



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:32 AM UTC

PDB ID : 4GA5 / pdb_00004ga5
Title : Crystal structure of AMP phosphorylase C-terminal deletion mutant in the apo-form
Authors : Nishitani, Y.; Aono, R.; Nakamura, A.; Sato, T.; Atomi, H.; Imanaka, T.; Miki, K.
Deposited on : 2012-07-25
Resolution : 3.25 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

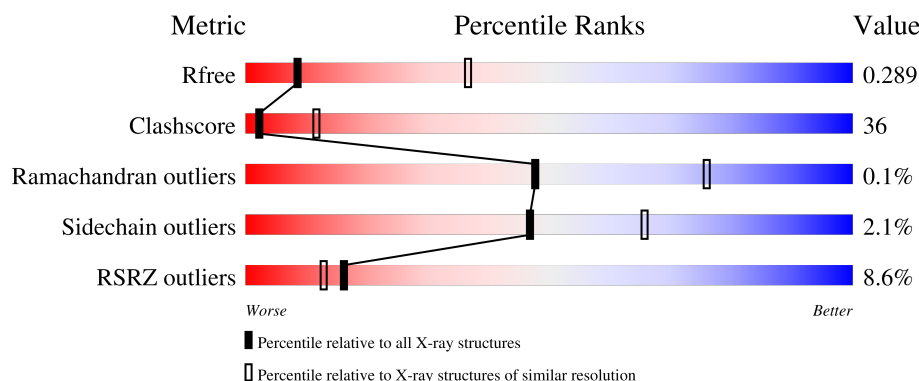
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1605 (3.30-3.22)
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)

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

Mol	Chain	Length	Quality of chain
1	A	513	4% 62% 33% ..
1	B	513	6% 60% 34% ..
1	C	513	6% 52% 42% ..
1	D	513	6% 55% 39% ..
1	E	513	7% 56% 39% ..

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Mol	Chain	Length	Quality of chain
1	F	513	4% 59% 35%
1	G	513	17% 50% 44%
1	H	513	17% 52% 42%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 26752 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 Putative thymidine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	493	Total	C	N	O	S	0	0	0
			3344	2123	560	647	14			
1	A	493	Total	C	N	O	S	0	0	0
			3344	2123	560	647	14			
1	C	493	Total	C	N	O	S	0	0	0
			3344	2123	560	647	14			
1	D	493	Total	C	N	O	S	0	0	0
			3344	2123	560	647	14			
1	E	493	Total	C	N	O	S	0	0	0
			3344	2123	560	647	14			
1	F	493	Total	C	N	O	S	0	0	0
			3344	2123	560	647	14			
1	G	493	Total	C	N	O	S	0	0	0
			3344	2123	560	647	14			
1	H	493	Total	C	N	O	S	0	0	0
			3344	2123	560	647	14			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	494	GLY	-	expression tag	UNP Q5JCX3
B	495	ASN	-	expression tag	UNP Q5JCX3
B	496	SER	-	expression tag	UNP Q5JCX3
B	497	SER	-	expression tag	UNP Q5JCX3
B	498	SER	-	expression tag	UNP Q5JCX3
B	499	VAL	-	expression tag	UNP Q5JCX3
B	500	ASP	-	expression tag	UNP Q5JCX3
B	501	LYS	-	expression tag	UNP Q5JCX3
B	502	LEU	-	expression tag	UNP Q5JCX3
B	503	ALA	-	expression tag	UNP Q5JCX3
B	504	ALA	-	expression tag	UNP Q5JCX3
B	505	ALA	-	expression tag	UNP Q5JCX3
B	506	LEU	-	expression tag	UNP Q5JCX3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	507	GLU	-	expression tag	UNP Q5JCX3
B	508	HIS	-	expression tag	UNP Q5JCX3
B	509	HIS	-	expression tag	UNP Q5JCX3
B	510	HIS	-	expression tag	UNP Q5JCX3
B	511	HIS	-	expression tag	UNP Q5JCX3
B	512	HIS	-	expression tag	UNP Q5JCX3
B	513	HIS	-	expression tag	UNP Q5JCX3
A	494	GLY	-	expression tag	UNP Q5JCX3
A	495	ASN	-	expression tag	UNP Q5JCX3
A	496	SER	-	expression tag	UNP Q5JCX3
A	497	SER	-	expression tag	UNP Q5JCX3
A	498	SER	-	expression tag	UNP Q5JCX3
A	499	VAL	-	expression tag	UNP Q5JCX3
A	500	ASP	-	expression tag	UNP Q5JCX3
A	501	LYS	-	expression tag	UNP Q5JCX3
A	502	LEU	-	expression tag	UNP Q5JCX3
A	503	ALA	-	expression tag	UNP Q5JCX3
A	504	ALA	-	expression tag	UNP Q5JCX3
A	505	ALA	-	expression tag	UNP Q5JCX3
A	506	LEU	-	expression tag	UNP Q5JCX3
A	507	GLU	-	expression tag	UNP Q5JCX3
A	508	HIS	-	expression tag	UNP Q5JCX3
A	509	HIS	-	expression tag	UNP Q5JCX3
A	510	HIS	-	expression tag	UNP Q5JCX3
A	511	HIS	-	expression tag	UNP Q5JCX3
A	512	HIS	-	expression tag	UNP Q5JCX3
A	513	HIS	-	expression tag	UNP Q5JCX3
C	494	GLY	-	expression tag	UNP Q5JCX3
C	495	ASN	-	expression tag	UNP Q5JCX3
C	496	SER	-	expression tag	UNP Q5JCX3
C	497	SER	-	expression tag	UNP Q5JCX3
C	498	SER	-	expression tag	UNP Q5JCX3
C	499	VAL	-	expression tag	UNP Q5JCX3
C	500	ASP	-	expression tag	UNP Q5JCX3
C	501	LYS	-	expression tag	UNP Q5JCX3
C	502	LEU	-	expression tag	UNP Q5JCX3
C	503	ALA	-	expression tag	UNP Q5JCX3
C	504	ALA	-	expression tag	UNP Q5JCX3
C	505	ALA	-	expression tag	UNP Q5JCX3
C	506	LEU	-	expression tag	UNP Q5JCX3
C	507	GLU	-	expression tag	UNP Q5JCX3
C	508	HIS	-	expression tag	UNP Q5JCX3

