



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 08:35 pm BST

PDB ID : 3DHW
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

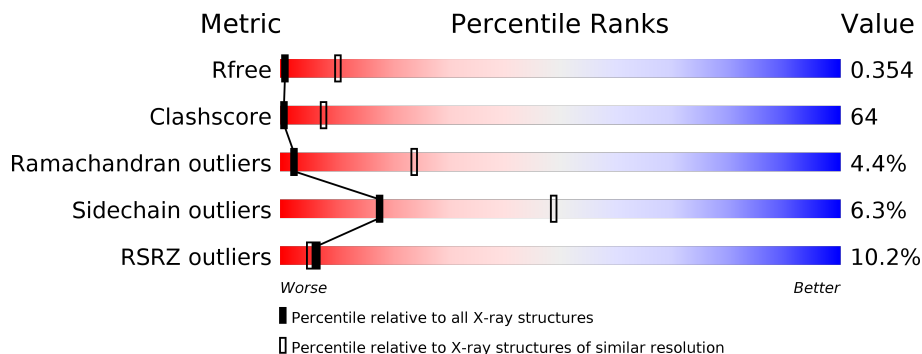
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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.



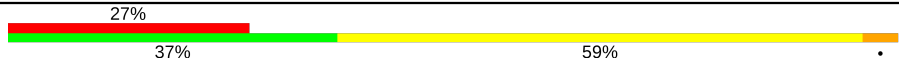

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1049 (3.88-3.52)
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (3.90-3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	
1	B	217	
1	E	217	
1	F	217	
2	C	343	
2	D	343	

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Mol	Chain	Length	Quality of chain
2	G	343	
2	H	343	

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
			Total	C	N	O	S			
1	A	203	1520	1014	244	254	8	0	0	0
1	B	203	1520	1014	244	254	8	0	0	0
1	E	203	1520	1014	244	254	8	0	0	0
1	F	203	1520	1014	244	254	8	0	0	0

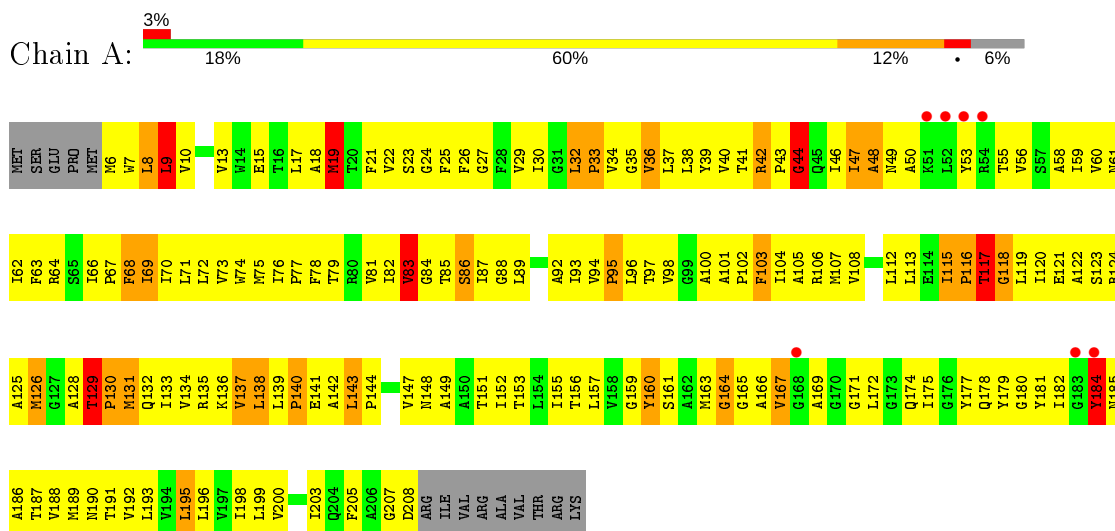
- Molecule 2 is a protein called Methionine import ATP-binding protein metN.

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

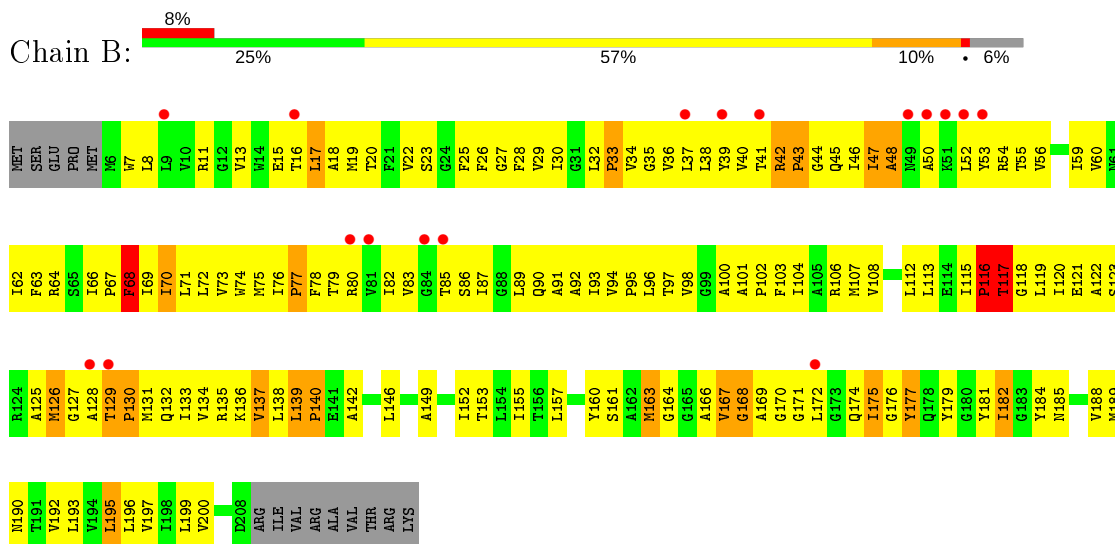
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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

