



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:08 AM UTC

PDB ID : 3DHW / pdb_00003dhw
Title : Crystal structure of methionine importer MetNI
Authors : Rees, D.C.; Kaiser, J.T.; Kadaba, N.S.; Johnson, E.; Lee, A.T.
Deposited on : 2008-06-18
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

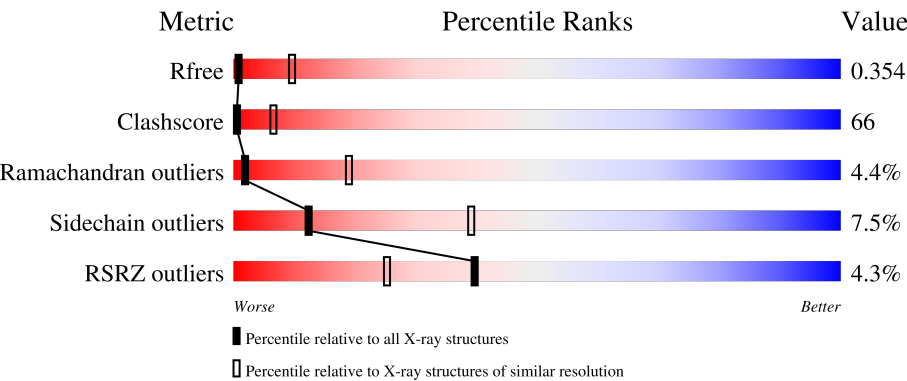
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1131 (3.80-3.60)
Clashscore	190562	1171 (3.80-3.60)
Ramachandran outliers	187476	1129 (3.80-3.60)
Sidechain outliers	187428	1126 (3.80-3.60)
RSRZ outliers	180081	1130 (3.80-3.60)

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

Mol	Chain	Length	Quality of chain
1	A	217	6% 16%47%25%6%6%
1	B	217	5% 18%52%21%•6%
1	E	217	2% 19%55%18%•6%
1	F	217	3% 15%50%26%•6%
2	C	343	3% 21%45%30%•

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Mol	Chain	Length	Quality of chain
2	D	343	4% 31% 49% 16%
2	G	343	5% 28% 56% 15%
2	H	343	5% 30% 50% 18%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16688 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called D-methionine transport system permease protein metI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	203	Total	C	N	O	S	0	0	0
			1520	1014	244	254	8			
1	B	203	Total	C	N	O	S	0	0	0
			1520	1014	244	254	8			
1	E	203	Total	C	N	O	S	0	0	0
			1520	1014	244	254	8			
1	F	203	Total	C	N	O	S	0	0	0
			1520	1014	244	254	8			

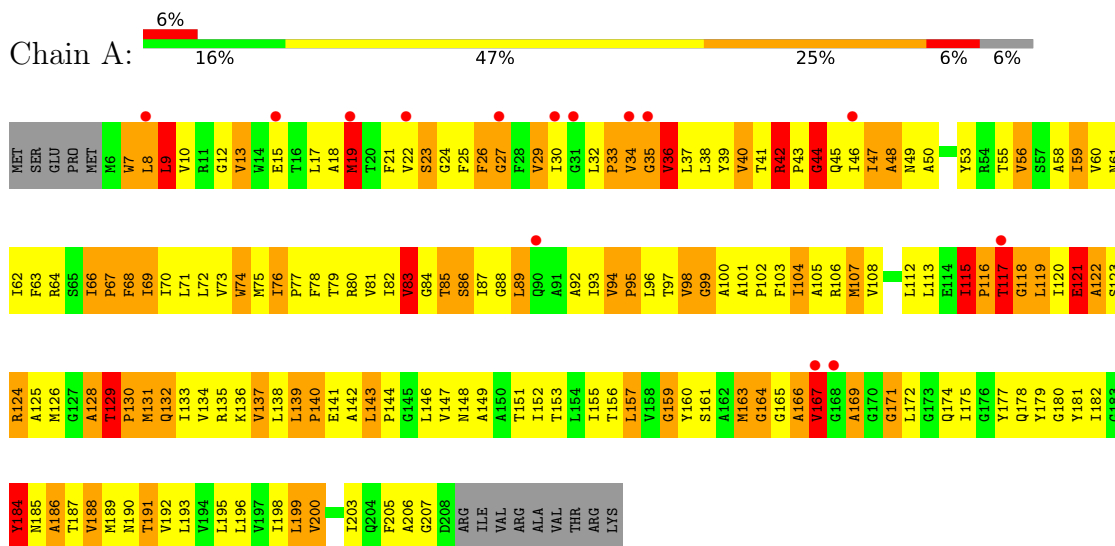
- Molecule 2 is a protein called Methionine import ATP-binding protein metN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	343	Total	C	N	O	S	0	0	0
			2652	1664	467	509	12			
2	D	343	Total	C	N	O	S	0	0	0
			2652	1664	467	509	12			
2	G	343	Total	C	N	O	S	0	0	0
			2652	1664	467	509	12			
2	H	343	Total	C	N	O	S	0	0	0
			2652	1664	467	509	12			

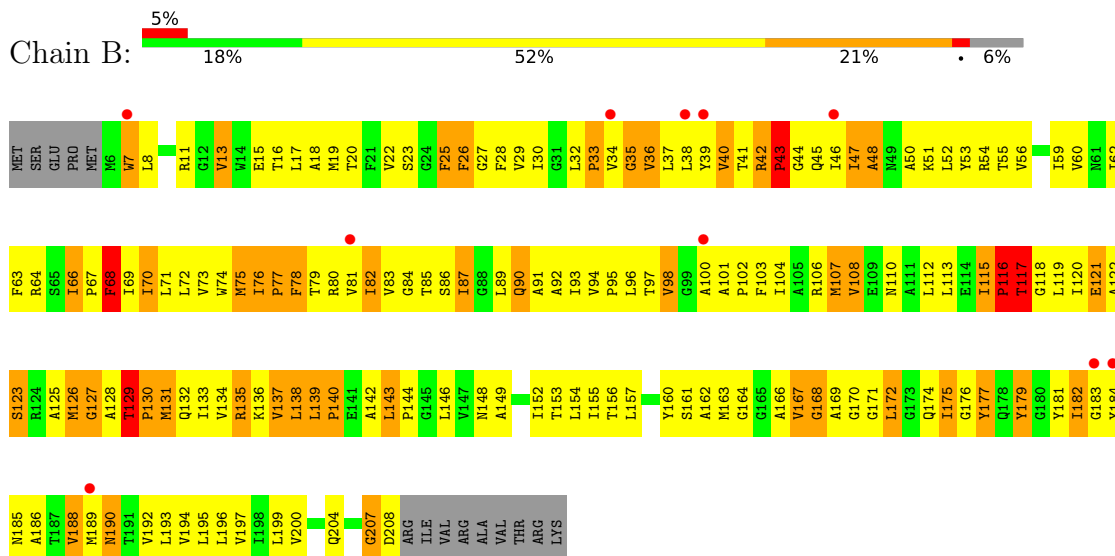
3 Residue-property plots

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

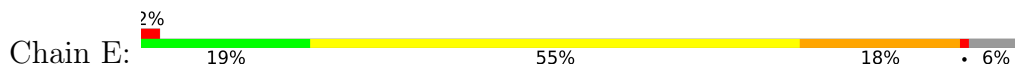
• Molecule 1: D-methionine transport system permease protein metI

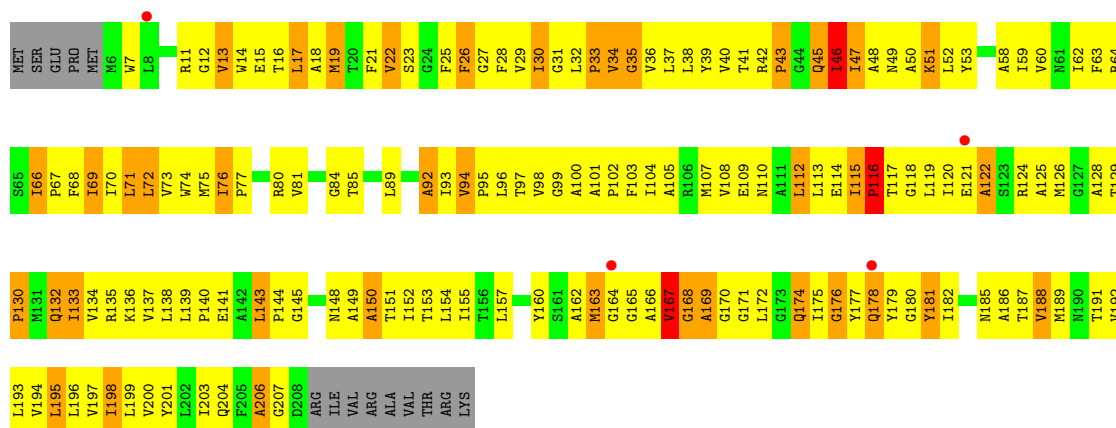


• Molecule 1: D-methionine transport system permease protein metI

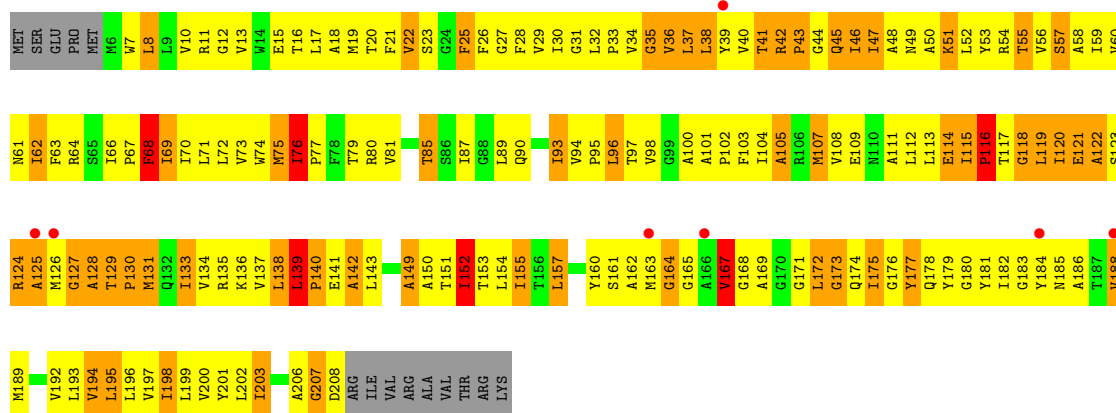
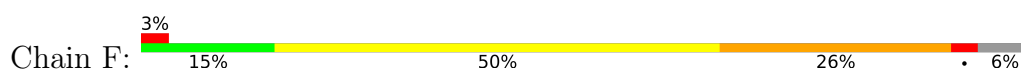


• Molecule 1: D-methionine transport system permease protein metI

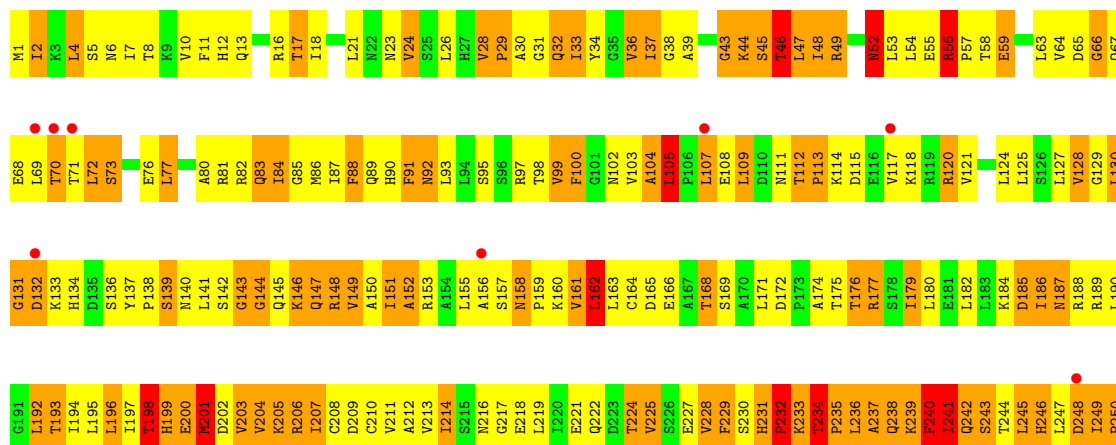
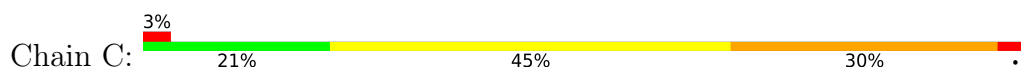


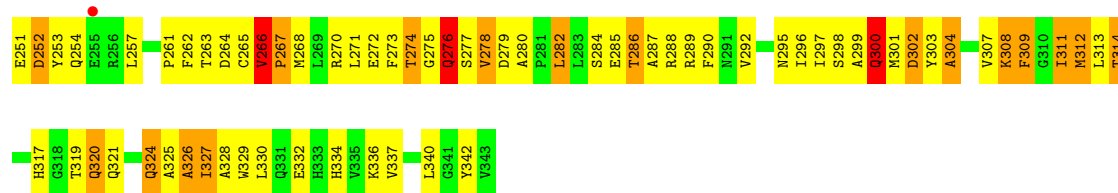


• Molecule 1: D-methionine transport system permease protein metI

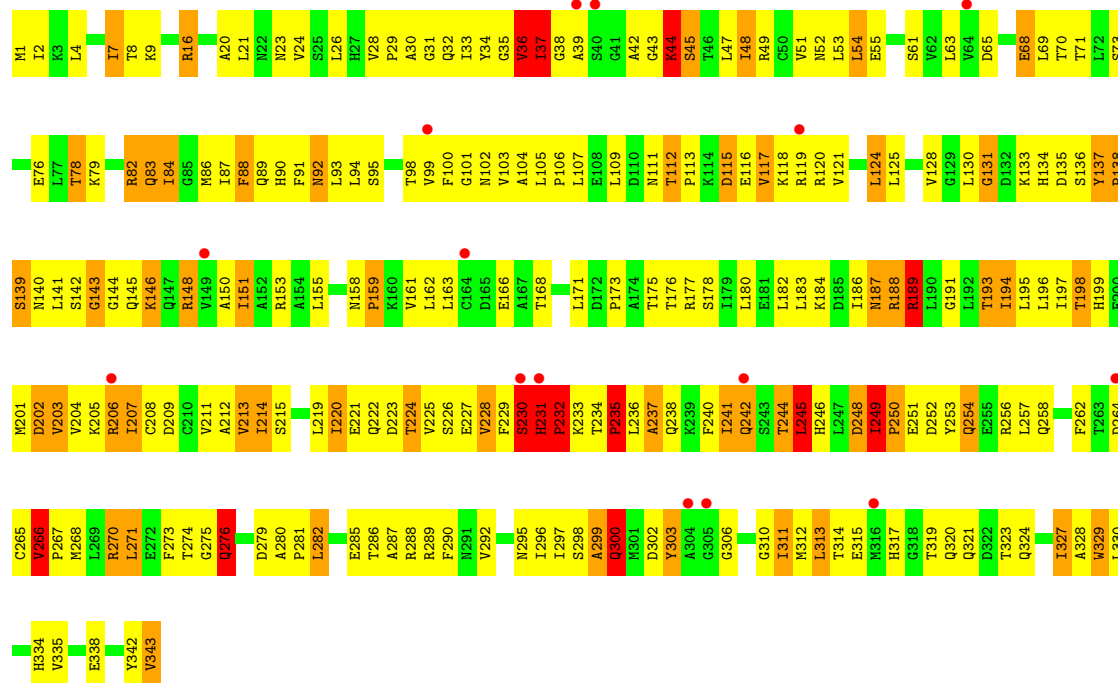


• Molecule 2: Methionine import ATP-binding protein metN

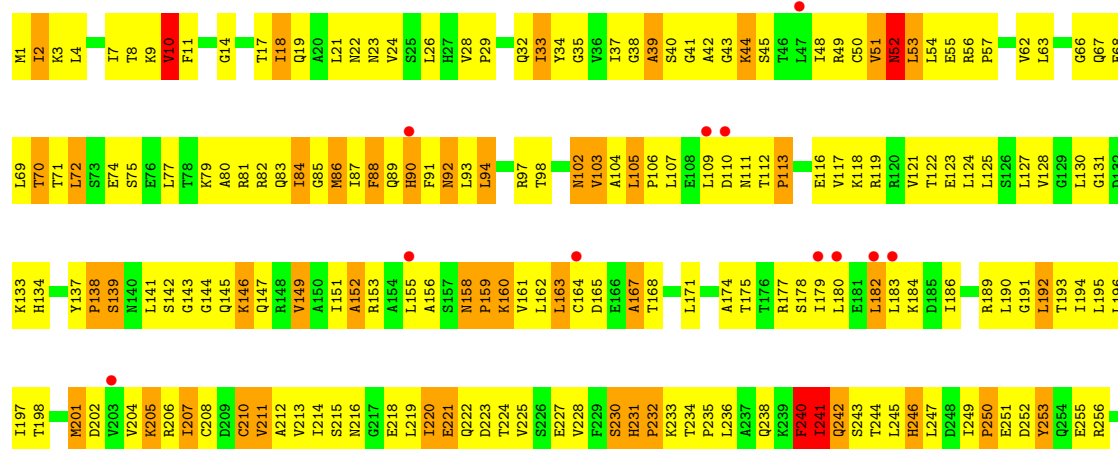


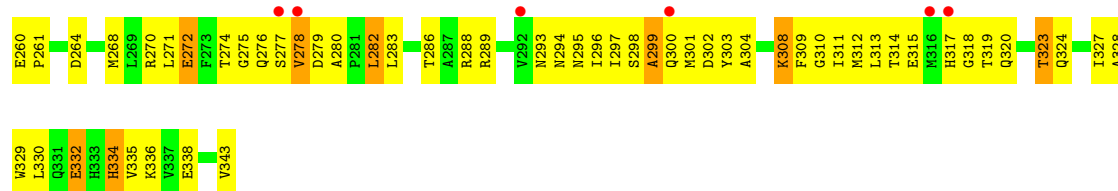


• Molecule 2: Methionine import ATP-binding protein metN

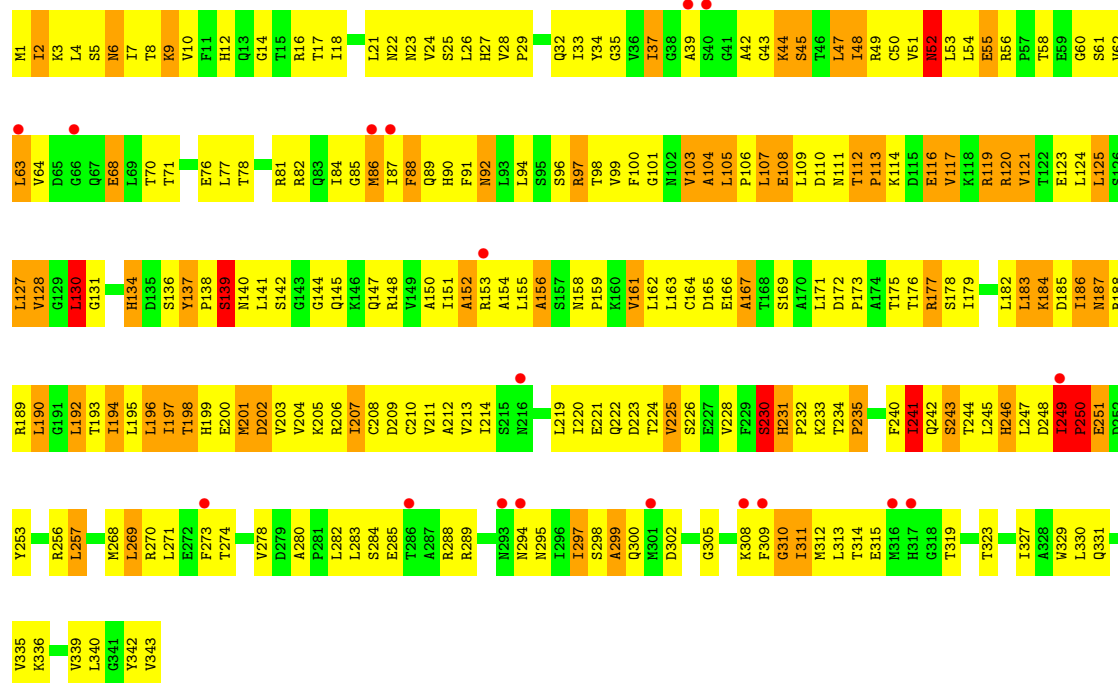


• Molecule 2: Methionine import ATP-binding protein metN





● Molecule 2: Methionine import ATP-binding protein metN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.70Å 165.40Å 289.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.90 – 3.70 39.90 – 3.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (39.90-3.70) 99.5 (39.90-3.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 3.66Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.310 , 0.347 0.319 , 0.354	Depositor DCC
R_{free} test set	5071 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	153.5	Xtriage
Anisotropy	0.575	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 120.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	16688	wwPDB-VP
Average B, all atoms (Å ²)	179.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.48	11/1552 (0.7%)	1.99	55/2122 (2.6%)
1	B	1.18	2/1552 (0.1%)	1.91	53/2122 (2.5%)
1	E	1.11	3/1552 (0.2%)	1.86	50/2122 (2.4%)
1	F	1.50	10/1552 (0.6%)	2.04	68/2122 (3.2%)
2	C	1.82	50/2691 (1.9%)	2.25	148/3647 (4.1%)
2	D	1.35	11/2691 (0.4%)	1.94	99/3647 (2.7%)
2	G	0.97	0/2691	1.76	82/3647 (2.2%)
2	H	1.26	17/2691 (0.6%)	1.87	103/3647 (2.8%)
All	All	1.36	104/16972 (0.6%)	1.96	658/23076 (2.9%)

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	0	3
1	B	0	1
1	E	0	2
2	C	0	2
All	All	0	8

All (104) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	228	VAL	C-O	16.07	1.41	1.23
2	C	201	MET	SD-CE	13.78	2.14	1.79
1	A	137	VAL	CA-C	11.29	1.65	1.52
1	F	115	ILE	CA-C	10.88	1.64	1.52
1	B	76	ILE	CA-CB	9.48	1.58	1.54
2	C	33	ILE	CA-CB	-9.09	1.43	1.54
2	D	311	ILE	CA-CB	-8.86	1.43	1.54
2	C	161	VAL	CA-CB	-8.76	1.43	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	238	GLN	CA-C	-8.69	1.42	1.53
2	C	309	PHE	CD2-CE2	8.50	1.64	1.38
2	C	309	PHE	CD1-CE1	8.36	1.63	1.38
2	C	234	THR	CA-CB	8.22	1.64	1.53
2	C	120	ARG	CA-C	-8.12	1.42	1.52
2	C	240	PHE	N-CA	-8.01	1.35	1.46
2	C	102	ASN	CA-C	-7.88	1.42	1.52
2	H	112	THR	CA-CB	7.84	1.58	1.52
1	F	120	ILE	CA-CB	7.83	1.64	1.54
2	H	249	ILE	CA-CB	7.55	1.58	1.54
2	C	32	GLN	CA-C	-7.48	1.44	1.52
1	A	137	VAL	CA-CB	-7.46	1.46	1.54
2	C	230	SER	CA-C	7.41	1.62	1.52
1	E	163	MET	SD-CE	7.24	1.97	1.79
2	C	24	VAL	CA-CB	-7.24	1.45	1.54
2	C	228	VAL	C-N	7.14	1.43	1.33
2	D	112	THR	CA-CB	7.12	1.58	1.52
1	E	76	ILE	CA-CB	7.10	1.57	1.54
2	C	194	ILE	CA-CB	-7.05	1.46	1.54
2	C	104	ALA	CA-C	6.95	1.61	1.52
1	E	94	VAL	CA-CB	-6.91	1.50	1.54
1	F	203	ILE	CA-CB	-6.86	1.46	1.54
2	C	45	SER	CA-C	6.79	1.61	1.52
2	C	229	PHE	N-CA	6.78	1.54	1.46
1	F	151	THR	CA-C	-6.75	1.44	1.52
2	C	229	PHE	CG-CD2	6.72	1.52	1.38
2	C	179	ILE	CA-CB	-6.60	1.46	1.54
2	C	213	VAL	CA-CB	-6.56	1.46	1.54
1	A	19	MET	CG-SD	6.52	1.97	1.80
2	C	33	ILE	N-CA	6.37	1.54	1.46
2	H	121	VAL	CA-CB	-6.37	1.47	1.54
1	F	138	LEU	CA-C	6.35	1.60	1.52
2	C	292	VAL	CA-CB	-6.35	1.45	1.55
1	A	94	VAL	CA-CB	6.34	1.57	1.54
2	H	78	THR	CA-CB	6.24	1.63	1.53
2	C	204	VAL	CA-C	6.23	1.60	1.52
2	D	151	ILE	CA-CB	6.18	1.62	1.54
2	H	128	VAL	CA-CB	-6.00	1.46	1.54
2	C	168	THR	C-O	5.95	1.31	1.24
2	C	39	ALA	CA-CB	5.94	1.62	1.53
2	D	205	LYS	CD-CE	5.91	1.70	1.52
1	F	76	ILE	CA-CB	5.88	1.57	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	139	LEU	N-CA	-5.84	1.41	1.46
2	C	232	PRO	CA-C	-5.79	1.44	1.52
2	D	214	ILE	CA-CB	-5.79	1.47	1.54
2	C	84	ILE	CA-C	5.78	1.60	1.52
2	D	7	ILE	CA-C	-5.75	1.46	1.53
1	F	195	LEU	CA-C	5.75	1.60	1.52
2	H	176	THR	CA-CB	5.74	1.62	1.53
2	C	324	GLN	C-O	-5.71	1.17	1.24
2	H	207	ILE	N-CA	-5.70	1.41	1.46
2	C	194	ILE	C-O	-5.69	1.17	1.24
1	F	149	ALA	CA-CB	-5.65	1.44	1.53
1	A	67	PRO	CA-C	5.65	1.59	1.52
1	A	146	LEU	CA-C	-5.63	1.45	1.52
2	C	304	ALA	CA-CB	-5.63	1.44	1.53
2	C	46	THR	CA-CB	5.58	1.62	1.53
2	C	266	VAL	CA-CB	5.56	1.59	1.55
2	C	33	ILE	C-O	5.56	1.30	1.24
2	H	120	ARG	CA-C	-5.54	1.45	1.52
2	D	207	ILE	CA-CB	-5.51	1.47	1.54
2	C	327	ILE	CA-CB	5.48	1.61	1.54
2	H	120	ARG	N-CA	-5.43	1.39	1.46
2	C	132	ASP	CA-CB	5.42	1.61	1.53
2	C	240	PHE	CA-C	-5.42	1.45	1.52
2	D	213	VAL	C-O	5.42	1.30	1.24
2	H	194	ILE	C-O	5.40	1.29	1.24
2	H	45	SER	CA-C	5.37	1.59	1.52
2	D	213	VAL	CA-CB	-5.34	1.47	1.54
2	H	167	ALA	N-CA	-5.34	1.40	1.46
2	D	244	THR	CA-C	5.30	1.57	1.52
2	C	71	THR	CA-CB	5.29	1.59	1.53
2	C	164	CYS	CA-C	-5.29	1.46	1.52
2	C	234	THR	CA-C	5.28	1.58	1.52
2	C	103	VAL	CA-CB	-5.27	1.47	1.54
2	C	237	ALA	CA-CB	5.27	1.62	1.53
2	C	48	ILE	CA-CB	-5.27	1.46	1.54
1	F	10	VAL	C-O	-5.26	1.18	1.24
1	A	19	MET	N-CA	5.25	1.52	1.46
2	H	104	ALA	CA-C	5.25	1.59	1.52
2	C	148	ARG	CA-C	-5.25	1.46	1.52
1	A	56	VAL	CA-CB	5.24	1.61	1.54
2	C	189	ARG	CA-C	-5.24	1.45	1.52
2	H	192	LEU	CA-C	-5.22	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	28	VAL	CA-CB	-5.21	1.48	1.53
2	C	229	PHE	C-O	-5.19	1.17	1.24
2	D	206	ARG	C-O	-5.19	1.18	1.24
1	F	115	ILE	N-CA	5.18	1.52	1.46
1	B	162	ALA	CA-CB	-5.18	1.45	1.53
1	A	167	VAL	CA-CB	5.16	1.60	1.54
1	A	166	ALA	CA-C	-5.11	1.46	1.53
2	C	225	VAL	CA-CB	-5.07	1.48	1.54
2	H	152	ALA	CA-CB	-5.03	1.45	1.53
2	C	309	PHE	CA-C	5.02	1.59	1.52
2	H	137	TYR	C-N	5.02	1.39	1.33
2	H	207	ILE	CA-CB	-5.02	1.48	1.54