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Chain	Residue	Modelled	Actual	Comment	Reference
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C	510	HIS	-	expression tag	UNP Q5JCX3
C	511	HIS	-	expression tag	UNP Q5JCX3
C	512	HIS	-	expression tag	UNP Q5JCX3
C	513	HIS	-	expression tag	UNP Q5JCX3
D	494	GLY	-	expression tag	UNP Q5JCX3
D	495	ASN	-	expression tag	UNP Q5JCX3
D	496	SER	-	expression tag	UNP Q5JCX3
D	497	SER	-	expression tag	UNP Q5JCX3
D	498	SER	-	expression tag	UNP Q5JCX3
D	499	VAL	-	expression tag	UNP Q5JCX3
D	500	ASP	-	expression tag	UNP Q5JCX3
D	501	LYS	-	expression tag	UNP Q5JCX3
D	502	LEU	-	expression tag	UNP Q5JCX3
D	503	ALA	-	expression tag	UNP Q5JCX3
D	504	ALA	-	expression tag	UNP Q5JCX3
D	505	ALA	-	expression tag	UNP Q5JCX3
D	506	LEU	-	expression tag	UNP Q5JCX3
D	507	GLU	-	expression tag	UNP Q5JCX3
D	508	HIS	-	expression tag	UNP Q5JCX3
D	509	HIS	-	expression tag	UNP Q5JCX3
D	510	HIS	-	expression tag	UNP Q5JCX3
D	511	HIS	-	expression tag	UNP Q5JCX3
D	512	HIS	-	expression tag	UNP Q5JCX3
D	513	HIS	-	expression tag	UNP Q5JCX3
E	494	GLY	-	expression tag	UNP Q5JCX3
E	495	ASN	-	expression tag	UNP Q5JCX3
E	496	SER	-	expression tag	UNP Q5JCX3
E	497	SER	-	expression tag	UNP Q5JCX3
E	498	SER	-	expression tag	UNP Q5JCX3
E	499	VAL	-	expression tag	UNP Q5JCX3
E	500	ASP	-	expression tag	UNP Q5JCX3
E	501	LYS	-	expression tag	UNP Q5JCX3
E	502	LEU	-	expression tag	UNP Q5JCX3
E	503	ALA	-	expression tag	UNP Q5JCX3
E	504	ALA	-	expression tag	UNP Q5JCX3
E	505	ALA	-	expression tag	UNP Q5JCX3
E	506	LEU	-	expression tag	UNP Q5JCX3
E	507	GLU	-	expression tag	UNP Q5JCX3
E	508	HIS	-	expression tag	UNP Q5JCX3
E	509	HIS	-	expression tag	UNP Q5JCX3
E	510	HIS	-	expression tag	UNP Q5JCX3