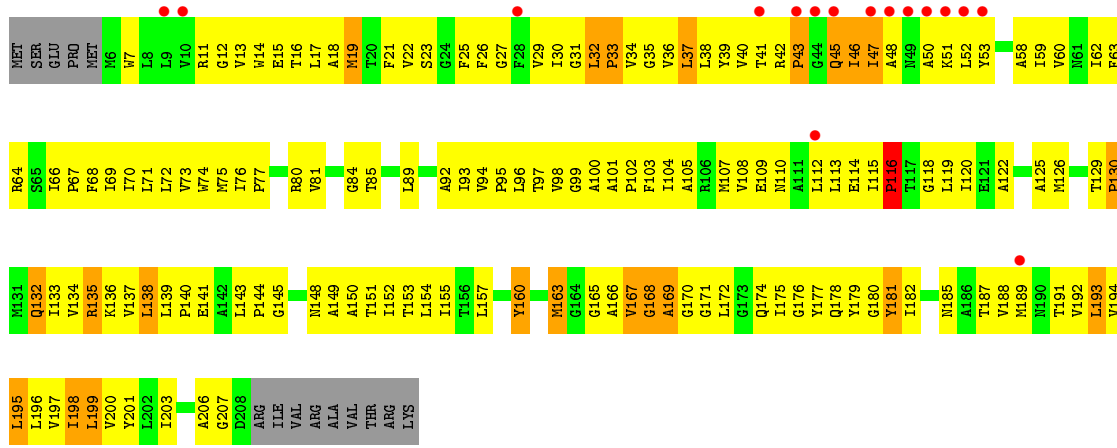


- Molecule 1: D-methionine transport system permease protein metI

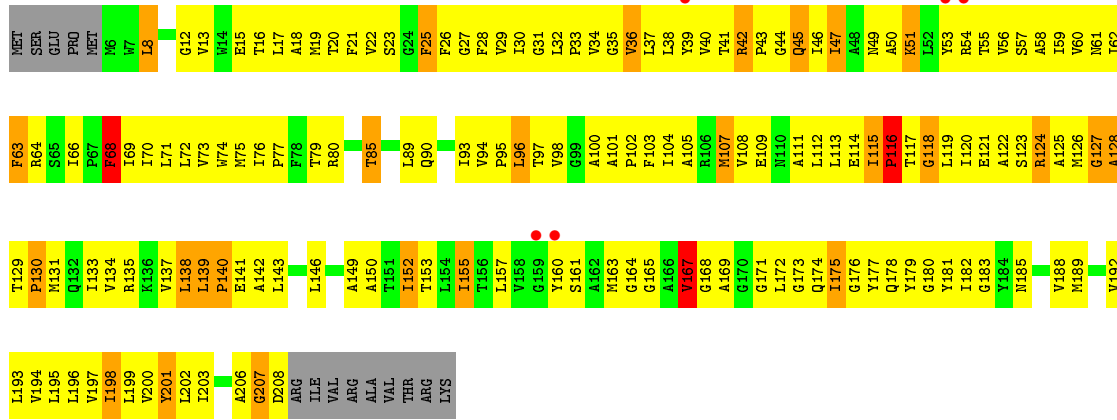


- Molecule 1: D-methionine transport system permease protein metI

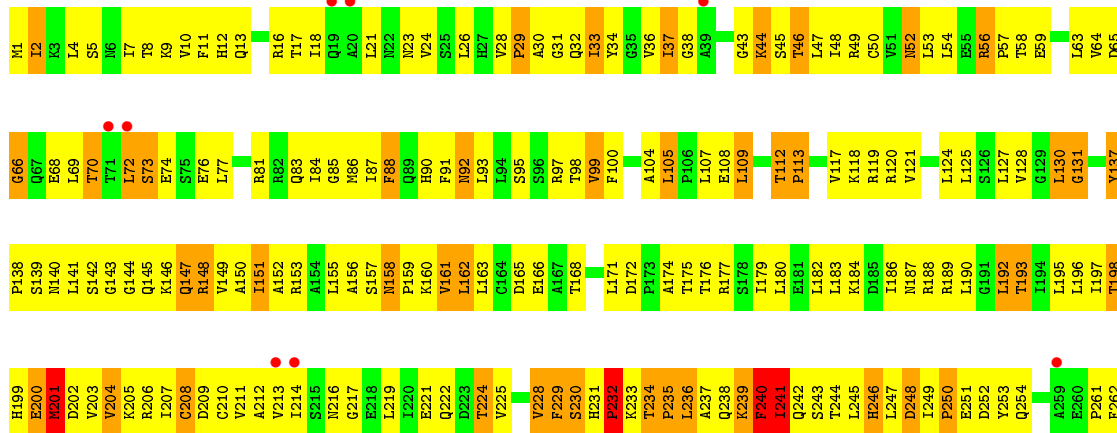


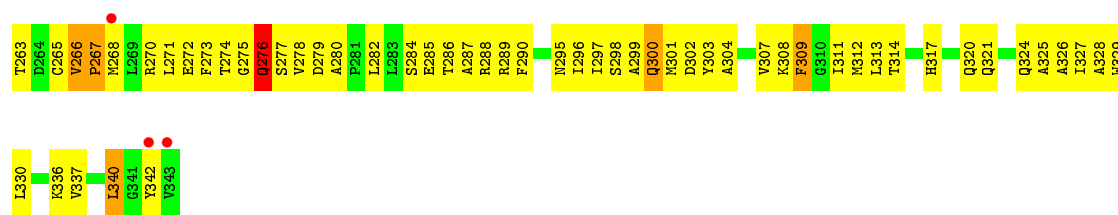


• Molecule 1: D-methionine transport system permease protein metI

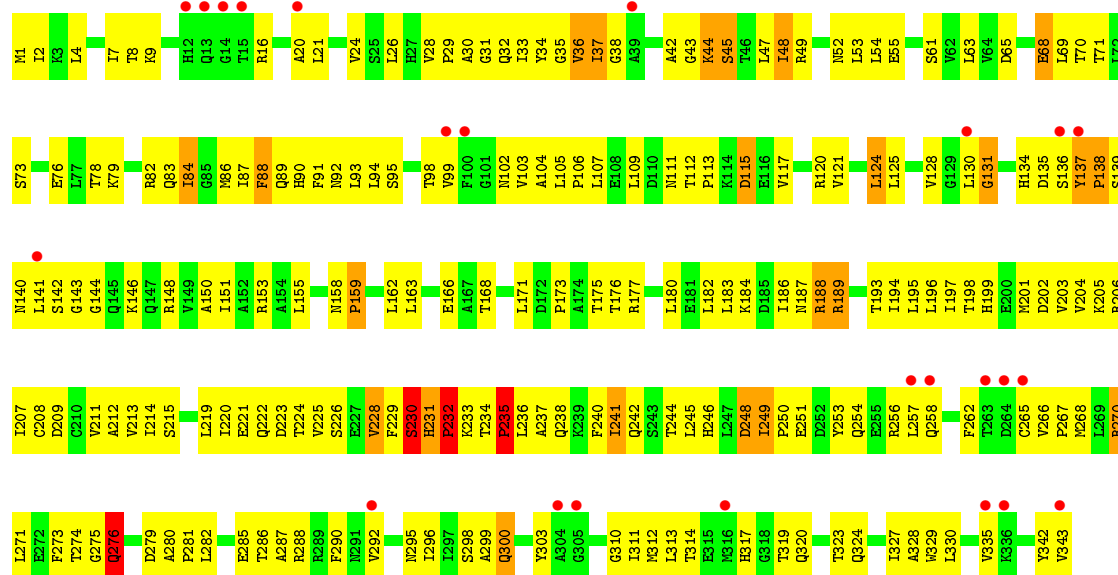


• Molecule 2: Methionine import ATP-binding protein metN

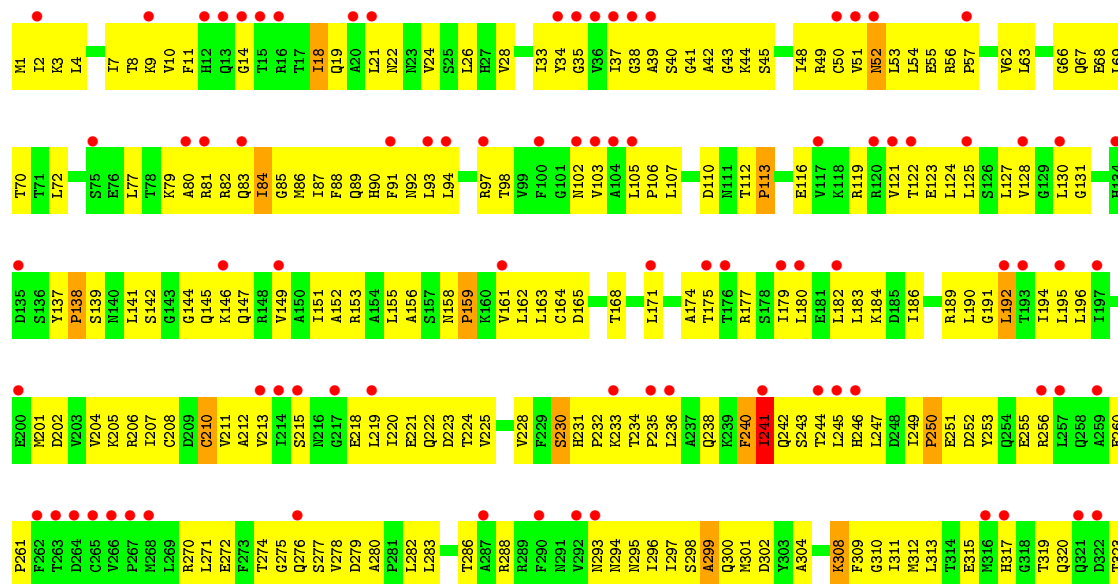




● Molecule 2: Methionine import ATP-binding protein metN

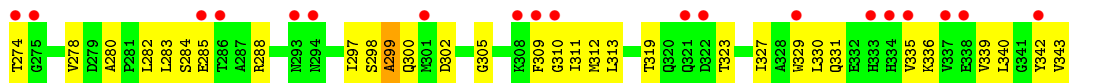
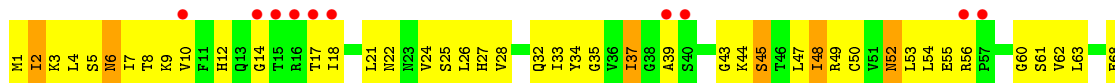


● Molecule 2: Methionine import ATP-binding protein metN





● 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 43.57 – 3.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (39.90-3.70) 99.6 (43.57-3.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 3.66Å)	Xtrriage
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 (10.01%)	wwPDB-VP
Wilson B-factor (Å ²)	153.5	Xtrriage
Anisotropy	0.575	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 95.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	16688	wwPDB-VP
Average B, all atoms (Å ²)	179.0	wwPDB-VP

Xtrriage'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.*

¹ Intensities estimated from amplitudes.

² Theoretical 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	1.08	2/1552 (0.1%)	1.33	16/2122 (0.8%)
1	B	0.88	0/1552	1.21	7/2122 (0.3%)
1	E	0.79	0/1552	1.22	9/2122 (0.4%)
1	F	1.12	1/1552 (0.1%)	1.36	10/2122 (0.5%)
2	C	1.40	13/2691 (0.5%)	1.50	35/3647 (1.0%)
2	D	1.01	1/2691 (0.0%)	1.27	18/3647 (0.5%)
2	G	0.70	0/2691	1.08	7/3647 (0.2%)
2	H	0.93	0/2691	1.24	13/3647 (0.4%)
All	All	1.02	17/16972 (0.1%)	1.28	115/23076 (0.5%)

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 (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	309	PHE	CD2-CE2	12.45	1.64	1.39
2	C	309	PHE	CD1-CE1	12.23	1.63	1.39
2	C	229	PHE	CG-CD2	9.48	1.52	1.38
2	C	228	VAL	C-O	9.44	1.41	1.23
2	D	205	LYS	CD-CE	7.57	1.70	1.51
2	C	204	VAL	CB-CG2	-7.19	1.37	1.52
2	C	201	MET	SD-CE	6.46	2.14	1.77
2	C	229	PHE	CE1-CZ	6.21	1.49	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	19	MET	CG-SD	6.12	1.97	1.81
1	F	201	TYR	CE2-CZ	5.90	1.46	1.38
1	A	68	PHE	CG-CD1	5.78	1.47	1.38
2	C	50	CYS	CB-SG	5.68	1.92	1.82
2	C	213	VAL	CB-CG2	-5.61	1.41	1.52
2	C	309	PHE	CE1-CZ	5.42	1.47	1.37
2	C	161	VAL	CA-CB	-5.42	1.43	1.54
2	C	74	GLU	CG-CD	5.29	1.59	1.51
2	C	240	PHE	N-CA	-5.25	1.35	1.46

All (115) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	116	PRO	N-CA-C	9.67	137.25	112.10
2	D	205	LYS	CD-CE-NZ	9.19	132.83	111.70
2	H	125	LEU	CB-CG-CD2	-9.11	95.52	111.00
1	F	115	ILE	C-N-CD	-9.07	100.66	120.60
2	C	239	LYS	CA-C-N	-8.79	97.87	117.20
2	C	230	SER	N-CA-C	8.49	133.93	111.00
1	E	195	LEU	CA-CB-CG	8.43	134.68	115.30
1	F	138	LEU	CA-CB-CG	-7.96	96.98	115.30
1	E	163	MET	CB-CG-SD	-7.80	88.99	112.40
2	C	99	VAL	CG1-CB-CG2	-7.13	99.50	110.90
2	D	89	GLN	N-CA-CB	-7.12	97.78	110.60
1	E	129	THR	N-CA-C	-7.07	91.92	111.00
2	D	70	THR	N-CA-C	-7.06	91.94	111.00
1	A	8	LEU	CB-CG-CD1	7.00	122.91	111.00
2	H	130	LEU	N-CA-C	-6.99	92.13	111.00
2	C	236	LEU	CA-CB-CG	6.97	131.34	115.30
2	C	239	LYS	CA-C-O	6.87	134.52	120.10
1	F	115	ILE	N-CA-C	6.81	129.38	111.00
2	C	241	ILE	N-CA-C	-6.71	92.89	111.00
1	A	143	LEU	C-N-CD	6.69	142.45	128.40
1	E	199	LEU	CA-CB-CG	6.67	130.64	115.30
1	B	50	ALA	N-CA-C	6.65	128.96	111.00
1	B	117	THR	N-CA-C	6.64	128.93	111.00
2	D	36	VAL	N-CA-C	-6.58	93.23	111.00
2	G	230	SER	N-CA-C	6.57	128.74	111.00
2	C	228	VAL	O-C-N	6.53	133.15	122.70
2	H	119	ARG	CB-CA-C	-6.49	97.41	110.40
2	C	183	LEU	CB-CG-CD2	-6.48	99.99	111.00
2	G	250	PRO	N-CA-C	-6.47	95.28	112.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	8	LEU	CB-CG-CD2	-6.43	100.07	111.00
2	D	88	PHE	N-CA-C	6.38	128.23	111.00
1	A	44	GLY	N-CA-C	-6.37	97.19	113.10
1	A	7	TRP	CB-CA-C	-6.29	97.83	110.40
2	C	148	ARG	NE-CZ-NH1	-6.23	117.19	120.30
1	F	167	VAL	N-CA-C	6.21	127.78	111.00
2	C	228	VAL	C-N-CA	6.12	137.01	121.70
2	G	320	GLN	N-CA-C	6.11	127.49	111.00
2	C	188	ARG	CB-CG-CD	-6.10	95.74	111.60
2	C	336	LYS	CA-CB-CG	6.08	126.78	113.40
2	C	289	ARG	N-CA-C	6.08	127.41	111.00
2	G	192	LEU	N-CA-C	-6.07	94.62	111.00
2	C	88	PHE	N-CA-C	6.03	127.29	111.00
2	C	340	LEU	CB-CG-CD2	-6.03	100.75	111.00
2	H	193	THR	N-CA-C	-6.01	94.77	111.00
1	F	146	LEU	CB-CG-CD2	-6.01	100.78	111.00
1	A	68	PHE	CB-CA-C	-5.95	98.49	110.40
1	A	32	LEU	CA-CB-CG	-5.94	101.64	115.30
1	F	124	ARG	N-CA-CB	5.93	121.28	110.60
1	F	63	PHE	CB-CG-CD2	-5.86	116.70	120.80
2	H	100	PHE	CB-CG-CD2	-5.86	116.70	120.80
1	A	10	VAL	N-CA-C	5.84	126.77	111.00
2	C	228	VAL	CA-C-N	-5.80	104.44	117.20
2	C	44	LYS	N-CA-C	-5.80	95.34	111.00
1	A	195	LEU	CA-CB-CG	5.76	128.54	115.30
1	A	208	ASP	CB-CG-OD2	-5.75	113.12	118.30
2	C	208	CYS	CA-CB-SG	-5.71	103.72	114.00
2	C	234	THR	N-CA-C	-5.71	95.59	111.00
1	F	127	GLY	N-CA-C	-5.67	98.92	113.10
2	C	33	ILE	CB-CA-C	-5.64	100.32	111.60
2	C	119	ARG	NE-CZ-NH1	-5.63	117.49	120.30
1	E	37	LEU	CA-CB-CG	5.63	128.25	115.30
1	A	138	LEU	CB-CG-CD2	-5.61	101.47	111.00
2	D	276	GLN	CB-CA-C	-5.60	99.20	110.40
2	G	251	GLU	N-CA-C	5.60	126.12	111.00
2	D	251	GLU	N-CA-C	5.59	126.11	111.00
2	C	248	ASP	N-CA-CB	-5.59	100.54	110.60
2	D	90	HIS	N-CA-C	-5.57	95.97	111.00
2	D	188	ARG	CB-CA-C	-5.56	99.28	110.40
2	G	168	THR	N-CA-C	5.55	125.98	111.00
2	C	250	PRO	N-CA-C	-5.54	97.69	112.10
1	F	107	MET	CA-CB-CG	5.53	122.70	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	90	HIS	N-CA-C	-5.50	96.16	111.00
2	C	235	PRO	N-CA-C	-5.49	97.82	112.10
2	D	136	SER	N-CA-C	5.49	125.83	111.00
2	C	202	ASP	CB-CG-OD1	-5.49	113.36	118.30
2	D	295	ASN	N-CA-C	-5.49	96.18	111.00
2	C	309	PHE	N-CA-C	-5.47	96.22	111.00
2	D	270	ARG	N-CA-C	-5.44	96.32	111.00
2	C	188	ARG	CA-CB-CG	5.43	125.35	113.40
2	H	100	PHE	CB-CG-CD1	5.40	124.58	120.80
1	A	9	LEU	N-CA-C	5.39	125.56	111.00
1	A	126	MET	CG-SD-CE	5.38	108.81	100.20
2	C	240	PHE	N-CA-CB	-5.35	100.97	110.60
2	C	92	ASN	N-CA-C	5.34	125.41	111.00
2	D	230	SER	N-CA-C	5.30	125.31	111.00
2	D	248	ASP	CB-CA-C	-5.30	99.80	110.40
2	H	188	ARG	CB-CA-C	-5.29	99.82	110.40
1	E	32	LEU	CA-CB-CG	-5.29	103.14	115.30
1	B	163	MET	CA-CB-CG	-5.28	104.33	113.30
2	D	68	GLU	N-CA-CB	5.27	120.08	110.60
2	C	295	ASN	N-CA-C	-5.25	96.81	111.00
2	G	308	LYS	N-CA-C	5.24	125.14	111.00
2	C	192	LEU	CB-CG-CD2	-5.23	102.10	111.00
2	H	45	SER	N-CA-CB	-5.23	102.66	110.50
2	H	125	LEU	CB-CG-CD1	5.22	119.87	111.00
2	D	189	ARG	NE-CZ-NH2	5.20	122.90	120.30
1	B	17	LEU	CA-CB-CG	-5.18	103.39	115.30
1	B	44	GLY	N-CA-C	-5.17	100.16	113.10
1	B	54	ARG	CB-CA-C	-5.17	100.06	110.40
2	H	247	LEU	CA-CB-CG	5.16	127.16	115.30
2	D	115	ASP	N-CA-C	5.13	124.85	111.00
2	C	66	GLY	N-CA-C	5.12	125.89	113.10
1	E	138	LEU	CA-CB-CG	-5.11	103.54	115.30
1	B	195	LEU	CA-CB-CG	5.11	127.05	115.30
2	C	216	ASN	N-CA-C	5.10	124.76	111.00
2	H	1	MET	N-CA-C	5.09	124.76	111.00
1	A	137	VAL	CG1-CB-CG2	5.09	119.05	110.90
1	A	24	GLY	N-CA-C	-5.08	100.40	113.10
2	C	189	ARG	N-CA-C	5.07	124.69	111.00
1	E	45	GLN	N-CA-C	5.07	124.69	111.00
2	H	187	ASN	N-CA-C	5.05	124.65	111.00
1	E	193	LEU	CA-CB-CG	5.03	126.86	115.30
1	A	6	MET	CG-SD-CE	5.02	108.23	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	276	GLN	N-CA-C	-5.01	97.46	111.00
2	D	232	PRO	N-CA-C	5.01	125.11	112.10

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	240	0
1	B	1520	0	1622	259	0
1	E	1520	0	1622	258	0
1	F	1520	0	1622	301	0
2	C	2652	0	2705	375	0
2	D	2652	0	2705	310	0
2	G	2652	0	2705	280	0
2	H	2652	0	2705	344	0
All	All	16688	0	17308	2189	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 64.