All (658) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	230	SER	N-CA-C	21.37	133.93	111.07
1	F	115	ILE	CA-C-N	17.33	141.50	119.84
1	F	115	ILE	C-N-CA	17.33	141.50	119.84
1	A	10	VAL	N-CA-C	17.27	126.77	110.53
2	G	320	GLN	N-CA-C	14.87	127.49	111.28
2	C	289	ARG	N-CA-C	14.73	127.41	111.36
1	E	115	ILE	CA-C-N	14.71	138.22	119.84
1	E	115	ILE	C-N-CA	14.71	138.22	119.84
2	C	44	LYS	N-CA-C	-14.10	95.34	112.54
2	G	251	GLU	N-CA-C	13.61	126.12	111.28
2	D	251	GLU	N-CA-C	13.60	126.11	111.28
1	A	143	LEU	CA-C-N	-13.55	104.37	119.28
1	A	143	LEU	C-N-CA	-13.55	104.37	119.28
2	D	136	SER	N-CA-C	13.34	125.83	111.28
1	B	50	ALA	N-CA-C	13.20	128.96	112.86
1	A	9	LEU	N-CA-C	13.10	125.56	111.28
2	H	187	ASN	N-CA-C	12.69	124.65	111.07
2	C	234	THR	N-CA-C	-12.51	95.59	112.35
1	E	178	GLN	N-CA-C	-12.20	97.98	111.28
1	A	8	LEU	N-CA-C	12.12	124.49	111.28
1	F	116	PRO	N-CA-C	12.03	137.25	112.47
2	G	133	LYS	N-CA-C	11.93	124.29	111.28
2	C	91	PHE	N-CA-C	11.74	124.15	111.36
2	C	136	SER	N-CA-C	11.67	124.08	111.36
2	C	115	ASP	N-CA-C	11.66	124.07	111.36
2	D	88	PHE	N-CA-C	11.63	128.23	109.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	66	ILE	N-CA-C	11.52	120.23	108.95
2	C	88	PHE	N-CA-C	11.47	127.29	109.52
2	C	237	ALA	N-CA-C	-11.42	99.33	113.38
1	E	46	ILE	N-CA-C	11.38	122.21	110.72
2	H	44	LYS	N-CA-C	-11.30	98.60	112.38
2	H	130	LEU	N-CA-C	-11.29	92.13	109.96
2	G	278	VAL	N-CA-C	-11.18	99.22	110.62
2	G	111	ASN	N-CA-C	11.16	123.53	111.36
2	G	205	LYS	N-CA-C	11.13	123.42	111.28
1	F	87	ILE	N-CA-C	11.09	121.93	110.62
2	C	132	ASP	N-CA-C	-10.97	99.33	111.28
1	A	119	LEU	N-CA-C	-10.96	99.33	111.28
2	C	111	ASN	N-CA-C	10.96	123.31	111.36
1	F	43	PRO	N-CA-C	-10.88	101.14	114.20
2	G	117	VAL	N-CA-C	-10.86	100.00	110.42
2	H	201	MET	N-CA-C	10.77	124.10	111.71
1	A	68	PHE	N-CA-C	10.75	122.57	111.07
2	H	47	LEU	N-CA-C	10.72	122.54	111.07
2	D	220	ILE	N-CA-C	10.70	121.20	110.82
2	G	332	GLU	N-CA-C	-10.47	99.86	111.28
2	C	241	ILE	N-CA-C	-10.47	92.89	108.17
2	G	44	LYS	N-CA-C	-10.46	99.77	112.54
2	H	128	VAL	N-CA-C	10.43	121.25	110.72
2	D	70	THR	N-CA-C	-10.40	91.94	108.90
2	G	289	ARG	N-CA-C	10.32	122.61	111.36
2	G	308	LYS	N-CA-C	10.28	125.14	110.23
2	G	323	THR	N-CA-C	10.28	122.56	111.36
1	A	24	GLY	N-CA-C	-10.27	100.40	112.73
2	G	168	THR	N-CA-C	10.16	125.98	113.17
2	D	88	PHE	CA-C-N	10.16	133.89	120.28
2	D	88	PHE	C-N-CA	10.16	133.89	120.28
1	A	45	GLN	N-CA-C	-10.14	100.23	111.28
2	C	92	ASN	N-CA-C	10.13	125.41	111.74
2	C	309	PHE	N-CA-C	-10.13	96.22	110.50
1	B	35	GLY	N-CA-C	-10.11	102.08	115.32
2	D	189	ARG	N-CA-C	10.07	122.01	111.14
2	C	186	ILE	N-CA-C	-10.06	98.52	111.09
1	F	127	GLY	N-CA-C	-10.05	98.92	114.10
1	A	23	SER	N-CA-C	10.03	122.22	111.28
2	D	139	SER	N-CA-C	10.01	122.19	111.28
1	B	115	ILE	CA-C-N	9.99	132.33	119.84
1	B	115	ILE	C-N-CA	9.99	132.33	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	146	LYS	N-CA-C	-9.93	100.45	111.28
2	H	246	HIS	N-CA-C	9.82	122.06	111.36
2	C	239	LYS	CA-C-O	9.79	134.52	120.51
2	C	216	ASN	N-CA-C	9.69	124.76	111.39
1	E	129	THR	N-CA-C	-9.67	91.92	108.94
2	C	45	SER	N-CA-C	-9.66	100.75	111.28
2	D	248	ASP	N-CA-C	9.65	123.18	111.40
2	C	46	THR	N-CA-C	9.64	123.16	111.40
2	C	228	VAL	O-C-N	9.61	133.15	122.68
1	F	120	ILE	N-CA-C	-9.60	101.02	110.72
1	B	66	ILE	CA-C-N	9.53	131.75	119.84
1	B	66	ILE	C-N-CA	9.53	131.75	119.84
1	F	115	ILE	N-CA-C	9.49	129.38	108.88
2	C	278	VAL	N-CA-C	-9.35	101.08	110.62
2	D	133	LYS	N-CA-C	9.27	121.46	111.36
2	H	134	HIS	N-CA-C	9.26	123.89	112.59
2	G	201	MET	N-CA-C	9.22	121.33	111.28
1	F	76	ILE	CB-CA-C	-9.21	104.95	113.70
2	G	118	LYS	N-CA-C	9.20	121.39	111.36
2	C	47	LEU	N-CA-C	9.17	121.27	111.28
2	C	105	LEU	CA-C-N	-9.17	108.38	119.84
2	C	105	LEU	C-N-CA	-9.17	108.38	119.84
2	H	88	PHE	N-CA-C	9.15	123.70	109.52
2	H	103	VAL	N-CA-C	-9.11	101.33	110.62
1	B	7	TRP	N-CA-C	-9.09	101.45	111.36
2	G	92	ASN	N-CA-C	9.05	124.19	111.52
2	G	192	LEU	N-CA-C	-9.02	94.62	108.96
2	D	231	HIS	CA-C-N	8.99	131.07	119.84
2	D	231	HIS	C-N-CA	8.99	131.07	119.84
2	C	242	GLN	N-CA-C	-8.93	101.48	112.38
1	F	125	ALA	N-CA-C	-8.91	100.55	111.33
2	G	88	PHE	N-CA-C	8.89	123.62	110.46
2	C	238	GLN	N-CA-C	-8.88	99.36	111.87
1	F	167	VAL	N-CA-C	8.86	127.78	109.34
2	D	90	HIS	N-CA-C	-8.85	95.97	109.41
2	D	36	VAL	N-CA-C	-8.84	93.23	107.28
2	H	198	THR	N-CA-C	8.83	122.92	109.23
2	H	119	ARG	CB-CA-C	-8.80	97.41	110.96
2	C	189	ARG	N-CA-C	8.79	124.69	113.88
2	C	276	GLN	N-CA-C	-8.76	97.46	111.04
2	D	101	GLY	N-CA-C	8.73	123.21	112.73
2	H	289	ARG	N-CA-C	8.72	120.87	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	241	ILE	N-CA-C	-8.71	101.73	110.62
1	F	139	LEU	N-CA-C	-8.71	101.35	113.45
1	E	72	LEU	N-CA-C	8.70	120.84	111.36
1	F	22	VAL	N-CA-C	8.69	119.50	110.72
2	G	146	LYS	N-CA-C	-8.69	101.81	111.28
2	H	225	VAL	N-CA-C	8.69	119.48	110.62
2	H	90	HIS	N-CA-C	-8.67	96.16	109.95
2	H	193	THR	N-CA-C	-8.67	94.77	108.90
1	A	35	GLY	N-CA-C	-8.64	100.91	115.34
1	E	35	GLY	N-CA-C	-8.64	102.36	112.73
2	C	206	ARG	N-CA-C	8.60	120.66	111.28
2	H	202	ASP	N-CA-C	-8.58	101.92	111.28
1	B	81	VAL	N-CA-C	8.58	119.39	110.72
2	D	289	ARG	N-CA-C	8.56	120.69	111.36
2	H	114	LYS	N-CA-C	8.54	120.59	111.28
1	B	117	THR	N-CA-C	8.51	128.93	110.80
2	D	44	LYS	N-CA-C	-8.44	102.00	111.71
2	G	230	SER	N-CA-C	8.42	128.74	110.80
2	G	216	ASN	N-CA-C	8.42	122.99	111.54
2	C	235	PRO	N-CA-C	-8.42	97.82	111.21
2	C	49	ARG	N-CA-C	8.40	120.44	111.28
2	D	89	GLN	N-CA-CB	-8.40	97.78	110.12
2	H	121	VAL	N-CA-C	-8.38	102.37	110.42
2	H	97	ARG	N-CA-C	8.36	123.10	110.14
2	G	250	PRO	N-CA-C	-8.34	95.28	112.47
2	C	80	ALA	N-CA-C	8.23	120.33	111.36
2	C	66	GLY	N-CA-C	8.22	125.89	115.21
2	C	149	VAL	N-CA-C	-8.22	102.24	110.62
2	D	83	GLN	N-CA-C	8.21	120.31	111.36
2	D	252	ASP	N-CA-C	-8.21	102.82	112.92
1	E	76	ILE	CB-CA-C	-8.21	105.90	113.70
2	C	198	THR	N-CA-C	8.20	121.34	108.79
2	D	161	VAL	N-CA-C	8.20	119.64	108.17
2	H	205	LYS	N-CA-C	8.19	119.83	111.07
1	A	85	THR	N-CA-C	-8.17	102.88	113.17
2	G	214	ILE	N-CA-C	8.17	119.55	108.11
2	G	227	GLU	N-CA-C	8.17	122.03	112.72
2	G	143	GLY	N-CA-C	8.12	121.92	112.50
2	C	228	VAL	CA-C-N	8.10	137.01	121.54
2	C	228	VAL	C-N-CA	8.10	137.01	121.54
1	F	122	ALA	N-CA-C	-8.09	102.43	111.82
1	E	162	ALA	N-CA-C	-8.07	102.48	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	152	ALA	N-CA-C	-8.06	102.50	111.28
1	E	121	GLU	N-CA-C	-8.04	102.72	112.54
1	A	29	VAL	N-CA-C	8.03	118.81	110.62
2	G	220	ILE	N-CA-C	-8.01	102.73	110.42
1	F	38	LEU	N-CA-C	-7.98	102.58	111.28
1	A	12	GLY	N-CA-C	7.97	122.97	112.77
1	B	107	MET	N-CA-C	-7.96	102.61	111.28
2	C	214	ILE	N-CA-C	7.93	119.33	107.75
1	A	143	LEU	N-CA-C	7.92	124.46	113.45
1	B	51	LYS	N-CA-C	7.91	122.42	111.74
2	D	54	LEU	N-CA-C	-7.91	102.66	111.28
1	E	163	MET	CB-CG-SD	-7.90	88.99	112.70
1	E	163	MET	N-CA-C	7.90	119.89	111.28
1	A	68	PHE	CB-CA-C	-7.89	98.49	110.88
1	E	30	ILE	N-CA-C	7.88	122.02	113.43
2	H	92	ASN	N-CA-C	7.88	121.92	111.28
2	D	249	ILE	CA-C-N	-7.85	111.26	120.13
2	D	249	ILE	C-N-CA	-7.85	111.26	120.13
2	C	282	LEU	N-CA-C	7.84	119.83	111.28
2	D	227	GLU	N-CA-C	7.83	119.90	111.36
2	G	231	HIS	CA-C-N	7.82	129.62	119.84
2	G	231	HIS	C-N-CA	7.82	129.62	119.84
2	H	158	ASN	CA-C-N	7.81	129.04	119.98
2	H	158	ASN	C-N-CA	7.81	129.04	119.98
1	A	7	TRP	CB-CA-C	-7.81	97.83	110.79
1	A	132	GLN	N-CA-C	-7.81	102.77	111.28
1	E	117	THR	N-CA-C	7.80	119.78	111.28
1	B	148	ASN	N-CA-C	-7.80	102.78	111.28
1	B	98	VAL	N-CA-C	7.79	118.59	110.72
1	A	122	ALA	N-CA-C	-7.79	103.66	113.01
2	C	33	ILE	CB-CA-C	-7.78	100.32	110.98
1	F	67	PRO	N-CA-C	7.75	122.87	110.40
1	F	195	LEU	N-CA-C	-7.74	102.85	111.28
2	H	63	LEU	N-CA-C	7.73	121.01	108.41
1	F	129	THR	CA-C-N	-7.72	110.19	119.84
1	F	129	THR	C-N-CA	-7.72	110.19	119.84
2	C	218	GLU	N-CA-C	-7.70	97.58	109.52
2	C	179	ILE	N-CA-C	7.69	118.49	110.72
2	D	143	GLY	N-CA-C	7.62	122.13	112.83
1	E	66	ILE	CB-CA-C	-7.62	102.66	110.89
2	D	270	ARG	N-CA-C	-7.61	96.32	108.73
1	B	123	SER	N-CA-C	-7.60	103.27	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	178	SER	N-CA-C	7.60	119.57	111.28
1	E	26	PHE	N-CA-C	7.60	123.23	113.88
2	D	116	GLU	N-CA-C	-7.60	103.89	113.01
1	F	55	THR	N-CA-C	7.60	120.67	111.40
2	D	295	ASN	N-CA-C	-7.57	96.18	108.52
2	H	127	LEU	N-CA-C	7.53	119.48	111.28
1	F	124	ARG	N-CA-CB	7.52	121.28	110.16
2	C	56	ARG	CA-C-N	7.51	129.23	119.84
2	C	56	ARG	C-N-CA	7.51	129.23	119.84
2	D	115	ASP	N-CA-C	7.50	124.85	113.61
1	B	156	THR	N-CA-C	-7.49	103.19	111.36
1	B	129	THR	CA-C-N	-7.48	110.49	119.84
1	B	129	THR	C-N-CA	-7.48	110.49	119.84
2	H	120	ARG	N-CA-C	7.47	119.43	111.28
1	B	90	GLN	N-CA-C	-7.47	103.14	111.28
2	C	249	ILE	N-CA-C	-7.46	103.40	112.35
2	C	231	HIS	CA-C-N	7.46	129.16	119.84
2	C	231	HIS	C-N-CA	7.46	129.16	119.84
2	C	274	THR	N-CA-C	-7.45	100.49	110.55
2	C	89	GLN	N-CA-C	-7.44	103.17	111.28
2	G	282	LEU	N-CA-C	7.43	119.38	111.28
2	D	187	ASN	N-CA-C	7.40	118.98	111.07
2	D	188	ARG	CB-CA-C	-7.39	99.28	110.88
2	H	251	GLU	N-CA-C	7.39	122.42	113.41
2	D	334	HIS	N-CA-C	7.38	121.80	111.92
2	C	134	HIS	N-CA-C	7.37	120.31	110.88
1	A	169	ALA	N-CA-C	7.35	120.28	109.69
2	H	207	ILE	N-CA-C	7.34	120.88	113.47
2	D	206	ARG	N-CA-C	7.34	119.28	111.28
1	A	76	ILE	CB-CA-C	-7.31	106.75	113.70
2	C	295	ASN	N-CA-C	-7.31	96.81	108.73
2	D	146	LYS	N-CA-C	-7.29	103.33	111.28
1	B	7	TRP	CA-C-N	7.26	130.01	120.28
1	B	7	TRP	C-N-CA	7.26	130.01	120.28
2	C	67	GLN	CA-C-N	-7.24	113.14	122.77
2	C	67	GLN	C-N-CA	-7.24	113.14	122.77
2	D	254	GLN	N-CA-C	7.24	120.03	111.71
2	D	100	PHE	N-CA-C	-7.23	103.40	111.28
2	G	74	GLU	N-CA-C	7.23	118.80	111.07
1	B	76	ILE	CB-CA-C	-7.21	106.85	113.70
2	D	264	ASP	N-CA-C	7.21	121.33	111.39
2	D	119	ARG	N-CA-C	7.18	118.75	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	250	PRO	N-CA-C	-7.17	97.69	112.47
2	G	303	TYR	N-CA-C	7.14	120.15	108.52
2	G	51	VAL	N-CA-C	7.12	117.26	110.42
2	G	152	ALA	N-CA-C	7.12	118.69	111.07
1	E	206	ALA	N-CA-C	-7.12	103.52	111.28
2	C	233	LYS	CA-C-N	7.11	128.60	119.78
2	C	233	LYS	C-N-CA	7.11	128.60	119.78
2	D	295	ASN	CA-C-N	-7.11	113.79	122.90
2	D	295	ASN	C-N-CA	-7.11	113.79	122.90
2	C	227	GLU	CA-C-N	-7.11	111.92	122.01
2	C	227	GLU	C-N-CA	-7.11	111.92	122.01
2	C	55	GLU	N-CA-C	-7.06	99.47	110.42
2	D	16	ARG	N-CA-C	7.05	120.95	109.59
1	A	186	ALA	N-CA-C	-7.05	103.78	112.38
2	C	319	THR	CA-C-N	-7.04	110.85	120.28
2	C	319	THR	C-N-CA	-7.04	110.85	120.28
2	C	326	ALA	N-CA-C	7.03	118.59	111.07
2	H	295	ASN	CA-C-N	-7.01	113.78	123.10
2	H	295	ASN	C-N-CA	-7.01	113.78	123.10
2	G	17	THR	N-CA-C	-6.98	97.52	108.90
1	B	121	GLU	N-CA-C	-6.96	103.69	111.28
2	H	42	ALA	N-CA-C	6.95	118.86	111.28
2	C	88	PHE	CA-C-N	6.95	129.59	120.28
2	C	88	PHE	C-N-CA	6.95	129.59	120.28
2	G	207	ILE	N-CA-C	6.95	119.87	113.20
1	E	94	VAL	N-CA-C	6.93	121.33	112.67
2	D	321	GLN	N-CA-C	6.92	118.91	111.36
2	D	198	THR	N-CA-C	6.91	119.94	109.23
2	G	158	ASN	CA-C-N	6.91	128.47	119.84
2	G	158	ASN	C-N-CA	6.91	128.47	119.84
1	F	42	ARG	CA-C-N	-6.91	112.45	120.12
1	F	42	ARG	C-N-CA	-6.91	112.45	120.12
1	B	54	ARG	CB-CA-C	-6.89	100.06	110.88
2	C	334	HIS	CA-C-N	-6.89	114.17	123.12
2	C	334	HIS	C-N-CA	-6.89	114.17	123.12
1	E	34	VAL	N-CA-C	-6.85	105.67	112.17
1	F	41	THR	N-CA-C	-6.84	103.82	111.28
2	C	327	ILE	N-CA-C	-6.84	103.81	110.72
2	G	242	GLN	N-CA-C	-6.83	102.24	111.54
1	B	82	ILE	N-CA-C	6.83	117.62	110.72
1	B	162	ALA	N-CA-C	-6.82	103.07	111.33
2	H	9	LYS	N-CA-C	6.82	120.29	108.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	300	GLN	N-CA-C	6.82	119.43	109.07
1	B	138	LEU	N-CA-C	6.82	118.36	111.07
2	D	230	SER	N-CA-C	6.81	125.31	110.80
2	G	75	SER	N-CA-C	6.81	118.78	111.36
1	B	87	ILE	N-CA-C	6.80	119.56	112.83
1	E	22	VAL	N-CA-C	-6.80	103.90	110.42
2	G	72	LEU	N-CA-C	6.80	119.69	108.48
1	A	124	ARG	N-CA-C	-6.77	103.90	111.28
2	C	188	ARG	CB-CG-CD	-6.76	95.74	111.30
2	C	334	HIS	N-CA-C	6.76	120.73	111.54
1	F	162	ALA	N-CA-C	-6.75	104.76	112.87
1	A	44	GLY	N-CA-C	-6.75	97.19	113.18
2	G	240	PHE	N-CA-C	6.74	118.71	111.36
1	F	136	LYS	N-CA-C	6.73	118.62	111.28
2	C	100	PHE	N-CA-C	-6.73	103.87	111.07
2	C	248	ASP	N-CA-CB	-6.72	100.54	110.49
2	D	242	GLN	N-CA-C	-6.71	105.09	113.28
2	G	102	ASN	N-CA-C	6.70	118.24	111.07
2	G	70	THR	N-CA-C	-6.70	98.98	108.96
2	H	311	ILE	N-CA-C	6.69	117.51	107.75
2	G	314	THR	N-CA-C	6.67	118.90	108.96
1	A	27	GLY	N-CA-C	-6.67	104.39	113.27
1	A	121	GLU	N-CA-C	-6.67	105.01	113.01
2	H	249	ILE	N-CA-C	-6.67	104.35	112.35
2	H	107	LEU	N-CA-C	-6.66	104.03	111.28
2	H	249	ILE	CA-C-N	6.65	128.16	119.84
2	H	249	ILE	C-N-CA	6.65	128.16	119.84
1	F	173	GLY	N-CA-C	-6.64	104.72	112.83
2	H	68	GLU	N-CA-C	-6.62	98.45	109.24
2	H	188	ARG	CB-CA-C	-6.61	99.82	110.79
2	G	178	SER	N-CA-C	6.60	118.27	111.14
2	G	198	THR	N-CA-C	6.58	119.43	109.23
2	G	86	MET	N-CA-C	6.58	120.24	109.06
1	B	143	LEU	N-CA-C	6.55	121.77	113.25
2	H	310	GLY	N-CA-C	6.55	122.68	111.15
2	C	133	LYS	N-CA-C	6.55	121.44	113.38
2	H	231	HIS	CA-C-N	6.55	128.03	119.84
2	H	231	HIS	C-N-CA	6.55	128.03	119.84
2	D	205	LYS	CD-CE-NZ	6.54	132.83	111.90
2	D	248	ASP	CB-CA-C	-6.54	99.80	110.79
2	G	23	ASN	N-CA-C	6.52	120.39	111.39
1	E	45	GLN	N-CA-C	6.52	124.69	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	156	ALA	N-CA-C	6.50	118.36	111.28
1	F	105	ALA	N-CA-C	6.49	118.01	111.07
2	G	94	LEU	N-CA-C	-6.49	100.23	109.96
2	D	329	TRP	N-CA-C	-6.48	104.13	111.07
2	G	104	ALA	N-CA-C	6.48	118.34	111.28
2	H	86	MET	N-CA-C	6.46	119.00	109.24
1	A	128	ALA	N-CA-C	6.46	118.32	111.28
2	C	240	PHE	CA-C-N	6.44	132.09	122.75
2	C	240	PHE	C-N-CA	6.44	132.09	122.75
2	G	39	ALA	N-CA-C	6.44	118.30	111.28
2	C	162	LEU	CA-C-N	-6.44	113.83	122.72
2	C	162	LEU	C-N-CA	-6.44	113.83	122.72
1	A	26	PHE	N-CA-C	6.43	121.79	113.88
2	C	194	ILE	N-CA-C	6.42	117.16	108.17
2	C	199	HIS	N-CA-C	6.41	118.34	111.36
1	B	154	LEU	N-CA-C	6.39	118.33	111.36
1	B	135	ARG	N-CA-C	-6.39	104.32	111.28
1	A	99	GLY	N-CA-C	-6.39	105.07	112.73
2	D	194	ILE	N-CA-C	6.39	117.97	108.46
1	A	163	MET	N-CA-C	-6.38	104.37	111.71
1	F	142	ALA	N-CA-C	6.38	120.90	113.18
1	E	143	LEU	N-CA-C	6.37	121.53	113.25
1	F	52	LEU	N-CA-C	6.37	118.23	111.28
2	D	315	GLU	N-CA-C	-6.37	100.41	109.96
1	B	188	VAL	N-CA-C	6.37	117.37	111.45
1	F	46	ILE	N-CA-C	6.36	118.61	109.51
1	F	154	LEU	N-CA-C	6.36	118.21	111.28
1	F	42	ARG	N-CA-C	6.35	123.85	109.81
2	C	152	ALA	N-CA-C	-6.34	104.28	111.07
2	C	336	LYS	CA-CB-CG	6.34	126.78	114.10
1	E	51	LYS	N-CA-C	-6.34	105.96	113.38
1	E	124	ARG	N-CA-C	-6.33	104.38	111.28
1	E	164	GLY	N-CA-C	-6.31	105.16	112.73
2	H	116	GLU	N-CA-C	6.30	118.15	111.28
2	G	109	LEU	N-CA-C	6.29	118.14	111.28
2	C	17	THR	N-CA-C	-6.29	98.65	108.90
2	G	318	GLY	N-CA-C	6.27	119.05	110.58
2	G	139	SER	N-CA-C	6.25	120.22	112.59
1	E	13	VAL	N-CA-C	-6.25	104.25	110.62
2	C	185	ASP	N-CA-C	6.23	118.07	111.28
2	D	191	GLY	N-CA-C	-6.23	104.14	114.48
2	H	196	LEU	N-CA-C	6.23	119.85	109.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	306	GLY	N-CA-C	6.22	123.30	115.21
2	G	33	ILE	N-CA-C	-6.22	98.91	107.99
2	D	203	VAL	CB-CA-C	-6.21	103.75	112.14
1	A	200	VAL	CB-CA-C	-6.21	104.02	111.97
1	A	115	ILE	CA-C-N	6.21	127.60	119.84
1	A	115	ILE	C-N-CA	6.21	127.60	119.84
2	D	117	VAL	N-CA-C	-6.21	104.46	110.42
1	A	191	THR	N-CA-C	-6.20	104.52	111.28
2	C	104	ALA	N-CA-C	6.19	118.03	111.28
2	G	241	ILE	N-CA-C	6.17	122.18	109.34
2	D	299	ALA	N-CA-C	6.17	117.92	108.42
1	E	133	ILE	N-CA-C	6.16	116.94	110.72
2	D	205	LYS	N-CA-C	6.15	117.98	111.28
1	B	172	LEU	N-CA-C	-6.14	105.05	112.54
1	F	157	LEU	CB-CA-C	-6.14	101.24	110.88
2	D	232	PRO	N-CA-C	6.14	125.11	112.47
1	A	13	VAL	N-CA-C	-6.12	104.54	110.72
1	F	186	ALA	N-CA-C	6.12	118.03	111.36
2	C	240	PHE	O-C-N	6.08	130.68	122.59
1	E	188	VAL	N-CA-C	6.08	116.86	110.72
2	D	237	ALA	CA-C-N	6.07	129.53	120.31
2	D	237	ALA	C-N-CA	6.07	129.53	120.31
2	D	148	ARG	N-CA-C	-6.06	104.67	111.28
2	C	177	ARG	N-CA-CB	6.06	119.13	110.16
2	D	188	ARG	N-CA-C	-6.04	104.60	111.07
2	H	64	VAL	N-CA-C	6.02	116.79	108.12
1	A	94	VAL	CB-CA-C	-6.01	107.99	113.70
1	F	37	LEU	N-CA-C	-6.01	105.71	113.16
2	D	266	VAL	N-CA-C	6.00	121.83	108.88
2	D	51	VAL	N-CA-C	6.00	116.73	110.62
1	E	112	LEU	CA-C-N	5.99	128.30	120.28
1	E	112	LEU	C-N-CA	5.99	128.30	120.28
1	E	71	LEU	N-CA-C	-5.98	104.67	111.07
2	H	137	TYR	N-CA-C	5.98	117.42	109.83
1	A	36	VAL	N-CA-C	-5.96	105.94	112.80
1	B	43	PRO	N-CA-C	-5.96	100.19	112.47
2	D	223	ASP	N-CA-C	5.96	117.20	108.14
2	C	176	THR	CA-C-N	-5.96	111.83	120.29
2	C	176	THR	C-N-CA	-5.96	111.83	120.29
1	A	104	ILE	N-CA-C	5.95	116.73	110.72
1	A	66	ILE	CB-CA-C	-5.95	105.17	111.00
1	F	115	ILE	C-N-CD	-5.94	100.66	125.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	39	ALA	N-CA-C	-5.93	103.11	110.41
2	C	114	LYS	N-CA-C	5.92	117.60	111.03
2	H	139	SER	N-CA-C	5.92	123.41	110.80
2	H	117	VAL	CA-C-N	-5.91	112.75	120.44
2	H	117	VAL	C-N-CA	-5.91	112.75	120.44
1	E	186	ALA	N-CA-C	-5.91	106.03	113.18
2	C	144	GLY	N-CA-C	-5.91	105.64	112.73
1	A	171	GLY	N-CA-C	5.89	124.90	112.17
2	G	134	HIS	N-CA-C	5.88	119.77	112.59
2	G	264	ASP	N-CA-C	5.88	119.51	111.39
1	B	25	PHE	CB-CA-C	-5.87	101.66	110.88
1	F	57	SER	N-CA-C	-5.87	105.38	112.54
1	B	13	VAL	CB-CA-C	-5.86	104.22	112.14
2	C	128	VAL	CB-CA-C	-5.86	102.77	112.26
1	B	190	ASN	N-CA-C	-5.86	104.90	111.28
1	F	194	VAL	N-CA-C	5.85	116.03	110.42
2	C	239	LYS	CA-C-N	5.84	132.69	121.54
2	C	239	LYS	C-N-CA	5.84	132.69	121.54
2	G	103	VAL	N-CA-C	-5.84	104.82	110.72
1	F	184	TYR	N-CA-C	-5.83	101.77	110.23
2	C	52	ASN	N-CA-C	-5.83	105.75	112.92
1	E	17	LEU	N-CA-C	-5.83	104.93	111.28
2	C	196	LEU	N-CA-C	5.82	119.57	110.32
1	F	177	TYR	N-CA-C	5.81	117.29	111.07
2	D	117	VAL	CA-C-N	-5.80	112.50	120.28
2	D	117	VAL	C-N-CA	-5.80	112.50	120.28
1	A	34	VAL	N-CA-C	-5.80	106.66	112.17
2	D	68	GLU	N-CA-CB	5.80	120.08	110.63
2	C	245	LEU	N-CA-C	5.79	117.67	111.36
1	E	204	GLN	N-CA-C	5.79	117.59	111.28
1	B	204	GLN	N-CA-C	5.77	117.24	111.07
2	D	23	ASN	N-CA-C	5.77	119.20	111.24
1	A	107	MET	N-CA-C	-5.76	105.00	111.28
1	F	93	ILE	N-CA-C	5.76	116.49	110.62
2	H	144	GLY	N-CA-C	-5.74	105.84	112.73
2	C	43	GLY	CA-C-O	5.72	125.55	119.03
2	C	59	GLU	N-CA-C	5.71	117.76	109.07
2	C	312	MET	N-CA-C	5.71	117.81	108.55
2	D	78	THR	N-CA-C	-5.70	105.06	111.28
2	C	84	ILE	N-CA-CB	-5.70	104.28	111.46
2	H	107	LEU	O-C-N	5.69	128.16	122.12
2	D	92	ASN	N-CA-C	5.68	119.41	111.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	303	TYR	N-CA-C	-5.68	99.48	108.73
2	H	76	GLU	CA-C-N	5.67	127.88	120.28
2	H	76	GLU	C-N-CA	5.67	127.88	120.28
1	B	183	GLY	N-CA-C	5.67	119.53	112.73
2	D	202	ASP	N-CA-C	-5.66	105.11	111.28
1	E	195	LEU	N-CA-C	-5.66	105.02	111.07
2	C	231	HIS	N-CA-C	5.66	118.80	109.58
1	F	107	MET	N-CA-C	-5.65	105.12	111.28
2	G	272	GLU	N-CA-C	-5.65	99.81	109.24
2	G	338	GLU	CA-C-N	-5.64	115.53	122.93
2	G	338	GLU	C-N-CA	-5.64	115.53	122.93
2	G	2	ILE	N-CA-C	5.64	116.53	107.73
2	D	276	GLN	CB-CA-C	-5.64	99.20	110.42
2	C	240	PHE	N-CA-CB	-5.63	100.97	110.49
2	C	207	ILE	N-CA-C	5.63	119.16	113.47
2	C	188	ARG	CA-CB-CG	5.62	125.35	114.10
2	C	4	LEU	N-CA-C	-5.62	100.02	109.07
1	E	94	VAL	CB-CA-C	-5.62	108.37	113.70
2	D	237	ALA	N-CA-C	-5.61	105.26	111.71
1	B	26	PHE	N-CA-C	5.61	118.32	111.82
2	C	129	GLY	CA-C-N	-5.60	115.07	122.85
2	C	129	GLY	C-N-CA	-5.60	115.07	122.85
2	C	320	GLN	N-CA-C	5.58	117.37	111.28
2	D	37	ILE	N-CA-C	-5.58	99.74	108.95
1	F	22	VAL	CB-CA-C	-5.58	104.52	112.22
2	G	253	TYR	N-CA-C	-5.58	105.28	111.36
2	C	319	THR	N-CA-C	-5.58	103.02	110.55
2	H	231	HIS	N-CA-C	5.58	118.23	110.20
1	E	28	PHE	N-CA-C	5.57	117.36	111.28
2	G	53	LEU	N-CA-C	5.57	119.11	111.54
2	C	264	ASP	N-CA-C	5.56	119.24	111.74
2	H	55	GLU	N-CA-C	-5.53	99.89	108.90
2	G	10	VAL	N-CA-C	-5.52	99.68	107.75
2	C	202	ASP	N-CA-C	-5.52	105.26	111.28
1	F	138	LEU	CA-CB-CG	-5.52	96.98	116.30
2	G	334	HIS	N-CA-C	5.52	119.19	111.74
2	H	271	LEU	N-CA-C	-5.52	99.74	108.73
2	H	269	LEU	N-CA-C	5.51	118.20	109.50
2	C	286	THR	N-CA-C	-5.50	105.44	111.82
1	F	62	ILE	N-CA-C	-5.50	105.17	110.72
2	H	16	ARG	N-CA-C	5.50	118.05	108.76
1	B	44	GLY	N-CA-C	-5.49	100.16	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	29	VAL	CA-C-N	-5.49	115.24	122.16
1	A	29	VAL	C-N-CA	-5.49	115.24	122.16
1	E	115	ILE	N-CA-C	5.49	120.74	108.88
1	A	89	LEU	N-CA-C	5.49	117.26	111.28
2	C	143	GLY	CA-C-N	-5.49	113.89	119.98
2	C	143	GLY	C-N-CA	-5.49	113.89	119.98
1	F	11	ARG	CB-CA-C	-5.49	101.68	110.79
2	C	91	PHE	CA-C-N	-5.49	114.45	122.19
2	C	91	PHE	C-N-CA	-5.49	114.45	122.19
1	F	93	ILE	CB-CA-C	-5.48	104.74	112.14
2	C	71	THR	N-CA-C	-5.47	100.19	108.67
2	G	149	VAL	N-CA-C	-5.47	105.04	110.62
2	H	297	ILE	N-CA-C	5.46	116.24	110.72
1	E	176	GLY	N-CA-C	-5.46	105.79	112.77
1	F	138	LEU	N-CA-C	5.46	120.81	113.72
2	C	107	LEU	N-CA-C	-5.45	105.34	111.28
2	C	302	ASP	N-CA-C	-5.45	100.45	108.79
2	D	207	ILE	N-CA-C	5.45	120.67	109.34
2	H	197	ILE	O-C-N	-5.43	117.39	123.26
2	G	211	VAL	N-CA-C	5.43	116.48	108.45
2	C	188	ARG	CB-CA-C	-5.42	101.79	110.79
2	C	36	VAL	N-CA-C	-5.42	100.52	108.11
1	B	116	PRO	N-CA-C	5.42	123.63	112.47
2	G	221	GLU	N-CA-C	5.41	117.62	109.23
2	D	224	THR	N-CA-C	-5.41	102.87	110.50
1	F	81	VAL	N-CA-C	5.41	116.19	110.72
2	D	297	ILE	N-CA-C	5.41	115.61	110.42
2	H	186	ILE	N-CA-C	-5.41	104.33	111.09
2	H	308	LYS	N-CA-CB	5.40	117.99	109.83
2	G	105	LEU	N-CA-C	5.40	120.09	112.75
1	E	150	ALA	N-CA-C	-5.40	105.40	111.28
2	H	23	ASN	N-CA-C	5.39	118.83	111.39
2	C	252	ASP	N-CA-C	-5.39	105.41	111.28
2	H	103	VAL	CB-CA-C	5.38	119.41	112.14
2	D	118	LYS	N-CA-CB	5.38	118.03	110.12
2	D	302	ASP	CA-C-N	-5.38	115.62	122.77
2	D	302	ASP	C-N-CA	-5.38	115.62	122.77
2	C	238	GLN	CA-C-N	-5.37	111.29	121.54
2	C	238	GLN	C-N-CA	-5.37	111.29	121.54
1	A	98	VAL	N-CA-C	5.36	116.13	110.72
2	H	108	GLU	CA-C-N	5.35	127.89	120.29
2	H	108	GLU	C-N-CA	5.35	127.89	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	82	ARG	N-CA-C	-5.35	105.45	111.28
1	F	124	ARG	N-CA-C	5.35	117.19	111.36
2	H	314	THR	N-CA-C	5.35	117.31	109.24
2	G	163	LEU	N-CA-C	5.34	117.95	109.24
1	F	131	MET	CA-C-N	5.34	127.44	120.28
1	F	131	MET	C-N-CA	5.34	127.44	120.28
2	G	324	GLN	N-CA-CB	5.34	117.97	110.12
2	C	314	THR	N-CA-C	5.33	117.09	109.14
1	F	172	LEU	N-CA-C	-5.33	105.47	111.28
1	A	146	LEU	N-CA-C	5.33	117.17	111.36
2	H	206	ARG	N-CA-C	5.32	117.16	111.36
1	A	74	TRP	N-CA-C	-5.32	105.48	111.28
2	C	169	SER	N-CA-C	5.32	117.08	111.28
1	F	37	LEU	N-CA-CB	5.32	118.58	110.44
1	F	114	GLU	N-CA-C	-5.31	105.49	111.28
1	B	108	VAL	CB-CA-C	-5.31	105.17	111.97
1	F	133	ILE	CA-C-N	-5.31	113.19	120.46
1	F	133	ILE	C-N-CA	-5.31	113.19	120.46
1	E	129	THR	CA-C-N	5.30	126.47	119.84
1	E	129	THR	C-N-CA	5.30	126.47	119.84
1	B	179	TYR	N-CA-C	5.30	117.97	111.82
2	H	92	ASN	N-CA-CB	-5.30	103.36	111.74
2	H	184	LYS	CB-CA-C	-5.30	102.00	110.79
1	E	128	ALA	N-CA-C	5.30	117.44	109.23
2	G	182	LEU	N-CA-C	-5.30	105.51	111.28
2	C	207	ILE	CA-C-N	-5.29	114.26	122.09
2	C	207	ILE	C-N-CA	-5.29	114.26	122.09
2	G	167	ALA	N-CA-C	-5.28	105.93	112.38
2	H	51	VAL	CB-CA-C	-5.28	105.01	112.14
2	D	327	ILE	CB-CA-C	-5.28	105.02	112.14
2	G	160	LYS	N-CA-CB	-5.28	103.57	110.59
1	B	194	VAL	N-CA-C	-5.27	105.39	110.72
2	H	136	SER	N-CA-C	5.26	117.01	111.28
1	F	124	ARG	CB-CG-CD	-5.26	99.21	111.30
1	E	195	LEU	CA-CB-CG	5.25	134.68	116.30
2	H	315	GLU	CA-C-N	-5.25	115.40	123.07
2	H	315	GLU	C-N-CA	-5.25	115.40	123.07
2	C	83	GLN	N-CA-C	5.25	117.00	111.28
1	F	164	GLY	N-CA-C	-5.25	106.43	112.73
1	E	92	ALA	N-CA-C	5.24	117.08	111.36
1	F	35	GLY	N-CA-C	-5.24	106.31	113.27
2	H	70	THR	N-CA-C	-5.22	100.38	108.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	206	ARG	CA-C-N	-5.21	116.35	122.14
2	H	206	ARG	C-N-CA	-5.21	116.35	122.14
1	F	121	GLU	N-CA-CB	-5.21	102.45	110.01
1	B	75	MET	CB-CA-C	5.21	120.26	110.63
2	D	82	ARG	N-CA-C	-5.20	105.61	111.28
2	H	234	THR	CA-C-N	5.20	126.34	119.84
2	H	234	THR	C-N-CA	5.20	126.34	119.84
2	C	289	ARG	CA-C-N	-5.20	114.37	122.37
2	C	289	ARG	C-N-CA	-5.20	114.37	122.37
2	G	23	ASN	CA-C-N	-5.19	116.75	123.19
2	G	23	ASN	C-N-CA	-5.19	116.75	123.19
2	H	1	MET	CA-C-N	-5.19	115.77	122.99
2	H	1	MET	C-N-CA	-5.19	115.77	122.99
1	F	152	ILE	CA-C-N	-5.19	113.33	120.28
1	F	152	ILE	C-N-CA	-5.19	113.33	120.28
1	A	157	LEU	N-CA-CB	5.18	117.74	110.12
2	C	192	LEU	N-CA-C	5.18	117.95	110.28
2	H	176	THR	N-CA-C	-5.18	105.63	111.28
2	D	250	PRO	N-CA-C	-5.18	102.10	110.55
2	G	52	ASN	CA-C-N	5.18	129.48	122.07
2	G	52	ASN	C-N-CA	5.18	129.48	122.07
2	D	300	GLN	N-CA-C	5.18	116.71	108.79
2	H	178	SER	N-CA-C	5.17	117.00	111.36
1	A	159	GLY	N-CA-C	-5.17	106.53	112.73
2	C	187	ASN	CB-CA-C	-5.17	102.77	110.88
2	H	120	ARG	CA-C-N	-5.17	114.05	120.56
2	H	120	ARG	C-N-CA	-5.17	114.05	120.56
2	D	205	LYS	CA-C-N	-5.17	113.36	120.28
2	D	205	LYS	C-N-CA	-5.17	113.36	120.28
2	C	139	SER	N-CA-C	5.16	121.80	110.80
1	A	59	ILE	CB-CA-C	-5.16	105.10	112.22
1	F	116	PRO	CA-N-CD	-5.16	104.78	112.00
2	C	308	LYS	CB-CA-C	-5.15	101.61	110.22
2	C	243	SER	CA-C-N	-5.15	113.44	120.44
2	C	243	SER	C-N-CA	-5.15	113.44	120.44
1	E	174	GLN	N-CA-C	5.14	119.54	113.16
2	D	282	LEU	N-CA-C	5.14	116.57	111.07
2	C	99	VAL	CG1-CB-CG2	-5.14	99.50	110.80
2	C	237	ALA	CA-C-O	5.14	125.01	119.15
2	D	311	ILE	N-CA-C	5.14	115.30	108.11
2	H	58	THR	N-CA-C	5.13	116.56	111.07
1	F	48	ALA	N-CA-C	5.13	118.47	111.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	188	VAL	CB-CA-C	-5.13	105.22	112.14
2	H	308	LYS	CA-CB-CG	5.13	124.35	114.10
2	H	117	VAL	N-CA-C	-5.12	105.39	110.62
2	D	271	LEU	N-CA-C	-5.11	100.19	108.52
1	A	206	ALA	N-CA-C	-5.11	105.71	111.28
1	E	167	VAL	N-CA-C	5.10	119.95	109.34
2	D	193	THR	N-CA-C	-5.10	101.39	109.76
1	B	78	PHE	N-CA-C	5.10	116.84	111.28
1	B	127	GLY	N-CA-C	-5.09	104.41	112.66
2	H	51	VAL	N-CA-C	5.09	115.81	110.62
2	H	52	ASN	N-CA-C	-5.09	106.66	112.92
2	C	203	VAL	CB-CA-C	-5.08	105.47	111.97
2	C	6	ASN	CA-C-N	-5.08	116.03	122.37
2	C	6	ASN	C-N-CA	-5.08	116.03	122.37
2	H	45	SER	N-CA-CB	-5.07	102.66	110.12
1	E	122	ALA	N-CA-C	-5.07	106.36	112.54
2	D	338	GLU	CA-C-N	-5.07	116.53	123.12
2	D	338	GLU	C-N-CA	-5.07	116.53	123.12
1	F	119	LEU	N-CA-C	5.06	116.88	111.36
2	H	125	LEU	CB-CG-CD2	-5.06	95.52	110.70
2	H	294	ASN	N-CA-C	5.06	117.69	109.24
2	H	308	LYS	CB-CA-C	-5.06	101.32	109.72
1	B	110	ASN	N-CA-C	5.06	116.87	111.36
2	G	246	HIS	N-CA-C	5.05	118.70	112.54
2	H	225	VAL	CB-CA-C	-5.05	105.33	112.14
2	G	197	ILE	N-CA-C	5.04	115.23	108.17
1	A	157	LEU	CB-CA-C	-5.04	102.43	110.79
1	E	28	PHE	CA-C-N	-5.04	114.11	120.56
1	E	28	PHE	C-N-CA	-5.04	114.11	120.56
2	C	213	VAL	N-CA-C	-5.03	100.51	107.80
1	B	84	GLY	N-CA-C	5.03	118.76	112.73
2	H	177	ARG	CB-CA-C	-5.03	102.99	110.88
1	B	186	ALA	N-CA-C	-5.02	105.81	111.28
2	H	230	SER	N-CA-C	5.02	121.48	110.80
1	A	80	ARG	CB-CA-C	-5.01	102.46	110.79
2	C	146	LYS	O-C-N	5.01	127.43	122.12
2	D	245	LEU	N-CA-C	5.01	116.82	111.36
1	B	207	GLY	N-CA-C	5.01	118.74	112.73
1	B	131	MET	N-CA-C	5.01	116.43	111.07
1	A	199	LEU	N-CA-C	-5.01	105.82	111.28
2	C	77	LEU	N-CA-C	-5.01	105.82	111.28
2	H	161	VAL	CB-CA-C	-5.01	103.22	110.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	23	ASN	CA-C-N	-5.00	116.63	122.93
2	D	23	ASN	C-N-CA	-5.00	116.63	122.93