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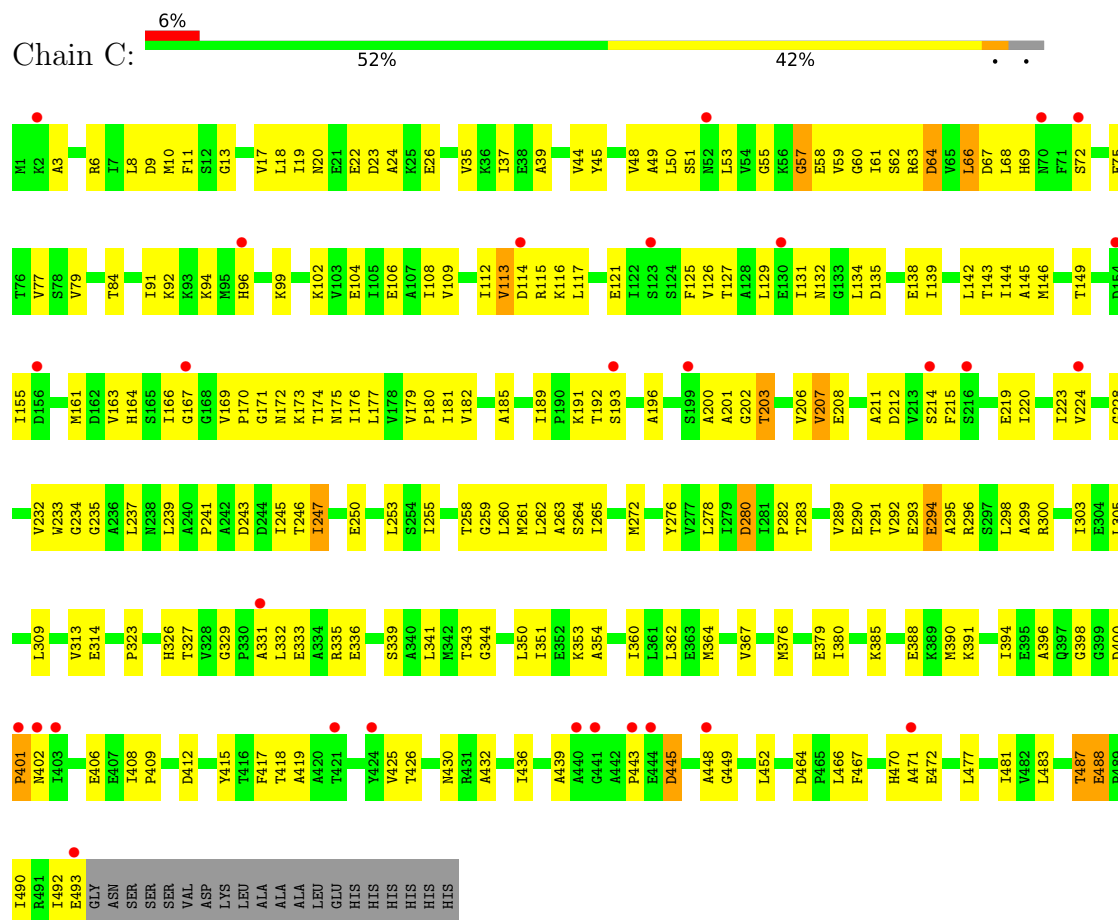
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F	494	GLY	-	expression tag	UNP Q5JCX3
F	495	ASN	-	expression tag	UNP Q5JCX3
F	496	SER	-	expression tag	UNP Q5JCX3
F	497	SER	-	expression tag	UNP Q5JCX3
F	498	SER	-	expression tag	UNP Q5JCX3
F	499	VAL	-	expression tag	UNP Q5JCX3
F	500	ASP	-	expression tag	UNP Q5JCX3
F	501	LYS	-	expression tag	UNP Q5JCX3
F	502	LEU	-	expression tag	UNP Q5JCX3
F	503	ALA	-	expression tag	UNP Q5JCX3
F	504	ALA	-	expression tag	UNP Q5JCX3
F	505	ALA	-	expression tag	UNP Q5JCX3
F	506	LEU	-	expression tag	UNP Q5JCX3
F	507	GLU	-	expression tag	UNP Q5JCX3
F	508	HIS	-	expression tag	UNP Q5JCX3
F	509	HIS	-	expression tag	UNP Q5JCX3
F	510	HIS	-	expression tag	UNP Q5JCX3
F	511	HIS	-	expression tag	UNP Q5JCX3
F	512	HIS	-	expression tag	UNP Q5JCX3
F	513	HIS	-	expression tag	UNP Q5JCX3
G	494	GLY	-	expression tag	UNP Q5JCX3
G	495	ASN	-	expression tag	UNP Q5JCX3
G	496	SER	-	expression tag	UNP Q5JCX3
G	497	SER	-	expression tag	UNP Q5JCX3
G	498	SER	-	expression tag	UNP Q5JCX3
G	499	VAL	-	expression tag	UNP Q5JCX3
G	500	ASP	-	expression tag	UNP Q5JCX3
G	501	LYS	-	expression tag	UNP Q5JCX3
G	502	LEU	-	expression tag	UNP Q5JCX3
G	503	ALA	-	expression tag	UNP Q5JCX3
G	504	ALA	-	expression tag	UNP Q5JCX3
G	505	ALA	-	expression tag	UNP Q5JCX3
G	506	LEU	-	expression tag	UNP Q5JCX3
G	507	GLU	-	expression tag	UNP Q5JCX3
G	508	HIS	-	expression tag	UNP Q5JCX3
G	509	HIS	-	expression tag	UNP Q5JCX3
G	510	HIS	-	expression tag	UNP Q5JCX3
G	511	HIS	-	expression tag	UNP Q5JCX3
G	512	HIS	-	expression tag	UNP Q5JCX3