All (2189) 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:SD	2:C:201:MET:CE	2.14	1.34
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:223:ASP:HB3	2:H:228:VAL:HG22	1.34	1.08
2:H:52:ASN:HD21	2:H:54:LEU:HG	1.12	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
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
1:A:126:MET:HE1	2:C:153:ARG:HD2	1.44	0.99
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:71:LEU:HG	1:A:75:MET:HE2	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: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:H	2:D:48:ILE:HD13	1.23	0.94
2:C:214:ILE:HD11	2:C:219:LEU:HD23	1.48	0.94
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:75:MET:HE3	1:A:95:PRO:HB3	1.53	0.91
1:F:104:ILE:HG22	1:F:153:THR:HG21	1.53	0.91
1:B:175:ILE:HG13	1:B:176:GLY:N	1.82	0.90
2:D:43:GLY:H	2:D:44:LYS:HZ2	1.12	0.90
2:C:87:ILE:HG22	2:C:88:PHE:N	1.83	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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:F:124:ARG:CZ	1:F:124:ARG:HB3	2.06	0.86
2:G:128:VAL:HG23	2:G:130:LEU:H	1.39	0.86
1:A:117:THR:C	1:A:119:LEU:H	1.79	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
1:E:69:ILE:HD12	1:E:163:MET:HE2	1.58	0.83
2:H:240:PHE:H	2:H:243:SER:HB3	1.40	0.83
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:D:240:PHE:C	2:D:242:GLN:H	1.81	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
1:B:119:LEU:HB3	2:D:92:ASN:CG	1.99	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
1:B:167:VAL:HG13	1:B:168:GLY:N	1.96	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:103:PHE:O	1:A:107:MET:HG2	1.81	0.80
1:A:46:ILE:HG13	1:A:135:ARG:HH22	1.46	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
2:C:201:MET:HB3	2:C:201:MET:HE3	1.63	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:241:ILE:HG23	2:D:244:THR:OG1	1.82	0.79
2:D:98:THR:HA	2:D:138:PRO:HB3	1.64	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:220:ILE:HG22	2:D:221:GLU:HG3	1.63	0.79
2:D:33:ILE:HG12	2:D:194:ILE:CD1	2.12	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:O	2:D:241:ILE:HG22	1.82	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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:B:167:VAL:HG22	1:B:168:GLY:N	2.00	0.76
2:D:1:MET:HG3	2:D:30:ALA:HB2	1.66	0.76
1:E:165:GLY:HA2	1:E:169:ALA:O	1.86	0.76
1:E:69:ILE:HG13	1:F:163:MET:SD	2.25	0.76
1:A:132:GLN:O	1:A:136:LYS:HB3	1.85	0.76
2:C:296:ILE:HA	2:C:314:THR:HG22	1.67	0.76
1:B:133:ILE:CG2	2:D:109:LEU:HD22	2.15	0.76
1:E:180:GLY:CA	1:F:73:VAL:HG13	2.15	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:G:1:MET:HE1	2:G:161:VAL:HG22	1.66	0.75
2:C:214:ILE:HD11	2:C:219:LEU:CD2	2.17	0.75
2:C:36:VAL:O	2:C:197:ILE:HD12	1.87	0.75
1:F:23:SER:HA	1:F:26:PHE:CZ	2.22	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:125:LEU:HB3	2:D:131:GLY:HA3	1.67	0.74
2:D:44:LYS:H	2:D:44:LYS:HD3	1.52	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: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:38:LEU:HD22	1:E:112:LEU:HD22	1.70	0.73
1:E:36:VAL:O	1:E:40:VAL:HG23	1.87	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
1:F:69:ILE:HG23	1:F:163:MET:HE2	1.69	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
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:E:189:MET:SD	1:F:73:VAL:HG12	2.28	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:196:LEU:HD23	1:E:199:LEU:HD23	1.71	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
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
1:F:42:ARG:C	1:F:44:GLY:H	1.94	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
1:F:12:GLY:C	1:F:172:LEU:HD11	2.10	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:180:GLY:HA3	1:B:73:VAL:HG11	1.73	0.71
1:A:42:ARG:HA	1:A:42:ARG:CZ	2.20	0.71
2:C:248:ASP:HB3	2:C:254:GLN:CG	2.20	0.71
2:D:43:GLY:N	2:D:44:LYS:HZ2	1.88	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
1:E:198:ILE:HG13	1:E:199:LEU:N	2.04	0.71
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:F:63:PHE:HA	1:F:66:ILE:HD12	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HG2	2:C:238:GLN:O	1.90	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
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: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:288:ARG:HA	2:H:288:ARG:HG2	1.72	0.70
2:G:70:THR:O	2:G:72:LEU:HG	1.92	0.70
1:A:124:ARG:HA	1:A:128:ALA:HB3	1.72	0.70
2:D:144:GLY:HA2	2:D:175:THR:HG21	1.73	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:234:THR:O	2:D:237:ALA:N	2.25	0.70
2:D:48:ILE:N	2:D:48:ILE:CD1	2.45	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
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:238:GLN:C	2:C:240:PHE:H	1.96	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
2:D:9:LYS:HE2	2:D:55:GLU:OE1	1.92	0.69
2:H:84:ILE:HD11	2:H:163:LEU:CD1	2.23	0.69
1:E:194:VAL:O	1:E:198:ILE:HG23	1.93	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
2:G:37:ILE:HD11	2:G:236:LEU:CD2	2.22	0.69
1:E:119:LEU:CD1	2:G:90:HIS:HB2	2.22	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
1:E:64:ARG:HH12	1:E:103:PHE:HD1	1.38	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:A:165:GLY:HA2	1:A:174:GLN:CG	2.23	0.68
1:A:38:LEU:HD22	1:A:112:LEU:HB3	1.75	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:N	2:D:197:ILE:HD12	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:E:85:THR:O	1:E:85:THR:HG22	1.94	0.68
1:F:172:LEU:HD12	1:F:172:LEU:N	2.09	0.68
1:F:124:ARG:HG3	2:H:54:LEU:HD21	1.76	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:A:139:LEU:HB2	1:A:140:PRO:HD3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:266:VAL:HG22	2:C:267:PRO:HD2	1.74	0.67
2:C:44:LYS:NZ	2:C:198:THR:O	2.25	0.67
2:G:144:GLY:HA2	2:G:171:LEU:HD22	1.76	0.67
1:A:115:ILE:HD13	1:A:115:ILE:O	1.94	0.67
1:B:69:ILE:HD11	1:B:163:MET:CE	2.24	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:A:189:MET:HE2	1:B:74:TRP:N	2.09	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:H	1:F:68:PHE:HD1	1.41	0.67
2:D:267:PRO:HB3	2:D:342:TYR:CE2	2.30	0.67
2:D:36:VAL:HG11	2:D:47:LEU:HD23	1.77	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
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:266:VAL:HG21	2:D:317:HIS:HA	1.77	0.67
2:D:36:VAL:HG12	2:D:214:ILE:HD13	1.77	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:HA	1:A:121:GLU:OE2	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: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:299:ALA:CB	2:H:312:MET:HG3	2.24	0.66
1:A:42:ARG:NE	1:A:42:ARG:HA	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:ILE:HG12	1:A:167:VAL:O	1.94	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:D:248:ASP:C	2:D:249:ILE:O	2.34	0.66
2:H:246:HIS:CE1	2:H:247:LEU:HD12	2.30	0.66
2:C:53:LEU:HD22	2:C:69:LEU:HB3	1.77	0.66
1:B:127:GLY:HA3	2:D:109:LEU:CD1	2.25	0.66
1:E:174:GLN:HA	1:E:177:TYR:CB	2.26	0.66
1:F:139:LEU:N	1:F:140:PRO:CD	2.59	0.66
1:F:19:MET:CB	1:F:157:LEU:HD11	2.24	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
1:E:30:ILE:C	1:E:33:PRO:HD2	2.16	0.65
2:G:205:LYS:NZ	2:G:304:ALA:HB2	2.10	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:D:98:THR:HA	2:D:138:PRO:CA	2.27	0.65
2:D:7:ILE:O	2:D:24:VAL:HG22	1.97	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:139:LEU:HG	1:F:140:PRO:HD3	1.78	0.65
1:F:90:GLN:O	1:F:93:ILE:HG12	1.95	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:36:VAL:CG1	2:C:214:ILE:HD13	2.27	0.65
2:C:4:LEU:HB2	2:C:26:LEU:HB3	1.78	0.65
1:F:185:ASN:ND2	1:F:188:VAL:HG22	2.12	0.65
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
1:F:35:GLY:C	1:F:37:LEU:H	2.00	0.64
1:F:42:ARG:C	1:F:44:GLY:N	2.49	0.64
1:A:172:LEU:HD23	1:A:172:LEU:O	1.97	0.64
2:C:12:HIS:HD2	2:C:17:THR:HG23	1.61	0.64
1:B:41:THR:C	1:B:43:PRO:HD3	2.18	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
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
2:H:220:ILE:CG2	2:H:233:LYS:HD3	2.27	0.64
1:B:155:ILE:CG2	1:B:200:VAL:HG13	2.27	0.64
1:A:181:TYR:CZ	1:B:167:VAL:HG23	2.32	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:279:ASP:O	2:D:280:ALA:C	2.36	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:252:ASP:HA	2:G:255:GLU:HG2	1.78	0.64
2:G:80:ALA:O	2:G:83:GLN:HB2	1.97	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:129:THR:O	1:F:129:THR:HG23	1.97	0.64
1:F:59:ILE:HA	1:F:62:ILE:HG12	1.78	0.64
2:G:93:LEU:HD11	2:G:149:VAL:HB	1.79	0.64
2:G:4:LEU:HB3	2:G:7:ILE:HG12	1.80	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
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
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:E:163:MET:SD	1:F:163:MET:HE1	2.38	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:67:PRO:O	1:E:71:LEU:HB2	1.98	0.63
1:E:26:PHE:HB3	1:E:97:THR:HB	1.79	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:324:GLN:O	2:D:327:ILE:HG12	1.99	0.63
2:D:265:CYS:HB2	2:D:343:VAL:OXT	1.98	0.63
1:E:115:ILE:HG23	1:E:116:PRO:HD2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:93:ILE:O	1:E:96:LEU:HB3	1.98	0.63
1:F:124:ARG:NH1	1:F:124:ARG:HB3	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:F:104:ILE:HD12	1:F:105:ALA:N	2.14	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: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:163:MET:O	1:B:167:VAL:HG12	2.00	0.62
1:B:93:ILE:HG13	1:B:94:VAL:N	2.12	0.62
2:C:171:LEU:HD13	2:C:179:ILE:HD12	1.80	0.62
2:C:288:ARG:NH1	2:D:287:ALA:HB1	2.15	0.62
2:C:36:VAL:HB	2:C:197:ILE:HD13	1.80	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
1:B:69:ILE:HD11	1:B:163:MET:HE3	1.79	0.62
2:D:250:PRO:O	2:D:253:TYR:HB3	2.00	0.62
2:D:36:VAL:HG11	2:D:47:LEU:CD2	2.30	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:F:107:MET:HE2	1:F:149:ALA:CB	2.30	0.62
1:B:23:SER:HA	1:B:26:PHE:CZ	2.35	0.62
2:C:201:MET:HG3	2:C:236:LEU:O	1.99	0.62
2:C:4:LEU:HD12	2:C:26:LEU:HD23	1.82	0.62
2:D:241:ILE:O	2:D:245:LEU:HD13	2.00	0.62
1:A:128:ALA:O	1:A:129:THR:HG23	2.00	0.61
1:A:68:PHE:CD2	1:A:163:MET:HG3	2.34	0.61
2:C:303:TYR:CA	2:C:307:VAL:O	2.48	0.61
2:C:44:LYS:HZ1	2:C:199:HIS:HA	1.65	0.61
1:E:73:VAL:CG2	1:F:180:GLY:HA3	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:VAL:HG22	1:A:93:ILE:HG22	1.82	0.61
1:A:22:VAL:HG12	1:A:26:PHE:CD2	2.35	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
2:H:82:ARG:HD3	2:H:110:ASP:CG	2.21	0.61
1:A:130:PRO:O	1:A:131:MET:O	2.18	0.61
2:C:201:MET:HB2	2:C:239:LYS:HB3	1.82	0.61
2:C:7:ILE:HB	2:C:24:VAL:CG2	2.30	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
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:130:PRO:CG	1:A:131:MET:H	2.07	0.61
1:A:75:MET:O	1:A:79:THR:N	2.30	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
1:A:126:MET:HE2	2:C:153:ARG:HD2	1.80	0.61
2:C:1:MET:HE1	2:C:161:VAL:HG23	1.81	0.61
2:D:125:LEU:O	2:D:128:VAL:HG22	2.01	0.61
2:D:91:PHE:CE1	2:D:171:LEU:HD21	2.35	0.61
2:G:122:THR:HA	2:G:125:LEU:HD12	1.81	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:C:238:GLN:C	2:C:240:PHE:N	2.51	0.61
2:D:91:PHE:HE1	2:D:171:LEU:HD21	1.64	0.61
2:D:29:PRO:HG2	2:D:32:GLN:CD	2.20	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
2:D:233:LYS:C	2:D:235:PRO:HD2	2.21	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:150:ALA:O	1:E:154:LEU:HG	2.00	0.60
1:E:109:GLU:O	1:E:113:LEU:HG	2.01	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: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:NH1	1:B:11:ARG:HB3	2.16	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: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
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
2:D:241:ILE:CG2	2:D:244:THR:OG1	2.49	0.60
1:E:174:GLN:CA	1:E:177:TYR:HB3	2.29	0.60
1:F:123:SER:HA	1:F:129:THR:CB	2.31	0.60
1:F:59:ILE:O	1:F:62:ILE:CG1	2.50	0.60
2:G:247:LEU:HG	2:H:300:GLN:HG3	1.83	0.60
1:E:122:ALA:HB1	2:G:88:PHE:CZ	2.36	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
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:135:ARG:H	1:E:135:ARG:HD2	1.64	0.60
1:E:71:LEU:O	1:E:75:MET:HB2	2.01	0.60
1:F:76:ILE:HB	1:F:77:PRO:HD3	1.82	0.60
1:A:130:PRO:HG2	1:A:131:MET:N	2.10	0.60
2:C:252:ASP:OD2	2:C:253:TYR:N	2.34	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:107:LEU:HB3	2:G:113:PRO:HG3	1.83	0.60
2:G:86:MET:SD	2:G:88:PHE:CZ	2.95	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:117:THR:C	1:A:119:LEU:N	2.46	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:233:LYS:HA	2:C:235:PRO:HD2	1.83	0.59
2:C:201:MET:HG3	2:C:236:LEU:HB2	1.84	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:182:LEU:O	2:H:186:ILE:HG23	2.02	0.59
2:H:28:VAL:HG22	2:H:34:TYR:CD2	2.37	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
2:C:165:ASP:HA	2:C:197:ILE:CG2	2.32	0.59
2:C:26:LEU:HD11	2:C:34:TYR:CZ	2.38	0.59
2:D:233:LYS:O	2:D:233:LYS:HG3	2.02	0.59
1:E:125:ALA:CA	2:G:54:LEU:HD21	2.32	0.59
1:E:32:LEU:C	1:E:34:VAL:H	2.05	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: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:23:SER:HA	1:A:26:PHE:CE2	2.38	0.59
1:A:22:VAL:HG22	1:A:93:ILE:CG2	2.33	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:155:LEU:HD21	2:D:186:ILE:HD12	1.84	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:E:69:ILE:N	1:E:69:ILE:HD13	2.17	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
1:A:71:LEU:HG	1:A:75:MET:CE	2.29	0.59
1:B:47:ILE:O	1:B:48:ALA:HB3	2.03	0.59
2:C:12:HIS:CD2	2:C:17:THR:HG23	2.37	0.59
2:D:274:THR:C	2:D:276:GLN:H	2.05	0.59
1:E:139:LEU:HB2	1:E:140:PRO:HD3	1.85	0.59