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	179	TYR	Sidechain
1	A	184	TYR	Sidechain
1	A	205	PHE	Sidechain
1	B	177	TYR	Sidechain
2	C	198	THR	Mainchain
2	C	309	PHE	Sidechain
1	E	179	TYR	Sidechain
1	E	181	TYR	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1520	0	1622	258	0
1	B	1520	0	1622	261	0
1	E	1520	0	1622	264	0
1	F	1520	0	1622	302	0
2	C	2652	0	2705	384	0
2	D	2652	0	2705	317	0
2	G	2652	0	2705	294	0
2	H	2652	0	2705	355	0
All	All	16688	0	17308	2254	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 66.

All (2254) 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)
2:C:201:MET:CE	2:C:201:MET:SD	2.14	1.34
1:A:126:MET:HE2	2:C:153:ARG:HD2	1.24	1.16
1:E:94:VAL:HG23	1:E:95:PRO:HD3	1.22	1.15
1:F:126:MET:SD	1:F:129:THR:HA	1.87	1.13
2:D:31:GLY:H	2:D:193:THR:HG22	1.08	1.12
1:B:72:LEU:HD22	1:B:95:PRO:HB2	1.28	1.08
1:E:75:MET:HG2	1:E:95:PRO:HB3	1.15	1.08
2:H:52:ASN:HD21	2:H:54:LEU:HG	1.12	1.08
2:H:223:ASP:HB3	2:H:228:VAL:HG22	1.34	1.08
2:D:33:ILE:HG12	2:D:194:ILE:HD11	1.31	1.07
2:D:36:VAL:HG12	2:D:214:ILE:HD11	1.36	1.06
1:F:94:VAL:HG23	1:F:95:PRO:HD3	1.33	1.04
2:C:44:LYS:HB2	2:C:197:ILE:HD11	1.34	1.04
2:C:200:GLU:HB3	2:C:239:LYS:HE2	1.39	1.03
2:C:247:LEU:HD21	2:C:298:SER:HB2	1.40	1.03
2:C:64:VAL:HG11	2:C:84:ILE:HD12	1.41	1.03
2:D:48:ILE:HD13	2:D:48:ILE:N	1.72	1.01
1:A:71:LEU:HG	1:A:75:MET:HE2	1.37	1.01
2:D:168:THR:HB	2:D:176:THR:HG23	1.38	1.01
2:D:240:PHE:O	2:D:242:GLN:N	1.92	1.01
2:D:48:ILE:CD1	2:D:197:ILE:HG12	1.92	1.00
1:B:69:ILE:HD11	1:B:163:MET:HB3	1.38	1.00
1:E:180:GLY:HA3	1:F:73:VAL:HG13	1.41	1.00
2:D:36:VAL:HG12	2:D:214:ILE:CD1	1.91	0.99
1:F:164:GLY:HA2	1:F:169:ALA:HB3	1.43	0.99
2:C:87:ILE:HG22	2:C:88:PHE:H	1.22	0.99
2:H:63:LEU:HB2	2:H:68:GLU:HG2	1.45	0.98
1:A:185:ASN:HB2	1:A:188:VAL:HG22	1.45	0.98
1:F:100:ALA:O	1:F:104:ILE:HG13	1.64	0.98
2:H:171:LEU:HD22	2:H:175:THR:HG21	1.44	0.98
2:G:300:GLN:HA	2:H:297:ILE:O	1.63	0.97
1:E:193:LEU:HD23	1:F:70:ILE:HG13	1.46	0.97
1:F:19:MET:HB3	1:F:157:LEU:HD11	1.45	0.97
1:E:38:LEU:HB2	1:E:112:LEU:HD13	1.44	0.97
1:F:69:ILE:HG23	1:F:163:MET:HE2	1.47	0.96
1:B:69:ILE:HD11	1:B:163:MET:HE3	1.47	0.96
1:A:130:PRO:HG2	1:A:131:MET:H	1.30	0.95
1:A:126:MET:CE	2:C:153:ARG:HD2	1.96	0.95
1:F:101:ALA:HA	1:F:104:ILE:HD11	1.48	0.95
2:D:48:ILE:HD12	2:D:197:ILE:HG12	1.46	0.95
2:D:48:ILE:HD13	2:D:48:ILE:H	1.23	0.94
2:C:214:ILE:HD11	2:C:219:LEU:HD23	1.48	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:TRP:O	1:B:77:PRO:HD2	1.65	0.94
1:E:40:VAL:HA	1:E:47:ILE:HD11	1.49	0.94
2:H:77:LEU:HD21	2:H:81:ARG:HH21	1.29	0.93
2:D:43:GLY:H	2:D:44:LYS:NZ	1.64	0.93
1:B:127:GLY:HA3	2:D:109:LEU:HD12	1.51	0.93
2:D:128:VAL:HG23	2:D:130:LEU:H	1.33	0.93
1:F:188:VAL:O	1:F:192:VAL:HG23	1.69	0.93
2:H:245:LEU:HD23	2:H:313:LEU:HG	1.50	0.92
2:C:241:ILE:HG13	2:C:300:GLN:HB2	1.50	0.92
2:D:4:LEU:HD22	2:D:7:ILE:HD11	1.51	0.92
1:B:172:LEU:HD11	1:B:195:LEU:HD21	1.51	0.92
2:C:246:HIS:HA	2:C:249:ILE:HG12	1.51	0.92
1:A:69:ILE:HG21	1:B:163:MET:SD	2.09	0.92
1:E:140:PRO:HA	1:E:143:LEU:HD12	1.51	0.92
2:G:241:ILE:HD11	2:H:248:ASP:HB2	1.49	0.92
1:B:35:GLY:HA3	1:B:108:VAL:HG11	1.52	0.91
2:D:166:GLU:OE2	2:D:199:HIS:HB2	1.70	0.91
2:D:131:GLY:O	2:D:135:ASP:HB2	1.70	0.91
2:D:213:VAL:HG11	2:D:233:LYS:HD2	1.52	0.91
2:C:247:LEU:HD11	2:C:298:SER:HB2	1.53	0.91
2:D:2:ILE:HG23	2:D:28:VAL:HB	1.49	0.91
1:F:104:ILE:HG22	1:F:153:THR:HG21	1.53	0.91
1:A:117:THR:C	1:A:119:LEU:H	1.79	0.90
1:B:107:MET:HE1	1:B:152:ILE:HD11	1.52	0.90
1:B:175:ILE:HG13	1:B:176:GLY:N	1.82	0.90
2:H:52:ASN:ND2	2:H:54:LEU:HG	1.87	0.90
1:B:22:VAL:HG11	1:B:93:ILE:HB	1.52	0.90
2:C:87:ILE:HG22	2:C:88:PHE:N	1.83	0.90
2:D:43:GLY:H	2:D:44:LYS:HZ2	1.13	0.90
2:C:247:LEU:HD11	2:C:298:SER:CB	2.02	0.89
1:E:116:PRO:HB2	1:E:120:ILE:HG12	1.54	0.89
2:H:108:GLU:O	2:H:112:THR:HG22	1.72	0.89
2:C:147:GLN:HE21	2:C:147:GLN:HA	1.38	0.89
2:C:247:LEU:CD2	2:C:298:SER:HB2	2.01	0.89
2:G:52:ASN:HB3	2:G:84:ILE:HD12	1.52	0.89
2:C:161:VAL:HG22	2:C:193:THR:HG22	1.52	0.89
2:H:299:ALA:HB2	2:H:312:MET:HG3	1.55	0.89
1:B:167:VAL:HG13	1:B:168:GLY:H	1.38	0.89
2:D:83:GLN:O	2:D:159:PRO:HB2	1.72	0.89
1:A:193:LEU:HD23	1:B:70:ILE:HD11	1.55	0.89
2:C:4:LEU:HB3	2:C:7:ILE:HD12	1.51	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:ILE:CD1	1:B:163:MET:HE3	2.04	0.88
1:E:63:PHE:HA	1:E:66:ILE:HD12	1.55	0.88
1:E:122:ALA:HB1	2:G:88:PHE:CE2	2.08	0.88
1:E:92:ALA:HB2	1:E:169:ALA:HB3	1.55	0.88
2:G:224:THR:O	2:G:228:VAL:HG23	1.74	0.88
1:B:172:LEU:HD21	1:B:195:LEU:HD23	1.55	0.88
2:D:240:PHE:C	2:D:242:GLN:H	1.81	0.88
2:G:3:LYS:HB3	2:G:63:LEU:HB3	1.54	0.87
2:D:31:GLY:N	2:D:193:THR:HG22	1.90	0.87
2:D:189:ARG:HH21	2:D:189:ARG:HG3	1.39	0.87
2:H:196:LEU:HD21	2:H:203:VAL:HG12	1.56	0.87
1:B:125:ALA:HB2	2:D:54:LEU:HD21	1.55	0.87
2:H:172:ASP:HB2	2:H:173:PRO:HD2	1.56	0.87
1:E:149:ALA:O	1:E:153:THR:HG23	1.74	0.87
1:F:124:ARG:NH2	2:H:85:GLY:HA2	1.89	0.87
2:C:234:THR:HA	2:C:237:ALA:HB3	1.55	0.87
1:A:193:LEU:HD11	1:B:74:TRP:CD1	2.10	0.86
1:F:193:LEU:O	1:F:197:VAL:HG23	1.75	0.86
2:G:128:VAL:HG11	2:G:152:ALA:HB2	1.55	0.86
2:G:49:ARG:HG2	2:G:54:LEU:HD12	1.54	0.86
1:B:119:LEU:HB3	2:D:92:ASN:CG	1.99	0.86
1:F:124:ARG:HB3	1:F:124:ARG:CZ	2.06	0.86
2:G:128:VAL:HG23	2:G:130:LEU:H	1.39	0.86
1:E:75:MET:CG	1:E:95:PRO:HB3	2.04	0.86
2:H:34:TYR:OH	2:H:212:ALA:HB2	1.76	0.86
2:H:223:ASP:HB3	2:H:228:VAL:CG2	2.06	0.86
2:C:105:LEU:O	2:C:109:LEU:HG	1.74	0.85
2:C:171:LEU:HD22	2:C:175:THR:HG21	1.56	0.85
1:E:58:ALA:O	1:E:62:ILE:HG23	1.77	0.85
1:E:16:THR:HG21	1:E:199:LEU:HD11	1.59	0.85
1:F:194:VAL:O	1:F:198:ILE:HG23	1.76	0.85
2:C:34:TYR:CD2	2:C:210:CYS:HB2	2.12	0.84
1:F:103:PHE:O	1:F:107:MET:HG2	1.77	0.84
2:H:249:ILE:HG23	2:H:250:PRO:HD3	1.59	0.84
2:C:125:LEU:HB3	2:C:131:GLY:HA3	1.59	0.84
1:E:188:VAL:O	1:E:192:VAL:HG23	1.77	0.84
2:G:98:THR:HG22	2:G:138:PRO:HB3	1.56	0.84
1:F:33:PRO:O	1:F:36:VAL:HB	1.78	0.84
1:E:174:GLN:HA	1:E:177:TYR:HB3	1.57	0.84
2:C:37:ILE:HD13	2:C:201:MET:HG2	1.60	0.83
2:H:240:PHE:H	2:H:243:SER:HB3	1.40	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:36:VAL:CG1	2:D:214:ILE:HD11	2.08	0.83
1:E:119:LEU:O	1:E:122:ALA:HB3	1.78	0.83
2:H:52:ASN:HD21	2:H:54:LEU:CG	1.92	0.83
1:E:22:VAL:HG12	1:E:26:PHE:HE2	1.44	0.83
1:B:89:LEU:HA	1:B:169:ALA:HB1	1.58	0.83
2:C:36:VAL:HG13	2:C:214:ILE:HD13	1.61	0.83
2:G:83:GLN:O	2:G:159:PRO:HB2	1.77	0.83
2:D:44:LYS:HE2	2:D:45:SER:OG	1.79	0.83
2:D:208:CYS:O	2:D:225:VAL:HG21	1.78	0.82
2:C:231:HIS:HB3	2:C:232:PRO:HD2	1.60	0.82
2:G:8:THR:HG23	2:G:21:LEU:O	1.79	0.82
2:C:236:LEU:HA	2:C:239:LYS:HB2	1.61	0.82
2:D:180:LEU:HA	2:D:183:LEU:HD12	1.59	0.82
2:G:162:LEU:O	2:G:194:ILE:HA	1.79	0.82
2:G:37:ILE:HD11	2:G:236:LEU:HD23	1.62	0.82
1:A:118:GLY:HA2	1:A:121:GLU:HG2	1.62	0.82
1:B:72:LEU:CD2	1:B:95:PRO:HB2	2.09	0.82
2:H:241:ILE:HD12	2:H:242:GLN:N	1.94	0.82
1:B:179:TYR:HB3	1:B:185:ASN:HD22	1.43	0.82
2:D:201:MET:HG3	2:D:236:LEU:O	1.79	0.82
1:E:22:VAL:HG22	1:E:93:ILE:HB	1.62	0.82
1:F:38:LEU:HD22	1:F:112:LEU:HB3	1.61	0.82
2:G:184:LYS:HG3	2:G:207:ILE:HG22	1.62	0.82
1:A:119:LEU:HB3	2:C:92:ASN:OD1	1.80	0.81
2:C:247:LEU:CG	2:C:298:SER:HB2	2.10	0.81
2:H:77:LEU:HD21	2:H:81:ARG:NH2	1.94	0.81
1:E:46:ILE:HG23	1:E:47:ILE:HG12	1.60	0.81
1:F:26:PHE:CD1	1:F:97:THR:HA	2.14	0.81
2:C:303:TYR:HA	2:C:307:VAL:O	1.80	0.81
1:F:124:ARG:NH1	2:H:86:MET:HB3	1.96	0.81
2:H:48:ILE:CG2	2:H:197:ILE:HD11	2.10	0.81
2:H:105:LEU:O	2:H:108:GLU:HB3	1.81	0.81
1:F:126:MET:HA	2:H:109:LEU:HD13	1.63	0.81
2:H:240:PHE:N	2:H:243:SER:HB3	1.96	0.81
1:A:163:MET:SD	1:B:163:MET:HG3	2.20	0.81
2:D:37:ILE:HD13	2:D:236:LEU:HD13	1.63	0.81
1:A:46:ILE:HG13	1:A:135:ARG:HH22	1.46	0.80
1:A:103:PHE:O	1:A:107:MET:HG2	1.81	0.80
2:D:235:PRO:O	2:D:238:GLN:HB2	1.79	0.80
1:A:117:THR:O	1:A:119:LEU:N	2.14	0.80
2:C:161:VAL:HG22	2:C:193:THR:CG2	2.11	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:106:PRO:HA	2:H:109:LEU:HD12	1.62	0.80
1:E:38:LEU:HD22	1:E:112:LEU:HB3	1.61	0.80
2:G:299:ALA:HB2	2:G:312:MET:HA	1.62	0.80
2:H:241:ILE:HG12	2:H:302:ASP:HB2	1.61	0.80
2:H:242:GLN:NE2	2:H:311:ILE:HD13	1.96	0.80
1:F:126:MET:HG2	2:H:109:LEU:HD13	1.61	0.80
1:E:199:LEU:O	1:E:203:ILE:HG12	1.82	0.80
1:F:26:PHE:CD2	1:F:97:THR:HG22	2.16	0.80
2:H:101:GLY:O	2:H:104:ALA:HB3	1.82	0.80
2:C:127:LEU:HD21	2:C:190:LEU:HD11	1.64	0.80
2:C:247:LEU:CD1	2:C:298:SER:HB2	2.10	0.80
2:D:98:THR:HA	2:D:138:PRO:HB3	1.64	0.79
2:D:241:ILE:HG23	2:D:244:THR:OG1	1.82	0.79
2:H:33:ILE:HD12	2:H:207:ILE:O	1.81	0.79
2:C:247:LEU:HD21	2:C:298:SER:CB	2.11	0.79
2:D:33:ILE:HG12	2:D:194:ILE:CD1	2.12	0.79
2:D:220:ILE:HG22	2:D:221:GLU:HG3	1.63	0.79
1:F:26:PHE:CE1	1:F:97:THR:HA	2.17	0.79
2:G:299:ALA:O	2:H:298:SER:HA	1.83	0.79
2:C:214:ILE:CD1	2:C:219:LEU:HD23	2.12	0.79
1:E:22:VAL:HG12	1:E:26:PHE:CE2	2.17	0.79
2:H:33:ILE:HG23	2:H:194:ILE:HD11	1.64	0.79
2:D:33:ILE:HA	2:D:194:ILE:HG13	1.65	0.79
1:B:22:VAL:HG21	1:B:93:ILE:HG21	1.65	0.79
1:B:69:ILE:CD1	1:B:163:MET:HB3	2.13	0.78
2:C:151:ILE:HG13	2:C:152:ALA:N	1.95	0.78
2:H:48:ILE:H	2:H:48:ILE:CD1	1.96	0.78
2:D:241:ILE:HG22	2:D:241:ILE:O	1.82	0.78
1:A:126:MET:HE2	2:C:153:ARG:CD	2.11	0.78
1:E:36:VAL:HG12	1:E:40:VAL:HG23	1.65	0.78
2:D:327:ILE:HG13	2:D:328:ALA:N	1.97	0.78
1:E:15:GLU:O	1:E:19:MET:HE2	1.84	0.78
1:A:67:PRO:O	1:A:70:ILE:HG22	1.83	0.78
2:C:130:LEU:HD13	2:C:148:ARG:HH11	1.47	0.78
2:C:196:LEU:HD12	2:C:197:ILE:H	1.48	0.78
2:C:234:THR:CA	2:C:237:ALA:HB3	2.14	0.78
2:D:95:SER:HA	2:D:139:SER:OG	1.84	0.78
2:C:44:LYS:HB2	2:C:197:ILE:CD1	2.13	0.77
2:D:120:ARG:O	2:D:124:LEU:HD13	1.83	0.77
2:G:125:LEU:HB3	2:G:131:GLY:HA3	1.66	0.77
1:F:46:ILE:HG22	1:F:47:ILE:HG23	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:196:LEU:HD12	2:C:197:ILE:N	1.99	0.77
2:D:198:THR:HG21	2:D:203:VAL:HB	1.64	0.77
2:H:48:ILE:HD13	2:H:48:ILE:N	2.00	0.77
1:E:75:MET:HG2	1:E:95:PRO:CB	2.08	0.77
2:H:128:VAL:HG11	2:H:152:ALA:HB2	1.66	0.77
2:H:241:ILE:HB	2:H:300:GLN:HB3	1.65	0.77
2:H:245:LEU:HG	2:H:298:SER:OG	1.83	0.77
1:F:51:LYS:HB2	1:F:54:ARG:HD2	1.66	0.77
2:G:276:GLN:HE22	2:G:282:LEU:HD11	1.50	0.77
1:B:27:GLY:O	1:B:104:ILE:HD12	1.84	0.77
2:D:103:VAL:O	2:D:106:PRO:HD2	1.84	0.77
1:E:119:LEU:HD13	2:G:90:HIS:HB2	1.65	0.77
2:G:2:ILE:HG23	2:G:28:VAL:HB	1.65	0.77
2:H:91:PHE:HZ	2:H:171:LEU:HD21	1.49	0.77
2:C:238:GLN:O	2:C:240:PHE:N	2.16	0.77
1:E:60:VAL:HG13	1:E:102:PRO:HB2	1.67	0.77
2:C:247:LEU:HD22	2:C:297:ILE:HG22	1.64	0.77
1:E:37:LEU:O	1:E:41:THR:HG23	1.85	0.76
1:F:69:ILE:CG2	1:F:163:MET:HE2	2.14	0.76
2:D:37:ILE:HG12	2:D:38:GLY:N	2.01	0.76
1:F:42:ARG:HD3	1:F:49:ASN:HA	1.65	0.76
1:F:42:ARG:C	1:F:44:GLY:H	1.94	0.76
1:F:107:MET:HE2	1:F:152:ILE:HD11	1.68	0.76
2:D:1:MET:HG3	2:D:30:ALA:HB2	1.66	0.76
1:F:12:GLY:C	1:F:172:LEU:HD11	2.10	0.76
2:G:1:MET:HE1	2:G:160:LYS:O	1.86	0.76
1:E:69:ILE:HG13	1:F:163:MET:SD	2.25	0.76
1:E:165:GLY:HA2	1:E:169:ALA:O	1.86	0.76
1:A:132:GLN:O	1:A:136:LYS:HB3	1.85	0.76
1:B:133:ILE:CG2	2:D:109:LEU:HD22	2.15	0.76
2:C:296:ILE:HA	2:C:314:THR:HG22	1.67	0.76
1:E:180:GLY:CA	1:F:73:VAL:HG13	2.15	0.76
1:B:167:VAL:HG13	1:B:168:GLY:N	1.96	0.76
1:A:94:VAL:HB	1:A:95:PRO:HD3	1.68	0.76
1:B:193:LEU:O	1:B:197:VAL:HG23	1.86	0.76
2:D:241:ILE:HG22	2:D:245:LEU:HD13	1.68	0.76
1:E:43:PRO:HA	1:E:48:ALA:HB3	1.65	0.76
1:E:71:LEU:HD11	1:E:99:GLY:HA2	1.67	0.76
2:G:180:LEU:O	2:G:207:ILE:HG21	1.85	0.75
1:B:134:VAL:O	1:B:137:VAL:HG22	1.85	0.75
2:C:214:ILE:HD11	2:C:219:LEU:CD2	2.17	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:36:VAL:O	2:C:197:ILE:HD12	1.87	0.75
2:C:86:MET:HE3	2:C:163:LEU:HD12	1.67	0.75
1:F:23:SER:HA	1:F:26:PHE:CZ	2.22	0.75
1:B:167:VAL:HG22	1:B:168:GLY:N	2.00	0.75
2:C:87:ILE:CG2	2:C:88:PHE:H	1.98	0.75
2:G:77:LEU:HD21	2:G:81:ARG:NH2	2.01	0.75
1:B:172:LEU:HD23	1:B:192:VAL:HG13	1.67	0.75
2:D:9:LYS:O	2:D:20:ALA:HB3	1.86	0.75
1:F:118:GLY:HA2	1:F:121:GLU:OE2	1.85	0.75
1:B:172:LEU:CD2	1:B:192:VAL:HG13	2.17	0.75
2:D:31:GLY:H	2:D:193:THR:CG2	1.95	0.75
1:B:134:VAL:HA	1:B:137:VAL:HG13	1.67	0.74
2:D:44:LYS:HD3	2:D:44:LYS:H	1.52	0.74
2:D:125:LEU:HB3	2:D:131:GLY:HA3	1.67	0.74
2:G:79:LYS:O	2:G:83:GLN:HG2	1.87	0.74
2:H:249:ILE:CG1	2:H:250:PRO:HD3	2.17	0.74
2:C:270:ARG:HG2	2:C:313:LEU:HD21	1.69	0.74
2:D:234:THR:CG2	2:D:238:GLN:HE21	2.01	0.74
2:G:298:SER:HA	2:H:299:ALA:O	1.88	0.74
1:E:174:GLN:O	1:E:178:GLN:HB2	1.87	0.74
2:C:2:ILE:HG23	2:C:28:VAL:HB	1.69	0.74
2:H:26:LEU:HD11	2:H:34:TYR:CE1	2.23	0.74
1:B:119:LEU:HB3	2:D:92:ASN:ND2	2.03	0.74
2:C:238:GLN:C	2:C:240:PHE:H	1.96	0.74
2:G:183:LEU:HD23	2:G:194:ILE:HD12	1.70	0.74
2:H:49:ARG:HB3	2:H:54:LEU:HB2	1.69	0.74
1:E:62:ILE:HG13	1:E:63:PHE:N	2.01	0.73
1:E:36:VAL:O	1:E:40:VAL:HG23	1.87	0.73
1:E:38:LEU:HD22	1:E:112:LEU:HD22	1.70	0.73
1:F:124:ARG:HD2	2:H:52:ASN:OD1	1.88	0.73
1:A:22:VAL:HG12	1:A:26:PHE:CE2	2.23	0.73
2:C:278:VAL:HA	2:C:308:LYS:HE2	1.70	0.73
1:F:34:VAL:O	1:F:37:LEU:HG	1.87	0.73
2:C:107:LEU:HD22	2:C:120:ARG:HH11	1.54	0.73
1:B:177:TYR:O	1:B:181:TYR:HB3	1.87	0.73
2:C:186:ILE:HB	2:C:190:LEU:HD12	1.70	0.73
2:G:82:ARG:HH21	2:G:110:ASP:HB3	1.54	0.73
2:H:48:ILE:HG21	2:H:197:ILE:HD11	1.70	0.73
1:F:44:GLY:O	1:F:45:GLN:O	2.06	0.73
2:C:201:MET:N	2:C:239:LYS:HD3	2.03	0.72
2:C:241:ILE:HG21	2:C:300:GLN:HG3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:ILE:HG13	1:B:116:PRO:HD2	1.69	0.72
2:C:130:LEU:HD22	2:C:148:ARG:HB2	1.70	0.72
2:C:165:ASP:HA	2:C:197:ILE:HG22	1.72	0.72
2:C:266:VAL:HG21	2:C:317:HIS:HA	1.71	0.72
1:E:19:MET:O	1:E:22:VAL:HB	1.88	0.72
2:H:150:ALA:O	2:H:153:ARG:HB3	1.88	0.72
1:A:68:PHE:HD2	1:A:163:MET:HG3	1.54	0.72
1:A:117:THR:C	1:A:119:LEU:N	2.46	0.72
1:E:189:MET:SD	1:F:73:VAL:HG12	2.28	0.72
2:H:214:ILE:HG12	2:H:219:LEU:HD23	1.70	0.72
1:E:193:LEU:O	1:E:197:VAL:HG23	1.88	0.72
2:C:270:ARG:HA	2:C:313:LEU:HD23	1.71	0.72
1:E:102:PRO:O	1:E:105:ALA:HB3	1.90	0.72
1:E:32:LEU:O	1:E:35:GLY:N	2.19	0.72
1:E:60:VAL:HG13	1:E:102:PRO:CB	2.20	0.72
1:E:196:LEU:HD23	1:E:199:LEU:HD23	1.71	0.72
2:H:283:LEU:HD21	2:H:312:MET:SD	2.29	0.72
2:C:241:ILE:HG13	2:C:300:GLN:CB	2.20	0.72
1:B:92:ALA:HB2	1:B:169:ALA:HB2	1.69	0.72
2:D:98:THR:HA	2:D:138:PRO:CB	2.19	0.72
2:G:302:ASP:OD2	2:H:251:GLU:HG3	1.90	0.72
2:C:201:MET:CE	2:C:201:MET:HB3	2.19	0.72
1:E:94:VAL:CG2	1:E:95:PRO:HD3	2.12	0.72
2:G:223:ASP:HB2	2:G:228:VAL:HG22	1.71	0.72
1:B:37:LEU:HD21	1:B:56:VAL:CG1	2.19	0.71
1:F:179:TYR:O	1:F:185:ASN:HB2	1.90	0.71
2:G:77:LEU:HD21	2:G:81:ARG:CZ	2.20	0.71
2:D:162:LEU:HB3	2:D:194:ILE:HG22	1.71	0.71
1:E:70:ILE:HD12	1:F:192:VAL:HG12	1.72	0.71
2:H:249:ILE:CG2	2:H:250:PRO:HD3	2.19	0.71
2:H:245:LEU:CD2	2:H:311:ILE:HG22	2.19	0.71
2:H:273:PHE:HB2	2:H:310:GLY:O	1.89	0.71
1:F:37:LEU:HD21	1:F:56:VAL:HG11	1.72	0.71
2:G:4:LEU:HD23	2:G:62:VAL:HG13	1.70	0.71
2:H:249:ILE:CB	2:H:250:PRO:HD3	2.20	0.71
1:A:42:ARG:HA	1:A:42:ARG:CZ	2.20	0.71
1:A:180:GLY:HA3	1:B:73:VAL:HG11	1.73	0.71
2:C:248:ASP:HB3	2:C:254:GLN:CG	2.20	0.71
2:H:245:LEU:HD22	2:H:311:ILE:HG22	1.71	0.71
2:H:268:MET:O	2:H:339:VAL:HG13	1.90	0.71
2:C:196:LEU:HD22	2:C:207:ILE:HD11	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:ILE:CG2	1:B:163:MET:SD	2.77	0.71
1:E:172:LEU:O	1:E:175:ILE:HG12	1.90	0.71
1:E:80:ARG:HG3	1:E:85:THR:HG23	1.71	0.71
1:F:45:GLN:HE21	1:F:46:ILE:HG12	1.56	0.71
1:A:75:MET:HE3	1:A:95:PRO:HB3	1.72	0.71
1:F:63:PHE:HA	1:F:66:ILE:HD12	1.71	0.71
2:C:130:LEU:HD21	2:C:145:GLN:HA	1.73	0.71
2:C:234:THR:HG23	2:C:272:GLU:OE1	1.91	0.71
2:C:288:ARG:HG2	2:D:288:ARG:HA	1.73	0.71
2:D:124:LEU:O	2:D:128:VAL:HG13	1.89	0.71
2:C:238:GLN:O	2:C:238:GLN:HG2	1.90	0.70
2:G:268:MET:HE3	2:G:343:VAL:HG22	1.73	0.70
2:D:99:VAL:HG23	2:D:137:TYR:O	1.92	0.70
1:E:46:ILE:O	1:E:47:ILE:HG23	1.90	0.70
1:E:198:ILE:HG13	1:E:199:LEU:N	2.04	0.70
2:H:48:ILE:CD1	2:H:48:ILE:N	2.53	0.70
2:H:84:ILE:HD11	2:H:163:LEU:HD11	1.73	0.70
1:B:22:VAL:HG21	1:B:93:ILE:CG2	2.22	0.70
2:C:214:ILE:CG1	2:C:219:LEU:HD23	2.21	0.70
2:D:163:LEU:HD23	2:D:195:LEU:HB3	1.72	0.70
2:D:248:ASP:C	2:D:249:ILE:O	2.34	0.70
2:G:283:LEU:HD11	2:G:312:MET:SD	2.31	0.70
1:F:124:ARG:HH22	2:H:85:GLY:HA2	1.57	0.70
1:F:164:GLY:CA	1:F:169:ALA:HB3	2.21	0.70
2:G:70:THR:O	2:G:72:LEU:HG	1.92	0.70
2:G:288:ARG:HA	2:H:288:ARG:HG2	1.72	0.70
1:A:124:ARG:HA	1:A:128:ALA:HB3	1.72	0.70
2:D:43:GLY:N	2:D:44:LYS:HZ2	1.89	0.70
2:D:144:GLY:HA2	2:D:175:THR:HG21	1.73	0.70
1:E:30:ILE:C	1:E:33:PRO:HD2	2.16	0.70
1:E:171:GLY:O	1:E:175:ILE:HG23	1.90	0.70
1:F:19:MET:HB3	1:F:157:LEU:CD1	2.21	0.70
2:H:87:ILE:HG23	2:H:147:GLN:NE2	2.06	0.70
2:H:241:ILE:HG12	2:H:302:ASP:CB	2.22	0.70
1:B:8:LEU:H	1:B:8:LEU:HD12	1.57	0.70
2:C:201:MET:H	2:C:239:LYS:HD3	1.55	0.70
2:D:48:ILE:N	2:D:48:ILE:CD1	2.45	0.70
2:D:234:THR:O	2:D:237:ALA:N	2.25	0.70
1:F:42:ARG:C	1:F:44:GLY:N	2.49	0.70
1:A:132:GLN:O	1:A:136:LYS:CB	2.39	0.70
1:B:20:THR:O	1:B:23:SER:HB2	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:269:LEU:CD2	2:H:339:VAL:HG22	2.21	0.70
2:C:244:THR:O	2:C:247:LEU:HG	1.92	0.70
2:C:63:LEU:HB2	2:C:68:GLU:HG2	1.74	0.70
2:G:215:SER:HB3	2:G:220:ILE:HD11	1.74	0.70
2:H:26:LEU:HD11	2:H:34:TYR:CZ	2.26	0.69
1:F:120:ILE:O	1:F:123:SER:HB2	1.93	0.69
1:E:11:ARG:O	1:E:14:TRP:HB3	1.91	0.69
1:A:131:MET:O	1:A:135:ARG:HG2	1.92	0.69
1:B:89:LEU:HA	1:B:169:ALA:CB	2.23	0.69
2:C:290:PHE:CE2	2:C:329:TRP:HB2	2.27	0.69
2:D:37:ILE:HD11	2:D:236:LEU:HD22	1.74	0.69
2:H:249:ILE:HG12	2:H:250:PRO:CD	2.22	0.69
1:E:31:GLY:O	1:E:34:VAL:HG22	1.93	0.69
1:F:35:GLY:C	1:F:37:LEU:H	2.00	0.69
2:C:44:LYS:NZ	2:C:198:THR:O	2.25	0.69
2:D:171:LEU:HD22	2:D:175:THR:HG21	1.75	0.69
1:E:12:GLY:O	1:E:15:GLU:HB2	1.91	0.69
1:B:41:THR:C	1:B:43:PRO:HD3	2.18	0.69
2:D:9:LYS:HE2	2:D:55:GLU:OE1	1.92	0.69
1:E:50:ALA:O	1:E:51:LYS:HG2	1.92	0.69
1:E:59:ILE:O	1:E:62:ILE:HG12	1.93	0.69
1:E:119:LEU:CD1	2:G:90:HIS:HB2	2.22	0.69
1:E:194:VAL:O	1:E:198:ILE:HG23	1.93	0.69
2:G:37:ILE:HD11	2:G:236:LEU:CD2	2.22	0.69
2:H:84:ILE:HD11	2:H:163:LEU:CD1	2.23	0.69
1:A:75:MET:CE	1:A:95:PRO:HB3	2.23	0.69
2:H:47:LEU:O	2:H:50:CYS:HB2	1.91	0.69
1:A:40:VAL:HA	1:A:49:ASN:CB	2.23	0.68
1:B:139:LEU:HB2	1:B:140:PRO:HD3	1.75	0.68
2:C:77:LEU:HD21	2:C:81:ARG:NH2	2.07	0.68
2:D:26:LEU:HD11	2:D:34:TYR:CZ	2.27	0.68
2:D:279:ASP:O	2:D:280:ALA:C	2.36	0.68
1:E:64:ARG:HH12	1:E:103:PHE:HD1	1.38	0.68
1:E:126:MET:HE1	2:G:153:ARG:HG2	1.74	0.68
1:F:122:ALA:HB1	1:F:126:MET:HE2	1.74	0.68
2:G:208:CYS:O	2:G:225:VAL:HG21	1.93	0.68
2:H:121:VAL:HG12	2:H:125:LEU:HD12	1.75	0.68
2:H:199:HIS:ND1	2:H:200:GLU:HG3	2.07	0.68
2:H:242:GLN:HE21	2:H:311:ILE:HD13	1.57	0.68
1:E:69:ILE:HD12	1:E:163:MET:HE2	1.73	0.68
1:A:38:LEU:HD22	1:A:112:LEU:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:GLY:HA2	1:A:174:GLN:CG	2.23	0.68
1:B:118:GLY:O	1:B:121:GLU:HB2	1.92	0.68
1:F:130:PRO:HD2	1:F:133:ILE:HB	1.73	0.68
1:B:85:THR:HG22	1:B:87:ILE:HG12	1.74	0.68
2:D:197:ILE:HD12	2:D:197:ILE:N	2.08	0.68
2:C:273:PHE:HD1	2:C:276:GLN:NE2	1.91	0.68
2:D:26:LEU:HD11	2:D:34:TYR:OH	1.93	0.68
2:G:38:GLY:HA3	2:G:44:LYS:HD3	1.75	0.68
2:H:249:ILE:HG12	2:H:250:PRO:HD3	1.74	0.68
1:B:177:TYR:O	1:B:181:TYR:CB	2.41	0.68
1:F:124:ARG:HG3	2:H:54:LEU:HD21	1.76	0.68
1:F:172:LEU:HD12	1:F:172:LEU:N	2.09	0.68
2:H:37:ILE:HB	2:H:204:VAL:HG21	1.75	0.68
2:C:270:ARG:CG	2:C:313:LEU:HD21	2.23	0.68
1:F:69:ILE:HD12	1:F:70:ILE:H	1.59	0.68
1:A:165:GLY:HA2	1:A:174:GLN:HG3	1.75	0.68
1:E:85:THR:O	1:E:85:THR:HG22	1.94	0.68
1:A:139:LEU:HB2	1:A:140:PRO:HD3	1.76	0.67
2:C:266:VAL:HG22	2:C:267:PRO:HD2	1.74	0.67
2:G:144:GLY:HA2	2:G:171:LEU:HD22	1.76	0.67
1:A:115:ILE:O	1:A:115:ILE:HD13	1.94	0.67
2:H:85:GLY:O	2:H:162:LEU:HA	1.94	0.67
2:C:48:ILE:HD11	2:C:163:LEU:HB3	1.76	0.67
1:F:45:GLN:NE2	1:F:46:ILE:HG12	2.09	0.67
1:B:60:VAL:HG13	1:B:102:PRO:HA	1.76	0.67
1:B:104:ILE:O	1:B:107:MET:HB2	1.94	0.67
2:D:143:GLY:HA2	2:D:146:LYS:CD	2.23	0.67
1:F:128:ALA:O	1:F:130:PRO:HD3	1.95	0.67
1:B:69:ILE:HD11	1:B:163:MET:CE	2.24	0.67
2:D:330:LEU:HB3	2:D:335:VAL:HB	1.77	0.67
1:E:135:ARG:HD2	1:E:135:ARG:N	2.08	0.67
1:E:163:MET:SD	1:F:69:ILE:HG12	2.34	0.67
1:F:68:PHE:HD1	1:F:68:PHE:H	1.41	0.67
2:D:36:VAL:HG11	2:D:47:LEU:HD23	1.77	0.67
2:D:267:PRO:HB3	2:D:342:TYR:CE2	2.30	0.67
1:F:30:ILE:HD11	1:F:101:ALA:CB	2.25	0.67
1:A:116:PRO:O	1:A:117:THR:O	2.13	0.67
1:B:63:PHE:HB3	1:B:102:PRO:HG3	1.76	0.67
2:C:274:THR:O	2:C:276:GLN:HG3	1.94	0.67
1:F:115:ILE:N	1:F:116:PRO:HD2	2.10	0.67
1:F:198:ILE:HG13	1:F:199:LEU:N	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:121:VAL:O	2:G:125:LEU:HG	1.94	0.67
2:C:166:GLU:OE2	2:C:198:THR:HA	1.95	0.67
2:C:200:GLU:HB3	2:C:239:LYS:CE	2.22	0.67
2:D:36:VAL:HG12	2:D:214:ILE:HD13	1.77	0.67
2:D:266:VAL:HG21	2:D:317:HIS:HA	1.77	0.67
2:G:1:MET:HE2	2:G:193:THR:OG1	1.94	0.67
1:A:39:TYR:CD2	1:A:48:ALA:HB3	2.30	0.67
1:B:185:ASN:HB2	1:B:188:VAL:HG22	1.77	0.67
2:D:98:THR:HG22	2:D:138:PRO:HD3	1.77	0.67
1:A:121:GLU:OE2	1:A:121:GLU:HA	1.95	0.66
1:E:38:LEU:CB	1:E:112:LEU:HD13	2.24	0.66
2:C:127:LEU:CD2	2:C:190:LEU:HD11	2.24	0.66
2:C:201:MET:HB3	2:C:201:MET:HE3	1.78	0.66
2:G:276:GLN:NE2	2:G:282:LEU:HD11	2.10	0.66
1:E:66:ILE:HG12	1:F:193:LEU:HD21	1.76	0.66
1:F:22:VAL:HG23	1:F:23:SER:N	2.09	0.66
2:H:82:ARG:HD3	2:H:110:ASP:CG	2.21	0.66
2:H:299:ALA:CB	2:H:312:MET:HG3	2.24	0.66
1:A:42:ARG:HA	1:A:42:ARG:NE	2.11	0.66
1:A:87:ILE:HG12	1:A:167:VAL:O	1.94	0.66
2:D:233:LYS:C	2:D:235:PRO:HD2	2.21	0.66
1:E:155:ILE:HB	1:E:200:VAL:HG13	1.77	0.66
2:H:4:LEU:HD23	2:H:62:VAL:HG13	1.78	0.66
2:C:246:HIS:HA	2:C:249:ILE:CG1	2.24	0.66
2:D:189:ARG:HH21	2:D:189:ARG:CG	2.07	0.66
2:D:98:THR:HA	2:D:138:PRO:HA	1.78	0.66
1:F:36:VAL:O	1:F:36:VAL:HG12	1.96	0.66
2:G:213:VAL:HG21	2:G:233:LYS:HD2	1.78	0.66
1:E:81:VAL:HG23	1:E:84:GLY:H	1.60	0.66
2:G:63:LEU:HD12	2:G:68:GLU:HG2	1.77	0.66
2:G:241:ILE:CD1	2:H:248:ASP:HB2	2.24	0.66
1:A:35:GLY:HA3	1:A:108:VAL:HG11	1.78	0.66
2:H:246:HIS:CE1	2:H:247:LEU:HD12	2.30	0.66
1:B:127:GLY:HA3	2:D:109:LEU:CD1	2.25	0.66
2:C:53:LEU:HD22	2:C:69:LEU:HB3	1.77	0.66
1:E:174:GLN:HA	1:E:177:TYR:CB	2.26	0.66
1:F:19:MET:CB	1:F:157:LEU:HD11	2.24	0.66
1:F:139:LEU:N	1:F:140:PRO:CD	2.59	0.66
2:G:63:LEU:HA	2:G:67:GLN:O	1.96	0.66
2:H:84:ILE:HD11	2:H:163:LEU:CG	2.26	0.66
1:A:59:ILE:HA	1:A:62:ILE:HG12	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:205:LYS:NZ	2:G:304:ALA:HB2	2.10	0.65
2:G:268:MET:HE2	2:G:297:ILE:HD11	1.78	0.65
2:G:295:ASN:HD21	2:G:317:HIS:CD2	2.14	0.65
2:H:125:LEU:HB3	2:H:131:GLY:HA3	1.76	0.65
1:A:15:GLU:OE1	1:A:171:GLY:HA2	1.95	0.65
2:C:238:GLN:C	2:C:240:PHE:N	2.51	0.65
2:D:7:ILE:O	2:D:24:VAL:HG22	1.97	0.65
2:D:29:PRO:HG2	2:D:32:GLN:CD	2.20	0.65
2:D:98:THR:HA	2:D:138:PRO:CA	2.27	0.65
1:F:196:LEU:O	1:F:199:LEU:HB3	1.96	0.65
2:H:171:LEU:HD13	2:H:179:ILE:HD12	1.78	0.65
2:C:100:PHE:HZ	2:C:118:LYS:HA	1.62	0.65
2:H:112:THR:N	2:H:113:PRO:HD3	2.12	0.65
2:C:299:ALA:O	2:C:300:GLN:HG2	1.97	0.65
1:F:20:THR:N	1:F:157:LEU:HD21	2.10	0.65
1:F:90:GLN:O	1:F:93:ILE:HG12	1.95	0.65
1:F:139:LEU:HG	1:F:140:PRO:HD3	1.78	0.65
2:G:137:TYR:HB3	2:G:141:LEU:HD11	1.77	0.65
1:A:64:ARG:NH1	1:A:106:ARG:HD2	2.12	0.65
1:E:32:LEU:C	1:E:34:VAL:H	2.05	0.65
2:H:98:THR:HA	2:H:138:PRO:HA	1.77	0.65
1:B:93:ILE:O	1:B:96:LEU:HB3	1.97	0.65
1:F:171:GLY:O	1:F:174:GLN:HB3	1.97	0.65
2:G:97:ARG:NH1	2:G:105:LEU:HD21	2.12	0.65
1:A:181:TYR:CE2	1:B:167:VAL:HG23	2.32	0.65
2:C:241:ILE:HG21	2:C:300:GLN:CG	2.27	0.65
2:D:250:PRO:HG2	2:D:253:TYR:CG	2.32	0.65
2:H:119:ARG:O	2:H:123:GLU:N	2.26	0.65
2:H:164:CYS:HB3	2:H:167:ALA:HB2	1.79	0.65
1:A:139:LEU:HA	1:A:142:ALA:HB3	1.79	0.65
2:D:33:ILE:HD13	2:D:207:ILE:HB	1.77	0.65
2:G:125:LEU:HB3	2:G:131:GLY:CA	2.27	0.65
2:G:164:CYS:SG	2:G:183:LEU:HD21	2.36	0.65
2:G:231:HIS:O	2:G:233:LYS:N	2.28	0.65
1:B:131:MET:HG3	1:B:132:GLN:H	1.62	0.65
2:C:4:LEU:HB2	2:C:26:LEU:HB3	1.78	0.65
2:C:36:VAL:CG1	2:C:214:ILE:HD13	2.27	0.65
1:F:185:ASN:ND2	1:F:188:VAL:HG22	2.12	0.65
2:D:54:LEU:HD11	2:D:86:MET:HE1	1.79	0.64
1:B:126:MET:SD	2:D:153:ARG:HD2	2.37	0.64
1:F:139:LEU:O	1:F:142:ALA:N	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:LEU:O	1:A:172:LEU:HD23	1.97	0.64
2:C:12:HIS:HD2	2:C:17:THR:HG23	1.61	0.64
2:H:2:ILE:HG23	2:H:28:VAL:HB	1.79	0.64
1:B:167:VAL:HG22	1:B:168:GLY:H	1.61	0.64
2:D:7:ILE:HB	2:D:24:VAL:HG23	1.78	0.64
1:F:137:VAL:HG23	1:F:138:LEU:HG	1.79	0.64
2:G:52:ASN:HD21	2:G:54:LEU:HG	1.63	0.64
2:H:24:VAL:HG12	2:H:219:LEU:HG	1.78	0.64
1:A:38:LEU:HA	1:A:41:THR:HG23	1.80	0.64
1:A:58:ALA:O	1:A:62:ILE:HG23	1.98	0.64
1:F:22:VAL:HG11	1:F:93:ILE:HG21	1.80	0.64
2:G:93:LEU:HD22	2:G:102:ASN:ND2	2.12	0.64
2:C:43:GLY:C	2:C:45:SER:N	2.51	0.64
1:E:201:TYR:OH	1:F:62:ILE:HG22	1.96	0.64
2:C:201:MET:H	2:C:239:LYS:CD	2.10	0.64
2:C:247:LEU:HD11	2:C:298:SER:HB3	1.77	0.64
1:E:74:TRP:HA	1:F:189:MET:HE1	1.78	0.64
2:H:220:ILE:CG2	2:H:233:LYS:HD3	2.27	0.64
1:A:181:TYR:CZ	1:B:167:VAL:HG23	2.32	0.64
1:B:155:ILE:CG2	1:B:200:VAL:HG13	2.27	0.64
2:C:234:THR:N	2:C:235:PRO:HD2	2.13	0.64
2:D:184:LYS:O	2:D:187:ASN:HB3	1.98	0.64
1:F:115:ILE:HG22	1:F:116:PRO:N	2.13	0.64
1:F:123:SER:HA	1:F:129:THR:HG21	1.80	0.64
2:G:80:ALA:O	2:G:83:GLN:HB2	1.97	0.64
2:G:252:ASP:HA	2:G:255:GLU:HG2	1.78	0.64
1:B:68:PHE:HB3	1:B:160:TYR:CE2	2.31	0.64
2:D:151:ILE:HD11	2:D:182:LEU:HD21	1.80	0.64
1:F:59:ILE:HA	1:F:62:ILE:HG12	1.78	0.64
1:F:129:THR:O	1:F:129:THR:HG23	1.97	0.64
2:G:4:LEU:HB3	2:G:7:ILE:HG12	1.80	0.64
2:G:93:LEU:HD11	2:G:149:VAL:HB	1.79	0.64
2:H:87:ILE:HG22	2:H:88:PHE:N	2.11	0.64
2:C:157:SER:O	2:C:158:ASN:HB2	1.98	0.63
2:C:233:LYS:O	2:C:237:ALA:HB2	1.98	0.63
2:D:273:PHE:CE1	2:D:335:VAL:HG13	2.32	0.63
2:D:274:THR:C	2:D:276:GLN:H	2.05	0.63
1:F:74:TRP:O	1:F:77:PRO:HD2	1.97	0.63
2:G:37:ILE:HD11	2:G:236:LEU:HB3	1.79	0.63
2:C:2:ILE:CG2	2:C:28:VAL:HB	2.29	0.63
1:E:76:ILE:HB	1:E:77:PRO:HD3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:152:ILE:HA	1:F:155:ILE:HG23	1.80	0.63
2:H:84:ILE:HD11	2:H:163:LEU:HG	1.80	0.63
1:A:69:ILE:HG21	1:B:163:MET:CE	2.27	0.63
2:C:44:LYS:NZ	2:C:199:HIS:HA	2.13	0.63
2:H:91:PHE:CZ	2:H:171:LEU:HD21	2.31	0.63
2:C:158:ASN:H	2:C:159:PRO:HD3	1.64	0.63
1:F:16:THR:OG1	1:F:172:LEU:HD13	1.98	0.63
2:H:221:GLU:OE1	2:H:230:SER:HB2	1.96	0.63
1:B:89:LEU:HD13	1:B:170:GLY:O	1.98	0.63
1:F:55:THR:O	1:F:58:ALA:HB3	1.97	0.63
2:G:151:ILE:O	2:G:155:LEU:HG	1.98	0.63
1:E:26:PHE:HB3	1:E:97:THR:HB	1.79	0.63
1:E:67:PRO:O	1:E:71:LEU:HB2	1.98	0.63
1:F:30:ILE:HD11	1:F:101:ALA:HB1	1.81	0.63
2:G:3:LYS:HD3	2:G:63:LEU:HD13	1.79	0.63
2:H:63:LEU:HD13	2:H:68:GLU:HG3	1.79	0.63
1:B:94:VAL:HA	1:B:97:THR:HG23	1.79	0.63
2:C:168:THR:HG21	2:C:176:THR:HG23	1.81	0.63
2:D:265:CYS:HB2	2:D:343:VAL:OXT	1.98	0.63
2:D:324:GLN:O	2:D:327:ILE:HG12	1.99	0.63
1:E:93:ILE:O	1:E:96:LEU:HB3	1.98	0.63
1:E:115:ILE:HG23	1:E:116:PRO:HD2	1.79	0.63
1:F:124:ARG:HB3	1:F:124:ARG:NH1	2.13	0.63
1:B:64:ARG:HG3	1:B:102:PRO:HB2	1.81	0.62
2:C:249:ILE:CG2	2:D:206:ARG:NH1	2.62	0.62
1:E:64:ARG:NH1	1:E:103:PHE:HD1	1.97	0.62
1:F:93:ILE:HG13	1:F:94:VAL:N	2.14	0.62
1:B:177:TYR:O	1:B:181:TYR:N	2.31	0.62
1:E:73:VAL:HG21	1:F:180:GLY:HA3	1.80	0.62
1:F:59:ILE:O	1:F:62:ILE:HG12	1.99	0.62
1:F:104:ILE:HD12	1:F:105:ALA:N	2.14	0.62
1:A:40:VAL:HA	1:A:49:ASN:HB3	1.82	0.62
1:B:90:GLN:O	1:B:93:ILE:HG12	2.00	0.62
2:C:29:PRO:HG3	2:C:32:GLN:OE1	1.99	0.62
2:G:98:THR:HA	2:G:138:PRO:HA	1.80	0.62
1:E:22:VAL:HG21	1:E:96:LEU:HD23	1.80	0.62
2:G:22:ASN:HB2	2:G:218:GLU:HG2	1.81	0.62
1:B:93:ILE:HG13	1:B:94:VAL:N	2.12	0.62
1:B:163:MET:O	1:B:167:VAL:HG12	2.00	0.62
2:C:36:VAL:HB	2:C:197:ILE:HD13	1.80	0.62
2:C:171:LEU:HD13	2:C:179:ILE:HD12	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:288:ARG:NH1	2:D:287:ALA:HB1	2.15	0.62
2:C:303:TYR:O	2:C:304:ALA:C	2.40	0.62
1:E:25:PHE:O	1:E:29:VAL:HB	1.98	0.62
1:F:25:PHE:O	1:F:29:VAL:HG23	2.00	0.62
2:D:36:VAL:HG11	2:D:47:LEU:CD2	2.30	0.62
2:D:250:PRO:O	2:D:253:TYR:HB3	2.00	0.62
1:F:89:LEU:O	1:F:93:ILE:HG23	2.00	0.62
2:G:174:ALA:HA	2:G:177:ARG:NH1	2.13	0.62
1:A:26:PHE:CZ	1:A:157:LEU:HD11	2.34	0.62
2:C:168:THR:CG2	2:C:176:THR:HG23	2.30	0.62
2:D:196:LEU:HD21	2:D:203:VAL:HG12	1.81	0.62
1:B:23:SER:HA	1:B:26:PHE:CZ	2.35	0.62
2:C:4:LEU:HD12	2:C:26:LEU:HD23	1.82	0.62
2:C:201:MET:HG3	2:C:236:LEU:O	1.99	0.62
2:D:241:ILE:O	2:D:245:LEU:HD13	2.00	0.62
1:A:68:PHE:CD2	1:A:163:MET:HG3	2.34	0.61
1:A:128:ALA:O	1:A:129:THR:HG23	2.00	0.61
2:C:303:TYR:CA	2:C:307:VAL:O	2.48	0.61
1:E:73:VAL:CG2	1:F:180:GLY:HA3	2.30	0.61
1:A:22:VAL:HG12	1:A:26:PHE:CD2	2.35	0.61
1:A:22:VAL:HG22	1:A:93:ILE:HG22	1.82	0.61
1:A:40:VAL:HG22	1:A:48:ALA:O	2.00	0.61
1:A:76:ILE:HG21	1:B:184:TYR:CE1	2.35	0.61
1:E:15:GLU:O	1:E:18:ALA:HB3	2.00	0.61
1:A:128:ALA:C	1:A:129:THR:HG23	2.26	0.61
1:A:130:PRO:O	1:A:131:MET:O	2.18	0.61
2:C:7:ILE:HB	2:C:24:VAL:CG2	2.30	0.61
2:C:201:MET:HB2	2:C:239:LYS:HB3	1.82	0.61
2:C:240:PHE:C	2:C:241:ILE:HD13	2.24	0.61
2:G:288:ARG:HG2	2:H:288:ARG:HA	1.82	0.61
1:B:15:GLU:HB3	1:B:89:LEU:HD21	1.81	0.61
2:D:48:ILE:HD11	2:D:197:ILE:HG12	1.81	0.61
1:E:23:SER:HA	1:E:26:PHE:CE2	2.36	0.61
1:F:104:ILE:CG2	1:F:153:THR:HG21	2.29	0.61
2:G:33:ILE:HG12	2:G:194:ILE:CG1	2.30	0.61
2:D:93:LEU:HD11	2:D:146:LYS:O	2.01	0.61
1:A:137:VAL:C	1:A:140:PRO:HD2	2.25	0.61
2:C:168:THR:HB	2:C:176:THR:HG23	1.83	0.61
2:D:143:GLY:HA2	2:D:146:LYS:HE3	1.82	0.61
2:D:234:THR:HG22	2:D:238:GLN:HE21	1.64	0.61
1:A:75:MET:O	1:A:79:THR:N	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:PRO:CG	1:A:131:MET:H	2.07	0.61
1:B:85:THR:CG2	1:B:87:ILE:HG12	2.29	0.61
2:C:91:PHE:CE2	2:C:146:LYS:HD2	2.36	0.61
2:D:91:PHE:CE1	2:D:171:LEU:HD21	2.35	0.61
2:D:125:LEU:O	2:D:128:VAL:HG22	2.01	0.61
1:F:137:VAL:C	1:F:138:LEU:HG	2.24	0.61
2:G:122:THR:HA	2:G:125:LEU:HD12	1.81	0.61
2:G:247:LEU:HG	2:H:300:GLN:CD	2.26	0.61
2:H:173:PRO:O	2:H:177:ARG:HG3	2.01	0.61
2:C:273:PHE:HB3	2:C:276:GLN:NE2	2.15	0.61
2:C:104:ALA:O	2:C:107:LEU:N	2.33	0.61
2:D:91:PHE:HE1	2:D:171:LEU:HD21	1.64	0.61
2:H:106:PRO:CA	2:H:109:LEU:HD12	2.30	0.61
2:H:189:ARG:O	2:H:190:LEU:O	2.19	0.61
1:A:34:VAL:O	1:A:37:LEU:HG	2.01	0.61
2:C:196:LEU:HD21	2:C:203:VAL:HG12	1.83	0.61
2:G:26:LEU:HD11	2:G:34:TYR:CE1	2.35	0.60
1:B:75:MET:SD	1:B:95:PRO:HA	2.41	0.60
1:E:150:ALA:O	1:E:154:LEU:HG	2.00	0.60
1:E:38:LEU:HB2	1:E:112:LEU:CD1	2.25	0.60
1:E:70:ILE:CD1	1:F:193:LEU:HA	2.31	0.60
1:E:109:GLU:O	1:E:113:LEU:HG	2.01	0.60
1:F:94:VAL:HA	1:F:97:THR:HG23	1.83	0.60
1:A:112:LEU:O	1:A:115:ILE:HG23	2.00	0.60
1:B:11:ARG:HB3	1:B:11:ARG:NH1	2.16	0.60
1:B:41:THR:C	1:B:42:ARG:HG3	2.26	0.60
1:B:83:VAL:HG11	1:B:91:ALA:HB1	1.83	0.60
1:E:38:LEU:HD13	1:E:112:LEU:HB3	1.83	0.60
1:B:26:PHE:CD2	1:B:97:THR:HG22	2.37	0.60
1:B:80:ARG:HB2	1:B:86:SER:HB3	1.83	0.60
1:B:149:ALA:O	1:B:153:THR:HG23	2.01	0.60
1:B:172:LEU:HD11	1:B:195:LEU:CD2	2.27	0.60
2:D:241:ILE:CG2	2:D:244:THR:OG1	2.49	0.60
1:E:122:ALA:HB1	2:G:88:PHE:CZ	2.36	0.60
1:E:174:GLN:CA	1:E:177:TYR:HB3	2.29	0.60
1:F:59:ILE:O	1:F:62:ILE:CG1	2.50	0.60
1:F:123:SER:HA	1:F:129:THR:CB	2.31	0.60
2:G:247:LEU:HG	2:H:300:GLN:HG3	1.83	0.60
2:H:12:HIS:NE2	2:H:14:GLY:HA2	2.16	0.60
1:B:92:ALA:CB	1:B:169:ALA:HB2	2.32	0.60
2:C:13:GLN:HB2	2:C:16:ARG:HG2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:231:HIS:CB	2:C:232:PRO:HD2	2.32	0.60
2:D:125:LEU:HB3	2:D:131:GLY:CA	2.31	0.60
1:E:71:LEU:O	1:E:75:MET:HB2	2.01	0.60
1:E:135:ARG:HD2	1:E:135:ARG:H	1.64	0.60
1:F:76:ILE:HB	1:F:77:PRO:HD3	1.82	0.60
2:C:252:ASP:OD2	2:C:253:TYR:N	2.34	0.60
1:E:118:GLY:C	1:E:119:LEU:HG	2.26	0.60
1:A:149:ALA:O	1:A:152:ILE:HG12	2.02	0.60
1:B:16:THR:HG21	1:B:199:LEU:HD21	1.84	0.60
2:G:86:MET:SD	2:G:88:PHE:CZ	2.95	0.60
2:G:107:LEU:HB3	2:G:113:PRO:HG3	1.83	0.60
2:H:241:ILE:O	2:H:300:GLN:HG3	2.02	0.60
2:C:186:ILE:HD12	2:C:192:LEU:HD23	1.83	0.60
2:C:248:ASP:HB3	2:C:254:GLN:HG3	1.83	0.60
1:A:104:ILE:HG22	1:A:153:THR:HG21	1.84	0.60
2:C:234:THR:O	2:C:238:GLN:N	2.35	0.60
2:H:8:THR:HG23	2:H:22:ASN:HA	1.84	0.60
1:A:42:ARG:HB3	1:A:43:PRO:HD3	1.83	0.59
2:C:201:MET:HG3	2:C:236:LEU:HB2	1.84	0.59
2:C:233:LYS:HA	2:C:235:PRO:HD2	1.83	0.59
1:E:116:PRO:HB2	1:E:120:ILE:CG1	2.30	0.59
1:F:71:LEU:O	1:F:75:MET:HB2	2.01	0.59
2:H:204:VAL:HA	2:H:208:CYS:SG	2.41	0.59
1:A:55:THR:O	1:A:59:ILE:HG23	2.01	0.59
1:B:112:LEU:O	1:B:115:ILE:HG22	2.02	0.59
2:C:97:ARG:NH2	2:C:108:GLU:OE2	2.27	0.59
2:C:138:PRO:O	2:C:140:ASN:N	2.35	0.59
2:C:234:THR:O	2:C:237:ALA:N	2.34	0.59
2:C:262:PHE:O	2:C:265:CYS:SG	2.60	0.59
1:F:16:THR:O	1:F:19:MET:HB2	2.02	0.59
1:F:41:THR:HG22	1:F:53:TYR:CE2	2.37	0.59
2:H:28:VAL:HG22	2:H:34:TYR:CD2	2.37	0.59
2:H:182:LEU:O	2:H:186:ILE:HG23	2.02	0.59
1:A:189:MET:HE2	1:B:74:TRP:N	2.18	0.59
2:C:231:HIS:O	2:C:233:LYS:N	2.35	0.59
2:C:290:PHE:CD1	2:C:325:ALA:HB1	2.37	0.59
1:E:46:ILE:HD13	1:E:47:ILE:HG23	1.83	0.59
1:A:78:PHE:O	1:A:81:VAL:HG22	2.03	0.59
1:B:76:ILE:O	1:B:77:PRO:C	2.44	0.59
2:C:26:LEU:HD11	2:C:34:TYR:CZ	2.38	0.59
2:C:165:ASP:HA	2:C:197:ILE:CG2	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:83:GLN:C	2:D:159:PRO:HB2	2.27	0.59