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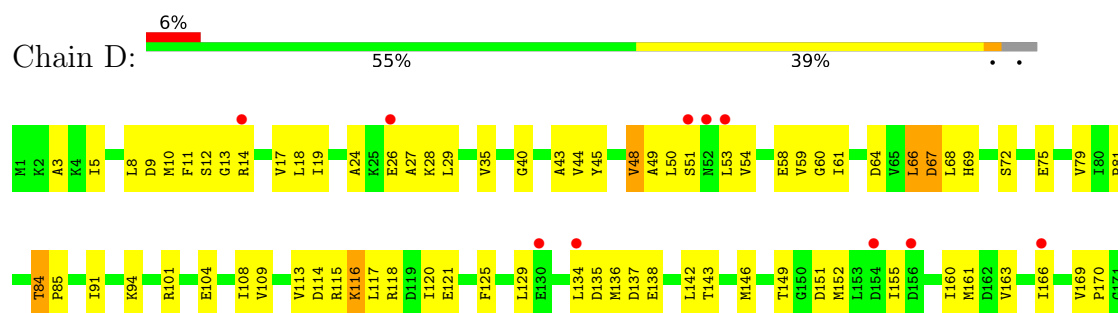
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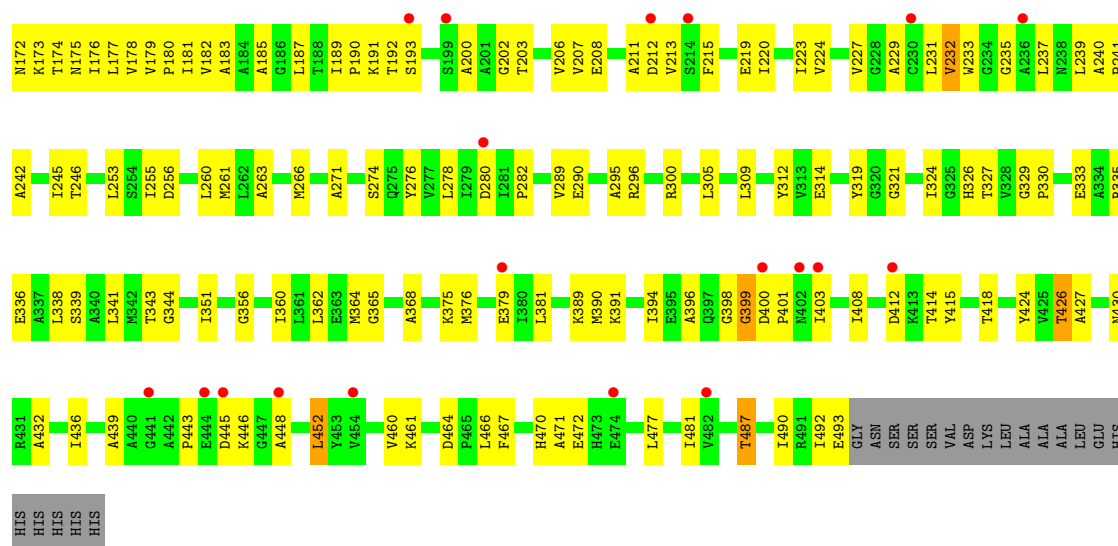
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H	494	GLY	-	expression tag	UNP Q5JCX3
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H	496	SER	-	expression tag	UNP Q5JCX3
H	497	SER	-	expression tag	UNP Q5JCX3
H	498	SER	-	expression tag	UNP Q5JCX3
H	499	VAL	-	expression tag	UNP Q5JCX3
H	500	ASP	-	expression tag	UNP Q5JCX3
H	501	LYS	-	expression tag	UNP Q5JCX3
H	502	LEU	-	expression tag	UNP Q5JCX3
H	503	ALA	-	expression tag	UNP Q5JCX3
H	504	ALA	-	expression tag	UNP Q5JCX3
H	505	ALA	-	expression tag	UNP Q5JCX3
H	506	LEU	-	expression tag	UNP Q5JCX3
H	507	GLU	-	expression tag	UNP Q5JCX3
H	508	HIS	-	expression tag	UNP Q5JCX3
H	509	HIS	-	expression tag	UNP Q5JCX3
H	510	HIS	-	expression tag	UNP Q5JCX3
H	511	HIS	-	expression tag	UNP Q5JCX3
H	512	HIS	-	expression tag	UNP Q5JCX3
H	513	HIS	-	expression tag	UNP Q5JCX3