1:E:70:ILE:HD13	1:F:193:LEU:HA	1.84	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
1:A:26:PHE:HE1	1:A:104:ILE:HG21	1.68	0.58
1:F:126:MET:SD	1:F:129:THR:CA	2.79	0.58
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
2:C:36:VAL:HG13	2:C:214:ILE:CD1	2.33	0.58
2:C:43:GLY:C	2:C:45:SER:N	2.51	0.58
1:A:134:VAL:O	1:A:138:LEU:HG	2.03	0.58
1:A:19:MET:O	1:A:22:VAL:HB	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
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: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:158:ASN:N	2:G:159:PRO:HD3	2.18	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:60:VAL:O	1:A:64:ARG:HG3	2.04	0.58
1:A:15:GLU:HB3	1:A:89:LEU:HD11	1.85	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:300:GLN:HE22	2:H:244:THR:HB	1.68	0.58
2:G:246:HIS:O	2:H:241:ILE:HG22	2.04	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
1:B:69:ILE:CD1	1:B:163:MET:HE3	2.33	0.57
2:C:121:VAL:O	2:C:125:LEU:HG	2.04	0.57
2:C:7:ILE:O	2:C:24:VAL:HG22	2.04	0.57
1:F:122:ALA:HB1	1:F:126:MET:HE2	1.87	0.57
2:G:97:ARG:HD2	2:G:105:LEU:HD11	1.86	0.57
2:G:77:LEU:HD21	2:G:81:ARG:NH1	2.19	0.57
1:A:74:TRP:O	1:A:77:PRO:HD2	2.03	0.57
1:B:35:GLY:CA	1:B:108:VAL:HG11	2.31	0.57
1:B:32:LEU:O	1:B:35:GLY:N	2.33	0.57
1:B:67:PRO:O	1:B:70:ILE:HG23	2.04	0.57
2:C:303:TYR:O	2:C:304:ALA:C	2.40	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:94:VAL:CG2	1:F:95:PRO:HD3	2.22	0.57
2:G:220:ILE:HD12	2:G:220:ILE:H	1.70	0.57
2:G:282:LEU:HD13	2:G:330:LEU:HD22	1.85	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:H:179:ILE:O	2:H:183:LEU:HD22	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:300:GLN:HE22	2:H:244:THR:CB	2.17	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
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
2:C:230:SER:HG	2:C:231:HIS:CE1	2.22	0.57
2:C:240:PHE:C	2:C:241:ILE:HD13	2.24	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:72:LEU:HD11	1:F:160:TYR:CE1	2.40	0.57
1:F:42:ARG:NH2	1:F:51:LYS:HA	2.19	0.57
2:G:106:PRO:HD3	2:G:153:ARG:HG3	1.87	0.57
1:A:128:ALA:C	1:A:129:THR:HG23	2.26	0.56
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:137:VAL:C	1:F:138:LEU:HG	2.24	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:137:VAL:C	1:A:140:PRO:HD2	2.25	0.56
2:C:228:VAL:O	2:C:229:PHE:CD2	2.59	0.56
1:E:47:ILE:O	1:E:48:ALA:HB3	2.05	0.56
2:G:247:LEU:HG	2:H:300:GLN:CD	2.26	0.56
2:H:52:ASN:O	2:H:53:LEU:HB3	2.04	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:HD22	2:C:52:ASN:H	1.51	0.56
2:D:282:LEU:HD13	2:D:335:VAL:HG21	1.88	0.56
1:E:192:VAL:O	1:E:195:LEU:HB3	2.04	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
2:G:206:ARG:HH22	2:G:242:GLN:NE2	2.03	0.56
1:A:128:ALA:HB1	1:A:134:VAL:CG2	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:CG2	2:D:241:ILE:O	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
2:H:33:ILE:HD13	2:H:207:ILE:HB	1.88	0.56
1:B:107:MET:CE	1:B:152:ILE:HD11	2.36	0.56
1:B:59:ILE:HG13	1:B:60:VAL:N	2.21	0.56
1:B:69:ILE:HG13	1:B:163:MET:HE2	1.87	0.56
1:A:193:LEU:HD11	1:B:74:TRP:NE1	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: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:41:THR:C	1:B:42:ARG:HG3	2.26	0.56
1:B:68:PHE:N	1:B:68:PHE:CD1	2.73	0.56
2:C:244:THR:HA	2:C:298:SER:OG	2.06	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:E:40:VAL:HG12	1:E:53:TYR:HD2	1.72	0.55
2:G:299:ALA:CB	2:G:312:MET:HG3	2.36	0.55
2:H:151:ILE:HD11	2:H:182:LEU:HD21	1.87	0.55
2:H:186:ILE:HB	2:H:192:LEU:HD12	1.87	0.55
2:H:183:LEU:O	2:H:186:ILE:HG12	2.06	0.55
2:H:28:VAL:HG22	2:H:34:TYR:CG	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:E:118:GLY:C	1:E:119:LEU:HG	2.26	0.55
1:F:69:ILE:CG2	1:F:163:MET:HE2	2.35	0.55
1:A:87:ILE:HG22	1:A:88:GLY:N	2.22	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:B:89:LEU:CA	1:B:169:ALA:HB1	2.33	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:299:ALA:HB1	2:D:312:MET:HG2	1.87	0.55
2:D:249:ILE:HG22	2:D:313:LEU:HD12	1.88	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
2:D:52:ASN:ND2	2:D:86:MET:HE3	2.22	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
2:G:82:ARG:NH2	2:G:110:ASP:HB3	2.20	0.55
1:E:122:ALA:HB1	2:G:88:PHE:CD2	2.42	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: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:F:93:ILE:O	1:F:96:LEU:HB2	2.07	0.55
1:E:125:ALA:HA	2:G:54:LEU:HD21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:B:76:ILE:O	1:B:77:PRO:C	2.44	0.55
2:D:83:GLN:C	2:D:159:PRO:HB2	2.27	0.55
2:D:196:LEU:C	2:D:197:ILE:HD12	2.27	0.55
1:E:119:LEU:HD13	2:G:90:HIS:CB	2.36	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
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
1:B:118:GLY:HA2	1:B:121:GLU:CD	2.27	0.54
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
2:H:241:ILE:HD13	2:H:300:GLN:C	2.28	0.54
1:A:185:ASN:CB	1:A:188:VAL:HG22	2.30	0.54
1:A:40:VAL:HG12	1:A:53:TYR:HB2	1.87	0.54
1:A:9:LEU:O	1:A:13:VAL:HG23	2.07	0.54
2:D:82:ARG:O	2:D:159:PRO:HB3	2.06	0.54
1:F:139:LEU:CG	1:F:140:PRO:HD3	2.36	0.54
1:F:36:VAL:HG13	1:F:39:TYR:CE1	2.43	0.54
2:G:63:LEU:HD12	2:G:68:GLU:CG	2.36	0.54
2:H:43:GLY:C	2:H:45:SER:N	2.56	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
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:189:MET:HE1	1:F:74:TRP:HA	1.89	0.54
1:E:32:LEU:C	1:E:34:VAL:N	2.61	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:D:276:GLN:OE1	2:D:280:ALA:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:87:ILE:HG22	2:D:88:PHE:N	2.22	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:G:241:ILE:C	2:G:241:ILE:HD13	2.28	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: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:27:HIS:H	2:H:222:GLN:NE2	2.06	0.54
2:H:3:LYS:HA	2:H:26:LEU:O	2.08	0.54
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:118:GLY:HA2	1:B:121:GLU:OE1	2.08	0.54
1:B:78:PHE:O	1:B:82:ILE:HG12	2.08	0.54
2:C:158:ASN:N	2:C:159:PRO:HD3	2.21	0.54
2:D:248:ASP:O	2:D:249:ILE:HG13	2.08	0.54
2:D:2:ILE:CG2	2:D:28:VAL:HB	2.31	0.54
1:E:34:VAL:HB	1:E:37:LEU:HG	1.90	0.54
1:E:75:MET:HE2	1:E:98:VAL:HG21	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:196:LEU:HD21	2:H:203:VAL:CG1	2.34	0.54
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:C:235:PRO:C	2:C:237:ALA:H	2.11	0.53
2:D:196:LEU:HD23	2:D:208:CYS:SG	2.47	0.53
2:H:105:LEU:O	2:H:109:LEU:HG	2.07	0.53
2:H:84:ILE:HG13	2:H:161:VAL:O	2.08	0.53
2:H:21:LEU:HD21	2:H:47:LEU:HB2	1.90	0.53
1:A:22:VAL:HG12	1:A:26:PHE:HE2	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:271:LEU:HD23	2:C:337:VAL:HG13	1.90	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
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
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:201:MET:O	2:G:202:ASP:C	2.45	0.53
2:G:282:LEU:HD13	2:G:330:LEU:CD2	2.38	0.53
1:B:185:ASN:HB2	1:B:188:VAL:CG2	2.38	0.53
1:B:56:VAL:O	1:B:60:VAL:HG23	2.08	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: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:97:THR:O	1:E:101:ALA:N	2.42	0.53
1:E:34:VAL:HG21	1:E:105:ALA:HA	1.91	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:158:ASN:N	2:G:159:PRO:CD	2.71	0.53
2:G:86:MET:SD	2:G:88:PHE:CE2	3.02	0.53
2:H:105:LEU:HD22	2:H:109:LEU:HD21	1.91	0.53
2:C:48:ILE:HD13	2:C:165:ASP:HB2	1.91	0.53
2:C:44:LYS:CB	2:C:197:ILE:HD11	2.24	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
1:F:126:MET:HB3	1:F:128:ALA:C	2.28	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:241:ILE:HG21	2:H:302:ASP:HB2	1.91	0.53
2:H:33:ILE:CD1	2:H:207:ILE:HB	2.39	0.53
1:A:23:SER:HA	1:A:26:PHE:CD2	2.43	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
1:F:12:GLY:C	1:F:172:LEU:CD1	2.78	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
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
2:H:100:PHE:C	2:H:100:PHE:CD2	2.81	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:42:ARG:HH21	1:F:50:ALA:C	2.12	0.52
2:H:33:ILE:HG23	2:H:194:ILE:CD1	2.38	0.52
1:B:69:ILE:CD1	1:B:163:MET:CE	2.87	0.52
1:F:111:ALA:O	1:F:114:GLU:HB3	2.08	0.52
1:F:59:ILE:CA	1:F:62:ILE:HG12	2.39	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
1:A:69:ILE:HG21	1:B:163:MET:HE1	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
1:B:69:ILE:CG1	1:B:163:MET:HE2	2.39	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
2:C:137:TYR:HD2	2:C:138:PRO:N	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:86:MET:HE3	2:C:163:LEU:HD12	1.90	0.52
1:B:133:ILE:HG21	2:D:109:LEU:HD22	1.91	0.52
2:D:273:PHE:N	2:D:310:GLY:O	2.34	0.52
2:D:44:LYS:CE	2:D:45:SER:OG	2.55	0.52
1:F:107:MET:HE2	1:F:149:ALA:HB1	1.90	0.52
1:F:42:ARG:HE	1:F:49:ASN:C	2.13	0.52
2:H:165:ASP:O	2:H:166:GLU:C	2.47	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:61:ASN:HB2	1:A:106:ARG:HH22	1.75	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
2:C:288:ARG:HH11	2:D:287:ALA:HB1	1.75	0.52
1:F:107:MET:CE	1:F:152:ILE:HD11	2.40	0.52
1:F:36:VAL:O	1:F:36:VAL:CG1	2.58	0.52
2:H:141:LEU:HG	2:H:145:GLN:CB	2.39	0.52
2:H:87:ILE:CG2	2:H:88:PHE:N	2.73	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: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:C:4:LEU:HD22	2:C:7:ILE:CD1	2.40	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: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:B:131:MET:O	1:B:135:ARG:HG2	2.10	0.51
1:B:40:VAL:HG11	1:B:52:LEU:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:VAL:HG12	1:B:53:TYR:HB2	1.92	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:HZ3	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
1:F:126:MET:HE1	1:F:134:VAL:HB	1.93	0.51
2:G:271:LEU:HD22	2:G:335:VAL:HG12	1.92	0.51
2:H:105:LEU:CD2	2:H:109:LEU:HD21	2.41	0.51
2:H:49:ARG:HG2	2:H:54:LEU:HD12	1.93	0.51
1:B:155:ILE:HB	1:B:200:VAL:HG13	1.93	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:C:52:ASN:N	2:C:52:ASN:HD22	2.06	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:187:THR:O	1:E:191:THR:HG23	2.10	0.51
1:E:19:MET:HA	1:E:22:VAL:CG2	2.40	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:O	2:G:241:ILE:HD13	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:B:134:VAL:HA	1:B:137:VAL:CG1	2.36	0.51
2:D:234:THR:HG22	2:D:238:GLN:HG2	1.92	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: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
2:G:241:ILE:O	2:G:241:ILE:HG23	2.11	0.51
1:A:180:GLY:CA	1:B:73:VAL:HG11	2.39	0.51
1:A:56:VAL:O	1:A:59:ILE:HG12	2.10	0.51
1:B:18:ALA:O	1:B:22:VAL:HG23	2.10	0.51
2:C:278:VAL:C	2:C:280:ALA:H	2.13	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:GLU:OE2	2:C:95:SER:N	2.44	0.51
2:D:248:ASP:O	2:D:249:ILE:C	2.49	0.51
1:E:192:VAL:HA	1:E:195:LEU:CD2	2.41	0.51
1:F:41:THR:C	1:F:43:PRO:HD3	2.30	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:196:LEU:HD21	2:C:203:VAL:CG1	2.41	0.51
2:D:83:GLN:NE2	2:D:159:PRO:HA	2.26	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
2:G:113:PRO:HB2	2:G:116:GLU:HB2	1.91	0.51
2:G:220:ILE:N	2:G:220:ILE:HD12	2.25	0.51
1:A:18:ALA:O	1:A:22:VAL:HG23	2.11	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
1:E:26:PHE:CD1	1:E:104:ILE:HD13	2.46	0.50
2:H:141:LEU:HG	2:H:145:GLN:HB3	1.91	0.50
2:H:128:VAL:CG1	2:H:152:ALA:HB2	2.38	0.50
2:H:91:PHE:CE1	2:H:147:GLN:HB2	2.46	0.50
1:B:107:MET:HE2	1:B:152:ILE:HD11	1.93	0.50
2:C:239:LYS:O	2:C:240:PHE:O	2.30	0.50
2:D:209:ASP:O	2:D:225:VAL:HG23	2.10	0.50
2:D:26:LEU:HD11	2:D:34:TYR:CE1	2.47	0.50
2:D:273:PHE:HE1	2:D:335:VAL:HG13	1.74	0.50
2:D:265:CYS:SG	2:D:342:TYR:HB3	2.51	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:HZ1	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:G:10:VAL:O	2:G:10:VAL:HG13	2.11	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:130:PRO:HD2	1:F:133:ILE:CB	2.41	0.50
1:F:15:GLU:O	1:F:18:ALA:HB3	2.11	0.50
2:G:35:GLY:O	2:G:212:ALA:N	2.38	0.50
2:G:89:GLN:HG3	2:G:165:ASP:CG	2.32	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:A:34:VAL:C	1:A:36:VAL:H	2.12	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
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:173:GLY:O	1:F:177:TYR:CB	2.59	0.50
1:F:165:GLY:HA2	1:F:174:GLN:CA	2.41	0.50
1:F:63:PHE:O	1:F:66:ILE:HB	2.12	0.50
2:G:247:LEU:HD11	2:H:244:THR:HG23	1.93	0.50
1:A:79:THR:O	1:A:82:ILE:O	2.29	0.50
1:A:69:ILE:HG13	1:B:163:MET:SD	2.51	0.50
1:B:40:VAL:CG1	1:B:52:LEU:HB2	2.42	0.50
1:B:26:PHE:CB	1:B:97:THR:HB	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:122:ALA:HB1	1:F:126:MET:CE	2.42	0.50
1:F:30:ILE:HD11	1:F:101:ALA:HA	1.94	0.50
2:G:7:ILE:HD11	2:G:62:VAL:HG22	1.94	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
2:G:243:SER:HA	2:H:244:THR:HG21	1.92	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
1:E:160:TYR:C	1:E:160:TYR:CD1	2.84	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:107:LEU:CD1	2:C:121:VAL:HG23	2.43	0.49
2:C:36:VAL:HB	2:C:197:ILE:CD1	2.42	0.49
2:C:2:ILE:HD11	2:C:195:LEU:CD2	2.40	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:125:LEU:O	2:H:130:LEU:O	2.29	0.49
2:H:87:ILE:HD12	2:H:162:LEU:HD21	1.95	0.49
1:B:161:SER:O	1:B:164:GLY:N	2.46	0.49
1:A:159:GLY:O	1:B:68:PHE:HE1	1.96	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: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:C:145:GLN:O	2:C:146:LYS:C	2.51	0.49
2:D:184:LYS:CE	2:D:207:ILE:HG22	2.42	0.49
1:F:126:MET:C	1:F:128:ALA:N	2.64	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:147:GLN:NE2	2:C:147:GLN:HA	2.19	0.49
2:C:147:GLN:O	2:C:150:ALA:HB3	2.12	0.49
2:C:10:VAL:HG23	2:C:18:ILE:O	2.13	0.49