1:E:125:ALA:CA	2:G:54:LEU:HD21	2.32	0.59
2:G:97:ARG:CD	2:G:105:LEU:HD11	2.32	0.59
2:H:53:LEU:HD23	2:H:77:LEU:CD2	2.31	0.59
1:B:118:GLY:HA2	1:B:121:GLU:CD	2.27	0.59
2:D:196:LEU:C	2:D:197:ILE:HD12	2.27	0.59
1:F:165:GLY:HA2	1:F:174:GLN:HA	1.84	0.59
2:H:84:ILE:CD1	2:H:163:LEU:HD11	2.32	0.59
1:B:129:THR:HA	1:B:133:ILE:HB	1.85	0.59
2:C:273:PHE:CD1	2:C:276:GLN:NE2	2.71	0.59
2:H:209:ASP:O	2:H:224:THR:HG23	2.02	0.59
1:A:22:VAL:HG22	1:A:93:ILE:CG2	2.33	0.59
1:A:23:SER:HA	1:A:26:PHE:CE2	2.38	0.59
1:B:131:MET:HG3	1:B:132:GLN:N	2.17	0.59
2:D:234:THR:HG21	2:D:238:GLN:HE21	1.66	0.59
2:G:295:ASN:HB2	2:G:315:GLU:HB2	1.85	0.59
2:H:198:THR:HG21	2:H:204:VAL:HG23	1.85	0.59
1:A:59:ILE:HG13	1:A:60:VAL:N	2.17	0.59
1:A:82:ILE:O	1:A:84:GLY:N	2.36	0.59
2:C:128:VAL:HG11	2:C:152:ALA:HB2	1.85	0.59
2:C:296:ILE:HG23	2:C:314:THR:HG22	1.83	0.59
2:D:155:LEU:HD21	2:D:186:ILE:HD12	1.84	0.59
1:E:69:ILE:HD13	1:E:69:ILE:N	2.17	0.59
1:E:175:ILE:HG13	1:E:176:GLY:N	2.17	0.59
1:E:203:ILE:O	1:E:206:ALA:HB3	2.03	0.59
1:F:206:ALA:O	1:F:207:GLY:O	2.21	0.59
2:H:213:VAL:HB	2:H:233:LYS:HD2	1.84	0.59
1:A:132:GLN:HB3	1:A:136:LYS:HD2	1.85	0.59
2:C:12:HIS:CD2	2:C:17:THR:HG23	2.37	0.59
1:E:32:LEU:C	1:E:34:VAL:N	2.61	0.59
1:E:70:ILE:HD13	1:F:193:LEU:HA	1.84	0.59
1:E:139:LEU:HB2	1:E:140:PRO:HD3	1.85	0.59
2:H:4:LEU:CD2	2:H:62:VAL:HG13	2.32	0.59
1:A:64:ARG:HH11	1:A:106:ARG:HD2	1.67	0.59
1:B:179:TYR:HB3	1:B:185:ASN:ND2	2.18	0.59
2:C:7:ILE:HB	2:C:24:VAL:HG23	1.85	0.59
2:G:228:VAL:CG1	2:G:233:LYS:HE3	2.33	0.58
2:G:241:ILE:C	2:G:241:ILE:HD13	2.28	0.58
2:H:43:GLY:C	2:H:45:SER:N	2.56	0.58
1:A:26:PHE:HE1	1:A:104:ILE:HG21	1.68	0.58
2:C:44:LYS:HZ1	2:C:199:HIS:HA	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:69:ILE:HD12	1:F:70:ILE:N	2.18	0.58
1:F:69:ILE:O	1:F:73:VAL:HG23	2.03	0.58
1:F:126:MET:SD	1:F:129:THR:CA	2.79	0.58
2:C:36:VAL:HG13	2:C:214:ILE:CD1	2.33	0.58
1:A:19:MET:O	1:A:22:VAL:HB	2.03	0.58
1:A:134:VAL:O	1:A:138:LEU:HG	2.03	0.58
1:B:42:ARG:N	1:B:43:PRO:HD3	2.19	0.58
2:C:142:SER:O	2:C:145:GLN:HB2	2.03	0.58
2:D:103:VAL:HG12	2:D:121:VAL:HG22	1.86	0.58
1:A:70:ILE:HG13	1:B:193:LEU:HD23	1.86	0.58
1:B:47:ILE:O	1:B:48:ALA:HB3	2.03	0.58
2:C:234:THR:CG2	2:C:272:GLU:OE1	2.51	0.58
2:G:9:LYS:HB2	2:G:57:PRO:HB3	1.86	0.58
2:C:235:PRO:C	2:C:237:ALA:H	2.11	0.58
2:D:93:LEU:HD22	2:D:102:ASN:HD22	1.69	0.58
1:E:36:VAL:HG12	1:E:40:VAL:CG2	2.33	0.58
1:E:72:LEU:CD2	1:E:95:PRO:HB2	2.33	0.58
1:F:36:VAL:HG13	1:F:39:TYR:CD1	2.38	0.58
2:G:51:VAL:CG1	2:G:163:LEU:HD11	2.34	0.58
2:G:127:LEU:HD11	2:G:186:ILE:HG22	1.85	0.58
2:G:158:ASN:N	2:G:159:PRO:HD3	2.18	0.58
2:H:285:GLU:HG2	2:H:329:TRP:CH2	2.39	0.58
1:B:181:TYR:HD1	1:B:182:ILE:HG12	1.69	0.58
2:D:143:GLY:HA2	2:D:146:LYS:CE	2.34	0.58
1:F:72:LEU:CD2	1:F:95:PRO:HB2	2.33	0.58
2:H:241:ILE:HD13	2:H:300:GLN:C	2.28	0.58
1:A:193:LEU:HD23	1:B:70:ILE:CD1	2.32	0.58
2:D:7:ILE:HB	2:D:24:VAL:CG2	2.34	0.58
1:F:133:ILE:O	1:F:137:VAL:HG22	2.03	0.58
2:G:18:ILE:HD13	2:G:19:GLN:N	2.19	0.58
2:G:22:ASN:HB2	2:G:218:GLU:CG	2.34	0.58
1:F:72:LEU:HD23	1:F:95:PRO:CB	2.34	0.58
1:A:15:GLU:HB3	1:A:89:LEU:HD11	1.85	0.58
1:A:60:VAL:O	1:A:64:ARG:HG3	2.04	0.58
2:C:124:LEU:CD2	2:C:156:ALA:HA	2.33	0.58
2:C:144:GLY:O	2:C:147:GLN:HB3	2.04	0.58
2:C:196:LEU:HD23	2:C:208:CYS:SG	2.44	0.58
2:D:73:SER:HB2	2:D:76:GLU:HG2	1.86	0.58
1:E:104:ILE:HG22	1:E:153:THR:CG2	2.33	0.58
2:G:26:LEU:HD12	2:G:222:GLN:NE2	2.19	0.58
2:G:246:HIS:O	2:H:241:ILE:HG22	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:300:GLN:HE22	2:H:244:THR:HB	1.68	0.58
1:B:119:LEU:O	1:B:122:ALA:HB3	2.04	0.57
1:F:31:GLY:CA	1:F:104:ILE:HD13	2.34	0.57
2:C:7:ILE:O	2:C:24:VAL:HG22	2.04	0.57
2:C:121:VAL:O	2:C:125:LEU:HG	2.04	0.57
1:F:126:MET:HB3	1:F:128:ALA:C	2.28	0.57
2:G:77:LEU:HD21	2:G:81:ARG:NH1	2.19	0.57
2:G:97:ARG:HD2	2:G:105:LEU:HD11	1.86	0.57
1:A:74:TRP:O	1:A:77:PRO:HD2	2.03	0.57
1:B:32:LEU:O	1:B:35:GLY:N	2.33	0.57
1:B:35:GLY:CA	1:B:108:VAL:HG11	2.31	0.57
1:B:67:PRO:O	1:B:70:ILE:HG23	2.04	0.57
2:D:45:SER:O	2:D:49:ARG:NH1	2.37	0.57
2:D:180:LEU:O	2:D:183:LEU:HB2	2.04	0.57
2:D:268:MET:CE	2:D:313:LEU:HB3	2.34	0.57
1:F:12:GLY:C	1:F:172:LEU:CD1	2.78	0.57
1:F:94:VAL:CG2	1:F:95:PRO:HD3	2.22	0.57
2:G:220:ILE:H	2:G:220:ILE:HD12	1.70	0.57
2:G:282:LEU:HD13	2:G:330:LEU:HD22	1.85	0.57
1:A:34:VAL:C	1:A:36:VAL:H	2.12	0.57
1:B:60:VAL:O	1:B:102:PRO:HB2	2.05	0.57
1:E:32:LEU:O	1:E:34:VAL:N	2.37	0.57
1:F:179:TYR:O	1:F:183:GLY:O	2.22	0.57
2:G:201:MET:O	2:G:202:ASP:C	2.45	0.57
2:H:100:PHE:C	2:H:100:PHE:CD2	2.81	0.57
1:F:126:MET:HE3	1:F:129:THR:OG1	2.04	0.57
2:G:300:GLN:HE22	2:H:244:THR:CB	2.17	0.57
2:H:179:ILE:O	2:H:183:LEU:HD22	2.04	0.57
2:H:274:THR:HG21	2:H:336:LYS:HE2	1.87	0.57
2:C:214:ILE:HG13	2:C:219:LEU:HA	1.86	0.57
1:F:42:ARG:HH21	1:F:50:ALA:C	2.12	0.57
2:G:97:ARG:HH11	2:G:105:LEU:HD21	1.68	0.57
2:H:86:MET:HG2	2:H:87:ILE:N	2.19	0.57
1:B:185:ASN:CB	1:B:188:VAL:HG22	2.34	0.57
1:A:178:GLN:O	1:A:182:ILE:O	2.22	0.57
1:F:175:ILE:HD11	1:F:192:VAL:CG2	2.35	0.57
2:H:257:LEU:HA	2:H:342:TYR:O	2.05	0.57
2:C:168:THR:CB	2:C:176:THR:HG23	2.34	0.57
1:E:74:TRP:O	1:E:77:PRO:HD2	2.05	0.57
1:F:42:ARG:NH2	1:F:51:LYS:HA	2.19	0.57
1:F:72:LEU:HD11	1:F:160:TYR:CE1	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:106:PRO:HD3	2:G:153:ARG:HG3	1.87	0.57
1:B:23:SER:HA	1:B:26:PHE:CE2	2.40	0.56
2:C:303:TYR:HH	2:D:253:TYR:HD2	1.53	0.56
2:D:4:LEU:HB3	2:D:7:ILE:CD1	2.36	0.56
2:D:63:LEU:HD13	2:D:68:GLU:HG3	1.88	0.56
1:F:42:ARG:HE	1:F:49:ASN:C	2.13	0.56
2:H:165:ASP:O	2:H:166:GLU:C	2.47	0.56
2:H:240:PHE:H	2:H:243:SER:CB	2.15	0.56
1:A:191:THR:O	1:A:195:LEU:HB2	2.05	0.56
2:C:221:GLU:OE2	2:C:231:HIS:HB2	2.05	0.56
1:F:126:MET:HG2	2:H:109:LEU:CD1	2.31	0.56
2:H:87:ILE:HD12	2:H:164:CYS:SG	2.45	0.56
1:A:129:THR:OG1	1:A:133:ILE:HD12	2.06	0.56
1:B:16:THR:O	1:B:19:MET:HB2	2.04	0.56
2:C:52:ASN:H	2:C:52:ASN:HD22	1.51	0.56
2:C:228:VAL:O	2:C:229:PHE:CD2	2.59	0.56
2:D:282:LEU:HD13	2:D:335:VAL:HG21	1.88	0.56
1:E:19:MET:HA	1:E:22:VAL:HG23	1.88	0.56
1:E:42:ARG:CD	1:E:45:GLN:HB3	2.35	0.56
1:E:47:ILE:O	1:E:48:ALA:HB3	2.05	0.56
1:E:192:VAL:O	1:E:195:LEU:HB3	2.04	0.56
2:G:206:ARG:HH22	2:G:242:GLN:NE2	2.03	0.56
2:H:52:ASN:O	2:H:53:LEU:HB3	2.04	0.56
1:A:128:ALA:HB1	1:A:134:VAL:CG2	2.35	0.56
1:A:152:ILE:HG13	1:A:153:THR:N	2.20	0.56
1:B:83:VAL:HG11	1:B:91:ALA:CB	2.36	0.56
2:D:151:ILE:HD11	2:D:182:LEU:CD2	2.35	0.56
2:D:241:ILE:O	2:D:241:ILE:CG2	2.53	0.56
2:G:63:LEU:HD21	2:G:66:GLY:HA2	1.88	0.56
2:H:184:LYS:O	2:H:187:ASN:HB3	2.06	0.56
1:A:26:PHE:CD1	1:A:104:ILE:HD13	2.41	0.56
1:A:94:VAL:CB	1:A:95:PRO:HD3	2.34	0.56
2:C:33:ILE:HD13	2:C:207:ILE:O	2.06	0.56
1:F:72:LEU:HD23	1:F:95:PRO:HB2	1.86	0.56
2:H:256:ARG:O	2:H:343:VAL:HG12	2.05	0.56
1:A:167:VAL:HG11	1:B:181:TYR:O	2.04	0.56
1:B:22:VAL:CG1	1:B:93:ILE:HD12	2.35	0.56
2:C:302:ASP:O	2:C:308:LYS:HA	2.05	0.56
2:D:148:ARG:HA	2:D:151:ILE:HG12	1.87	0.56
1:F:175:ILE:HG13	1:F:176:GLY:N	2.20	0.56
2:C:11:PHE:HB2	2:C:18:ILE:HG23	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:33:ILE:HD13	2:H:207:ILE:HB	1.88	0.56
1:A:193:LEU:HD11	1:B:74:TRP:NE1	2.21	0.56
1:B:59:ILE:HG13	1:B:60:VAL:N	2.21	0.56
2:D:198:THR:OG1	2:D:203:VAL:HG21	2.05	0.56
1:E:27:GLY:HA2	1:E:104:ILE:HD12	1.86	0.56
1:E:41:THR:HG22	1:E:53:TYR:CE2	2.41	0.56
1:F:41:THR:C	1:F:43:PRO:HD3	2.30	0.56
1:F:32:LEU:HD23	1:F:108:VAL:HG21	1.88	0.56
2:G:144:GLY:CA	2:G:175:THR:HG21	2.36	0.56
2:H:48:ILE:HD13	2:H:49:ARG:H	1.71	0.56
1:B:68:PHE:CD1	1:B:68:PHE:N	2.73	0.56
2:C:244:THR:HA	2:C:298:SER:OG	2.06	0.56
2:C:278:VAL:C	2:C:280:ALA:H	2.13	0.56
2:D:248:ASP:O	2:D:249:ILE:C	2.49	0.56
1:E:71:LEU:HD22	1:E:160:TYR:OH	2.06	0.56
1:F:124:ARG:NH2	2:H:85:GLY:CA	2.67	0.56
2:H:242:GLN:NE2	2:H:311:ILE:CD1	2.68	0.56
2:H:299:ALA:HA	2:H:312:MET:HA	1.86	0.56
1:A:68:PHE:HB2	1:A:163:MET:HE3	1.87	0.55
1:A:72:LEU:HA	1:A:75:MET:HE3	1.87	0.55
1:E:40:VAL:HG12	1:E:53:TYR:HD2	1.72	0.55
1:E:69:ILE:HD12	1:E:163:MET:CE	2.36	0.55
2:G:89:GLN:HG3	2:G:165:ASP:CG	2.32	0.55
2:G:299:ALA:CB	2:G:312:MET:HG3	2.36	0.55
2:H:28:VAL:HG22	2:H:34:TYR:CG	2.41	0.55
2:H:151:ILE:HD11	2:H:182:LEU:HD21	1.87	0.55
2:H:183:LEU:O	2:H:186:ILE:HG12	2.06	0.55
2:H:186:ILE:HB	2:H:192:LEU:HD12	1.87	0.55
1:B:167:VAL:CG1	1:B:168:GLY:H	2.07	0.55
2:D:37:ILE:CD1	2:D:236:LEU:HD13	2.35	0.55
1:A:87:ILE:HG22	1:A:88:GLY:N	2.22	0.55
1:B:89:LEU:CA	1:B:169:ALA:HB1	2.33	0.55
1:B:101:ALA:HA	1:B:104:ILE:HG12	1.88	0.55
1:B:128:ALA:HB1	2:D:78:THR:HG23	1.87	0.55
1:F:101:ALA:HA	1:F:104:ILE:CD1	2.30	0.55
1:F:173:GLY:O	1:F:177:TYR:N	2.29	0.55
2:G:171:LEU:HD13	2:G:179:ILE:HG13	1.88	0.55
2:G:288:ARG:HA	2:H:288:ARG:CG	2.36	0.55
1:B:130:PRO:O	1:B:134:VAL:HG12	2.07	0.55
2:D:150:ALA:O	2:D:153:ARG:HB3	2.06	0.55
2:D:233:LYS:HG3	2:D:233:LYS:O	2.02	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:249:ILE:HG22	2:D:313:LEU:HD12	1.88	0.55
2:D:299:ALA:HB1	2:D:312:MET:HG2	1.87	0.55
2:C:137:TYR:OH	2:C:140:ASN:HB3	2.07	0.55
1:E:104:ILE:HG22	1:E:153:THR:HG21	1.89	0.55
1:F:178:GLN:O	1:F:182:ILE:O	2.24	0.55
2:G:299:ALA:HB2	2:G:312:MET:HG3	1.87	0.55
2:H:124:LEU:HD22	2:H:152:ALA:O	2.07	0.55
1:B:69:ILE:HD11	1:B:163:MET:CB	2.25	0.55
2:H:138:PRO:O	2:H:140:ASN:N	2.40	0.55
2:C:300:GLN:NE2	2:D:298:SER:HB2	2.21	0.55
2:D:221:GLU:OE1	2:D:231:HIS:O	2.25	0.55
1:E:192:VAL:HA	1:E:195:LEU:HD22	1.87	0.55
1:F:176:GLY:O	1:F:180:GLY:HA3	2.07	0.55
2:H:224:THR:O	2:H:228:VAL:HG23	2.06	0.55
1:B:22:VAL:HG12	1:B:26:PHE:CE2	2.42	0.55
2:C:241:ILE:HD11	2:C:311:ILE:HD11	1.89	0.55
2:D:248:ASP:O	2:D:249:ILE:CG1	2.55	0.55
1:E:75:MET:HE1	1:E:98:VAL:HG21	1.88	0.55
1:E:122:ALA:HB1	2:G:88:PHE:CD2	2.42	0.55
2:G:82:ARG:NH2	2:G:110:ASP:HB3	2.20	0.55
2:G:246:HIS:HB3	2:H:241:ILE:HG23	1.87	0.55
2:H:319:THR:O	2:H:323:THR:HG23	2.07	0.55
2:C:241:ILE:C	2:C:243:SER:N	2.64	0.55
2:D:103:VAL:CG1	2:D:121:VAL:HG22	2.36	0.55
2:D:208:CYS:O	2:D:225:VAL:CG2	2.52	0.55
1:E:13:VAL:CG2	1:E:195:LEU:HD11	2.36	0.55
1:E:125:ALA:HA	2:G:54:LEU:HD21	1.88	0.55
1:F:93:ILE:O	1:F:96:LEU:HB2	2.07	0.55
2:G:1:MET:HE3	2:G:161:VAL:HG22	1.88	0.55
2:H:48:ILE:HG13	2:H:197:ILE:HD11	1.88	0.55
2:H:220:ILE:HB	2:H:233:LYS:HD3	1.88	0.55
1:E:16:THR:HA	1:E:19:MET:HG2	1.88	0.55
1:E:73:VAL:HG13	1:E:74:TRP:N	2.22	0.55
1:E:119:LEU:HD13	2:G:90:HIS:CB	2.36	0.55
2:G:301:MET:HG2	2:G:310:GLY:HA3	1.88	0.55
2:H:77:LEU:HG	2:H:81:ARG:HE	1.71	0.55
2:C:99:VAL:HG22	2:C:149:VAL:CG2	2.36	0.54
2:D:250:PRO:HG2	2:D:253:TYR:CD2	2.42	0.54
1:E:12:GLY:O	1:E:172:LEU:HD21	2.07	0.54
2:G:84:ILE:HA	2:G:161:VAL:O	2.06	0.54
1:A:9:LEU:O	1:A:13:VAL:HG23	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:VAL:HG12	1:A:53:TYR:HB2	1.87	0.54
1:A:185:ASN:CB	1:A:188:VAL:HG22	2.30	0.54
2:D:82:ARG:O	2:D:159:PRO:HB3	2.06	0.54
1:E:19:MET:HE3	1:E:172:LEU:HD12	1.89	0.54
1:F:36:VAL:HG13	1:F:39:TYR:CE1	2.43	0.54
1:F:139:LEU:CG	1:F:140:PRO:HD3	2.36	0.54
2:G:63:LEU:HD12	2:G:68:GLU:CG	2.36	0.54
2:H:87:ILE:HG23	2:H:147:GLN:HE22	1.69	0.54
1:A:132:GLN:O	1:A:136:LYS:N	2.34	0.54
2:C:249:ILE:N	2:C:250:PRO:HD2	2.23	0.54
2:D:173:PRO:O	2:D:177:ARG:HG3	2.07	0.54
1:E:160:TYR:CD1	1:E:160:TYR:C	2.84	0.54
2:H:103:VAL:HB	2:H:121:VAL:HG13	1.89	0.54
2:C:153:ARG:O	2:C:156:ALA:HB3	2.07	0.54
1:E:38:LEU:CD2	1:E:112:LEU:HB3	2.36	0.54
1:F:119:LEU:N	1:F:119:LEU:HD12	2.23	0.54
1:F:139:LEU:N	1:F:140:PRO:HD2	2.22	0.54
2:D:254:GLN:O	2:D:257:LEU:HB3	2.07	0.54
1:E:42:ARG:HD2	1:E:45:GLN:HB3	1.88	0.54
2:G:189:ARG:O	2:G:191:GLY:N	2.41	0.54
2:H:105:LEU:HD22	2:H:109:LEU:HD11	1.90	0.54
1:A:155:ILE:HG13	1:A:156:THR:N	2.23	0.54
2:C:145:GLN:O	2:C:146:LYS:C	2.51	0.54
2:D:87:ILE:HG22	2:D:88:PHE:N	2.22	0.54
2:D:276:GLN:OE1	2:D:280:ALA:HB2	2.07	0.54
1:E:101:ALA:HB3	1:E:102:PRO:CD	2.37	0.54
1:A:141:GLU:O	1:A:144:PRO:HD2	2.08	0.54
1:B:15:GLU:O	1:B:19:MET:HG2	2.08	0.54
1:B:37:LEU:HD21	1:B:56:VAL:HB	1.88	0.54
1:F:35:GLY:HA3	1:F:108:VAL:CG1	2.37	0.54
2:H:105:LEU:CB	2:H:106:PRO:CD	2.86	0.54
1:A:107:MET:HB3	1:A:149:ALA:HB1	1.89	0.54
1:B:55:THR:O	1:B:59:ILE:HG12	2.07	0.54
2:C:33:ILE:HD12	2:C:209:ASP:OD2	2.08	0.54
2:C:249:ILE:HG22	2:D:206:ARG:NH1	2.22	0.54
2:C:303:TYR:C	2:C:307:VAL:O	2.50	0.54
2:D:246:HIS:ND1	2:D:270:ARG:NH1	2.56	0.54
1:F:123:SER:HA	1:F:129:THR:CG2	2.37	0.54
2:G:112:THR:N	2:G:113:PRO:HD3	2.23	0.54
2:H:3:LYS:HA	2:H:26:LEU:O	2.08	0.54
2:H:27:HIS:H	2:H:222:GLN:NE2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:VAL:O	1:A:33:PRO:HG2	2.07	0.54
1:A:63:PHE:HB3	1:A:102:PRO:HG3	1.88	0.54
1:B:7:TRP:H	1:B:7:TRP:CD1	2.23	0.54
1:B:78:PHE:O	1:B:82:ILE:HG12	2.08	0.54
1:B:118:GLY:HA2	1:B:121:GLU:OE1	2.08	0.54
2:C:158:ASN:N	2:C:159:PRO:HD3	2.21	0.54
2:D:2:ILE:CG2	2:D:28:VAL:HB	2.31	0.54
2:D:29:PRO:CG	2:D:32:GLN:CD	2.81	0.54
2:D:248:ASP:O	2:D:249:ILE:HG13	2.08	0.54
1:E:34:VAL:HB	1:E:37:LEU:HG	1.90	0.54
1:F:58:ALA:O	1:F:62:ILE:HG23	2.08	0.54
2:G:183:LEU:HD23	2:G:194:ILE:CD1	2.36	0.54
2:H:37:ILE:C	2:H:37:ILE:HD13	2.33	0.54
2:H:196:LEU:HD21	2:H:203:VAL:CG1	2.34	0.54
2:H:280:ALA:C	2:H:282:LEU:H	2.16	0.54
2:D:234:THR:O	2:D:235:PRO:C	2.50	0.53
1:E:40:VAL:HG22	1:E:47:ILE:HD11	1.90	0.53
1:E:125:ALA:HB2	2:G:54:LEU:HD21	1.90	0.53
2:H:242:GLN:HG3	2:H:311:ILE:HB	1.90	0.53
1:A:40:VAL:HA	1:A:49:ASN:HB2	1.89	0.53
1:B:60:VAL:HG13	1:B:102:PRO:CA	2.38	0.53
1:B:179:TYR:HE2	1:F:182:ILE:O	1.91	0.53
2:D:196:LEU:HD23	2:D:208:CYS:SG	2.47	0.53
2:H:21:LEU:HD21	2:H:47:LEU:HB2	1.90	0.53
2:H:84:ILE:HG13	2:H:161:VAL:O	2.08	0.53
2:H:105:LEU:O	2:H:109:LEU:HG	2.07	0.53
1:A:22:VAL:HG12	1:A:26:PHE:HE2	1.72	0.53
1:A:26:PHE:HD1	1:A:104:ILE:HD13	1.72	0.53
1:A:66:ILE:HG21	1:A:71:LEU:HB2	1.89	0.53
2:C:46:THR:HG22	2:C:47:LEU:N	2.22	0.53
2:C:69:LEU:N	2:C:69:LEU:HD12	2.23	0.53
2:C:271:LEU:HD23	2:C:337:VAL:HG13	1.90	0.53
1:E:126:MET:SD	2:G:106:PRO:HB3	2.48	0.53
2:G:206:ARG:HH22	2:G:242:GLN:HE22	1.57	0.53
2:G:260:GLU:HG2	2:G:261:PRO:HD2	1.90	0.53
2:H:48:ILE:CG1	2:H:197:ILE:HD11	2.38	0.53
1:B:120:ILE:HD12	2:D:94:LEU:CD2	2.38	0.53
2:C:224:THR:O	2:C:228:VAL:HG23	2.09	0.53
2:C:247:LEU:HD23	2:D:300:GLN:OE1	2.09	0.53
2:C:248:ASP:HB3	2:C:254:GLN:CD	2.33	0.53
1:E:12:GLY:C	1:E:172:LEU:HD21	2.33	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:143:LEU:N	1:E:144:PRO:HD2	2.24	0.53
1:F:19:MET:HB2	1:F:157:LEU:HD21	1.91	0.53
2:G:282:LEU:HD13	2:G:330:LEU:CD2	2.38	0.53
1:A:172:LEU:HD23	1:A:172:LEU:C	2.33	0.53
1:B:56:VAL:O	1:B:60:VAL:HG23	2.08	0.53
1:B:185:ASN:HB2	1:B:188:VAL:CG2	2.38	0.53
2:C:47:LEU:O	2:C:48:ILE:C	2.51	0.53
2:C:241:ILE:HB	2:C:243:SER:HB3	1.90	0.53
2:D:98:THR:HG22	2:D:138:PRO:CD	2.39	0.53
1:F:182:ILE:O	1:F:182:ILE:HG13	2.09	0.53
2:H:241:ILE:HD12	2:H:242:GLN:H	1.72	0.53
2:H:283:LEU:HD11	2:H:312:MET:HE1	1.90	0.53
2:C:162:LEU:HD23	2:C:163:LEU:N	2.24	0.53
2:C:247:LEU:HD13	2:C:297:ILE:CG2	2.38	0.53
2:D:163:LEU:CD2	2:D:195:LEU:HB3	2.37	0.53
1:E:34:VAL:HG21	1:E:105:ALA:HA	1.91	0.53
1:E:97:THR:O	1:E:101:ALA:N	2.42	0.53
1:F:126:MET:CE	1:F:129:THR:OG1	2.57	0.53
2:H:91:PHE:HE1	2:H:147:GLN:HB2	1.72	0.53
1:B:28:PHE:HB3	1:B:32:LEU:CD1	2.38	0.53
2:D:282:LEU:HD13	2:D:335:VAL:CG2	2.38	0.53
2:D:299:ALA:CB	2:D:312:MET:HG2	2.39	0.53
2:G:86:MET:SD	2:G:88:PHE:CE2	3.02	0.53
2:G:158:ASN:N	2:G:159:PRO:CD	2.71	0.53
2:H:105:LEU:HD22	2:H:109:LEU:HD21	1.91	0.53
2:C:44:LYS:CB	2:C:197:ILE:HD11	2.24	0.53
2:C:48:ILE:HD13	2:C:165:ASP:HB2	1.91	0.53
2:C:270:ARG:HG2	2:C:313:LEU:CD2	2.36	0.53
2:D:94:LEU:H	2:D:102:ASN:HD21	1.55	0.53
2:C:300:GLN:HE21	2:C:301:MET:H	1.57	0.53
2:H:33:ILE:CD1	2:H:207:ILE:HB	2.39	0.53
2:H:241:ILE:HG21	2:H:302:ASP:HB2	1.91	0.53
1:A:23:SER:HA	1:A:26:PHE:CD2	2.43	0.53
1:A:130:PRO:HG2	1:A:131:MET:N	2.10	0.53
1:B:92:ALA:C	1:B:95:PRO:HD2	2.34	0.53
2:D:148:ARG:O	2:D:151:ILE:HG12	2.09	0.53
1:E:22:VAL:O	1:E:26:PHE:CD2	2.62	0.53
1:E:75:MET:CE	1:E:98:VAL:HG21	2.39	0.53
2:G:247:LEU:HG	2:H:300:GLN:CG	2.39	0.53
2:H:124:LEU:CD2	2:H:152:ALA:O	2.57	0.53
1:A:13:VAL:HG21	1:A:195:LEU:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:68:PHE:CB	1:E:69:ILE:HD13	2.38	0.52
2:G:276:GLN:O	2:G:308:LYS:HD3	2.08	0.52
1:B:125:ALA:CB	2:D:54:LEU:HD21	2.33	0.52
1:E:27:GLY:HA2	1:E:104:ILE:CD1	2.40	0.52
2:H:269:LEU:HD23	2:H:339:VAL:HG22	1.91	0.52
1:A:135:ARG:HA	1:A:138:LEU:HD12	1.91	0.52
2:C:253:TYR:HD2	2:D:303:TYR:HE1	1.57	0.52
1:E:110:ASN:O	1:E:114:GLU:HG2	2.09	0.52
1:E:157:LEU:O	1:E:160:TYR:HB3	2.09	0.52
1:F:71:LEU:O	1:F:75:MET:HE3	2.09	0.52
1:F:161:SER:C	1:F:163:MET:N	2.65	0.52
2:H:33:ILE:HG23	2:H:194:ILE:CD1	2.38	0.52
1:F:59:ILE:C	1:F:62:ILE:HG12	2.34	0.52
1:F:59:ILE:CA	1:F:62:ILE:HG12	2.39	0.52
1:F:111:ALA:O	1:F:114:GLU:HB3	2.08	0.52
2:G:204:VAL:O	2:G:208:CYS:HB2	2.09	0.52
2:H:249:ILE:HG23	2:H:250:PRO:CD	2.36	0.52
1:B:38:LEU:HD22	1:B:112:LEU:HB3	1.91	0.52
2:D:130:LEU:HD11	2:D:134:HIS:HB2	1.90	0.52
1:E:16:THR:O	1:E:19:MET:HB2	2.09	0.52
1:E:40:VAL:CA	1:E:47:ILE:HD11	2.33	0.52
2:H:116:GLU:HA	2:H:119:ARG:HH11	1.73	0.52
1:A:41:THR:O	1:A:42:ARG:HB2	2.10	0.52
2:D:158:ASN:N	2:D:159:PRO:HD3	2.23	0.52
1:F:177:TYR:O	1:F:181:TYR:N	2.42	0.52
2:G:38:GLY:CA	2:G:44:LYS:HD3	2.40	0.52
2:H:97:ARG:NH2	2:H:108:GLU:OE1	2.39	0.52
1:A:122:ALA:HB1	2:C:88:PHE:CZ	2.45	0.52
1:A:180:GLY:C	1:B:73:VAL:HG13	2.35	0.52
1:B:133:ILE:HG21	2:D:109:LEU:HD22	1.91	0.52
2:C:137:TYR:HD2	2:C:138:PRO:N	2.08	0.52
2:D:44:LYS:CE	2:D:45:SER:OG	2.55	0.52
2:D:273:PHE:N	2:D:310:GLY:O	2.34	0.52
2:H:49:ARG:O	2:H:54:LEU:N	2.38	0.52
1:B:40:VAL:O	1:B:40:VAL:HG12	2.10	0.52
1:B:64:ARG:NE	1:B:103:PHE:HA	2.25	0.52
2:C:278:VAL:CA	2:C:308:LYS:HE2	2.39	0.52
2:G:298:SER:HB2	2:H:300:GLN:OE1	2.10	0.52
2:H:53:LEU:HD23	2:H:77:LEU:HD21	1.92	0.52
1:A:26:PHE:HZ	1:A:157:LEU:HD11	1.75	0.52
1:A:36:VAL:O	1:A:36:VAL:HG13	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:ASN:HB2	1:A:106:ARG:HH22	1.75	0.52
2:C:288:ARG:HH11	2:D:287:ALA:HB1	1.75	0.52
2:C:247:LEU:HD23	2:D:300:GLN:CD	2.35	0.52
2:D:61:SER:HB3	2:D:68:GLU:CD	2.35	0.52
1:F:36:VAL:O	1:F:36:VAL:CG1	2.58	0.52
2:H:87:ILE:CG2	2:H:88:PHE:N	2.73	0.52
2:H:141:LEU:HG	2:H:145:GLN:CB	2.39	0.52
1:A:100:ALA:O	1:A:104:ILE:HG12	2.10	0.51
1:B:123:SER:HB2	1:B:126:MET:CE	2.39	0.51
2:C:4:LEU:HD22	2:C:7:ILE:CD1	2.40	0.51
2:C:142:SER:N	2:C:145:GLN:OE1	2.35	0.51
2:C:151:ILE:CG1	2:C:152:ALA:N	2.69	0.51
2:C:247:LEU:HD13	2:C:297:ILE:HG22	1.91	0.51
2:D:212:ALA:HB1	2:D:219:LEU:HD11	1.91	0.51
2:D:238:GLN:HA	2:D:242:GLN:HB2	1.91	0.51
2:G:41:GLY:HA2	2:G:45:SER:OG	2.10	0.51
2:H:214:ILE:CG1	2:H:219:LEU:HD23	2.38	0.51
1:B:100:ALA:O	1:B:104:ILE:HG12	2.10	0.51
2:C:235:PRO:O	2:C:236:LEU:HG	2.10	0.51
2:D:52:ASN:OD1	2:D:54:LEU:HG	2.11	0.51
1:E:70:ILE:CD1	1:F:192:VAL:HG12	2.39	0.51
1:F:114:GLU:C	1:F:116:PRO:HD2	2.35	0.51
1:F:196:LEU:HD23	1:F:199:LEU:HD23	1.91	0.51
2:G:184:LYS:CG	2:G:207:ILE:HG22	2.35	0.51
2:H:33:ILE:HB	2:H:208:CYS:HA	1.92	0.51
1:A:100:ALA:HB2	1:A:157:LEU:HD21	1.93	0.51
1:A:180:GLY:C	1:B:73:VAL:CG1	2.83	0.51
1:B:40:VAL:HG12	1:B:53:TYR:HB2	1.92	0.51
1:B:40:VAL:HG11	1:B:52:LEU:HB2	1.92	0.51
1:B:131:MET:O	1:B:135:ARG:HG2	2.10	0.51
2:C:93:LEU:HD11	2:C:149:VAL:HB	1.92	0.51
1:E:18:ALA:O	1:E:22:VAL:HG23	2.11	0.51
2:G:205:LYS:HZ2	2:G:304:ALA:HB2	1.75	0.51
2:G:247:LEU:HD11	2:H:244:THR:CG2	2.39	0.51
1:A:122:ALA:O	1:A:125:ALA:HB3	2.11	0.51
1:A:148:ASN:O	1:A:151:THR:HG22	2.10	0.51
1:B:115:ILE:HG13	1:B:116:PRO:CD	2.39	0.51
1:E:67:PRO:HB2	1:E:70:ILE:HG22	1.92	0.51
2:G:271:LEU:HD22	2:G:335:VAL:HG12	1.92	0.51
2:H:49:ARG:HG2	2:H:54:LEU:HD12	1.93	0.51
2:H:105:LEU:CD2	2:H:109:LEU:HD21	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:ILE:HB	1:B:200:VAL:HG13	1.93	0.51
2:C:52:ASN:HD22	2:C:52:ASN:N	2.06	0.51
2:C:113:PRO:HD2	2:C:117:VAL:HG23	1.91	0.51
2:C:125:LEU:HB3	2:C:131:GLY:CA	2.36	0.51
2:D:1:MET:HE2	2:D:65:ASP:HA	1.91	0.51
2:D:206:ARG:HH11	2:D:206:ARG:HG3	1.75	0.51
2:D:266:VAL:CG2	2:D:317:HIS:HA	2.39	0.51
1:E:19:MET:HA	1:E:22:VAL:CG2	2.40	0.51
1:E:187:THR:O	1:E:191:THR:HG23	2.10	0.51
1:F:70:ILE:HG23	1:F:71:LEU:N	2.25	0.51
1:F:79:THR:HG22	1:F:85:THR:O	2.10	0.51
2:G:241:ILE:HD13	2:G:241:ILE:O	2.09	0.51
2:H:213:VAL:CB	2:H:233:LYS:HD2	2.40	0.51
1:A:131:MET:O	1:A:135:ARG:CG	2.57	0.51
1:A:185:ASN:HD22	1:A:188:VAL:CG2	2.22	0.51
1:A:189:MET:HE2	1:B:74:TRP:HB2	1.92	0.51
1:B:134:VAL:HA	1:B:137:VAL:CG1	2.36	0.51
2:C:162:LEU:C	2:C:162:LEU:CD2	2.83	0.51
2:D:234:THR:HG22	2:D:238:GLN:HG2	1.92	0.51
1:F:185:ASN:CG	1:F:188:VAL:HG22	2.36	0.51
2:H:113:PRO:O	2:H:117:VAL:HG23	2.10	0.51
1:B:128:ALA:HB1	2:D:78:THR:CG2	2.41	0.51
2:C:69:LEU:O	2:C:70:THR:HG23	2.11	0.51
2:C:91:PHE:CD2	2:C:146:LYS:HD2	2.46	0.51
2:D:162:LEU:C	2:D:162:LEU:HD23	2.35	0.51
2:D:204:VAL:HG13	2:D:208:CYS:HB2	1.93	0.51
1:E:196:LEU:O	1:E:199:LEU:HB3	2.10	0.51
1:F:35:GLY:HA3	1:F:108:VAL:HB	1.93	0.51
1:F:118:GLY:HA2	1:F:121:GLU:CD	2.35	0.51
2:G:241:ILE:O	2:G:241:ILE:HG23	2.11	0.51
1:A:56:VAL:O	1:A:59:ILE:HG12	2.10	0.51
1:A:141:GLU:OE2	2:C:95:SER:N	2.44	0.51
1:A:180:GLY:CA	1:B:73:VAL:HG11	2.39	0.51
1:B:18:ALA:O	1:B:22:VAL:HG23	2.10	0.51
1:E:192:VAL:HA	1:E:195:LEU:CD2	2.41	0.51
1:F:59:ILE:HG13	1:F:60:VAL:N	2.26	0.51
2:G:159:PRO:HG2	2:G:192:LEU:HD22	1.93	0.51
2:H:105:LEU:HB3	2:H:106:PRO:CD	2.41	0.51
1:A:81:VAL:HG23	1:A:82:ILE:HG13	1.92	0.51
2:C:1:MET:HE1	2:C:161:VAL:HG23	1.92	0.51
2:C:196:LEU:HD21	2:C:203:VAL:CG1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:83:GLN:NE2	2:D:159:PRO:HA	2.26	0.51
1:E:160:TYR:C	1:E:160:TYR:HD1	2.19	0.51
1:F:30:ILE:HD11	1:F:101:ALA:CA	2.41	0.51
1:F:126:MET:CG	2:H:109:LEU:HD13	2.38	0.51
1:A:19:MET:HA	1:A:22:VAL:HG23	1.92	0.51
2:C:30:ALA:HA	2:C:193:THR:OG1	2.10	0.51
2:D:84:ILE:HD11	2:D:163:LEU:CD1	2.41	0.51
1:E:15:GLU:C	1:E:19:MET:HE2	2.34	0.51
2:G:113:PRO:HB2	2:G:116:GLU:HB2	1.91	0.51
2:G:220:ILE:HD12	2:G:220:ILE:N	2.25	0.51
1:A:18:ALA:O	1:A:22:VAL:HG23	2.11	0.50
2:D:34:TYR:HH	2:D:222:GLN:HG3	1.76	0.50
2:D:201:MET:HG3	2:D:236:LEU:C	2.36	0.50
1:E:26:PHE:CD1	1:E:104:ILE:HD13	2.46	0.50
1:E:120:ILE:HD12	2:G:94:LEU:HD23	1.93	0.50
1:E:181:TYR:HD2	1:F:167:VAL:HG13	1.76	0.50
2:H:91:PHE:CE1	2:H:147:GLN:HB2	2.46	0.50
2:H:128:VAL:CG1	2:H:152:ALA:HB2	2.38	0.50
2:H:141:LEU:HG	2:H:145:GLN:HB3	1.91	0.50
1:A:163:MET:C	1:A:164:GLY:O	2.53	0.50
2:C:143:GLY:O	2:C:144:GLY:C	2.53	0.50
2:C:239:LYS:O	2:C:240:PHE:O	2.30	0.50
2:D:26:LEU:HD11	2:D:34:TYR:CE1	2.47	0.50
2:D:209:ASP:O	2:D:225:VAL:HG23	2.10	0.50
2:D:265:CYS:SG	2:D:342:TYR:HB3	2.51	0.50
2:D:273:PHE:HE1	2:D:335:VAL:HG13	1.74	0.50
1:E:39:TYR:HE2	1:E:46:ILE:HG13	1.76	0.50
1:E:70:ILE:HA	1:E:73:VAL:HG12	1.93	0.50
1:F:172:LEU:HD12	1:F:172:LEU:H	1.74	0.50
2:G:205:LYS:HZ3	2:G:304:ALA:HB2	1.74	0.50
2:H:37:ILE:HG23	2:H:213:VAL:HG22	1.92	0.50
1:B:33:PRO:O	1:B:36:VAL:HB	2.12	0.50
1:B:39:TYR:O	1:B:48:ALA:HB2	2.11	0.50
2:C:91:PHE:HE1	2:C:147:GLN:HB2	1.76	0.50
2:C:234:THR:N	2:C:235:PRO:CD	2.74	0.50
2:C:274:THR:O	2:C:276:GLN:N	2.44	0.50
1:E:98:VAL:O	1:E:102:PRO:HD2	2.10	0.50
1:B:37:LEU:HD21	1:B:56:VAL:CB	2.41	0.50
2:C:107:LEU:HD12	2:C:121:VAL:CG2	2.41	0.50
2:D:234:THR:N	2:D:235:PRO:HD2	2.27	0.50
1:E:39:TYR:CE2	1:E:46:ILE:HG13	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:10:VAL:HG13	2:G:10:VAL:O	2.11	0.50
2:G:52:ASN:C	2:G:52:ASN:HD22	2.18	0.50
2:G:97:ARG:HH11	2:G:105:LEU:HD11	1.76	0.50
2:G:249:ILE:HD11	2:H:177:ARG:HH21	1.76	0.50
2:H:270:ARG:HA	2:H:313:LEU:CD2	2.41	0.50
1:A:198:ILE:HG13	1:A:199:LEU:N	2.26	0.50
2:C:205:LYS:HD2	2:C:304:ALA:HB2	1.92	0.50
1:E:108:VAL:HG12	1:E:112:LEU:HD11	1.92	0.50
1:F:15:GLU:O	1:F:18:ALA:HB3	2.11	0.50
1:F:107:MET:CE	1:F:152:ILE:HD11	2.40	0.50
1:F:130:PRO:HD2	1:F:133:ILE:CB	2.41	0.50
2:G:35:GLY:O	2:G:212:ALA:N	2.38	0.50
2:H:52:ASN:O	2:H:81:ARG:NH1	2.45	0.50
1:A:115:ILE:HG12	1:A:116:PRO:N	2.27	0.50
1:A:199:LEU:O	1:A:203:ILE:HG13	2.11	0.50
1:B:37:LEU:HD21	1:B:56:VAL:HG12	1.90	0.50
2:C:149:VAL:O	2:C:152:ALA:HB3	2.11	0.50
1:E:160:TYR:HD1	1:E:160:TYR:O	1.95	0.50
1:F:57:SER:O	1:F:61:ASN:HB2	2.12	0.50
1:F:100:ALA:C	1:F:104:ILE:HG13	2.36	0.50
2:G:241:ILE:HD13	2:G:242:GLN:HB2	1.93	0.50
2:H:28:VAL:HG13	2:H:34:TYR:HB2	1.94	0.50
2:H:89:GLN:HG2	2:H:166:GLU:HB2	1.94	0.50
1:B:22:VAL:HG11	1:B:93:ILE:CB	2.34	0.50
2:C:52:ASN:ND2	2:C:54:LEU:HG	2.27	0.50
1:E:92:ALA:HB2	1:E:169:ALA:CB	2.34	0.50
1:F:63:PHE:O	1:F:66:ILE:HB	2.12	0.50
1:F:165:GLY:HA2	1:F:174:GLN:CA	2.41	0.50
1:F:173:GLY:O	1:F:177:TYR:CB	2.59	0.50
2:G:247:LEU:HD11	2:H:244:THR:HG23	1.93	0.50
1:A:69:ILE:HG13	1:B:163:MET:SD	2.51	0.50
1:A:79:THR:O	1:A:82:ILE:O	2.29	0.50
1:B:26:PHE:CB	1:B:97:THR:HB	2.42	0.50
1:B:40:VAL:CG1	1:B:52:LEU:HB2	2.42	0.50
2:C:234:THR:H	2:C:235:PRO:HD2	1.77	0.50
2:D:241:ILE:HG22	2:D:245:LEU:CD1	2.38	0.50
2:D:249:ILE:HG22	2:D:313:LEU:CD1	2.42	0.50
2:D:327:ILE:CG1	2:D:328:ALA:N	2.70	0.50
1:F:30:ILE:HD11	1:F:101:ALA:HA	1.94	0.50
1:F:121:GLU:OE1	2:H:92:ASN:CG	2.54	0.50
1:F:122:ALA:HB1	1:F:126:MET:CE	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:7:ILE:HD11	2:G:62:VAL:HG22	1.94	0.50
2:G:243:SER:HA	2:H:244:THR:HG21	1.92	0.50
2:H:34:TYR:CZ	2:H:212:ALA:HB2	2.47	0.50
2:H:226:SER:OG	2:H:305:GLY:HA3	2.12	0.50
1:B:85:THR:HG22	1:B:87:ILE:H	1.77	0.50
2:C:21:LEU:HD11	2:C:46:THR:HG22	1.94	0.50
2:D:84:ILE:HD11	2:D:163:LEU:HG	1.94	0.50
2:H:130:LEU:HD11	2:H:148:ARG:HB2	1.93	0.50
2:H:245:LEU:HB3	2:H:313:LEU:HD11	1.93	0.50
1:B:122:ALA:HB1	2:D:88:PHE:CZ	2.47	0.49
2:C:2:ILE:HD11	2:C:195:LEU:CD2	2.40	0.49
2:C:36:VAL:HB	2:C:197:ILE:CD1	2.42	0.49
2:C:107:LEU:CD1	2:C:121:VAL:HG23	2.43	0.49
1:E:63:PHE:HB3	1:E:102:PRO:HG3	1.94	0.49
1:E:71:LEU:HD13	1:E:160:TYR:OH	2.11	0.49
1:F:124:ARG:O	1:F:127:GLY:N	2.45	0.49
2:G:49:ARG:HH11	2:G:49:ARG:HG3	1.77	0.49
2:H:87:ILE:HD12	2:H:162:LEU:HD21	1.95	0.49
2:H:125:LEU:O	2:H:130:LEU:O	2.29	0.49
1:A:159:GLY:O	1:B:68:PHE:HE1	1.96	0.49
1:B:161:SER:O	1:B:164:GLY:N	2.46	0.49
2:D:234:THR:N	2:D:235:PRO:CD	2.74	0.49
2:H:220:ILE:CB	2:H:233:LYS:HD3	2.42	0.49
1:A:123:SER:O	1:A:128:ALA:HB2	2.12	0.49
2:C:43:GLY:C	2:C:45:SER:H	2.09	0.49
2:C:239:LYS:HG3	2:C:240:PHE:CE1	2.48	0.49
1:E:34:VAL:HG21	1:E:105:ALA:CA	2.41	0.49
1:F:127:GLY:O	1:F:128:ALA:HB2	2.13	0.49
2:G:51:VAL:HG11	2:G:163:LEU:HD21	1.95	0.49
2:H:5:SER:HB2	2:H:61:SER:O	2.12	0.49
2:H:231:HIS:C	2:H:233:LYS:H	2.20	0.49
2:D:184:LYS:CE	2:D:207:ILE:HG22	2.42	0.49
1:F:130:PRO:CD	1:F:133:ILE:HB	2.42	0.49
2:H:12:HIS:CE1	2:H:14:GLY:HA2	2.47	0.49
2:C:10:VAL:HG23	2:C:18:ILE:O	2.13	0.49
2:C:147:GLN:HA	2:C:147:GLN:NE2	2.19	0.49
2:C:147:GLN:O	2:C:150:ALA:HB3	2.12	0.49
2:D:33:ILE:HG21	2:D:207:ILE:HD12	1.94	0.49
2:D:43:GLY:H	2:D:44:LYS:HZ3	1.58	0.49
1:B:123:SER:HB2	1:B:126:MET:HE2	1.94	0.49
2:D:34:TYR:OH	2:D:222:GLN:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:215:SER:HB3	2:D:220:ILE:CD1	2.42	0.49
1:F:56:VAL:O	1:F:59:ILE:HG12	2.12	0.49
2:G:147:GLN:HG2	2:G:171:LEU:HD11	1.94	0.49
2:G:245:LEU:HD23	2:H:173:PRO:HG3	1.94	0.49
1:B:80:ARG:CB	1:B:86:SER:HB3	2.43	0.49
2:C:47:LEU:C	2:C:49:ARG:N	2.70	0.49
2:C:321:GLN:O	2:C:324:GLN:HB2	2.13	0.49
2:D:52:ASN:ND2	2:D:86:MET:CE	2.75	0.49
2:D:184:LYS:HE2	2:D:207:ILE:HG22	1.94	0.49
2:D:1:MET:CE	2:D:65:ASP:HA	2.42	0.49
1:E:110:ASN:OD1	1:E:113:LEU:HD12	2.13	0.49
1:F:68:PHE:N	1:F:68:PHE:CD1	2.79	0.49
2:G:62:VAL:O	2:G:69:LEU:N	2.37	0.49
2:G:278:VAL:C	2:G:280:ALA:H	2.20	0.49
2:H:44:LYS:CG	2:H:45:SER:N	2.75	0.49
2:H:77:LEU:O	2:H:81:ARG:HG3	2.12	0.49
1:A:96:LEU:HD12	1:A:96:LEU:N	2.27	0.49
1:A:98:VAL:O	1:A:102:PRO:HD2	2.12	0.49
1:B:28:PHE:HB3	1:B:32:LEU:HD12	1.94	0.49
2:D:198:THR:HG21	2:D:203:VAL:CB	2.40	0.49
1:E:89:LEU:CD2	1:E:170:GLY:HA2	2.43	0.49
1:E:125:ALA:CB	2:G:54:LEU:HD21	2.43	0.49
1:F:98:VAL:O	1:F:102:PRO:HD2	2.13	0.49
2:G:1:MET:CE	2:G:161:VAL:HG22	2.43	0.49
2:G:293:ASN:HB2	2:G:317:HIS:HB2	1.94	0.49
1:A:185:ASN:HD22	1:A:188:VAL:HG21	1.78	0.49
2:C:7:ILE:HA	2:C:59:GLU:O	2.13	0.49
1:E:155:ILE:CD1	1:F:64:ARG:HH22	2.26	0.49
1:F:126:MET:HA	2:H:109:LEU:CD1	2.37	0.49
2:G:7:ILE:O	2:G:24:VAL:HG22	2.13	0.49
2:G:144:GLY:HA2	2:G:175:THR:HG21	1.94	0.49
2:G:145:GLN:O	2:G:149:VAL:HG23	2.12	0.49
2:H:56:ARG:HD3	2:H:71:THR:HG21	1.94	0.49
1:A:9:LEU:HD23	1:A:9:LEU:N	2.27	0.48
1:A:82:ILE:O	1:A:83:VAL:C	2.55	0.48
1:A:163:MET:O	1:A:164:GLY:O	2.31	0.48
1:B:92:ALA:O	1:B:95:PRO:HG2	2.13	0.48
2:C:298:SER:O	2:C:299:ALA:HB2	2.13	0.48
2:C:300:GLN:HE21	2:C:300:GLN:HA	1.77	0.48
2:D:249:ILE:HG13	2:D:250:PRO:O	2.13	0.48
2:D:268:MET:HE3	2:D:313:LEU:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:48:ALA:HA	1:E:53:TYR:H	1.77	0.48
2:G:299:ALA:HB2	2:G:312:MET:CA	2.39	0.48
2:H:223:ASP:OD1	2:H:224:THR:N	2.46	0.48
1:A:30:ILE:HD12	1:A:101:ALA:HB2	1.95	0.48
1:A:73:VAL:HG13	1:B:189:MET:SD	2.53	0.48
1:B:13:VAL:N	1:B:172:LEU:HD12	2.28	0.48
1:E:108:VAL:HG12	1:E:112:LEU:CD1	2.43	0.48
1:F:119:LEU:O	1:F:123:SER:N	2.46	0.48
2:G:56:ARG:NH1	2:G:56:ARG:HB2	2.28	0.48
2:H:183:LEU:HA	2:H:186:ILE:HG12	1.95	0.48
1:A:59:ILE:CA	1:A:62:ILE:HG12	2.43	0.48
2:C:1:MET:CE	2:C:161:VAL:HG23	2.43	0.48
2:C:77:LEU:HD21	2:C:81:ARG:CZ	2.43	0.48
2:C:148:ARG:O	2:C:149:VAL:C	2.54	0.48
2:C:177:ARG:CZ	2:C:206:ARG:NH2	2.77	0.48
2:C:290:PHE:CE2	2:C:329:TRP:CB	2.96	0.48
2:C:290:PHE:HE2	2:C:329:TRP:CB	2.26	0.48
1:E:74:TRP:HA	1:F:189:MET:CE	2.42	0.48
2:G:213:VAL:HG21	2:G:233:LYS:CD	2.43	0.48
2:H:274:THR:CG2	2:H:336:LYS:HE2	2.43	0.48
2:H:309:PHE:O	2:H:311:ILE:HD12	2.14	0.48
1:A:67:PRO:HD2	1:A:70:ILE:HG21	1.95	0.48
1:A:69:ILE:HD12	1:B:163:MET:SD	2.54	0.48
1:B:36:VAL:O	1:B:40:VAL:HG23	2.14	0.48
1:B:79:THR:HG22	1:B:86:SER:HA	1.94	0.48
2:D:141:LEU:HG	2:D:142:SER:N	2.29	0.48
1:F:32:LEU:HD23	1:F:108:VAL:CG2	2.42	0.48
1:A:74:TRP:HE1	1:B:190:ASN:ND2	2.11	0.48
1:A:85:THR:O	1:A:86:SER:HB3	2.14	0.48
2:C:211:VAL:CG1	2:C:228:VAL:HG21	2.43	0.48
2:D:35:GLY:O	2:D:212:ALA:N	2.41	0.48
1:F:80:ARG:HA	1:F:85:THR:HA	1.95	0.48
1:F:161:SER:C	1:F:163:MET:H	2.21	0.48
2:H:231:HIS:O	2:H:233:LYS:N	2.44	0.48
1:A:47:ILE:HG23	1:A:47:ILE:O	2.12	0.48
2:G:301:MET:HA	2:G:309:PHE:O	2.13	0.48
2:H:33:ILE:CG2	2:H:194:ILE:HD11	2.40	0.48
2:H:211:VAL:CG1	2:H:225:VAL:HG22	2.44	0.48
1:B:106:ARG:O	1:B:106:ARG:HG2	2.11	0.48
1:B:167:VAL:CG2	1:B:168:GLY:H	2.23	0.48
2:C:130:LEU:CD2	2:C:145:GLN:HA	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:266:VAL:HG21	2:D:317:HIS:CG	2.47	0.48
1:F:124:ARG:HD3	2:H:86:MET:SD	2.54	0.48
1:F:124:ARG:HH11	2:H:86:MET:HB3	1.75	0.48
1:F:126:MET:CA	2:H:109:LEU:HD13	2.40	0.48
2:G:9:LYS:HE2	2:G:55:GLU:HB3	1.95	0.48
2:G:124:LEU:CD1	2:G:156:ALA:HA	2.44	0.48
2:H:82:ARG:CD	2:H:110:ASP:CG	2.86	0.48
2:H:331:GLN:HA	2:H:335:VAL:O	2.14	0.48
1:A:130:PRO:CG	1:A:131:MET:N	2.72	0.48
1:B:59:ILE:O	1:B:62:ILE:HG12	2.14	0.48
2:C:99:VAL:HG22	2:C:149:VAL:HG22	1.96	0.48
2:D:33:ILE:CD1	2:D:207:ILE:HB	2.44	0.48
2:D:248:ASP:O	2:D:249:ILE:O	2.31	0.48
2:G:4:LEU:CD2	2:G:62:VAL:HG13	2.41	0.48
2:G:51:VAL:HB	2:G:163:LEU:HD11	1.94	0.48
2:G:196:LEU:HD23	2:G:208:CYS:SG	2.53	0.48
2:H:6:ASN:N	2:H:25:SER:OG	2.43	0.48
2:H:10:VAL:HG23	2:H:18:ILE:O	2.14	0.48
1:A:22:VAL:O	1:A:25:PHE:HB3	2.14	0.48
1:A:165:GLY:HA2	1:A:174:GLN:HG2	1.96	0.48
2:C:107:LEU:HD12	2:C:121:VAL:HG23	1.95	0.48
2:C:177:ARG:NE	2:C:206:ARG:NH2	2.62	0.48
2:D:42:ALA:N	2:D:44:LYS:HZ2	2.12	0.48
1:E:196:LEU:HD23	1:E:199:LEU:CD2	2.42	0.48
1:F:37:LEU:O	1:F:41:THR:HG23	2.13	0.48
1:F:172:LEU:N	1:F:172:LEU:CD1	2.75	0.48
2:H:44:LYS:HG3	2:H:45:SER:N	2.27	0.48
2:H:48:ILE:HG21	2:H:197:ILE:CD1	2.40	0.48
2:H:201:MET:O	2:H:204:VAL:N	2.47	0.48
2:H:243:SER:HA	2:H:246:HIS:CD2	2.49	0.48
1:B:132:GLN:O	1:B:136:LYS:HG2	2.13	0.48
2:C:253:TYR:HD2	2:D:303:TYR:CE1	2.32	0.48
1:F:22:VAL:CG2	1:F:23:SER:N	2.77	0.48
1:F:172:LEU:CD1	1:F:172:LEU:H	2.27	0.48
2:G:37:ILE:CD1	2:G:236:LEU:HB3	2.44	0.48
1:B:22:VAL:HG13	1:B:93:ILE:HD12	1.96	0.47
1:B:126:MET:SD	2:D:153:ARG:CD	3.01	0.47
2:C:214:ILE:HG13	2:C:219:LEU:HD23	1.96	0.47
1:F:121:GLU:O	1:F:125:ALA:HB2	2.14	0.47
2:H:53:LEU:HG	2:H:53:LEU:O	2.13	0.47
1:A:166:ALA:HB1	1:B:181:TYR:HE2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:PHE:CD1	1:B:97:THR:HA	2.48	0.47
1:B:70:ILE:O	1:B:70:ILE:HG13	2.09	0.47
1:B:72:LEU:HD22	1:B:95:PRO:CB	2.20	0.47
1:E:163:MET:O	1:E:166:ALA:HB3	2.14	0.47
1:F:118:GLY:C	1:F:121:GLU:HB2	2.40	0.47
2:G:249:ILE:HD13	2:H:177:ARG:HE	1.79	0.47
2:H:299:ALA:HA	2:H:311:ILE:O	2.15	0.47
1:A:76:ILE:HB	1:A:77:PRO:HD3	1.96	0.47
1:A:104:ILE:HG13	1:A:105:ALA:N	2.30	0.47
1:B:93:ILE:O	1:B:97:THR:HG23	2.14	0.47
2:C:28:VAL:O	2:C:29:PRO:O	2.32	0.47
2:D:143:GLY:HA2	2:D:146:LYS:HD2	1.94	0.47
1:E:174:GLN:HG2	1:E:177:TYR:CG	2.49	0.47
1:F:13:VAL:N	1:F:172:LEU:HD11	2.29	0.47
1:F:71:LEU:HD21	1:F:98:VAL:CG1	2.44	0.47
2:G:112:THR:N	2:G:113:PRO:CD	2.77	0.47
2:H:106:PRO:HA	2:H:109:LEU:HB2	1.96	0.47
1:A:87:ILE:CG2	1:A:88:GLY:N	2.77	0.47
1:B:68:PHE:O	1:B:71:LEU:HB3	2.14	0.47
2:C:31:GLY:N	2:C:193:THR:OG1	2.46	0.47
2:C:63:LEU:HD11	2:C:66:GLY:C	2.39	0.47
2:C:296:ILE:HD13	2:D:296:ILE:CD1	2.44	0.47
1:E:63:PHE:CB	1:E:102:PRO:HG3	2.45	0.47
1:F:37:LEU:CD2	1:F:56:VAL:HG11	2.43	0.47