- Molecule 1: Putative thymidine phosphorylase

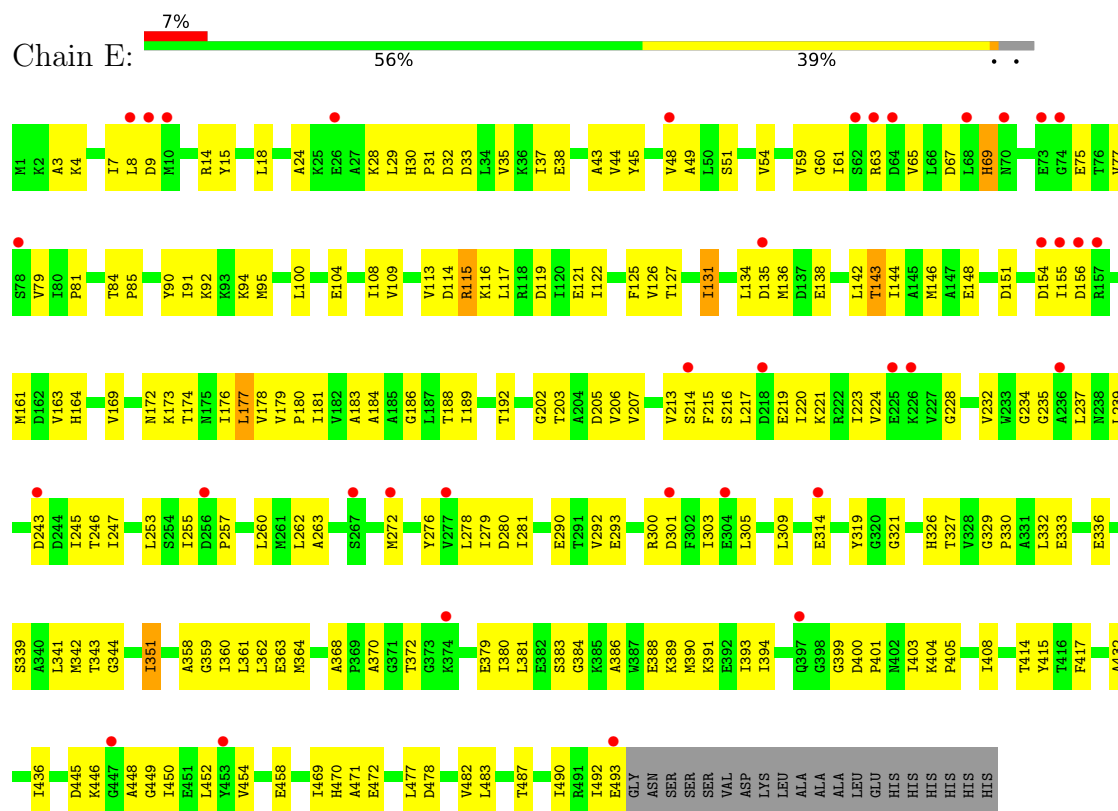


- Molecule 1: Putative thymidine phosphorylase

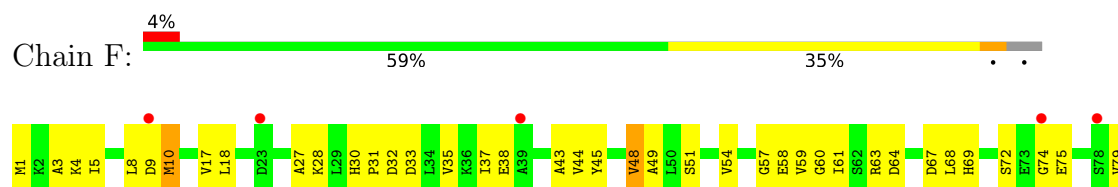


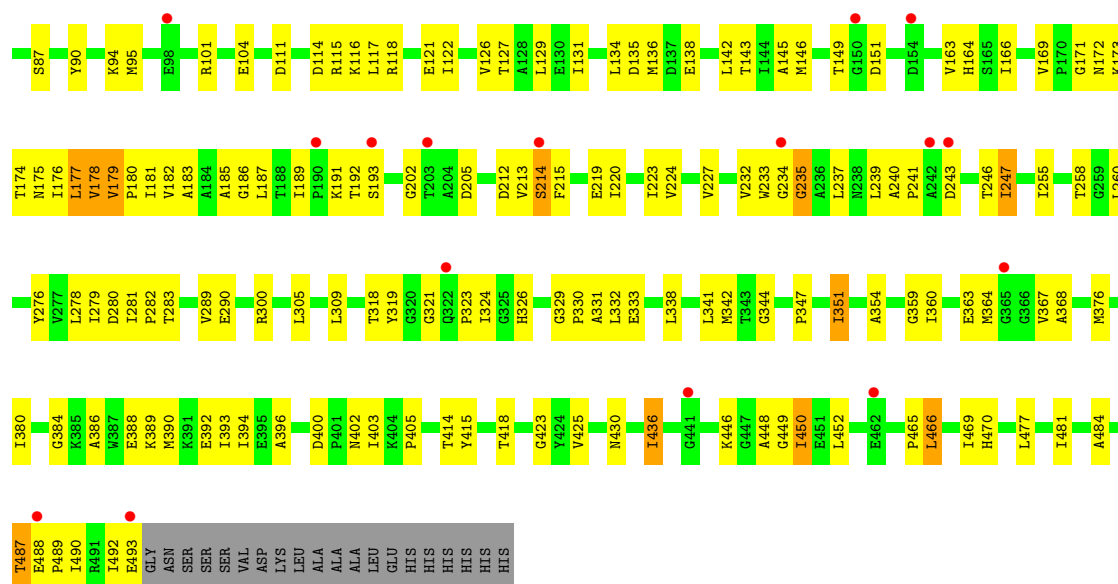


• Molecule 1: Putative thymidine phosphorylase

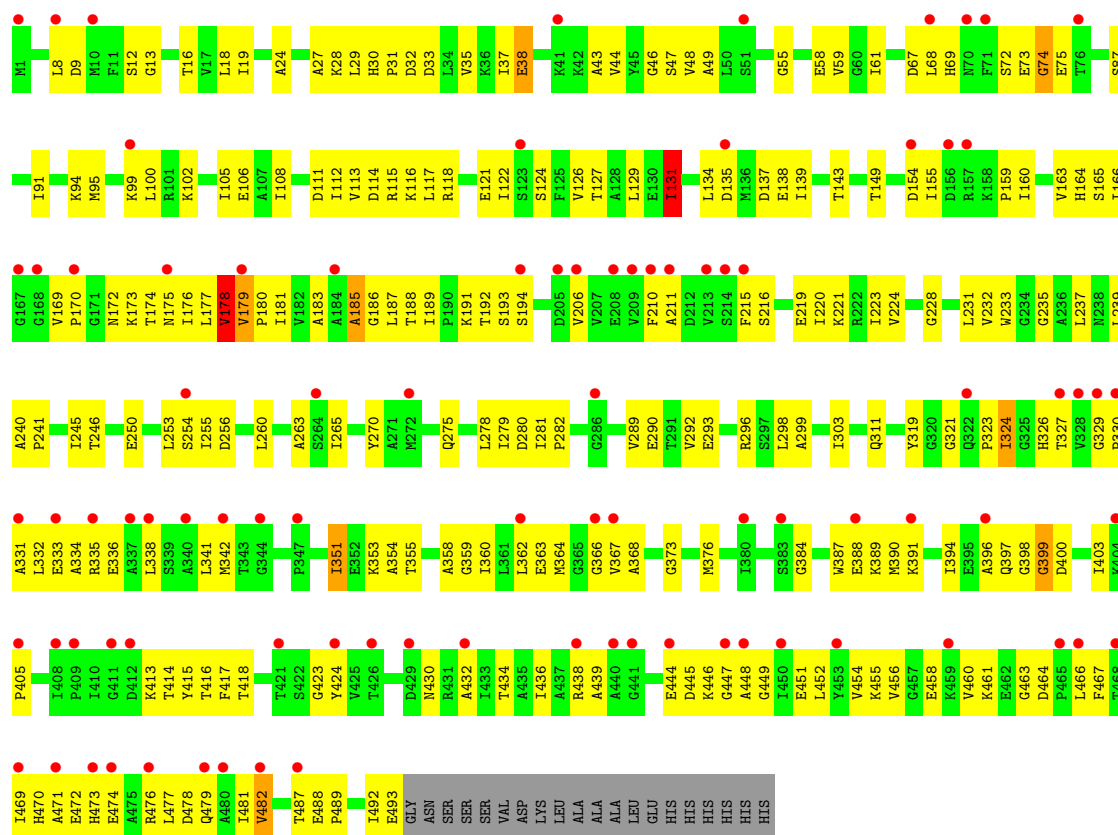


• Molecule 1: Putative thymidine phosphorylase





• Molecule 1: Putative thymidine phosphorylase



• Molecule 1: Putative thymidine phosphorylase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	124.33Å 249.48Å 162.37Å 90.00° 110.44° 90.00°	Depositor
Resolution (Å)	50.00 – 3.25 50.00 – 3.25	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.25) 99.7 (50.00-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 3.25Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.261 , 0.289 0.261 , 0.289	Depositor DCC
R_{free} test set	3680 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	65.6	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 85.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.055 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	26752	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.83	2/3391 (0.1%)	1.06	17/4637 (0.4%)
1	B	0.74	0/3391	1.03	15/4637 (0.3%)
1	C	0.80	0/3391	1.08	18/4637 (0.4%)
1	D	0.78	0/3391	1.08	18/4637 (0.4%)
1	E	0.77	0/3391	1.08	12/4637 (0.3%)
1	F	0.80	1/3391 (0.0%)	1.06	19/4637 (0.4%)
1	G	0.68	0/3391	1.07	15/4637 (0.3%)
1	H	0.68	0/3391	1.07	12/4637 (0.3%)
All	All	0.76	3/27128 (0.0%)	1.07	126/37096 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	188	THR	C-N	8.41	1.42	1.33
1	F	116	LYS	C-N	5.33	1.41	1.33
1	A	280	ASP	C-N	-5.12	1.27	1.33