2:D:33:ILE:HG21	2:D:207:ILE:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:303:TYR:C	2:C:307:VAL:O	2.50	0.49
2:D:215:SER:HB3	2:D:220:ILE:CD1	2.42	0.49
2:D:34:TYR:OH	2:D:222:GLN:HG3	2.12	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:321:GLN:O	2:C:324:GLN:HB2	2.13	0.49
2:D:184:LYS:HE2	2:D:207:ILE:HG22	1.94	0.49
2:D:52:ASN:ND2	2:D:86:MET:CE	2.75	0.49
2:C:241:ILE:C	2:C:243:SER:N	2.64	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:H:280:ALA:C	2:H:282:LEU:H	2.16	0.49
2:H:37:ILE:C	2:H:37:ILE:HD13	2.33	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:98:VAL:O	1:A:102:PRO:HD2	2.12	0.49
1:A:96:LEU:N	1:A:96:LEU:HD12	2.27	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
2:D:234:THR:O	2:D:235:PRO:C	2.50	0.49
1:E:125:ALA:CB	2:G:54:LEU:HD21	2.43	0.49
1:E:89:LEU:CD2	1:E:170:GLY:HA2	2.43	0.49
1:F:98:VAL:O	1:F:102:PRO:HD2	2.13	0.49
2:G:293:ASN:HB2	2:G:317:HIS:HB2	1.94	0.49
1:A:172:LEU:HD23	1:A:172:LEU:C	2.33	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: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:G:7:ILE:O	2:G:24:VAL:HG22	2.13	0.49
2:H:56:ARG:HD3	2:H:71:THR:HG21	1.94	0.49
1:A:163:MET:O	1:A:164:GLY:O	2.31	0.48
1:A:9:LEU:N	1:A:9:LEU:HD23	2.27	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:29:PRO:CG	2:D:32:GLN:CD	2.81	0.48
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
2:C:248:ASP:HB3	2:C:254:GLN:CD	2.33	0.48
1:E:108:VAL:HG12	1:E:112:LEU:CD1	2.43	0.48
1:E:12:GLY:C	1:E:172:LEU:HD21	2.33	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: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
2:C:77:LEU:HD21	2:C:81:ARG:CZ	2.43	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:C:47:LEU:O	2:C:48:ILE:C	2.51	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:35:GLY:C	1:F:37:LEU:N	2.67	0.48
1:F:80:ARG:HA	1:F:85:THR:HA	1.95	0.48
2:H:231:HIS:O	2:H:233:LYS:N	2.44	0.48
1:A:47:ILE:O	1:A:47:ILE:HG23	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:211:VAL:CG1	2:H:225:VAL:HG22	2.44	0.48
1:B:106:ARG:HG2	1:B:106:ARG:O	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
2:D:266:VAL:HG21	2:D:317:HIS:CG	2.47	0.48
2:D:43:GLY:H	2:D:44:LYS:HZ3	1.59	0.48
1:F:124:ARG:HD3	2:H:86:MET:SD	2.54	0.48
2:G:124:LEU:CD1	2:G:156:ALA:HA	2.44	0.48
2:G:9:LYS:HE2	2:G:55:GLU:HB3	1.95	0.48
1:F:126:MET:CA	2:H:109:LEU:HD13	2.40	0.48
2:H:331:GLN:HA	2:H:335:VAL:O	2.14	0.48
1:F:124:ARG:HH11	2:H:86:MET:HB3	1.75	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
1:B:92:ALA:C	1:B:95:PRO:HD2	2.34	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:196:LEU:HD23	2:G:208:CYS:SG	2.53	0.48
2:G:51:VAL:HB	2:G:163:LEU:HD11	1.94	0.48
2:G:4:LEU:CD2	2:G:62:VAL:HG13	2.41	0.48
2:H:10:VAL:HG23	2:H:18:ILE:O	2.14	0.48
2:H:6:ASN:N	2:H:25:SER:OG	2.43	0.48
1:A:165:GLY:HA2	1:A:174:GLN:HG2	1.96	0.48
1:A:22:VAL:O	1:A:25:PHE:HB3	2.14	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
1:E:196:LEU:HD23	1:E:199:LEU:CD2	2.42	0.48
1:F:161:SER:C	1:F:163:MET:N	2.65	0.48
1:F:172:LEU:CD1	1:F:172:LEU:N	2.75	0.48
1:F:37:LEU:O	1:F:41:THR:HG23	2.13	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
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
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:172:LEU:CD1	1:F:172:LEU:H	2.27	0.48
1:F:22:VAL:CG2	1:F:23:SER:N	2.77	0.48
2:G:37:ILE:CD1	2:G:236:LEU:HB3	2.44	0.48
1:B:126:MET:SD	2:D:153:ARG:CD	3.01	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:VAL:HG13	1:B:93:ILE:HD12	1.96	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:O	2:H:53:LEU:HG	2.13	0.47
1:A:166:ALA:HB1	1:B:181:TYR:HE2	1.79	0.47
1:B:26:PHE:CD1	1:B:97:THR:HA	2.48	0.47
1:B:70:ILE:HG13	1:B:70:ILE:O	2.09	0.47
1:B:72:LEU:HD22	1:B:95:PRO:CB	2.20	0.47
2:C:1:MET:CE	2:C:161:VAL:HG23	2.43	0.47
1:E:163:MET:O	1:E:166:ALA:HB3	2.14	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:104:ILE:HG13	1:A:105:ALA:N	2.30	0.47
1:A:76:ILE:HB	1:A:77:PRO:HD3	1.96	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: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:E:163:MET:CE	1:F:163:MET:HE1	2.44	0.47
1:F:37:LEU:CD2	1:F:56:VAL:HG11	2.43	0.47
2:H:125:LEU:HA	2:H:128:VAL:HG22	1.96	0.47
2:H:84:ILE:HG13	2:H:161:VAL:HB	1.96	0.47
2:H:245:LEU:HG	2:H:298:SER:CB	2.44	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:A:47:ILE:O	1:A:48:ALA:HB2	2.14	0.47
1:A:72:LEU:HA	1:A:75:MET:HE3	1.95	0.47
1:B:101:ALA:HA	1:B:104:ILE:CG1	2.45	0.47
1:A:180:GLY:C	1:B:73:VAL:HG13	2.35	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:132:GLN:O	1:E:136:LYS:HB2	2.15	0.47
1:E:69:ILE:HD12	1:E:163:MET:CE	2.36	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
2:H:37:ILE:HG23	2:H:37:ILE:O	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
2:C:124:LEU:HD21	2:C:156:ALA:HA	1.96	0.47
2:D:98:THR:CA	2:D:138:PRO:HB3	2.41	0.47
2:D:43:GLY:N	2:D:44:LYS:NZ	2.48	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:H:121:VAL:HG12	2:H:125:LEU:CD1	2.43	0.47
2:H:34:TYR:CE1	2:H:212:ALA:HB2	2.50	0.47
2:G:246:HIS:HB3	2:H:241:ILE:CG2	2.45	0.47
2:C:211:VAL:HG22	2:C:212:ALA:N	2.29	0.47
2:C:2:ILE:HG23	2:C:28:VAL:O	2.14	0.47
1:F:59:ILE:C	1:F:62:ILE:HG12	2.34	0.47
1:F:26:PHE:CE2	1:F:97:THR:HG22	2.50	0.47
2:H:125:LEU:HA	2:H:128:VAL:CG2	2.45	0.47
2:H:91:PHE:O	2:H:92:ASN:HB2	2.14	0.47
1:A:41:THR:HG21	1:A:113:LEU:HD21	1.97	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:D:162:LEU:HB3	2:D:194:ILE:CG2	2.41	0.47
2:D:128:VAL:HA	2:D:182:LEU:HD11	1.97	0.47
2:D:42:ALA:N	2:D:44:LYS:HZ2	2.13	0.47
1:F:118:GLY:O	1:F:121:GLU:HB2	2.15	0.47
1:F:39:TYR:OH	1:F:135:ARG:HD2	2.15	0.47
1:F:179:TYR:O	1:F:185:ASN:CB	2.59	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: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:8:THR:HG23	2:C:21:LEU:O	2.15	0.47
2:D:37:ILE:HD12	2:D:201:MET:SD	2.55	0.47
2:D:44:LYS:CD	2:D:44:LYS:H	2.21	0.47
2:D:53:LEU:HG	2:D:53:LEU:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:G:48:ILE:HD12	2:G:86:MET:HE2	1.96	0.47
2:H:33:ILE:CD1	2:H:207:ILE:O	2.57	0.47
1:A:180:GLY:C	1:B:73:VAL:CG1	2.83	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: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: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:N	1:A:17:LEU:HD23	2.30	0.46
2:C:2:ILE:HD11	2:C:195:LEU:HD22	1.97	0.46
2:C:247:LEU:HD23	2:D:300:GLN:CD	2.35	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: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:C:162:LEU:CD2	2:C:162:LEU:C	2.83	0.46
2:D:228:VAL:O	2:D:229:PHE:HD2	1.98	0.46
1:E:165:GLY:O	1:E:174:GLN:HG3	2.14	0.46
1:E:30:ILE:HA	1:E:33:PRO:HG2	1.97	0.46
1:F:30:ILE:CD1	1:F:101:ALA:HB1	2.43	0.46
1:F:60:VAL:HG13	1:F:102:PRO:HA	1.96	0.46
1:F:40:VAL:HG12	1:F:53:TYR:HB2	1.98	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:206:ARG:NH1	2:D:206:ARG:HG3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:61:SER:HB3	2:D:68:GLU:CD	2.35	0.46
2:D:73:SER:HB2	2:D:76:GLU:CG	2.44	0.46
1:E:188:VAL:HG23	1:E:189:MET:N	2.31	0.46
1:E:50:ALA:HB3	1:E:52:LEU:HD12	1.96	0.46
1:F:185:ASN:CG	1:F:188:VAL:HG22	2.36	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
2:G:33:ILE:HG12	2:G:194:ILE:HD11	1.97	0.46
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
2:D:162:LEU:HD23	2:D:162:LEU:C	2.35	0.46
1:F:126:MET:HE1	1:F:129:THR:OG1	2.16	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:250:PRO:HG2	2:H:253:TYR:HB2	1.97	0.46
2:H:56:ARG:CD	2:H:71:THR:HG21	2.45	0.46
2:C:130:LEU:CD2	2:C:148:ARG:HB2	2.43	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:118:GLY:HA2	1:F:121:GLU:CD	2.35	0.46
2:G:299:ALA:CB	2:G:312:MET:HA	2.39	0.46
2:G:7:ILE:HG21	2:G:50:CYS:SG	2.56	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:242:GLN:O	2:D:246:HIS:HB3	2.15	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
1:E:160:TYR:HD1	1:E:160:TYR:C	2.19	0.46
1:E:182:ILE:O	1:E:182:ILE:HG13	2.16	0.46
1:F:124:ARG:CZ	2:H:86:MET:CB	2.94	0.46
1:F:59:ILE:O	1:F:63:PHE:HD1	1.99	0.46
2:G:271:LEU:HD22	2:G:335:VAL:CG1	2.45	0.46
2:H:201:MET:SD	2:H:204:VAL:HB	2.55	0.46
2:H:48:ILE:HD13	2:H:48:ILE:H	1.64	0.46
1:A:163:MET:C	1:A:164:GLY:O	2.53	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:129:THR:HA	1:B:133:ILE:CB	2.46	0.46
2:C:327:ILE:HG13	2:C:328:ALA:N	2.31	0.46
2:C:97:ARG:NH1	2:C:105:LEU:HD23	2.31	0.46
1:F:123:SER:HA	1:F:129:THR:HB	1.96	0.46
1:F:152:ILE:HG13	1:F:152:ILE:H	1.50	0.46
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:201:MET:HG3	2:D:236:LEU:C	2.36	0.46
2:D:250:PRO:HG2	2:D:253:TYR:CB	2.46	0.46
1:F:8:LEU:H	1:F:8:LEU:HD23	1.81	0.46
1:A:74:TRP:CG	1:B:193:LEU:HD11	2.51	0.46
2:C:143:GLY:O	2:C:144:GLY:C	2.53	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:HA	2:C:313:LEU:HD23	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:162:LEU:HB3	2:G:194:ILE:HG22	1.97	0.46
2:G:52:ASN:C	2:G:52:ASN:HD22	2.18	0.46
2:G:83:GLN:O	2:G:159:PRO:CB	2.58	0.46
2:H:151:ILE:HG13	2:H:152:ALA:N	2.29	0.46
2:H:270:ARG:HB2	2:H:340:LEU:HD21	1.98	0.46
2:H:241:ILE:CG2	2:H:302:ASP:HB2	2.46	0.46
1:A:105:ALA:O	1:A:108:VAL:HB	2.15	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
2:D:34:TYR:HH	2:D:222:GLN:HG3	1.81	0.46
2:G:283:LEU:HB3	2:G:294:ASN:ND2	2.31	0.46
2:G:77:LEU:HD21	2:G:81:ARG:HH22	1.77	0.46
1:A:30:ILE:O	1:A:34:VAL:HG22	2.16	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
2:D:86:MET:HG2	2:D:87:ILE:N	2.31	0.45
1:E:40:VAL:HA	1:E:47:ILE:CD1	2.34	0.45
1:F:68:PHE:N	1:F:68:PHE:HD1	2.11	0.45
2:G:28:VAL:HG22	2:G:34:TYR:CD2	2.51	0.45
2:H:323:THR:O	2:H:327:ILE:HG12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:121:GLU:OE1	2:H:92:ASN:CG	2.54	0.45
1:A:153:THR:O	1:A:157:LEU:N	2.36	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
2:C:46:THR:CG2	2:C:47:LEU:N	2.78	0.45
1:E:138:LEU:O	1:E:141:GLU:HB2	2.16	0.45
1:E:66:ILE:HG12	1:F:193:LEU:CD2	2.45	0.45
1:F:114:GLU:C	1:F:116:PRO:HD2	2.35	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
2:H:256:ARG:O	2:H:257:LEU:HB2	2.16	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:HA	1:E:138:LEU:HD23	1.68	0.45
1:F:118:GLY:HA2	1:F:121:GLU:HB2	1.99	0.45
1:F:41:THR:HG22	1:F:53:TYR:HE2	1.80	0.45
2:G:35:GLY:N	2:G:210:CYS:O	2.40	0.45
2:G:35:GLY:O	2:G:211:VAL:HA	2.15	0.45
1:B:62:ILE:HG13	1:B:63:PHE:N	2.30	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
2:C:2:ILE:CG2	2:C:28:VAL:O	2.65	0.45
1:F:59:ILE:O	1:F:62:ILE:HG13	2.16	0.45
2:H:10:VAL:HG21	2:H:17:THR:HG23	1.98	0.45
2:D:240:PHE:HD2	2:D:242:GLN:HG2	1.82	0.45
2:D:95:SER:HA	2:D:139:SER:HG	1.80	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:313:LEU:HD22	2:C:340:LEU:HD11	1.99	0.45
2:C:93:LEU:HD11	2:C:146:LYS:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:188:VAL:HG23	1:F:189:MET:N	2.32	0.45
2:G:128:VAL:CG1	2:G:152:ALA:HB2	2.36	0.45
2:G:4:LEU:HB3	2:G:7:ILE:CG1	2.46	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:128:ALA:HB1	1:A:134:VAL:HG22	1.99	0.45
1:A:39:TYR:CD2	1:A:48:ALA:CB	2.98	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:270:ARG:HG3	2:G:313:LEU:CD2	2.46	0.45
2:G:87:ILE:HG23	2:G:147:GLN:NE2	2.31	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:NH2	2:D:189:ARG:HG3	2.20	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:231:HIS:C	2:H:233:LYS:H	2.20	0.45
1:F:124:ARG:CZ	2:H:86:MET:HB3	2.47	0.45
1:B:137:VAL:CG2	1:B:138:LEU:N	2.80	0.45
1:B:66:ILE:HA	1:B:67:PRO:HD3	1.57	0.45
2:C:99:VAL:HG22	2:C:149:VAL:HG21	1.98	0.45
2:D:16:ARG:HG3	2:D:16:ARG:HH11	1.82	0.45
2:D:189:ARG:NH2	2:D:189:ARG:CG	2.74	0.45
2:D:4:LEU:HB3	2:D:7:ILE:HD11	1.99	0.45
1:E:68:PHE:HB3	1:E:69:ILE:HD13	1.97	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
1:E:125:ALA:HB1	2:G:52:ASN:OD1	2.16	0.45
2:H:162:LEU:HD21	2:H:164:CYS:SG	2.56	0.45
1:A:188:VAL:O	1:A:192:VAL:HG23	2.17	0.44
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:B:97:THR:OG1	1:B:98:VAL:N	2.50	0.44
2:D:107:LEU:HD21	2:D:120:ARG:HD2	1.99	0.44
2:D:8:THR:HA	2:D:21:LEU:O	2.16	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:278:VAL:C	2:G:280:ALA:H	2.20	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:123:SER:HB2	1:B:126:MET:HE3	1.99	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:189:MET:O	1:F:192:VAL:HB	2.18	0.44
2:H:250:PRO:CG	2:H:253:TYR:HB2	2.47	0.44
2:H:4:LEU:O	2:H:25:SER:HA	2.17	0.44
1:F:124:ARG:HG3	2:H:54:LEU:HD11	1.99	0.44
1:A:131:MET:HB3	1:A:132:GLN:H	1.35	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:C:47:LEU:C	2:C:49:ARG:N	2.70	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
2:G:2:ILE:CG2	2:G:28:VAL:HB	2.41	0.44
2:H:107:LEU:HD21	2:H:156:ALA:O	2.17	0.44
2:H:82:ARG:HH12	2:H:111:ASN:ND2	2.16	0.44
2:H:298:SER:OG	2:H:313:LEU:HB2	2.17	0.44
2:H:35:GLY:HA3	2:H:208:CYS:SG	2.58	0.44
1:B:107:MET:HE3	1:B:149:ALA:HB1	2.00	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:172:LEU:HB3	1:F:192:VAL:HG13	2.00	0.44
1:F:17:LEU:HD23	1:F:17:LEU:HA	1.53	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:249:ILE:HG13	2:D:250:PRO:N	2.31	0.44
2:D:44:LYS:O	2:D:48:ILE:CD1	2.66	0.44
1:E:42:ARG:HB3	1:E:46:ILE:HG22	2.00	0.44
1:E:41:THR:O	1:E:43:PRO:HD3	2.17	0.44
2:G:238:GLN:NE2	2:G:311:ILE:HD13	2.33	0.44
2:G:28:VAL:HG13	2:G:34:TYR:CD2	2.53	0.44
2:H:103:VAL:CG2	2:H:152:ALA:HB3	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:ALA:O	1:B:104:ILE:HG23	2.18	0.44
1:B:130:PRO:HD2	1:B:133:ILE:CG1	2.47	0.44
2:C:130:LEU:HD21	2:C:145:GLN:HG2	1.98	0.44
2:C:11:PHE:HB2	2:C:18:ILE:CG2	2.47	0.44
2:D:1:MET:HB3	2:D:1:MET:HE2	1.86	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
1:A:82:ILE:O	1:A:83:VAL:C	2.55	0.44
1:B:134:VAL:CA	1:B:137:VAL:HG13	2.42	0.44