2:H:84:ILE:HG13	2:H:161:VAL:HB	1.96	0.47
2:H:125:LEU:HA	2:H:128:VAL:HG22	1.96	0.47
2:H:245:LEU:HG	2:H:298:SER:CB	2.44	0.47
1:A:47:ILE:O	1:A:48:ALA:HB2	2.14	0.47
1:A:139:LEU:O	1:A:143:LEU:N	2.46	0.47
1:A:161:SER:O	1:A:164:GLY:N	2.47	0.47
1:A:169:ALA:O	1:A:174:GLN:NE2	2.48	0.47
1:B:101:ALA:HA	1:B:104:ILE:CG1	2.45	0.47
2:C:168:THR:HB	2:C:176:THR:CG2	2.44	0.47
2:C:234:THR:HA	2:C:237:ALA:CB	2.38	0.47
1:E:132:GLN:O	1:E:136:LYS:HB2	2.15	0.47
1:F:31:GLY:HA3	1:F:104:ILE:HD13	1.95	0.47
2:G:298:SER:O	2:G:299:ALA:HB2	2.14	0.47
2:H:127:LEU:O	2:H:127:LEU:HD12	2.14	0.47
1:A:40:VAL:HG13	1:A:49:ASN:HA	1.97	0.47
1:B:128:ALA:CB	2:D:78:THR:HG23	2.45	0.47
1:B:166:ALA:HA	1:B:177:TYR:CD2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:124:LEU:HD21	2:C:156:ALA:HA	1.96	0.47
2:D:43:GLY:N	2:D:44:LYS:NZ	2.48	0.47
2:D:98:THR:CA	2:D:138:PRO:HB3	2.41	0.47
1:E:70:ILE:HD11	1:F:193:LEU:CA	2.45	0.47
1:F:123:SER:CA	1:F:129:THR:HG21	2.44	0.47
2:G:163:LEU:HD23	2:G:195:LEU:HB3	1.97	0.47
2:G:246:HIS:HB3	2:H:241:ILE:CG2	2.45	0.47
2:H:34:TYR:CE1	2:H:212:ALA:HB2	2.50	0.47
2:H:121:VAL:HG12	2:H:125:LEU:CD1	2.43	0.47
1:A:41:THR:HG21	1:A:113:LEU:HD21	1.97	0.47
2:C:2:ILE:HG23	2:C:28:VAL:O	2.14	0.47
2:C:58:THR:O	2:C:59:GLU:HG3	2.15	0.47
2:C:98:THR:HA	2:C:138:PRO:HB3	1.95	0.47
2:C:211:VAL:HG22	2:C:212:ALA:N	2.29	0.47
2:D:128:VAL:HA	2:D:182:LEU:HD11	1.97	0.47
2:D:162:LEU:HB3	2:D:194:ILE:CG2	2.41	0.47
2:D:274:THR:C	2:D:276:GLN:N	2.71	0.47
1:F:26:PHE:CE2	1:F:97:THR:HG22	2.50	0.47
1:F:39:TYR:OH	1:F:135:ARG:HD2	2.15	0.47
1:F:118:GLY:O	1:F:121:GLU:HB2	2.15	0.47
1:F:179:TYR:O	1:F:185:ASN:CB	2.59	0.47
1:F:206:ALA:O	1:F:207:GLY:C	2.57	0.47
2:G:241:ILE:HB	2:G:302:ASP:OD1	2.14	0.47
2:H:63:LEU:HD13	2:H:68:GLU:CG	2.44	0.47
2:H:91:PHE:O	2:H:92:ASN:HB2	2.14	0.47
2:H:125:LEU:HA	2:H:128:VAL:CG2	2.45	0.47
2:C:8:THR:HG23	2:C:21:LEU:O	2.15	0.47
2:C:104:ALA:O	2:C:107:LEU:HB2	2.15	0.47
2:C:130:LEU:HD22	2:C:148:ARG:HD2	1.97	0.47
2:C:247:LEU:C	2:C:250:PRO:HD2	2.39	0.47
2:D:37:ILE:HD12	2:D:201:MET:SD	2.55	0.47
2:D:44:LYS:H	2:D:44:LYS:CD	2.21	0.47
2:D:53:LEU:O	2:D:53:LEU:HG	2.15	0.47
2:H:37:ILE:HG23	2:H:37:ILE:O	2.14	0.47
2:H:139:SER:C	2:H:141:LEU:H	2.21	0.47
1:A:147:VAL:O	1:A:151:THR:HG22	2.15	0.47
2:C:247:LEU:CD2	2:C:297:ILE:O	2.62	0.47
2:C:249:ILE:O	2:C:251:GLU:N	2.48	0.47
1:E:153:THR:O	1:E:157:LEU:N	2.39	0.47
1:F:76:ILE:CB	1:F:77:PRO:HD3	2.45	0.47
1:F:117:THR:C	1:F:119:LEU:N	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:103:VAL:O	2:G:106:PRO:HD2	2.14	0.47
2:G:221:GLU:OE1	2:G:230:SER:HB3	2.14	0.47
2:H:33:ILE:CD1	2:H:207:ILE:O	2.57	0.47
1:B:117:THR:HB	1:B:118:GLY:H	1.43	0.47
2:C:247:LEU:HD22	2:C:297:ILE:O	2.14	0.47
2:D:144:GLY:HA2	2:D:171:LEU:HD22	1.97	0.47
1:E:75:MET:HE2	1:E:95:PRO:HA	1.97	0.47
1:E:104:ILE:O	1:E:107:MET:HB2	2.15	0.47
2:G:142:SER:O	2:G:146:LYS:HG3	2.14	0.47
2:G:245:LEU:N	2:G:245:LEU:HD12	2.29	0.47
2:G:283:LEU:HD13	2:G:296:ILE:HD11	1.97	0.47
2:H:189:ARG:C	2:H:190:LEU:O	2.57	0.47
2:H:242:GLN:HB2	2:H:311:ILE:HD13	1.95	0.47
2:H:283:LEU:HD11	2:H:312:MET:CE	2.45	0.47
1:A:17:LEU:HD23	1:A:17:LEU:N	2.30	0.46
2:C:2:ILE:HD11	2:C:195:LEU:HD22	1.97	0.46
2:D:102:ASN:O	2:D:105:LEU:HB2	2.15	0.46
2:D:285:GLU:HG2	2:D:329:TRP:CH2	2.50	0.46
1:F:75:MET:HB2	1:F:75:MET:HE3	1.84	0.46
1:F:138:LEU:HA	1:F:138:LEU:HD23	1.60	0.46
1:B:26:PHE:HB3	1:B:97:THR:HB	1.98	0.46
2:C:125:LEU:CB	2:C:131:GLY:HA3	2.38	0.46
2:D:228:VAL:O	2:D:229:PHE:HD2	1.98	0.46
1:E:30:ILE:HA	1:E:33:PRO:HG2	1.97	0.46
1:E:165:GLY:O	1:E:174:GLN:HG3	2.14	0.46
1:F:30:ILE:CD1	1:F:101:ALA:HB1	2.43	0.46
1:F:40:VAL:HG12	1:F:53:TYR:HB2	1.98	0.46
1:F:60:VAL:HG13	1:F:102:PRO:HA	1.96	0.46
2:G:282:LEU:O	2:G:286:THR:HG23	2.16	0.46
2:G:300:GLN:HG2	2:H:298:SER:CB	2.45	0.46
1:A:46:ILE:HG13	1:A:135:ARG:NH2	2.22	0.46
1:A:70:ILE:CG2	1:A:71:LEU:N	2.78	0.46
2:C:130:LEU:HD22	2:C:148:ARG:CB	2.43	0.46
2:C:204:VAL:HG13	2:C:208:CYS:HB2	1.96	0.46
2:D:73:SER:HB2	2:D:76:GLU:CG	2.44	0.46
2:D:115:ASP:C	2:D:117:VAL:N	2.70	0.46
2:D:206:ARG:NH1	2:D:206:ARG:HG3	2.30	0.46
1:E:50:ALA:HB3	1:E:52:LEU:HD12	1.96	0.46
2:G:33:ILE:HG12	2:G:194:ILE:HD11	1.97	0.46
2:G:186:ILE:HD12	2:G:192:LEU:HD12	1.97	0.46
2:G:300:GLN:NE2	2:H:244:THR:OG1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:147:GLN:HG2	2:H:179:ILE:HD13	1.97	0.46
2:H:243:SER:HA	2:H:246:HIS:NE2	2.30	0.46
1:B:63:PHE:CB	1:B:102:PRO:HG3	2.42	0.46
1:F:22:VAL:O	1:F:25:PHE:HB2	2.16	0.46
1:F:41:THR:HA	1:F:53:TYR:CD2	2.50	0.46
2:G:130:LEU:HD23	2:G:149:VAL:HG22	1.96	0.46
2:G:221:GLU:OE1	2:G:231:HIS:N	2.41	0.46
2:G:319:THR:O	2:G:323:THR:HG23	2.16	0.46
2:H:56:ARG:CD	2:H:71:THR:HG21	2.45	0.46
2:H:250:PRO:HG2	2:H:253:TYR:HB2	1.97	0.46
1:A:169:ALA:C	1:A:174:GLN:NE2	2.74	0.46
1:B:107:MET:HE3	1:B:149:ALA:HB1	1.96	0.46
2:C:130:LEU:CD2	2:C:148:ARG:HB2	2.43	0.46
2:D:52:ASN:HD21	2:D:86:MET:HE1	1.80	0.46
2:D:144:GLY:HA2	2:D:175:THR:CG2	2.44	0.46
2:D:224:THR:O	2:D:228:VAL:HG23	2.15	0.46
1:F:138:LEU:C	1:F:140:PRO:HD2	2.41	0.46
2:G:7:ILE:HG21	2:G:50:CYS:SG	2.56	0.46
2:G:268:MET:HE2	2:G:297:ILE:CD1	2.45	0.46
2:G:299:ALA:CB	2:G:312:MET:HA	2.39	0.46
1:A:26:PHE:CE2	1:A:157:LEU:HD11	2.50	0.46
2:C:37:ILE:HD12	2:C:198:THR:HG23	1.96	0.46
2:C:84:ILE:HG23	2:C:84:ILE:O	2.16	0.46
2:D:28:VAL:HG22	2:D:34:TYR:CD2	2.51	0.46
2:D:52:ASN:HD21	2:D:54:LEU:HG	1.81	0.46
2:D:76:GLU:O	2:D:79:LYS:HB2	2.16	0.46
2:D:242:GLN:O	2:D:246:HIS:HB3	2.15	0.46
1:E:182:ILE:O	1:E:182:ILE:HG13	2.16	0.46
1:F:59:ILE:O	1:F:63:PHE:HD1	1.99	0.46
1:F:124:ARG:CZ	2:H:86:MET:CB	2.94	0.46
1:F:126:MET:C	1:F:128:ALA:N	2.64	0.46
2:G:271:LEU:HD22	2:G:335:VAL:CG1	2.45	0.46
2:H:48:ILE:H	2:H:48:ILE:HD13	1.64	0.46
2:H:201:MET:SD	2:H:204:VAL:HB	2.55	0.46
1:A:132:GLN:O	1:A:133:ILE:C	2.57	0.46
1:B:129:THR:HA	1:B:133:ILE:CB	2.46	0.46
2:C:97:ARG:NH1	2:C:105:LEU:HD23	2.31	0.46
2:C:327:ILE:HG13	2:C:328:ALA:N	2.31	0.46
1:E:188:VAL:HG23	1:E:189:MET:N	2.31	0.46
1:F:123:SER:HA	1:F:129:THR:HB	1.96	0.46
1:F:152:ILE:H	1:F:152:ILE:HG13	1.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:211:VAL:HB	2:H:225:VAL:HG22	1.97	0.46
1:A:118:GLY:O	1:A:121:GLU:N	2.49	0.46
2:C:234:THR:O	2:C:237:ALA:HB3	2.15	0.46
2:D:163:LEU:HD21	2:D:195:LEU:HD23	1.98	0.46
2:D:250:PRO:HG2	2:D:253:TYR:CB	2.46	0.46
1:F:8:LEU:HD23	1:F:8:LEU:H	1.81	0.46
1:A:74:TRP:CG	1:B:193:LEU:HD11	2.51	0.46
2:C:26:LEU:HG	2:C:28:VAL:HG23	1.97	0.46
2:C:278:VAL:O	2:C:280:ALA:N	2.43	0.46
2:C:313:LEU:HD23	2:C:313:LEU:HA	1.62	0.46
1:E:70:ILE:HD11	1:F:193:LEU:N	2.30	0.46
1:F:71:LEU:HD11	1:F:98:VAL:HG12	1.97	0.46
2:G:83:GLN:O	2:G:159:PRO:CB	2.58	0.46
2:G:85:GLY:C	2:G:162:LEU:HD12	2.40	0.46
2:G:162:LEU:HB3	2:G:194:ILE:HG22	1.97	0.46
2:H:151:ILE:HG13	2:H:152:ALA:N	2.29	0.46
2:H:241:ILE:CG2	2:H:302:ASP:HB2	2.46	0.46
2:H:270:ARG:HB2	2:H:340:LEU:HD21	1.98	0.46
1:A:70:ILE:HD11	1:B:192:VAL:HG11	1.97	0.46
1:A:92:ALA:O	1:A:95:PRO:HD2	2.15	0.46
1:A:105:ALA:O	1:A:108:VAL:HB	2.15	0.46
1:A:143:LEU:O	1:A:144:PRO:C	2.55	0.46
1:F:126:MET:HE1	1:F:134:VAL:CB	2.46	0.46
2:G:77:LEU:HD21	2:G:81:ARG:HH22	1.77	0.46
2:G:283:LEU:HB3	2:G:294:ASN:ND2	2.31	0.46
2:H:5:SER:O	2:H:6:ASN:C	2.58	0.46
1:A:30:ILE:O	1:A:34:VAL:HG22	2.16	0.45
1:B:30:ILE:C	1:B:33:PRO:HD2	2.41	0.45
1:B:43:PRO:HG2	1:B:45:GLN:HG2	1.98	0.45
2:C:56:ARG:HA	2:C:57:PRO:HD2	1.71	0.45
2:D:120:ARG:O	2:D:124:LEU:HD22	2.16	0.45
2:D:245:LEU:O	2:D:313:LEU:HD11	2.16	0.45
1:E:40:VAL:HA	1:E:47:ILE:CD1	2.34	0.45
1:F:68:PHE:HD1	1:F:68:PHE:N	2.11	0.45
2:G:28:VAL:HG22	2:G:34:TYR:CD2	2.51	0.45
2:G:52:ASN:C	2:G:52:ASN:ND2	2.74	0.45
2:H:43:GLY:C	2:H:45:SER:H	2.10	0.45
2:H:323:THR:O	2:H:327:ILE:HG12	2.16	0.45
1:A:40:VAL:CG1	1:A:53:TYR:HB2	2.46	0.45
1:A:93:ILE:O	1:A:97:THR:HG23	2.16	0.45
1:A:153:THR:O	1:A:157:LEU:N	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:234:THR:C	2:C:237:ALA:HB3	2.40	0.45
1:E:66:ILE:HG12	1:F:193:LEU:CD2	2.45	0.45
1:E:138:LEU:O	1:E:141:GLU:HB2	2.16	0.45
1:F:35:GLY:C	1:F:37:LEU:N	2.67	0.45
2:G:184:LYS:NZ	2:G:206:ARG:O	2.49	0.45
2:G:244:THR:HB	2:G:247:LEU:CD1	2.46	0.45
2:G:301:MET:SD	2:G:308:LYS:HE3	2.57	0.45
2:G:329:TRP:O	2:G:332:GLU:HB2	2.16	0.45
1:A:66:ILE:HD13	1:B:193:LEU:HD13	1.98	0.45
2:C:73:SER:HB2	2:C:76:GLU:HB2	1.97	0.45
2:D:242:GLN:HE22	2:D:311:ILE:HD12	1.81	0.45
1:E:148:ASN:O	1:E:151:THR:HB	2.17	0.45
1:F:196:LEU:HD23	1:F:199:LEU:CD2	2.47	0.45
1:F:200:VAL:O	1:F:203:ILE:HB	2.16	0.45
2:G:240:PHE:HD1	2:G:241:ILE:H	1.64	0.45
1:B:108:VAL:O	1:B:112:LEU:HG	2.16	0.45
2:C:64:VAL:CG1	2:C:84:ILE:HD12	2.28	0.45
2:D:158:ASN:N	2:D:159:PRO:CD	2.78	0.45
1:E:115:ILE:HD11	1:E:141:GLU:O	2.16	0.45
1:E:138:LEU:HD23	1:E:138:LEU:HA	1.68	0.45
1:F:41:THR:HG22	1:F:53:TYR:HE2	1.80	0.45
1:F:118:GLY:HA2	1:F:121:GLU:HB2	1.99	0.45
2:G:35:GLY:O	2:G:211:VAL:HA	2.15	0.45
2:G:35:GLY:N	2:G:210:CYS:O	2.40	0.45
1:B:62:ILE:HG13	1:B:63:PHE:N	2.30	0.45
2:C:2:ILE:CG2	2:C:28:VAL:O	2.65	0.45
2:C:288:ARG:HD3	2:D:287:ALA:O	2.16	0.45
2:C:296:ILE:HG23	2:C:314:THR:CG2	2.46	0.45
1:F:59:ILE:O	1:F:62:ILE:HG13	2.16	0.45
1:F:193:LEU:HD13	1:F:193:LEU:C	2.42	0.45
2:G:41:GLY:C	2:G:43:GLY:H	2.24	0.45
2:H:10:VAL:HG21	2:H:17:THR:HG23	1.98	0.45
1:A:189:MET:HE2	1:B:74:TRP:CA	2.47	0.45
1:B:107:MET:CE	1:B:152:ILE:HD11	2.36	0.45
2:D:240:PHE:HD2	2:D:242:GLN:HG2	1.82	0.45
2:G:93:LEU:HD11	2:G:149:VAL:CB	2.46	0.45
2:H:37:ILE:HB	2:H:204:VAL:CG2	2.46	0.45
2:C:93:LEU:HD11	2:C:146:LYS:O	2.16	0.45
2:C:313:LEU:HD22	2:C:340:LEU:HD11	1.99	0.45
1:F:126:MET:HE1	1:F:134:VAL:HB	1.98	0.45
1:F:188:VAL:HG23	1:F:189:MET:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:4:LEU:HB3	2:G:7:ILE:CG1	2.46	0.45
2:G:128:VAL:CG1	2:G:152:ALA:HB2	2.36	0.45
2:G:276:GLN:CD	2:G:282:LEU:HD11	2.42	0.45
2:H:171:LEU:HD13	2:H:179:ILE:CD1	2.46	0.45
2:H:221:GLU:HB2	2:H:233:LYS:NZ	2.32	0.45
1:A:39:TYR:CD2	1:A:48:ALA:CB	2.98	0.45
1:A:128:ALA:HB1	1:A:134:VAL:HG22	1.99	0.45
1:B:28:PHE:O	1:B:32:LEU:HB2	2.17	0.45
1:E:72:LEU:HD23	1:E:95:PRO:HB2	1.98	0.45
1:E:181:TYR:CD2	1:F:167:VAL:HG13	2.52	0.45
2:G:87:ILE:HG23	2:G:147:GLN:NE2	2.31	0.45
2:G:270:ARG:HG3	2:G:313:LEU:CD2	2.46	0.45
1:B:41:THR:O	1:B:42:ARG:HG3	2.16	0.45
1:B:76:ILE:HA	1:B:79:THR:HB	1.99	0.45
2:C:97:ARG:HH11	2:C:105:LEU:HD23	1.82	0.45
2:C:145:GLN:O	2:C:148:ARG:N	2.50	0.45
2:C:320:GLN:HB3	2:C:324:GLN:HE21	1.82	0.45
2:D:189:ARG:HG3	2:D:189:ARG:NH2	2.20	0.45
1:F:124:ARG:CZ	2:H:86:MET:HB3	2.47	0.45
1:F:167:VAL:HG12	1:F:168:GLY:N	2.32	0.45
2:G:274:THR:HB	2:G:334:HIS:HB3	1.99	0.45
2:H:104:ALA:O	2:H:105:LEU:C	2.57	0.45
1:B:66:ILE:HA	1:B:67:PRO:HD3	1.57	0.45
1:B:137:VAL:CG2	1:B:138:LEU:N	2.80	0.45
2:C:99:VAL:HG22	2:C:149:VAL:HG21	1.98	0.45
2:D:4:LEU:HB3	2:D:7:ILE:HD11	1.99	0.45
2:D:16:ARG:HG3	2:D:16:ARG:HH11	1.82	0.45
2:D:189:ARG:CG	2:D:189:ARG:NH2	2.74	0.45
1:E:68:PHE:HB3	1:E:69:ILE:HD13	1.97	0.45
1:E:125:ALA:HB1	2:G:52:ASN:OD1	2.16	0.45
1:F:18:ALA:HA	1:F:21:PHE:HD2	1.81	0.45
1:F:32:LEU:HB2	1:F:33:PRO:HD3	1.99	0.45
2:G:196:LEU:HD22	2:G:207:ILE:HD11	1.98	0.45
2:G:283:LEU:CD1	2:G:296:ILE:HD11	2.47	0.45
2:H:162:LEU:HD21	2:H:164:CYS:SG	2.56	0.45
1:A:27:GLY:O	1:A:32:LEU:HD12	2.17	0.44
1:A:69:ILE:O	1:A:72:LEU:HB3	2.17	0.44
1:A:188:VAL:O	1:A:192:VAL:HG23	2.17	0.44
2:D:8:THR:HA	2:D:21:LEU:O	2.16	0.44
2:D:54:LEU:CD1	2:D:86:MET:HE1	2.47	0.44
2:D:107:LEU:HD21	2:D:120:ARG:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:139:LEU:N	1:E:140:PRO:CD	2.80	0.44
2:G:256:ARG:HH22	2:H:278:VAL:HG11	1.82	0.44
2:H:86:MET:CG	2:H:87:ILE:N	2.80	0.44
1:A:193:LEU:HD11	1:B:74:TRP:CG	2.52	0.44
1:B:97:THR:OG1	1:B:98:VAL:N	2.50	0.44
2:C:26:LEU:HD11	2:C:34:TYR:CE1	2.52	0.44
1:E:39:TYR:O	1:E:46:ILE:HG21	2.18	0.44
1:F:124:ARG:HG3	2:H:54:LEU:HD11	1.99	0.44
1:F:189:MET:O	1:F:192:VAL:HB	2.18	0.44
2:H:4:LEU:O	2:H:25:SER:HA	2.17	0.44
2:H:250:PRO:CG	2:H:253:TYR:HB2	2.47	0.44
1:A:123:SER:C	1:A:128:ALA:HB2	2.42	0.44
1:A:131:MET:HB3	1:A:132:GLN:H	1.35	0.44
1:A:189:MET:HE1	1:B:73:VAL:HB	2.00	0.44
1:B:68:PHE:HA	1:B:160:TYR:OH	2.18	0.44
2:C:172:ASP:OD2	2:C:174:ALA:HB3	2.17	0.44
2:C:300:GLN:NE2	2:C:301:MET:H	2.15	0.44
2:D:49:ARG:HG2	2:D:54:LEU:HD12	1.98	0.44
1:F:72:LEU:HD11	1:F:160:TYR:HE1	1.80	0.44
1:F:107:MET:HE2	1:F:149:ALA:HA	1.99	0.44
2:G:2:ILE:CG2	2:G:28:VAL:HB	2.41	0.44
2:H:35:GLY:HA3	2:H:208:CYS:SG	2.58	0.44
2:H:82:ARG:HH12	2:H:111:ASN:ND2	2.16	0.44
2:H:107:LEU:HD21	2:H:156:ALA:O	2.17	0.44
2:H:298:SER:OG	2:H:313:LEU:HB2	2.17	0.44
1:B:47:ILE:O	1:B:48:ALA:CB	2.65	0.44
2:C:97:ARG:NH1	2:C:105:LEU:CD2	2.81	0.44
2:D:87:ILE:HD12	2:D:162:LEU:HD21	1.99	0.44
1:F:17:LEU:HD23	1:F:17:LEU:HA	1.53	0.44
1:F:172:LEU:HB3	1:F:192:VAL:HG13	2.00	0.44
2:G:97:ARG:HD3	2:G:105:LEU:HD11	2.00	0.44
2:H:2:ILE:CG2	2:H:28:VAL:HB	2.47	0.44
2:H:6:ASN:H	2:H:25:SER:HG	1.65	0.44
1:B:188:VAL:O	1:B:192:VAL:HG23	2.18	0.44
2:D:44:LYS:O	2:D:48:ILE:CD1	2.66	0.44
1:E:41:THR:O	1:E:43:PRO:HD3	2.17	0.44
1:E:42:ARG:HB3	1:E:46:ILE:HG22	2.00	0.44
2:G:28:VAL:HG13	2:G:34:TYR:CD2	2.53	0.44
2:G:238:GLN:NE2	2:G:311:ILE:HD13	2.33	0.44
2:H:103:VAL:CG2	2:H:152:ALA:HB3	2.47	0.44
1:B:100:ALA:O	1:B:104:ILE:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:PRO:HD2	1:B:133:ILE:CG1	2.47	0.44
2:C:11:PHE:HB2	2:C:18:ILE:CG2	2.47	0.44
2:C:130:LEU:HD21	2:C:145:GLN:HG2	1.98	0.44
1:E:50:ALA:C	1:E:52:LEU:H	2.26	0.44
1:E:152:ILE:HA	1:E:155:ILE:HG12	2.00	0.44
1:E:189:MET:CE	1:F:74:TRP:HA	2.48	0.44
2:G:102:ASN:HD22	2:G:149:VAL:HG11	1.81	0.44
2:H:155:LEU:HA	2:H:159:PRO:HG3	1.98	0.44
2:H:256:ARG:O	2:H:257:LEU:HB2	2.16	0.44
1:B:134:VAL:CA	1:B:137:VAL:HG13	2.42	0.44
2:C:288:ARG:NH1	2:D:292:VAL:O	2.49	0.44
2:D:137:TYR:HD2	2:D:140:ASN:O	2.01	0.44
1:E:85:THR:O	1:E:85:THR:CG2	2.65	0.44
1:F:29:VAL:O	1:F:33:PRO:HG2	2.18	0.44
2:G:246:HIS:C	2:H:241:ILE:HG22	2.43	0.44
2:H:270:ARG:HA	2:H:313:LEU:HD23	1.99	0.44
1:A:174:GLN:HA	1:A:177:TYR:HB3	2.00	0.44
1:A:181:TYR:O	1:A:184:TYR:HE1	2.00	0.44
1:A:185:ASN:C	1:A:187:THR:N	2.72	0.44
1:B:146:LEU:O	1:B:149:ALA:HB3	2.18	0.44
2:C:63:LEU:HD11	2:C:66:GLY:CA	2.48	0.44
2:C:112:THR:N	2:C:113:PRO:HD3	2.33	0.44
2:C:257:LEU:HD12	2:C:342:TYR:C	2.43	0.44
1:E:140:PRO:HA	1:E:143:LEU:CD1	2.37	0.44
1:F:40:VAL:O	1:F:42:ARG:HG2	2.18	0.44
1:F:69:ILE:H	1:F:69:ILE:HG13	1.48	0.44
2:G:179:ILE:O	2:G:182:LEU:HB3	2.18	0.44
2:G:283:LEU:HD22	2:G:294:ASN:CG	2.42	0.44
2:H:186:ILE:HB	2:H:192:LEU:CD1	2.46	0.44
1:B:22:VAL:CG1	1:B:93:ILE:HB	2.36	0.44
1:B:133:ILE:O	1:B:136:LYS:HB2	2.18	0.44
2:C:285:GLU:HG2	2:C:329:TRP:CH2	2.53	0.44
2:D:184:LYS:O	2:D:188:ARG:HG3	2.18	0.44
2:G:85:GLY:O	2:G:162:LEU:HD12	2.18	0.44
1:A:161:SER:C	1:A:164:GLY:H	2.26	0.43
1:B:32:LEU:HB2	1:B:33:PRO:HD3	2.00	0.43
1:B:104:ILE:HA	1:B:107:MET:CG	2.49	0.43
1:B:179:TYR:CD2	1:B:185:ASN:ND2	2.86	0.43
2:C:190:LEU:HA	2:C:190:LEU:HD23	1.66	0.43
2:D:86:MET:HG2	2:D:87:ILE:N	2.31	0.43
1:E:32:LEU:N	1:E:33:PRO:CD	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:VAL:HG21	1:E:105:ALA:O	2.18	0.43
1:E:144:PRO:HG2	1:E:145:GLY:H	1.82	0.43
1:F:117:THR:O	1:F:119:LEU:N	2.51	0.43
1:F:126:MET:HG2	2:H:109:LEU:HD22	2.00	0.43
1:F:173:GLY:O	1:F:177:TYR:HB2	2.18	0.43
2:G:41:GLY:O	2:G:43:GLY:N	2.50	0.43
2:G:43:GLY:C	2:G:45:SER:N	2.73	0.43
2:G:119:ARG:O	2:G:123:GLU:HG3	2.18	0.43
2:G:276:GLN:OE1	2:G:282:LEU:HD11	2.18	0.43
2:H:33:ILE:HD13	2:H:207:ILE:HD12	2.00	0.43
2:H:52:ASN:HD22	2:H:52:ASN:C	2.26	0.43
2:C:85:GLY:O	2:C:163:LEU:N	2.47	0.43
2:C:246:HIS:O	2:C:250:PRO:HD2	2.18	0.43
2:D:113:PRO:O	2:D:117:VAL:HG23	2.18	0.43
2:D:290:PHE:N	2:D:290:PHE:CD2	2.86	0.43
2:G:84:ILE:HD13	2:G:84:ILE:C	2.43	0.43
2:G:91:PHE:HE1	2:G:171:LEU:CD2	2.31	0.43
2:G:242:GLN:O	2:H:244:THR:HG22	2.18	0.43
2:H:87:ILE:HG22	2:H:88:PHE:H	1.84	0.43
1:B:207:GLY:O	1:B:208:ASP:C	2.60	0.43
2:C:77:LEU:HD21	2:C:81:ARG:HH21	1.83	0.43
2:C:130:LEU:HD21	2:C:145:GLN:CA	2.46	0.43
2:C:300:GLN:HE21	2:C:300:GLN:CA	2.31	0.43
2:D:94:LEU:H	2:D:102:ASN:ND2	2.16	0.43
1:F:37:LEU:HB3	1:F:40:VAL:HB	1.98	0.43
1:F:141:GLU:OE2	2:H:96:SER:N	2.48	0.43
2:G:63:LEU:HD21	2:G:66:GLY:CA	2.48	0.43
2:H:48:ILE:H	2:H:48:ILE:HD12	1.78	0.43
2:H:87:ILE:CG2	2:H:147:GLN:NE2	2.77	0.43
2:H:130:LEU:HD22	2:H:130:LEU:C	2.43	0.43
1:A:18:ALA:HA	1:A:21:PHE:HD2	1.82	0.43
1:B:11:ARG:HB3	1:B:11:ARG:CZ	2.48	0.43
1:B:22:VAL:HG12	1:B:26:PHE:HE2	1.82	0.43
1:B:104:ILE:HA	1:B:107:MET:HG2	1.99	0.43
2:C:8:THR:O	2:C:58:THR:HB	2.17	0.43
2:C:86:MET:HG2	2:C:87:ILE:O	2.18	0.43
1:E:22:VAL:O	1:E:26:PHE:HD2	2.00	0.43
1:E:69:ILE:HG23	1:E:163:MET:CE	2.48	0.43
1:E:122:ALA:O	1:E:125:ALA:HB3	2.19	0.43
2:G:33:ILE:HG12	2:G:194:ILE:HG12	1.98	0.43
2:G:130:LEU:HG	2:G:130:LEU:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:252:ASP:O	2:G:256:ARG:HB2	2.18	0.43
2:H:125:LEU:O	2:H:128:VAL:CG2	2.66	0.43
1:A:69:ILE:CG1	1:B:163:MET:SD	3.07	0.43
1:A:133:ILE:O	1:A:137:VAL:HG22	2.19	0.43
2:C:1:MET:HG3	2:C:30:ALA:HB2	2.01	0.43
2:C:10:VAL:HG21	2:C:17:THR:HG22	1.99	0.43
2:C:284:SER:O	2:C:287:ALA:HB3	2.19	0.43
2:H:7:ILE:HD13	2:H:60:GLY:HA3	2.01	0.43
2:H:241:ILE:H	2:H:241:ILE:HG13	1.58	0.43
1:B:38:LEU:HD22	1:B:112:LEU:CB	2.49	0.43
1:B:96:LEU:HD11	1:B:157:LEU:HD11	2.00	0.43
2:C:29:PRO:HG2	2:C:32:GLN:HB2	2.00	0.43
2:C:137:TYR:CZ	2:C:140:ASN:O	2.72	0.43
2:C:278:VAL:HG21	2:D:256:ARG:HH22	1.83	0.43
2:D:224:THR:HG22	2:D:226:SER:H	1.84	0.43
2:D:233:LYS:O	2:D:234:THR:C	2.60	0.43
1:E:40:VAL:HG22	1:E:47:ILE:CD1	2.48	0.43
1:E:198:ILE:HG13	1:E:199:LEU:H	1.80	0.43
1:F:20:THR:N	1:F:157:LEU:CD2	2.81	0.43
2:H:124:LEU:HD23	2:H:155:LEU:HB2	2.01	0.43
2:H:163:LEU:HD23	2:H:195:LEU:HB3	2.00	0.43
1:A:22:VAL:O	1:A:26:PHE:CD2	2.71	0.43
2:C:193:THR:HG22	2:C:193:THR:O	2.19	0.43
2:D:48:ILE:HD12	2:D:197:ILE:CG1	2.33	0.43
1:E:100:ALA:O	1:E:103:PHE:HB3	2.18	0.43
1:F:19:MET:C	1:F:157:LEU:HD11	2.44	0.43
1:F:41:THR:O	1:F:43:PRO:HD3	2.18	0.43
1:F:138:LEU:HD21	2:H:94:LEU:CD2	2.49	0.43
2:H:142:SER:O	2:H:145:GLN:HB2	2.19	0.43
1:A:7:TRP:CD1	1:A:7:TRP:H	2.37	0.43
1:A:118:GLY:O	1:A:119:LEU:C	2.61	0.43
1:A:191:THR:O	1:A:195:LEU:CB	2.66	0.43
1:B:130:PRO:HD2	1:B:133:ILE:HG13	2.00	0.43
1:B:196:LEU:O	1:B:199:LEU:HB3	2.19	0.43
2:C:37:ILE:HG13	2:C:38:GLY:N	2.32	0.43
2:C:131:GLY:O	2:C:132:ASP:C	2.62	0.43
2:D:155:LEU:HD11	2:D:186:ILE:CD1	2.48	0.43
2:D:235:PRO:C	2:D:238:GLN:HB2	2.41	0.43
1:E:96:LEU:HD12	1:E:160:TYR:CD1	2.54	0.43
1:E:137:VAL:HG12	2:G:97:ARG:HH22	1.84	0.43
2:G:277:SER:O	2:G:280:ALA:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:120:ARG:O	2:H:121:VAL:C	2.57	0.43
1:B:25:PHE:O	1:B:29:VAL:HB	2.18	0.43
1:B:143:LEU:O	1:B:144:PRO:C	2.59	0.43
2:C:241:ILE:HG21	2:C:300:GLN:CD	2.44	0.43
2:D:24:VAL:HG23	2:D:24:VAL:O	2.19	0.43
2:D:330:LEU:HB3	2:D:335:VAL:CB	2.47	0.43
1:E:62:ILE:HG22	1:F:201:TYR:OH	2.19	0.43
1:F:68:PHE:O	1:F:160:TYR:OH	2.36	0.43
2:G:213:VAL:N	2:G:221:GLU:O	2.40	0.43
2:H:34:TYR:CD2	2:H:210:CYS:HB2	2.53	0.43
2:H:241:ILE:HD13	2:H:300:GLN:O	2.18	0.43
2:H:245:LEU:HD22	2:H:311:ILE:CG2	2.43	0.43
2:H:298:SER:O	2:H:299:ALA:HB2	2.17	0.43
1:B:139:LEU:CB	1:B:140:PRO:HD3	2.46	0.43
2:C:4:LEU:HD13	2:C:47:LEU:HD11	2.01	0.43
2:C:246:HIS:CE1	2:D:202:ASP:OD1	2.72	0.43
2:D:197:ILE:N	2:D:197:ILE:CD1	2.77	0.43
2:D:266:VAL:HG22	2:D:267:PRO:HD2	2.01	0.43
1:E:21:PHE:HB3	1:E:25:PHE:CE1	2.54	0.43
1:E:38:LEU:HD22	1:E:112:LEU:CB	2.40	0.43
1:E:133:ILE:HA	1:E:136:LYS:HB3	2.00	0.43
1:F:28:PHE:CZ	1:F:150:ALA:CB	3.02	0.43
2:G:250:PRO:HB2	2:G:253:TYR:CD2	2.54	0.43
2:H:37:ILE:CG2	2:H:213:VAL:HG22	2.49	0.43
2:H:130:LEU:CD1	2:H:148:ARG:HB2	2.49	0.43
2:H:242:GLN:O	2:H:244:THR:N	2.52	0.43
1:A:13:VAL:CG2	1:A:195:LEU:HD11	2.49	0.42
1:A:19:MET:HA	1:A:22:VAL:CG2	2.48	0.42
1:A:115:ILE:HD13	1:A:115:ILE:C	2.44	0.42
2:C:243:SER:O	2:D:300:GLN:OE1	2.36	0.42
2:C:312:MET:HG2	2:C:314:THR:HG23	2.00	0.42
2:D:145:GLN:O	2:D:146:LYS:C	2.61	0.42
2:D:215:SER:HB3	2:D:220:ILE:HD11	2.01	0.42
2:G:29:PRO:HG2	2:G:32:GLN:CD	2.43	0.42
2:G:212:ALA:HB1	2:G:219:LEU:HD23	1.99	0.42
2:G:272:GLU:HB3	2:G:336:LYS:HG3	2.01	0.42
2:H:29:PRO:HG2	2:H:32:GLN:CD	2.44	0.42
2:H:155:LEU:HA	2:H:159:PRO:CG	2.49	0.42
2:H:175:THR:HG22	2:H:179:ILE:HD12	2.00	0.42
1:A:92:ALA:O	1:A:96:LEU:HD13	2.20	0.42
1:A:130:PRO:O	1:A:131:MET:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:266:VAL:HG13	2:C:267:PRO:N	2.33	0.42
2:D:16:ARG:HG3	2:D:16:ARG:NH1	2.34	0.42
2:G:24:VAL:O	2:G:24:VAL:HG23	2.20	0.42
2:G:247:LEU:HA	2:H:300:GLN:NE2	2.35	0.42
2:G:250:PRO:HG2	2:G:297:ILE:CG2	2.49	0.42
2:H:52:ASN:HD21	2:H:54:LEU:CD2	2.32	0.42
1:A:101:ALA:HB3	1:A:102:PRO:CD	2.49	0.42
1:B:8:LEU:H	1:B:8:LEU:CD1	2.29	0.42
1:B:113:LEU:HD23	1:B:113:LEU:HA	1.76	0.42
2:C:155:LEU:HD23	2:C:155:LEU:HA	1.71	0.42
2:C:238:GLN:O	2:C:238:GLN:CG	2.53	0.42
2:C:245:LEU:O	2:C:247:LEU:N	2.53	0.42
2:D:107:LEU:O	2:D:111:ASN:HB2	2.19	0.42
2:D:319:THR:HG22	2:D:320:GLN:N	2.34	0.42
1:F:62:ILE:O	1:F:66:ILE:HG13	2.19	0.42
1:F:124:ARG:NH1	2:H:86:MET:CB	2.75	0.42
2:H:37:ILE:HG12	2:H:198:THR:HG23	2.00	0.42
2:H:128:VAL:HB	2:H:148:ARG:HB3	2.01	0.42
1:A:118:GLY:C	1:A:121:GLU:H	2.27	0.42
1:A:125:ALA:HA	2:C:54:LEU:HD21	2.02	0.42
2:C:235:PRO:C	2:C:237:ALA:N	2.77	0.42
2:D:35:GLY:HA3	2:D:208:CYS:SG	2.59	0.42
2:D:52:ASN:ND2	2:D:54:LEU:HG	2.35	0.42
2:D:87:ILE:CD1	2:D:162:LEU:HD21	2.50	0.42
1:F:134:VAL:HG13	1:F:135:ARG:HG3	2.02	0.42
2:G:295:ASN:ND2	2:G:317:HIS:CD2	2.86	0.42
2:H:163:LEU:CD2	2:H:195:LEU:HB3	2.50	0.42
1:A:15:GLU:O	1:A:18:ALA:HB3	2.19	0.42
1:A:126:MET:HE1	2:C:105:LEU:HB3	2.01	0.42
1:A:128:ALA:C	1:A:129:THR:CG2	2.92	0.42
2:D:36:VAL:O	2:D:197:ILE:HA	2.19	0.42
2:D:53:LEU:HD22	2:D:69:LEU:HB3	2.02	0.42
2:D:95:SER:HA	2:D:139:SER:HG	1.82	0.42
1:E:163:MET:HE3	1:E:163:MET:HB3	1.56	0.42
1:F:53:TYR:HE2	1:F:109:GLU:OE2	2.02	0.42
1:F:134:VAL:HG13	1:F:135:ARG:N	2.33	0.42
2:G:49:ARG:HG3	2:G:49:ARG:NH1	2.34	0.42
2:G:159:PRO:O	2:G:192:LEU:CD2	2.67	0.42
2:G:240:PHE:HD1	2:G:241:ILE:N	2.16	0.42
1:A:39:TYR:CG	1:A:48:ALA:HB3	2.54	0.42
1:A:96:LEU:N	1:A:96:LEU:CD1	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:ALA:O	1:A:190:ASN:OD1	2.38	0.42
2:C:10:VAL:HG22	2:C:11:PHE:N	2.34	0.42
2:C:186:ILE:CD1	2:C:192:LEU:HD23	2.49	0.42
1:E:47:ILE:C	1:E:49:ASN:H	2.27	0.42
1:F:172:LEU:HD23	1:F:195:LEU:HD23	2.01	0.42
2:G:9:LYS:HE3	2:G:11:PHE:HB2	2.02	0.42
2:G:18:ILE:HD13	2:G:19:GLN:C	2.44	0.42
2:G:53:LEU:HB3	2:G:81:ARG:HH21	1.84	0.42
2:G:247:LEU:HD21	2:H:244:THR:HG21	2.02	0.42
2:H:103:VAL:CG1	2:H:121:VAL:HG13	2.49	0.42
2:H:323:THR:O	2:H:327:ILE:HG23	2.20	0.42
1:B:40:VAL:HG11	1:B:53:TYR:N	2.35	0.42
1:B:149:ALA:O	1:B:152:ILE:HG12	2.19	0.42
1:B:171:GLY:O	1:B:174:GLN:HB3	2.19	0.42
2:D:173:PRO:HA	2:D:176:THR:HB	2.01	0.42
1:E:178:GLN:O	1:E:182:ILE:O	2.37	0.42
1:F:35:GLY:O	1:F:37:LEU:N	2.52	0.42
2:G:87:ILE:CD1	2:G:151:ILE:HD13	2.50	0.42
2:G:130:LEU:CD2	2:G:149:VAL:HG22	2.50	0.42
1:A:119:LEU:CB	2:C:92:ASN:OD1	2.60	0.42
1:A:159:GLY:O	1:B:68:PHE:CE1	2.73	0.42
1:B:119:LEU:HB3	2:D:92:ASN:OD1	2.18	0.42
1:B:132:GLN:O	1:B:135:ARG:HB2	2.20	0.42
2:C:4:LEU:HD12	2:C:26:LEU:HB3	2.02	0.42
2:C:107:LEU:HB3	2:C:117:VAL:HG22	2.02	0.42
2:C:162:LEU:HD23	2:C:162:LEU:C	2.44	0.42
2:C:253:TYR:OH	2:C:297:ILE:HD11	2.20	0.42
2:D:28:VAL:HG13	2:D:34:TYR:HB2	2.02	0.42
1:E:163:MET:HE2	1:F:163:MET:SD	2.60	0.42
1:F:37:LEU:HD22	1:F:40:VAL:HG21	2.02	0.42
1:F:38:LEU:HB2	1:F:112:LEU:HD13	2.02	0.42
1:F:70:ILE:CG2	1:F:71:LEU:N	2.82	0.42
1:F:121:GLU:OE2	2:H:92:ASN:HB3	2.20	0.42
2:H:201:MET:O	2:H:202:ASP:C	2.63	0.42
1:A:59:ILE:O	1:A:62:ILE:HG12	2.19	0.42
1:A:70:ILE:HG23	1:A:71:LEU:N	2.33	0.42
1:B:7:TRP:NE1	1:F:182:ILE:HG22	2.35	0.42
2:C:4:LEU:HA	2:C:7:ILE:HD11	2.02	0.42
2:C:268:MET:HA	2:C:314:THR:O	2.19	0.42
2:D:2:ILE:CD1	2:D:195:LEU:HD22	2.49	0.42
2:D:115:ASP:C	2:D:117:VAL:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:16:THR:HG21	1:E:199:LEU:HD21	2.01	0.42
1:E:26:PHE:HB2	1:E:30:ILE:CG1	2.49	0.42
2:G:240:PHE:CE1	2:G:243:SER:OG	2.72	0.42
2:G:241:ILE:O	2:G:242:GLN:C	2.62	0.42
1:A:89:LEU:HD23	1:A:89:LEU:HA	1.83	0.42
1:A:107:MET:HE2	1:A:152:ILE:HD11	2.01	0.42
1:B:120:ILE:HD12	2:D:94:LEU:HD21	2.01	0.42
1:B:123:SER:CB	1:B:126:MET:HE2	2.49	0.42
2:C:168:THR:HG21	2:C:180:LEU:HG	2.02	0.42
2:C:185:ASP:O	2:C:186:ILE:C	2.63	0.42
2:C:221:GLU:OE2	2:C:231:HIS:N	2.51	0.42
2:C:242:GLN:HA	2:C:242:GLN:NE2	2.34	0.42
2:D:313:LEU:HD23	2:D:313:LEU:N	2.34	0.42
1:E:101:ALA:HB3	1:E:102:PRO:HD3	2.01	0.42
1:E:108:VAL:O	1:E:112:LEU:HG	2.19	0.42
1:F:8:LEU:H	1:F:8:LEU:CD2	2.26	0.42
1:F:25:PHE:O	1:F:29:VAL:CG2	2.66	0.42
1:F:26:PHE:HA	1:F:29:VAL:HB	2.01	0.42
1:F:121:GLU:O	1:F:125:ALA:CB	2.68	0.42
1:F:130:PRO:HG2	1:F:133:ILE:CG1	2.50	0.42
2:G:234:THR:N	2:G:235:PRO:HD2	2.35	0.42
1:A:66:ILE:CG2	1:A:71:LEU:HB2	2.50	0.41
1:A:76:ILE:O	1:A:77:PRO:C	2.63	0.41
1:A:148:ASN:HA	1:A:151:THR:HG22	2.01	0.41
1:A:196:LEU:HD12	1:B:70:ILE:HD13	2.01	0.41
2:C:120:ARG:O	2:C:124:LEU:HD13	2.20	0.41
2:C:147:GLN:O	2:C:151:ILE:HG23	2.20	0.41
2:C:184:LYS:O	2:C:187:ASN:HB3	2.20	0.41
2:C:238:GLN:O	2:C:240:PHE:CD2	2.73	0.41
2:C:313:LEU:HD22	2:C:340:LEU:CD1	2.50	0.41
1:E:34:VAL:O	1:E:37:LEU:HB2	2.19	0.41
1:E:47:ILE:O	1:E:48:ALA:CB	2.68	0.41
2:G:103:VAL:HG22	2:G:152:ALA:HB1	2.02	0.41
2:G:144:GLY:HA3	2:G:175:THR:HG21	2.02	0.41
1:A:120:ILE:O	1:A:123:SER:HB3	2.20	0.41
1:A:139:LEU:N	1:A:140:PRO:CD	2.82	0.41
1:A:193:LEU:HA	1:B:70:ILE:HD11	2.01	0.41
2:D:143:GLY:HA2	2:D:146:LYS:HG3	2.03	0.41
2:D:282:LEU:O	2:D:286:THR:HG23	2.21	0.41
1:E:189:MET:O	1:E:192:VAL:HB	2.19	0.41
2:H:87:ILE:CG2	2:H:88:PHE:H	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:99:VAL:HB	2:H:134:HIS:O	2.20	0.41
2:H:141:LEU:CG	2:H:145:GLN:HB3	2.50	0.41
1:A:39:TYR:O	1:A:49:ASN:HB3	2.21	0.41
2:C:147:GLN:HG2	2:C:179:ILE:HD13	2.01	0.41
2:D:71:THR:O	2:D:71:THR:HG22	2.20	0.41
2:D:240:PHE:C	2:D:240:PHE:CD2	2.98	0.41
1:E:38:LEU:HD13	1:E:112:LEU:CB	2.48	0.41
2:G:39:ALA:HB2	2:G:236:LEU:HD21	2.01	0.41
2:H:52:ASN:ND2	2:H:52:ASN:C	2.78	0.41
2:H:87:ILE:CD1	2:H:151:ILE:HG22	2.49	0.41
1:A:39:TYR:O	1:A:44:GLY:HA2	2.21	0.41
1:A:180:GLY:CA	1:B:73:VAL:CG1	2.98	0.41
1:A:185:ASN:C	1:A:187:THR:H	2.28	0.41
1:B:129:THR:HA	1:B:133:ILE:CG2	2.50	0.41
2:C:249:ILE:N	2:C:250:PRO:CD	2.83	0.41
2:D:104:ALA:HA	2:D:107:LEU:HD12	2.02	0.41
2:D:287:ALA:HA	2:D:292:VAL:H	1.85	0.41
1:E:37:LEU:HA	1:E:40:VAL:HB	2.02	0.41
1:F:30:ILE:C	1:F:33:PRO:HD2	2.45	0.41
2:G:327:ILE:HG13	2:G:328:ALA:N	2.35	0.41
2:H:137:TYR:HE2	2:H:141:LEU:HA	1.85	0.41
2:C:34:TYR:HD2	2:C:210:CYS:HB2	1.80	0.41
2:C:270:ARG:HA	2:C:312:MET:O	2.21	0.41
1:E:107:MET:HE3	1:E:107:MET:HB3	1.86	0.41
1:E:168:GLY:O	1:E:169:ALA:HB2	2.20	0.41
2:G:293:ASN:HA	2:H:284:SER:CB	2.51	0.41
2:H:151:ILE:HA	2:H:154:ALA:HB3	2.02	0.41
1:A:115:ILE:HA	1:A:116:PRO:HD3	1.83	0.41
1:A:152:ILE:O	1:A:155:ILE:HG12	2.20	0.41
1:B:17:LEU:HD23	1:B:17:LEU:HA	1.75	0.41
1:B:93:ILE:CG1	1:B:94:VAL:N	2.81	0.41
2:D:4:LEU:CD2	2:D:7:ILE:HD11	2.36	0.41
1:E:16:THR:OG1	1:E:172:LEU:CD1	2.68	0.41
1:E:155:ILE:CB	1:E:200:VAL:HG13	2.48	0.41
1:E:165:GLY:O	1:E:166:ALA:C	2.62	0.41
2:G:138:PRO:HG2	2:G:139:SER:H	1.84	0.41
2:H:124:LEU:HD21	2:H:155:LEU:C	2.45	0.41
1:A:190:ASN:HA	1:A:193:LEU:HD12	2.02	0.41
1:B:32:LEU:HA	1:B:32:LEU:HD23	1.88	0.41
1:B:42:ARG:N	1:B:43:PRO:CD	2.83	0.41
1:B:167:VAL:CG1	1:B:168:GLY:N	2.65	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:LEU:CD2	1:B:195:LEU:HD23	2.37	0.41
2:C:208:CYS:O	2:C:225:VAL:HG21	2.21	0.41
2:C:247:LEU:N	2:D:300:GLN:OE1	2.54	0.41
2:C:271:LEU:HB2	2:C:312:MET:HB3	2.03	0.41
2:D:44:LYS:HG2	2:D:45:SER:N	2.35	0.41
1:E:66:ILE:HA	1:E:67:PRO:HD3	1.91	0.41
1:E:200:VAL:O	1:E:203:ILE:HB	2.20	0.41
1:F:72:LEU:HD23	1:F:95:PRO:HB3	2.01	0.41
1:F:113:LEU:O	1:F:116:PRO:CD	2.68	0.41
1:F:179:TYR:HD2	1:F:185:ASN:HD22	1.68	0.41
2:G:124:LEU:HD11	2:G:156:ALA:HA	2.02	0.41
2:G:243:SER:HA	2:H:244:THR:CG2	2.50	0.41
2:H:32:GLN:HG2	2:H:209:ASP:OD1	2.20	0.41
1:A:121:GLU:C	1:A:123:SER:N	2.78	0.41
1:B:69:ILE:CD1	1:B:163:MET:CE	2.87	0.41
2:C:21:LEU:HD23	2:C:217:GLY:HA2	2.02	0.41
2:C:177:ARG:CZ	2:C:206:ARG:HH21	2.33	0.41
2:C:326:ALA:O	2:C:330:LEU:HG	2.20	0.41
2:D:35:GLY:O	2:D:211:VAL:HA	2.21	0.41
1:E:14:TRP:CZ3	1:E:17:LEU:HD12	2.56	0.41
1:F:42:ARG:CD	1:F:49:ASN:HA	2.44	0.41
2:H:33:ILE:O	2:H:209:ASP:N	2.54	0.41
2:H:62:VAL:O	2:H:68:GLU:HA	2.21	0.41
2:H:105:LEU:C	2:H:109:LEU:HG	2.46	0.41
2:H:198:THR:HG21	2:H:200:GLU:O	2.20	0.41
1:A:32:LEU:HB2	1:A:33:PRO:HD3	2.03	0.41
1:A:196:LEU:O	1:A:200:VAL:HG23	2.21	0.41
1:B:115:ILE:CG1	1:B:116:PRO:HD2	2.45	0.41
2:C:5:SER:O	2:C:7:ILE:HG13	2.21	0.41
2:C:98:THR:HA	2:C:138:PRO:HA	2.01	0.41
2:C:235:PRO:O	2:C:236:LEU:CG	2.69	0.41
2:C:245:LEU:C	2:C:247:LEU:N	2.79	0.41
2:C:282:LEU:O	2:C:286:THR:HG23	2.21	0.41
2:C:290:PHE:CZ	2:C:329:TRP:HB2	2.54	0.41
2:D:230:SER:HB3	2:D:231:HIS:H	1.52	0.41
2:D:258:GLN:HG3	2:D:262:PHE:CD2	2.56	0.41
2:D:290:PHE:N	2:D:290:PHE:HD2	2.19	0.41
1:E:26:PHE:O	1:E:27:GLY:C	2.61	0.41
1:E:73:VAL:O	1:E:77:PRO:HD3	2.20	0.41
1:E:97:THR:OG1	1:E:98:VAL:N	2.54	0.41
1:E:134:VAL:HB	1:E:135:ARG:NH2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:46:ILE:CG2	1:F:47:ILE:HG23	2.45	0.41
2:G:28:VAL:HG13	2:G:34:TYR:HD2	1.86	0.41
2:G:87:ILE:HD12	2:G:151:ILE:HD13	2.03	0.41
2:G:91:PHE:HE1	2:G:171:LEU:HD21	1.86	0.41
2:G:103:VAL:HG12	2:G:121:VAL:HG22	2.03	0.41
2:G:112:THR:O	2:G:112:THR:HG22	2.21	0.41
2:H:9:LYS:HE3	2:H:55:GLU:HB3	2.02	0.41
2:H:330:LEU:O	2:H:335:VAL:HB	2.21	0.41
1:A:42:ARG:HB3	1:A:43:PRO:CD	2.49	0.41
1:A:160:TYR:HD1	1:A:160:TYR:O	2.04	0.41
1:B:22:VAL:HG21	1:B:93:ILE:CB	2.51	0.41
1:B:118:GLY:HA2	1:B:121:GLU:HB2	2.03	0.41
1:B:142:ALA:O	1:B:146:LEU:N	2.46	0.41
2:C:253:TYR:HE1	2:C:268:MET:CE	2.34	0.41
2:D:38:GLY:O	2:D:39:ALA:C	2.64	0.41
2:D:271:LEU:HB3	2:D:273:PHE:CE1	2.56	0.41
1:E:118:GLY:O	1:E:119:LEU:HG	2.21	0.41
1:E:119:LEU:O	2:G:92:ASN:ND2	2.54	0.41
1:E:175:ILE:HG13	1:E:176:GLY:H	1.85	0.41
1:F:124:ARG:HD2	2:H:86:MET:HE3	2.03	0.41
2:G:105:LEU:N	2:G:106:PRO:HD2	2.35	0.41
2:G:147:GLN:CD	2:G:167:ALA:HB1	2.46	0.41
2:G:247:LEU:HD21	2:G:300:GLN:NE2	2.36	0.41
1:A:98:VAL:O	1:A:99:GLY:C	2.64	0.40
1:A:177:TYR:O	1:A:181:TYR:N	2.42	0.40
2:C:34:TYR:OH	2:C:222:GLN:HG3	2.21	0.40
2:C:83:GLN:O	2:C:159:PRO:CB	2.70	0.40
2:C:120:ARG:O	2:C:121:VAL:C	2.64	0.40
2:C:228:VAL:C	2:C:229:PHE:CD2	2.99	0.40
2:C:261:PRO:HB3	2:C:342:TYR:CE1	2.55	0.40
1:E:76:ILE:CB	1:E:77:PRO:HD3	2.51	0.40
1:F:64:ARG:HD2	1:F:103:PHE:CZ	2.56	0.40
1:F:143:LEU:HD23	1:F:143:LEU:HA	1.84	0.40
2:G:298:SER:HB3	2:H:300:GLN:NE2	2.36	0.40
2:C:247:LEU:CD2	2:C:297:ILE:HG22	2.44	0.40
2:C:249:ILE:HD13	2:C:249:ILE:HA	1.97	0.40
2:C:286:THR:O	2:C:287:ALA:C	2.63	0.40
2:D:36:VAL:CG2	2:D:197:ILE:HG13	2.51	0.40
1:E:7:TRP:CE3	1:E:11:ARG:HD2	2.56	0.40
1:E:21:PHE:O	1:E:25:PHE:CD1	2.74	0.40
2:G:276:GLN:OE1	2:G:282:LEU:CD1	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:343:VAL:HG12	2:G:343:VAL:OXT	2.21	0.40
2:H:185:ASP:OD1	2:H:189:ARG:NH2	2.54	0.40
1:A:69:ILE:HD13	1:A:70:ILE:H	1.86	0.40
1:A:75:MET:HE1	1:A:95:PRO:HB3	2.03	0.40
1:A:118:GLY:HA2	1:A:121:GLU:CG	2.44	0.40
1:B:38:LEU:HD11	1:B:113:LEU:HD21	2.04	0.40
2:C:69:LEU:HD12	2:C:69:LEU:H	1.86	0.40
2:C:100:PHE:C	2:C:100:PHE:CD2	2.99	0.40
2:C:100:PHE:CZ	2:C:118:LYS:HA	2.49	0.40
2:C:236:LEU:HA	2:C:239:LYS:CB	2.43	0.40
1:F:26:PHE:CD1	1:F:27:GLY:N	2.89	0.40
1:F:208:ASP:OD1	1:F:208:ASP:N	2.54	0.40
2:G:70:THR:O	2:G:71:THR:C	2.64	0.40
2:H:166:GLU:HB3	2:H:169:SER:OG	2.22	0.40
1:A:112:LEU:HA	1:A:112:LEU:HD23	1.89	0.40
1:B:167:VAL:O	1:B:169:ALA:N	2.55	0.40
2:C:65:ASP:OD2	2:C:160:LYS:HD2	2.20	0.40
2:D:91:PHE:CD1	2:D:146:LYS:HB2	2.56	0.40
2:D:102:ASN:HA	2:D:105:LEU:CD1	2.51	0.40
1:E:50:ALA:O	1:E:52:LEU:HG	2.21	0.40
1:E:114:GLU:OE1	1:E:114:GLU:HA	2.21	0.40
1:F:126:MET:HE3	1:F:129:THR:CB	2.52	0.40
1:F:126:MET:HE1	1:F:134:VAL:HG23	2.03	0.40
1:F:127:GLY:O	1:F:128:ALA:CB	2.69	0.40
2:G:37:ILE:HD11	2:G:236:LEU:CB	2.48	0.40
2:H:105:LEU:O	2:H:108:GLU:CB	2.63	0.40
1:A:75:MET:HE3	1:A:75:MET:HB2	1.91	0.40
2:C:151:ILE:O	2:C:152:ALA:C	2.65	0.40
2:C:171:LEU:HD13	2:C:179:ILE:CD1	2.49	0.40
2:C:245:LEU:C	2:C:247:LEU:H	2.29	0.40
2:D:2:ILE:HD13	2:D:195:LEU:HD22	2.04	0.40
1:E:14:TRP:CE3	1:E:17:LEU:HD12	2.57	0.40
1:E:59:ILE:HG13	1:E:60:VAL:N	2.35	0.40
1:F:196:LEU:CD2	1:F:199:LEU:HD23	2.51	0.40
2:G:18:ILE:HD13	2:G:18:ILE:C	2.46	0.40
2:G:19:GLN:HB3	2:G:22:ASN:HD21	1.86	0.40
2:G:51:VAL:HA	2:G:62:VAL:HG11	2.04	0.40
2:G:159:PRO:O	2:G:192:LEU:HD23	2.22	0.40
2:H:33:ILE:HG21	2:H:207:ILE:HG13	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	201/217 (93%)	178 (89%)	9 (4%)	14 (7%)	1	12
1	B	201/217 (93%)	187 (93%)	3 (2%)	11 (6%)	1	16
1	E	201/217 (93%)	180 (90%)	11 (6%)	10 (5%)	1	17
1	F	201/217 (93%)	177 (88%)	10 (5%)	14 (7%)	1	12
2	C	341/343 (99%)	307 (90%)	19 (6%)	15 (4%)	2	19
2	D	341/343 (99%)	323 (95%)	8 (2%)	10 (3%)	3	26
2	G	341/343 (99%)	317 (93%)	14 (4%)	10 (3%)	3	26
2	H	341/343 (99%)	316 (93%)	14 (4%)	11 (3%)	3	25
All	All	2168/2240 (97%)	1985 (92%)	88 (4%)	95 (4%)	2	19