All (126) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	213	VAL	N-CA-C	9.33	120.14	110.72
1	E	213	VAL	N-CA-C	9.22	120.03	110.72
1	B	487	THR	N-CA-C	8.47	120.59	111.36
1	H	344	GLY	N-CA-C	-8.30	104.33	115.36
1	E	234	GLY	N-CA-C	8.06	123.09	112.77
1	H	376	MET	N-CA-C	-7.97	102.59	111.28
1	A	235	GLY	N-CA-C	7.91	122.23	112.73
1	H	396	ALA	N-CA-C	-7.82	102.76	111.28
1	G	384	GLY	N-CA-C	-7.77	104.48	115.43
1	G	351	ILE	N-CA-C	7.74	117.80	110.53
1	G	487	THR	N-CA-C	7.62	119.58	111.28
1	E	351	ILE	N-CA-C	7.53	117.60	110.53
1	D	13	GLY	N-CA-C	-7.29	105.67	115.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	290	GLU	N-CA-C	7.27	119.28	111.36
1	B	290	GLU	N-CA-C	7.14	118.72	111.07
1	C	344	GLY	N-CA-C	-7.04	105.61	115.32
1	D	487	THR	N-CA-C	6.91	118.89	111.36
1	F	487	THR	N-CA-C	6.87	118.85	111.36
1	B	344	GLY	N-CA-C	-6.81	106.30	115.36
1	F	351	ILE	N-CA-C	6.80	116.93	110.53
1	G	178	VAL	N-CA-C	6.55	117.30	110.62
1	D	116	LYS	N-CA-C	-6.54	104.15	111.28
1	G	13	GLY	N-CA-C	-6.52	106.32	115.32
1	G	74	GLY	N-CA-C	-6.50	106.72	115.36
1	H	401	PRO	N-CA-C	-6.47	106.07	114.03
1	C	401	PRO	N-CA-C	-6.42	106.13	114.03
1	E	235	GLY	N-CA-C	6.41	120.42	112.73
1	G	185	ALA	N-CA-C	-6.39	104.58	112.38
1	F	290	GLU	N-CA-C	6.33	118.18	111.28
1	E	384	GLY	N-CA-C	-6.32	106.60	115.32
1	F	178	VAL	N-CA-C	6.28	117.02	110.62
1	F	384	GLY	N-CA-C	-6.27	106.67	115.32
1	B	373	GLY	N-CA-C	6.22	120.19	112.73
1	H	351	ILE	N-CA-C	6.21	116.99	110.72
1	D	67	ASP	N-CA-C	6.15	117.65	111.07
1	B	401	PRO	N-CA-C	-6.13	106.49	114.03
1	D	48	VAL	N-CA-C	6.12	117.94	109.80
1	A	174	THR	N-CA-C	6.03	117.86	111.28
1	A	173	LYS	N-CA-C	-6.02	105.52	112.92
1	A	191	LYS	O-C-N	-6.01	116.37	123.22
1	C	351	ILE	N-CA-C	6.00	116.17	110.53
1	F	48	VAL	N-CA-C	6.00	118.26	109.63
1	C	57	GLY	N-CA-C	-5.99	106.97	115.30
1	D	213	VAL	N-CA-C	5.96	119.66	112.80
1	B	168	GLY	N-CA-C	-5.91	106.49	115.00
1	C	13	GLY	N-CA-C	-5.90	107.52	115.36
1	A	351	ILE	N-CA-C	5.89	116.54	110.36
1	G	366	GLY	N-CA-C	-5.88	106.98	115.27
1	A	290	GLU	N-CA-C	5.86	117.75	111.36
1	A	13	GLY	N-CA-C	-5.81	107.22	115.30
1	H	178	VAL	N-CA-C	5.81	116.55	110.62
1	G	290	GLU	N-CA-C	5.78	117.58	111.28
1	D	290	GLU	N-CA-C	5.75	117.63	111.36
1	C	116	LYS	N-CA-C	-5.75	104.61	111.69