2:D:137:TYR:HD2	2:D:140:ASN:O	2.01	0.44
2:C:288:ARG:NH1	2:D:292:VAL:O	2.49	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: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:B:146:LEU:O	1:B:149:ALA:HB3	2.18	0.44
2:C:112:THR:N	2:C:113:PRO:HD3	2.33	0.44
2:C:63:LEU:HD11	2:C:66:GLY:CA	2.48	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:HG13	1:F:69:ILE:H	1.48	0.44
2:G:179:ILE:O	2:G:182:LEU:HB3	2.18	0.44
2:H:186:ILE:HB	2:H:192:LEU:CD1	2.46	0.44
2:H:241:ILE:HD13	2:H:300:GLN:O	2.18	0.44
1:B:133:ILE:O	1:B:136:LYS:HB2	2.18	0.44
1:B:22:VAL:CG1	1:B:93:ILE:HB	2.36	0.44
2:C:285:GLU:HG2	2:C:329:TRP:CH2	2.53	0.44
2:C:43:GLY:C	2:C:45:SER:H	2.09	0.44
2:C:9:LYS:HZ2	2:C:56:ARG:H	1.65	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: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
1:B:32:LEU:HB2	1:B:33:PRO:HD3	2.00	0.43
2:C:148:ARG:O	2:C:149:VAL:C	2.54	0.43
2:C:190:LEU:HD23	2:C:190:LEU:HA	1.66	0.43
1:E:144:PRO:HG2	1:E:145:GLY:H	1.82	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:F:117:THR:O	1:F:119:LEU:N	2.51	0.43
1:F:122:ALA:O	1:F:126:MET:HE3	2.18	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: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:G:41:GLY:O	2:G:43:GLY:N	2.50	0.43
2:H:33:ILE:HD13	2:H:207:ILE:HD12	2.00	0.43
2:C:246:HIS:O	2:C:250:PRO:HD2	2.18	0.43
2:C:85:GLY:O	2:C:163:LEU:N	2.47	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: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
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:C:77:LEU:HD21	2:C:81:ARG:HH21	1.83	0.43
2:D:94:LEU:H	2:D:102:ASN:ND2	2.16	0.43
1:F:141:GLU:OE2	2:H:96:SER:N	2.48	0.43
1:F:37:LEU:HB3	1:F:40:VAL:HB	1.98	0.43
2:G:63:LEU:HD21	2:G:66:GLY:CA	2.48	0.43
2:H:82:ARG:CD	2:H:110:ASP:CG	2.86	0.43
2:H:87:ILE:CG2	2:H:147:GLN:NE2	2.77	0.43
2:H:48:ILE:H	2:H:48:ILE:HD12	1.78	0.43
1:A:18:ALA:HA	1:A:21:PHE:HD2	1.82	0.43
1:B:104:ILE:HA	1:B:107:MET:HG2	1.99	0.43
1:B:11:ARG:CZ	1:B:11:ARG:HB3	2.48	0.43
1:B:22:VAL:HG12	1:B:26:PHE:HE2	1.82	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:122:ALA:O	1:E:125:ALA:HB3	2.19	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
2:G:130:LEU:O	2:G:130:LEU:HG	2.19	0.43
2:G:252:ASP:O	2:G:256:ARG:HB2	2.18	0.43
2:G:33:ILE:HG12	2:G:194:ILE:HG12	1.98	0.43
2:H:125:LEU:O	2:H:128:VAL:CG2	2.66	0.43
1:A:133:ILE:O	1:A:137:VAL:HG22	2.19	0.43
1:A:69:ILE:CG1	1:B:163:MET:SD	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:1:MET:HG3	2:C:30:ALA:HB2	2.01	0.43
2:H:241:ILE:H	2:H:241:ILE:HG13	1.58	0.43
2:H:7:ILE:HD13	2:H:60:GLY:HA3	2.01	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:137:TYR:CZ	2:C:140:ASN:O	2.72	0.43
2:C:29:PRO:HG2	2:C:32:GLN:HB2	2.00	0.43
2:D:224:THR:HG22	2:D:226:SER:H	1.84	0.43
2:C:278:VAL:HG21	2:D:256:ARG:HH22	1.83	0.43
1:E:198:ILE:HG13	1:E:199:LEU:H	1.80	0.43
1:E:40:VAL:HG22	1:E:47:ILE:CD1	2.48	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:C:266:VAL:HG13	2:C:267:PRO:N	2.33	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:117:THR:C	1:F:119:LEU:N	2.72	0.43
1:F:138:LEU:HD21	2:H:94:LEU:CD2	2.49	0.43
1:F:41:THR:O	1:F:43:PRO:HD3	2.18	0.43
2:H:142:SER:O	2:H:145:GLN:HB2	2.19	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:D:155:LEU:HD11	2:D:186:ILE:CD1	2.48	0.43
1:E:137:VAL:HG12	2:G:97:ARG:HH22	1.84	0.43
1:E:96:LEU:HD12	1:E:160:TYR:CD1	2.54	0.43
2:G:277:SER:O	2:G:280:ALA:HB3	2.19	0.43
1:B:25:PHE:O	1:B:29:VAL:HB	2.18	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:118:GLY:C	1:F:121:GLU:HB2	2.40	0.43
1:F:68:PHE:O	1:F:160:TYR:OH	2.36	0.43
1:F:161:SER:C	1:F:163:MET:H	2.21	0.43
2:G:213:VAL:N	2:G:221:GLU:O	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:34:TYR:CD2	2:H:210:CYS:HB2	2.53	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:246:HIS:CE1	2:D:202:ASP:OD1	2.72	0.43
2:C:253:TYR:HE1	2:C:268:MET:HE1	1.84	0.43
2:C:4:LEU:HD13	2:C:47:LEU:HD11	2.01	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:133:ILE:HA	1:E:136:LYS:HB3	2.00	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: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:130:LEU:CD1	2:H:148:ARG:HB2	2.49	0.43
2:H:37:ILE:CG2	2:H:213:VAL:HG22	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
2:C:312:MET:HG2	2:C:314:THR:HG23	2.00	0.42
2:C:63:LEU:HD11	2:C:66:GLY:C	2.39	0.42
2:D:215:SER:HB3	2:D:220:ILE:HD11	2.01	0.42
2:C:243:SER:O	2:D:300:GLN:OE1	2.36	0.42
1:E:126:MET:HE2	2:G:153:ARG:HG2	2.01	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: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
2:D:16:ARG:HG3	2:D:16:ARG:NH1	2.34	0.42
1:E:74:TRP:HA	1:F:189:MET:HE1	2.01	0.42
2:G:247:LEU:HA	2:H:300:GLN:NE2	2.35	0.42
2:G:24:VAL:O	2:G:24:VAL:HG23	2.20	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:113:LEU:HA	1:B:113:LEU:HD23	1.76	0.42
1:B:8:LEU:H	1:B:8:LEU:CD1	2.29	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:107:LEU:O	2:D:111:ASN:HB2	2.19	0.42
2:D:115:ASP:C	2:D:117:VAL:N	2.70	0.42
2:D:268:MET:HE2	2:D:313:LEU:HB3	2.02	0.42
2:D:319:THR:HG22	2:D:320:GLN:N	2.34	0.42
1:F:124:ARG:NH1	2:H:86:MET:CB	2.75	0.42
1:F:62:ILE:O	1:F:66:ILE:HG13	2.19	0.42
2:H:128:VAL:HB	2:H:148:ARG:HB3	2.01	0.42
2:H:37:ILE:HG12	2:H:198:THR:HG23	2.00	0.42
1:A:125:ALA:HA	2:C:54:LEU:HD21	2.02	0.42
2:D:274:THR:C	2:D:276:GLN:N	2.71	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:139:SER:C	2:H:141:LEU:H	2.21	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
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
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: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
2:G:49:ARG:NH1	2:G:49:ARG:HG3	2.34	0.42
2:H:43:GLY:C	2:H:45:SER:H	2.10	0.42
1:A:186:ALA:O	1:A:190:ASN:OD1	2.38	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
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
2:C:247:LEU:C	2:C:250:PRO:HD2	2.39	0.42
1:F:172:LEU:HD23	1:F:195:LEU:HD23	2.01	0.42
1:F:206:ALA:O	1:F:207:GLY:C	2.57	0.42
1:F:76:ILE:HG22	1:F:77:PRO:N	2.35	0.42
2:G:9:LYS:HE3	2:G:11:PHE:HB2	2.02	0.42
2:G:247:LEU:HD21	2:H:244:THR:HG21	2.02	0.42
2:G:53:LEU:HB3	2:G:81:ARG:HH21	1.84	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:149:ALA:O	1:B:152:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:GLY:O	1:B:174:GLN:HB3	2.19	0.42
1:B:40:VAL:HG11	1:B:53:TYR:N	2.35	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:130:LEU:CD2	2:G:149:VAL:HG22	2.50	0.42
2:G:87:ILE:CD1	2:G:151:ILE:HD13	2.50	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:107:LEU:HB3	2:C:117:VAL:HG22	2.02	0.42
2:C:253:TYR:OH	2:C:297:ILE:HD11	2.20	0.42
2:C:4:LEU:HD12	2:C:26:LEU:HB3	2.02	0.42
1:A:119:LEU:CB	2:C:92:ASN:OD1	2.60	0.42
2:D:28:VAL:HG13	2:D:34:TYR:HB2	2.02	0.42
1:F:121:GLU:OE2	2:H:92:ASN:HB3	2.20	0.42
1:F:38:LEU:HB2	1:F:112:LEU:HD13	2.02	0.42
1:F:37:LEU:HD22	1:F:40:VAL:HG21	2.02	0.42
1:F:70:ILE:CG2	1:F:71:LEU:N	2.82	0.42
2:H:189:ARG:C	2:H:190:LEU:O	2.57	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:268:MET:HA	2:C:314:THR:O	2.19	0.42
2:C:4:LEU:HA	2:C:7:ILE:HD11	2.02	0.42
2:D:2:ILE:CD1	2:D:195:LEU:HD22	2.49	0.42
1:E:163:MET:HB3	1:E:163:MET:HE3	1.68	0.42
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
1:A:89:LEU:HD23	1:A:89:LEU:HA	1.83	0.42
2:C:168:THR:HG21	2:C:180:LEU:HG	2.02	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:N	2:D:313:LEU:HD23	2.34	0.42
1:B:120:ILE:HD12	2:D:94:LEU:HD21	2.01	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: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
1:F:25:PHE:O	1:F:29:VAL:CG2	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:26:PHE:HA	1:F:29:VAL:HB	2.01	0.42
1:F:8:LEU:H	1:F:8:LEU:CD2	2.26	0.42
2:G:234:THR:N	2:G:235:PRO:HD2	2.35	0.42
1:A:148:ASN:HA	1:A:151:THR:HG22	2.01	0.41
1:A:66:ILE:CG2	1:A:71:LEU:HB2	2.50	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
2:H:104:ALA:O	2:H:105:LEU:C	2.57	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
1:B:36:VAL:CG1	1:B:36:VAL:O	2.68	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:141:LEU:CG	2:H:145:GLN:HB3	2.50	0.41
2:H:87:ILE:CG2	2:H:88:PHE:H	2.32	0.41
2:H:99:VAL:HB	2:H:134:HIS:O	2.20	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
1:E:38:LEU:HD13	1:E:112:LEU:CB	2.48	0.41
1:F:138:LEU:C	1:F:140:PRO:HD2	2.41	0.41
2:G:39:ALA:HB2	2:G:236:LEU:HD21	2.01	0.41
2:H:87:ILE:CD1	2:H:151:ILE:HG22	2.49	0.41
1:A:180:GLY:CA	1:B:73:VAL:CG1	2.98	0.41
1:A:39:TYR:O	1:A:44:GLY:HA2	2.21	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:208:ASP:N	1:F:208:ASP:OD1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:132:GLN:O	1:A:133:ILE:C	2.57	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:168:GLY:O	1:E:169:ALA:HB2	2.20	0.41
2:G:1:MET:CE	2:G:161:VAL:HG22	2.43	0.41
2:H:151:ILE:HA	2:H:154:ALA:HB3	2.02	0.41
2:G:293:ASN:HA	2:H:284:SER:CB	2.51	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:A:185:ASN:C	1:A:187:THR:N	2.72	0.41
1:B:17:LEU:HA	1:B:17:LEU:HD23	1.75	0.41
1:B:93:ILE:CG1	1:B:94:VAL:N	2.81	0.41
2:C:86:MET:CE	2:C:163:LEU:HD12	2.48	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:F:69:ILE:HG23	1:F:163:MET:CE	2.44	0.41
2:G:138:PRO:HG2	2:G:139:SER:H	1.84	0.41
1:A:169:ALA:C	1:A:174:GLN:NE2	2.74	0.41
1:A:190:ASN:HA	1:A:193:LEU:HD12	2.02	0.41
1:B:167:VAL:CG1	1:B:168:GLY:N	2.65	0.41
1:B:172:LEU:CD2	1:B:195:LEU:HD23	2.37	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
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:200:VAL:O	1:E:203:ILE:HB	2.20	0.41
1:E:66:ILE:HA	1:E:67:PRO:HD3	1.91	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
1:F:72:LEU:HD23	1:F:95:PRO:HB3	2.01	0.41
2:G:124:LEU:HD11	2:G:156:ALA:HA	2.02	0.41
2:G:85:GLY:C	2:G:162:LEU:HD12	2.40	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
2:C:177:ARG:CZ	2:C:206:ARG:HH21	2.33	0.41
2:C:21:LEU:HD23	2:C:217:GLY:HA2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:198:THR:HG21	2:H:200:GLU:O	2.20	0.41
2:H:33:ILE:O	2:H:209:ASP:N	2.54	0.41
2:H:5:SER:O	2:H:6:ASN:C	2.58	0.41
2:H:62:VAL:O	2:H:68:GLU:HA	2.21	0.41
1:A:196:LEU:O	1:A:200:VAL:HG23	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:5:SER:O	2:C:7:ILE:HG13	2.21	0.41
1:E:97:THR:OG1	1:E:98:VAL:N	2.54	0.41
1:F:46:ILE:CG2	1:F:47:ILE:HG23	2.45	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:G:28:VAL:HG13	2:G:34:TYR:HD2	1.86	0.41
2:G:43:GLY:C	2:G:45:SER:N	2.73	0.41
2:G:52:ASN:C	2:G:52:ASN:ND2	2.74	0.41
2:G:87:ILE:HD12	2:G:151:ILE:HD13	2.03	0.41
1:A:32:LEU:HB2	1:A:33:PRO:HD3	2.03	0.41
1:B:115:ILE:CG1	1:B:116:PRO:HD2	2.45	0.41
2:C:234:THR:C	2:C:237:ALA:HB3	2.40	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:134:VAL:HB	1:E:135:ARG:NH2	2.36	0.41
1:E:73:VAL:O	1:E:77:PRO:HD3	2.20	0.41
2:G:91:PHE:HE1	2:G:171:LEU:HD21	1.86	0.41
2:H:330:LEU:O	2:H:335:VAL:HB	2.21	0.41
2:H:9:LYS:HE3	2:H:55:GLU:HB3	2.02	0.41
1:A:160:TYR:HD1	1:A:160:TYR:O	2.04	0.41
1:A:42:ARG:HB3	1:A:43:PRO:CD	2.49	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
1:B:22:VAL:HG21	1:B:93:ILE:CB	2.51	0.41
2:C:253:TYR:HE1	2:C:268:MET:CE	2.34	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:G:105:LEU:N	2:G:106:PRO:HD2	2.35	0.41
2:G:247:LEU:HD21	2:G:300:GLN:NE2	2.36	0.41
1:A:177:TYR:O	1:A:181:TYR:N	2.42	0.40
2:C:261:PRO:HB3	2:C:342:TYR:CE1	2.55	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
1:E:76:ILE:CB	1:E:77:PRO:HD3	2.51	0.40
1:F:143:LEU:HD23	1:F:143:LEU:HA	1.84	0.40
1:F:64:ARG:HD2	1:F:103:PHE:CZ	2.56	0.40
1:F:71:LEU:O	1:F:75:MET:HE3	2.21	0.40
2:G:298:SER:HB3	2:H:300:GLN:NE2	2.36	0.40
1:B:126:MET:HB2	1:B:126:MET:HE3	1.90	0.40
2:C:249:ILE:HA	2:C:249:ILE:HD13	1.97	0.40
2:C:247:LEU:CD2	2:C:297:ILE:HG22	2.44	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
1:F:193:LEU:C	1:F:193:LEU:HD13	2.42	0.40
2:G:276:GLN:OE1	2:G:282:LEU:CD1	2.69	0.40
2:G:343:VAL:HG12	2:G:343:VAL:OXT	2.21	0.40
2:G:41:GLY:C	2:G:43:GLY:H	2.24	0.40
2:H:185:ASP:OD1	2:H:189:ARG:NH2	2.54	0.40
1:A:118:GLY:HA2	1:A:121:GLU:CG	2.44	0.40
1:A:143:LEU:O	1:A:144:PRO:C	2.55	0.40
1:A:69:ILE:HD13	1:A:70:ILE:H	1.86	0.40
1:B:30:ILE:C	1:B:33:PRO:HD2	2.41	0.40
1:B:38:LEU:HD11	1:B:113:LEU:HD21	2.04	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
2:C:69:LEU:H	2:C:69:LEU:HD12	1.86	0.40
1:E:69:ILE:CD1	1:E:163:MET:HE2	2.38	0.40
1:F:26:PHE:CD1	1:F:27:GLY:N	2.89	0.40
2:H:166:GLU:HB3	2:H:169:SER:OG	2.22	0.40
1:A:112:LEU:HD23	1:A:112:LEU:HA	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:102:ASN:HA	2:D:105:LEU:CD1	2.51	0.40
2:D:91:PHE:CD1	2:D:146:LYS:HB2	2.56	0.40
1:E:114:GLU:OE1	1:E:114:GLU:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:50:ALA:O	1:E:52:LEU:HG	2.21	0.40
1:F:107:MET:HE2	1:F:152:ILE:HD11	2.03	0.40
1:F:126:MET:HE1	1:F:134:VAL:CB	2.50	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
2:C:171:LEU:HD13	2:C:179:ILE:CD1	2.49	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:159:PRO:O	2:G:192:LEU:HD23	2.22	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:H:33:ILE:HG21	2:H:207:ILE:HG13	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	201/217 (93%)	178 (89%)	9 (4%)	14 (7%)	1	15
1	B	201/217 (93%)	187 (93%)	3 (2%)	11 (6%)	2	20
1	E	201/217 (93%)	180 (90%)	11 (6%)	10 (5%)	2	22
1	F	201/217 (93%)	177 (88%)	10 (5%)	14 (7%)	1	15
2	C	341/343 (99%)	307 (90%)	19 (6%)	15 (4%)	2	24
2	D	341/343 (99%)	323 (95%)	8 (2%)	10 (3%)	4	32
2	G	341/343 (99%)	317 (93%)	14 (4%)	10 (3%)	4	32
2	H	341/343 (99%)	316 (93%)	14 (4%)	11 (3%)	4	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2168/2240 (97%)	1985 (92%)	88 (4%)	95 (4%)	2	24

