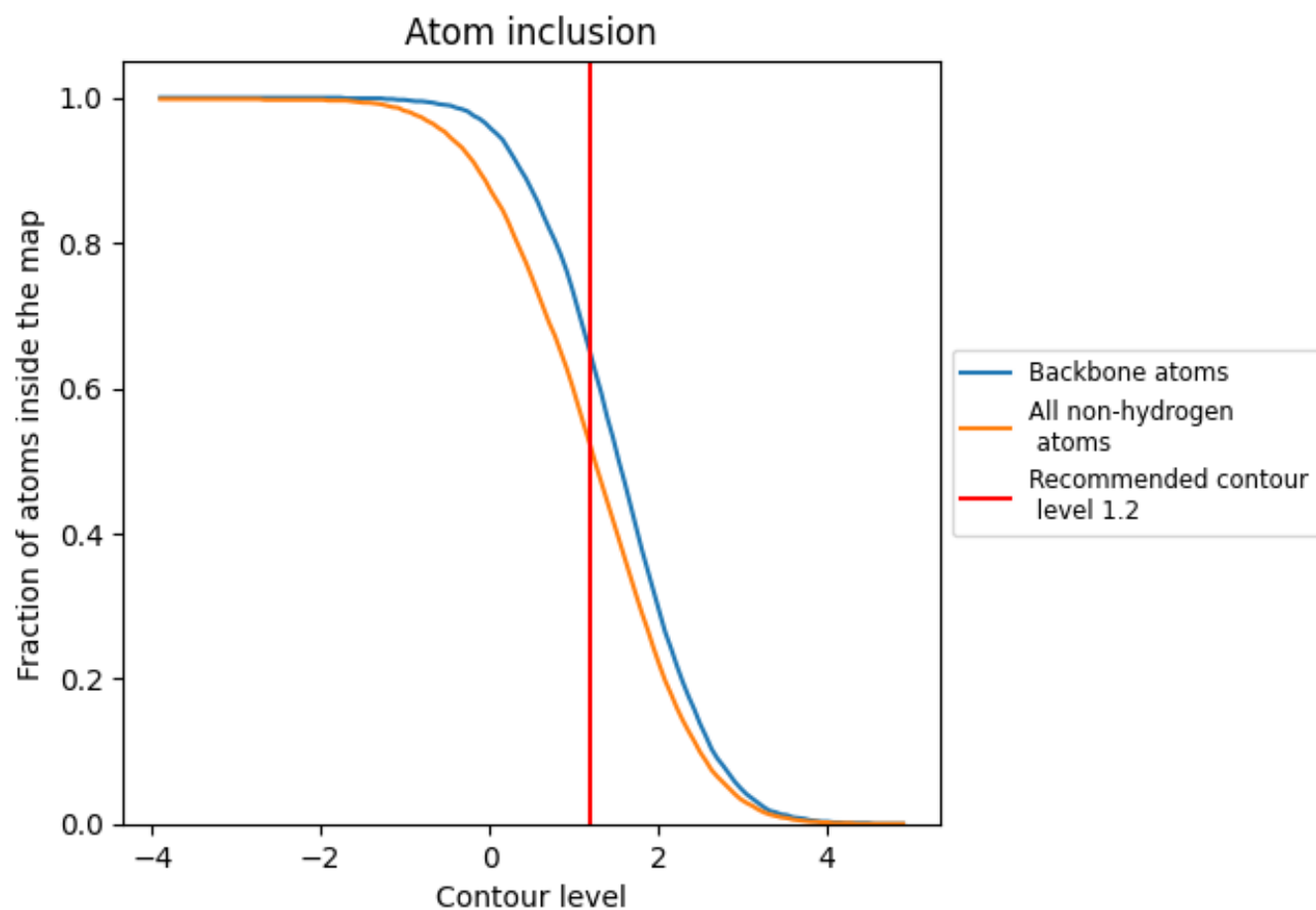
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 52% 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 (1.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5200	0.1050
A	0.5320	0.1070
B	0.4930	0.0950
C	0.4880	0.0980
D	0.5340	0.1100
E	0.5530	0.1160