All (95) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	ARG
1	A	47	ILE
1	A	48	ALA
1	A	83	VAL
1	A	117	THR
1	A	118	GLY
1	A	131	MET
1	B	43	PRO
1	B	47	ILE
1	B	48	ALA
1	B	68	PHE
1	B	117	THR
1	B	167	VAL
2	C	29	PRO
2	C	109	LEU
2	C	139	SER
2	C	232	PRO

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Mol	Chain	Res	Type
2	C	240	PHE
2	C	275	GLY
2	D	138	PRO
2	D	228	VAL
2	D	230	SER
2	D	232	PRO
2	D	241	ILE
2	D	249	ILE
1	E	47	ILE
1	E	130	PRO
1	E	132	GLN
1	F	36	VAL
1	F	45	GLN
1	F	47	ILE
1	F	51	LYS
1	F	68	PHE
1	F	85	THR
1	F	116	PRO
1	F	128	ALA
1	F	130	PRO
1	F	131	MET
1	F	207	GLY
2	G	138	PRO
2	G	190	LEU
2	G	232	PRO
2	H	139	SER
2	H	232	PRO
2	H	250	PRO
1	A	50	ALA
1	A	164	GLY
1	A	207	GLY
1	B	46	ILE
1	B	168	GLY
2	C	23	ASN
2	C	72	LEU
2	C	246	HIS
2	C	279	ASP
1	E	116	PRO
2	G	42	ALA
2	H	6	ASN
2	H	39	ALA
2	H	243	SER