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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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 [i](#)

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%)	140 (89%)	18 (11%)	5	27
1	B	158/172 (92%)	145 (92%)	13 (8%)	11	41
1	E	158/172 (92%)	149 (94%)	9 (6%)	20	52
1	F	158/172 (92%)	146 (92%)	12 (8%)	13	43
2	C	298/298 (100%)	269 (90%)	29 (10%)	8	33
2	D	298/298 (100%)	281 (94%)	17 (6%)	20	52
2	G	298/298 (100%)	290 (97%)	8 (3%)	44	68
2	H	298/298 (100%)	289 (97%)	9 (3%)	41	66
All	All	1824/1880 (97%)	1709 (94%)	115 (6%)	18	49

All (115) 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	69	ILE
1	A	83	VAL
1	A	86	SER
1	A	95	PRO
1	A	103	PHE
1	A	115	ILE
1	A	117	THR
1	A	129	THR
1	A	140	PRO
1	A	160	TYR
1	A	167	VAL
1	A	175	ILE
1	A	184	TYR
1	B	33	PRO
1	B	34	VAL
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	137	TYR

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Mol	Chain	Res	Type
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	224	THR
2	C	232	PRO
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
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	223	ASP
2	D	231	HIS
2	D	232	PRO
2	D	235	PRO
2	D	281	PRO
2	D	300	GLN
2	D	314	THR
2	D	323	THR
1	E	19	MET
1	E	46	ILE
1	E	116	PRO
1	E	130	PRO
1	E	135	ARG
1	E	160	TYR
1	E	167	VAL
1	E	185	ASN

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Mol	Chain	Res	Type
1	E	198	ILE
1	F	8	LEU
1	F	42	ARG
1	F	68	PHE
1	F	96	LEU
1	F	116	PRO
1	F	139	LEU
1	F	140	PRO
1	F	152	ILE
1	F	155	ILE
1	F	175	ILE
1	F	198	ILE
1	F	202	LEU
2	G	18	ILE
2	G	40	SER
2	G	52	ASN
2	G	84	ILE
2	G	159	PRO
2	G	210	CYS
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	130	LEU
2	H	183	LEU
2	H	235	PRO
2	H	249	ILE
2	H	250	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	ASN
1	A	190	ASN
1	B	178	GLN
1	B	185	ASN
1	B	190	ASN
2	C	12	HIS
2	C	52	ASN
2	C	147	GLN

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Mol	Chain	Res	Type
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	320	GLN
2	C	324	GLN
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	E	174	GLN
1	F	45	GLN
1	F	110	ASN
1	F	190	ASN
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	147	GLN
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	52	ASN
2	H	67	GLN
2	H	111	ASN
2	H	147	GLN
2	H	158	ASN
2	H	222	GLN
2	H	242	GLN

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Mol	Chain	Res	Type
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 carbohydrates 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%)	0.01	7 (3%) 45 34	113, 166, 210, 234	0
1	B	203/217 (93%)	0.24	17 (8%) 11 8	135, 195, 245, 259	0
1	E	203/217 (93%)	0.27	16 (7%) 12 9	136, 202, 249, 260	0
1	F	203/217 (93%)	-0.06	5 (2%) 57 45	106, 166, 222, 244	0
2	C	343/343 (100%)	0.04	11 (3%) 47 35	74, 133, 194, 241	0
2	D	343/343 (100%)	0.27	24 (6%) 16 11	105, 170, 214, 229	0
2	G	343/343 (100%)	1.17	94 (27%) 0 0	157, 209, 249, 265	0
2	H	343/343 (100%)	0.65	48 (13%) 2 3	94, 186, 234, 253	0
All	All	2184/2240 (97%)	0.38	222 (10%) 6 5	74, 179, 238, 265	0

All (222) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	214	ILE	8.9
2	H	17	THR	8.4
1	E	44	GLY	6.7
2	G	91	PHE	6.6
1	B	52	LEU	6.3
2	G	292	VAL	6.3
2	G	343	VAL	6.3
2	G	13	GLN	6.2
2	H	248	ASP	6.1
2	H	274	THR	5.9
2	G	246	HIS	5.8
2	G	215	SER	5.8
2	G	179	ILE	5.8
2	D	343	VAL	5.7
2	H	286	THR	5.7
1	A	168	GLY	5.7

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Mol	Chain	Res	Type	RSRZ
2	H	15	THR	5.6
2	G	266	VAL	5.6
2	G	83	GLN	5.5
2	H	261	PRO	5.5
2	G	121	VAL	5.4
2	G	264	ASP	5.2
2	D	304	ALA	5.1
2	G	217	GLY	5.1
2	G	130	LEU	5.1
2	H	333	HIS	4.9
2	G	317	HIS	4.9
2	H	212	ALA	4.8
2	H	16	ARG	4.8
2	H	310	GLY	4.8
1	E	49	ASN	4.8
1	B	51	LYS	4.7
2	G	267	PRO	4.7
2	G	103	VAL	4.7
2	G	182	LEU	4.6
2	H	309	PHE	4.6
1	B	39	TYR	4.6
1	A	51	LYS	4.6
1	E	28	PHE	4.6
1	B	50	ALA	4.6
2	G	316	MET	4.6
2	G	263	THR	4.5
2	G	176	THR	4.5
2	G	93	LEU	4.5
2	D	316	MET	4.3
2	G	135	ASP	4.3
2	G	236	LEU	4.2
2	G	161	VAL	4.2
2	H	249	ILE	4.1
2	G	265	CYS	4.1
2	H	293	ASN	4.0
2	G	259	ALA	4.0
2	D	263	THR	4.0
2	D	141	LEU	4.0
2	H	213	VAL	3.9
1	A	184	TYR	3.9
2	G	235	PRO	3.9
1	E	50	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
2	H	71	THR	3.9
2	G	104	ALA	3.8
2	H	220	ILE	3.7
2	C	71	THR	3.7
2	D	99	VAL	3.7
2	G	100	PHE	3.7
2	G	80	ALA	3.6
2	G	51	VAL	3.6
2	D	13	GLN	3.6
2	D	39	ALA	3.5
2	H	337	VAL	3.5
2	H	40	SER	3.5
2	G	244	THR	3.4
1	E	53	TYR	3.4
2	G	16	ARG	3.4
1	B	84	GLY	3.4
2	G	15	THR	3.4
2	H	273	PHE	3.4
2	G	122	THR	3.4
2	G	245	LEU	3.4
1	E	10	VAL	3.4
2	H	334	HIS	3.4
2	D	305	GLY	3.3
2	G	35	GLY	3.3
2	G	36	VAL	3.2
2	G	171	LEU	3.2
2	G	102	ASN	3.2
2	H	214	ILE	3.2
1	E	52	LEU	3.2
2	G	97	ARG	3.2
2	G	213	VAL	3.2
2	G	276	GLN	3.1
2	D	130	LEU	3.1
2	G	268	MET	3.1
2	G	175	THR	3.1
2	G	2	ILE	3.1
2	G	322	ASP	3.1
2	H	294	ASN	3.0
2	G	180	LEU	3.0
2	G	14	GLY	3.0
2	H	242	GLN	3.0
2	C	259	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
2	D	15	THR	2.9
2	G	21	LEU	2.9
1	B	172	LEU	2.9
2	G	193	THR	2.9
2	C	72	LEU	2.9
1	B	128	ALA	2.9
1	E	48	ALA	2.9
2	G	81	ARG	2.9
2	D	257	LEU	2.9
2	D	100	PHE	2.9
1	B	49	ASN	2.9
2	C	214	ILE	2.8
2	G	146	LYS	2.8
1	B	81	VAL	2.8
2	G	293	ASN	2.8
2	G	105	LEU	2.8
2	G	37	ILE	2.8
2	G	75	SER	2.8
2	H	14	GLY	2.8
1	E	51	LYS	2.8
2	G	9	LYS	2.8
2	H	342	TYR	2.8
2	G	328	ALA	2.7
1	A	53	TYR	2.7
2	H	301	MET	2.7
2	G	149	VAL	2.7
2	H	308	LYS	2.7
2	H	211	VAL	2.7
2	H	321	GLN	2.7
2	G	342	TYR	2.6
2	G	39	ALA	2.6
2	H	72	LEU	2.6
2	H	285	GLU	2.6
2	G	12	HIS	2.6
2	H	322	ASP	2.6
2	H	56	ARG	2.6
2	G	200	GLU	2.6
2	G	128	VAL	2.6
2	H	39	ALA	2.6
2	D	137	TYR	2.5
2	C	20	ALA	2.5
2	H	275	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	43	PRO	2.5
2	D	14	GLY	2.5
2	G	50	CYS	2.5
2	C	268	MET	2.5
2	D	20	ALA	2.5
2	H	57	PRO	2.5
2	G	287	ALA	2.5
2	G	321	GLN	2.4
2	H	18	ILE	2.4
2	G	219	LEU	2.4
2	G	290	PHE	2.4
1	B	85	THR	2.4
2	C	19	GLN	2.4
1	E	45	GLN	2.4
2	G	257	LEU	2.4
2	C	342	TYR	2.4
1	B	53	TYR	2.4
2	D	12	HIS	2.4
2	G	256	ARG	2.4
2	H	245	LEU	2.4
2	H	222	GLN	2.4
2	G	134	HIS	2.4
1	B	129	THR	2.3
2	H	10	VAL	2.3
2	G	241	ILE	2.3
2	D	258	GLN	2.3
2	G	120	ARG	2.3
2	H	240	PHE	2.3
1	E	47	ILE	2.3
2	G	327	ILE	2.3
1	A	52	LEU	2.3
2	C	343	VAL	2.3
1	B	9	LEU	2.3
2	G	197	ILE	2.3
1	E	112	LEU	2.3
2	G	20	ALA	2.3
2	G	192	LEU	2.3
2	H	250	PRO	2.3
2	G	262	PHE	2.3
2	G	233	LYS	2.2
2	G	117	VAL	2.2
2	G	57	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
2	G	329	TRP	2.2
1	F	159	GLY	2.2
2	D	292	VAL	2.2
2	D	265	CYS	2.2
1	E	9	LEU	2.2
2	H	335	VAL	2.2
2	D	264	ASP	2.2
2	H	329	TRP	2.2
2	G	94	LEU	2.2
1	A	183	GLY	2.2
1	E	189	MET	2.2
2	D	336	LYS	2.2
2	C	213	VAL	2.1
2	G	340	LEU	2.1
1	E	41	THR	2.1
2	C	39	ALA	2.1
2	G	325	ALA	2.1
2	G	337	VAL	2.1
1	A	54	ARG	2.1
2	G	195	LEU	2.1
2	G	52	ASN	2.1
2	G	125	LEU	2.1
1	F	39	TYR	2.1
1	B	41	THR	2.1
2	H	241	ILE	2.1
2	H	216	ASN	2.1
2	H	338	GLU	2.1
2	G	34	TYR	2.0
2	H	157	SER	2.0
1	B	16	THR	2.0
1	F	54	ARG	2.0
2	D	335	VAL	2.0
1	F	53	TYR	2.0
1	F	160	TYR	2.0
2	D	136	SER	2.0
1	B	80	ARG	2.0
1	B	37	LEU	2.0
2	G	38	GLY	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 carbohydrates 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.