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Mol	Chain	Res	Type
1	A	129	THR
1	B	116	PRO
1	B	126	MET
1	B	130	PRO
2	C	277	SER
2	D	235	PRO
2	D	276	GLN
1	E	43	PRO
1	E	168	GLY
2	G	279	ASP
2	G	299	ALA
2	H	113	PRO
2	H	235	PRO
2	H	299	ALA
2	C	113	PRO
2	D	275	GLY
1	E	33	PRO
1	E	169	ALA
1	F	25	PHE
1	F	118	GLY
2	H	257	LEU
1	A	130	PRO
1	E	167	VAL
2	G	275	GLY
2	H	190	LEU
2	C	2	ILE
1	F	167	VAL
2	G	241	ILE
2	G	113	PRO
1	A	116	PRO
2	C	158	ASN
2	D	131	GLY
1	A	44	GLY
1	E	207	GLY
2	C	131	GLY
2	G	14	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	158/172 (92%)	138 (87%)	20 (13%)	4	21
1	B	158/172 (92%)	143 (90%)	15 (10%)	8	31
1	E	158/172 (92%)	150 (95%)	8 (5%)	21	47
1	F	158/172 (92%)	143 (90%)	15 (10%)	8	31
2	C	298/298 (100%)	265 (89%)	33 (11%)	6	25
2	D	298/298 (100%)	276 (93%)	22 (7%)	13	39
2	G	298/298 (100%)	286 (96%)	12 (4%)	28	52
2	H	298/298 (100%)	286 (96%)	12 (4%)	28	52
All	All	1824/1880 (97%)	1687 (92%)	137 (8%)	12	39

All (137) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	9	LEU
1	A	19	MET
1	A	33	PRO
1	A	36	VAL
1	A	40	VAL
1	A	42	ARG
1	A	69	ILE
1	A	83	VAL
1	A	86	SER
1	A	95	PRO
1	A	115	ILE
1	A	117	THR
1	A	121	GLU
1	A	129	THR
1	A	140	PRO
1	A	167	VAL
1	A	175	ILE
1	A	184	TYR
1	A	188	VAL
1	B	33	PRO
1	B	34	VAL
1	B	36	VAL
1	B	40	VAL

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Mol	Chain	Res	Type
1	B	42	ARG
1	B	68	PHE
1	B	70	ILE
1	B	77	PRO
1	B	116	PRO
1	B	129	THR
1	B	137	VAL
1	B	139	LEU
1	B	140	PRO
1	B	175	ILE
1	B	182	ILE
2	C	37	ILE
2	C	46	THR
2	C	52	ASN
2	C	56	ARG
2	C	70	THR
2	C	72	LEU
2	C	73	SER
2	C	90	HIS
2	C	105	LEU
2	C	112	THR
2	C	130	LEU
2	C	141	LEU
2	C	147	GLN
2	C	151	ILE
2	C	162	LEU
2	C	182	LEU
2	C	193	THR
2	C	200	GLU
2	C	201	MET
2	C	205	LYS
2	C	224	THR
2	C	232	PRO
2	C	234	THR
2	C	236	LEU
2	C	240	PHE
2	C	241	ILE
2	C	263	THR
2	C	266	VAL
2	C	267	PRO
2	C	276	GLN
2	C	300	GLN

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Mol	Chain	Res	Type
2	C	311	ILE
2	C	332	GLU
2	D	36	VAL
2	D	37	ILE
2	D	44	LYS
2	D	45	SER
2	D	48	ILE
2	D	84	ILE
2	D	112	THR
2	D	124	LEU
2	D	137	TYR
2	D	159	PRO
2	D	189	ARG
2	D	231	HIS
2	D	232	PRO
2	D	235	PRO
2	D	245	LEU
2	D	266	VAL
2	D	281	PRO
2	D	300	GLN
2	D	313	LEU
2	D	314	THR
2	D	323	THR
2	D	343	VAL
1	E	19	MET
1	E	46	ILE
1	E	69	ILE
1	E	116	PRO
1	E	130	PRO
1	E	167	VAL
1	E	185	ASN
1	E	198	ILE
1	F	7	TRP
1	F	8	LEU
1	F	68	PHE
1	F	69	ILE
1	F	75	MET
1	F	76	ILE
1	F	96	LEU
1	F	116	PRO
1	F	139	LEU
1	F	140	PRO

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Mol	Chain	Res	Type
1	F	152	ILE
1	F	155	ILE
1	F	175	ILE
1	F	198	ILE
1	F	202	LEU
2	G	10	VAL
2	G	18	ILE
2	G	40	SER
2	G	48	ILE
2	G	52	ASN
2	G	84	ILE
2	G	90	HIS
2	G	159	PRO
2	G	210	CYS
2	G	232	PRO
2	G	240	PHE
2	G	241	ILE
2	H	2	ILE
2	H	37	ILE
2	H	48	ILE
2	H	52	ASN
2	H	105	LEU
2	H	130	LEU
2	H	183	LEU
2	H	230	SER
2	H	235	PRO
2	H	241	ILE
2	H	249	ILE
2	H	250	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	ASN
1	A	190	ASN
1	A	204	GLN
1	B	174	GLN
1	B	185	ASN
1	B	190	ASN
2	C	12	HIS
2	C	52	ASN
2	C	134	HIS

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Mol	Chain	Res	Type
2	C	147	GLN
2	C	187	ASN
2	C	199	HIS
2	C	242	GLN
2	C	246	HIS
2	C	295	ASN
2	C	300	GLN
2	C	317	HIS
2	C	320	GLN
2	C	324	GLN
2	C	331	GLN
2	D	23	ASN
2	D	111	ASN
2	D	134	HIS
2	D	140	ASN
2	D	147	GLN
2	D	187	ASN
2	D	216	ASN
2	D	238	GLN
2	D	242	GLN
2	D	320	GLN
2	D	334	HIS
1	F	45	GLN
1	F	110	ASN
1	F	190	ASN
2	G	19	GLN
2	G	22	ASN
2	G	52	ASN
2	G	67	GLN
2	G	92	ASN
2	G	102	ASN
2	G	111	ASN
2	G	134	HIS
2	G	147	GLN
2	G	187	ASN
2	G	242	GLN
2	G	246	HIS
2	G	294	ASN
2	G	295	ASN
2	G	300	GLN
2	G	320	GLN
2	H	32	GLN

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Mol	Chain	Res	Type
2	H	52	ASN
2	H	67	GLN
2	H	83	GLN
2	H	111	ASN
2	H	147	GLN
2	H	158	ASN
2	H	222	GLN
2	H	242	GLN
2	H	300	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	203/217 (93%)	0.28	14 (6%) 23 17	113, 166, 210, 234	0
1	B	203/217 (93%)	0.31	10 (4%) 35 23	135, 195, 245, 259	0
1	E	203/217 (93%)	0.20	4 (1%) 65 41	136, 202, 249, 260	0
1	F	203/217 (93%)	0.17	7 (3%) 48 30	106, 166, 222, 244	0
2	C	343/343 (100%)	0.03	9 (2%) 57 35	74, 133, 194, 241	0
2	D	343/343 (100%)	0.26	15 (4%) 39 25	105, 170, 214, 229	0
2	G	343/343 (100%)	0.43	17 (4%) 34 22	157, 209, 249, 265	0
2	H	343/343 (100%)	0.36	18 (5%) 33 22	94, 186, 234, 253	0
All	All	2184/2240 (97%)	0.26	94 (4%) 40 25	74, 179, 238, 265	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	39	TYR	6.3
2	G	179	ILE	6.1
2	H	66	GLY	6.1
2	D	39	ALA	6.0
1	A	168	GLY	6.0
2	D	304	ALA	5.5
2	G	277	SER	4.8
1	F	125	ALA	4.7
1	F	126	MET	4.6
2	D	316	MET	4.4
2	H	309	PHE	4.4
2	G	182	LEU	4.1
1	A	27	GLY	4.0
1	E	121	GLU	3.9
1	A	167	VAL	3.8
2	G	278	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
2	H	294	ASN	3.8
2	G	316	MET	3.6
2	H	249	ILE	3.5
2	H	301	MET	3.4
2	H	293	ASN	3.3
2	C	132	ASP	3.3
1	A	34	VAL	3.2
2	H	40	SER	3.2
2	C	248	ASP	3.2
1	F	163	MET	3.2
2	C	156	ALA	3.1
2	G	317	HIS	3.1
1	F	166	ALA	3.0
2	H	216	ASN	3.0
2	H	273	PHE	3.0
2	H	39	ALA	2.9
1	F	188	VAL	2.9
1	A	15	GLU	2.9
1	A	35	GLY	2.9
2	G	47	LEU	2.9
2	G	292	VAL	2.8
2	D	164	CYS	2.8
2	D	206	ARG	2.8
2	G	183	LEU	2.8
1	B	184	TYR	2.7
1	A	90	GLN	2.7
2	D	119	ARG	2.7
1	B	38	LEU	2.7
2	G	180	LEU	2.6
1	B	81	VAL	2.6
2	C	70	THR	2.6
2	C	71	THR	2.6
2	D	64	VAL	2.6
2	D	242	GLN	2.6
1	A	46	ILE	2.5
1	B	7	TRP	2.5
2	G	110	ASP	2.5
1	A	22	VAL	2.5
2	D	264	ASP	2.5
2	D	99	VAL	2.5
2	C	255	GLU	2.4
2	G	300	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
2	H	317	HIS	2.4
2	H	286	THR	2.4
1	A	31	GLY	2.4
2	D	149	VAL	2.4
1	A	19	MET	2.4
1	B	100	ALA	2.4
2	H	308	LYS	2.4
2	H	87	ILE	2.3
1	E	164	GLY	2.3
2	H	63	LEU	2.3
1	F	184	TYR	2.3
2	G	109	LEU	2.2
2	G	164	CYS	2.2
1	F	39	TYR	2.2
2	G	155	LEU	2.2
2	D	305	GLY	2.2
2	C	69	LEU	2.2
2	H	86	MET	2.2
2	C	117	VAL	2.2
1	B	189	MET	2.2
1	E	178	GLN	2.1
1	B	46	ILE	2.1
1	B	183	GLY	2.1
1	A	8	LEU	2.1
2	H	316	MET	2.1
2	G	90	HIS	2.1
2	C	107	LEU	2.1
2	D	40	SER	2.1
2	D	231	HIS	2.1
1	B	34	VAL	2.1
1	A	30	ILE	2.1
1	E	8	LEU	2.0
2	H	153	ARG	2.0
1	A	117	THR	2.0
2	D	230	SER	2.0
2	G	203	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.