1	B	351	ILE	N-CA-C	5.73	116.50	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	203	THR	N-CA-C	-5.71	105.05	111.28
1	G	131	ILE	N-CA-C	5.71	116.49	110.72
1	H	116	LYS	N-CA-C	-5.70	105.04	112.23
1	E	131	ILE	N-CA-C	5.65	115.84	110.53
1	C	66	LEU	N-CA-C	5.65	117.44	111.28
1	E	344	GLY	N-CA-C	-5.64	107.53	115.32
1	A	131	ILE	N-CA-C	5.62	116.40	110.72
1	A	487	THR	N-CA-C	5.62	117.40	111.28
1	G	399	GLY	N-CA-C	-5.57	105.13	112.82
1	D	396	ALA	N-CA-C	-5.54	105.24	111.28
1	B	13	GLY	N-CA-C	-5.54	107.60	115.30
1	E	303	ILE	CB-CA-C	-5.53	104.67	112.14
1	D	351	ILE	N-CA-C	5.53	116.30	110.72
1	E	7	ILE	N-CA-C	5.51	116.51	108.53
1	F	466	LEU	N-CA-C	5.50	117.08	111.14
1	F	116	LYS	N-CA-C	-5.50	104.92	111.69
1	C	487	THR	N-CA-C	5.50	117.36	111.36
1	F	487	THR	CA-C-N	-5.49	116.91	122.83
1	F	487	THR	C-N-CA	-5.49	116.91	122.83
1	A	5	ILE	N-CA-C	5.46	116.13	109.30
1	F	235	GLY	N-CA-C	5.45	119.27	112.73
1	E	136	MET	N-CA-C	5.44	117.21	111.28
1	C	385	LYS	N-CA-C	-5.42	105.38	111.28
1	G	116	LYS	N-CA-C	-5.39	105.06	111.69
1	H	290	GLU	N-CA-C	5.38	117.22	111.36
1	B	167	GLY	N-CA-C	5.36	120.83	111.78
1	H	213	VAL	N-CA-C	5.34	118.03	112.90
1	A	423	GLY	N-CA-C	5.34	117.79	110.69
1	C	388	GLU	N-CA-C	-5.33	105.47	111.28
1	A	373	GLY	N-CA-C	5.33	119.12	112.73
1	G	179	VAL	CB-CA-C	-5.32	107.03	114.00
1	A	74	GLY	N-CA-C	-5.30	108.00	115.32
1	D	66	LEU	N-CA-C	5.29	117.04	111.28
1	B	408	ILE	CA-C-N	5.28	125.04	119.76
1	B	408	ILE	C-N-CA	5.28	125.04	119.76
1	F	234	GLY	N-CA-C	5.26	119.04	112.73
1	A	168	GLY	N-CA-C	-5.26	107.99	115.30
1	F	214	SER	N-CA-C	5.24	117.82	109.96
1	D	412	ASP	N-CA-C	5.24	116.99	111.28
1	C	64	ASP	N-CA-C	-5.22	105.59	111.28
1	D	40	GLY	N-CA-C	-5.21	105.15	112.13
1	D	399	GLY	N-CA-C	-5.21	104.47	112.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	460	VAL	N-CA-C	5.20	115.40	108.11
1	C	290	GLU	N-CA-C	5.20	117.03	111.36
1	B	67	ASP	N-CA-C	5.19	117.34	111.11
1	A	213	VAL	N-CA-C	5.18	117.96	112.83
1	H	394	ILE	CB-CA-C	-5.17	105.16	112.14
1	A	441	GLY	N-CA-C	5.16	122.44	115.00
1	C	406	GLU	N-CA-C	-5.16	105.77	111.71
1	C	412	ASP	N-CA-C	5.16	116.91	111.28
1	F	74	GLY	N-CA-C	-5.15	108.51	115.36
1	C	396	ALA	N-CA-C	-5.13	105.69	111.28
1	F	185	ALA	N-CA-C	-5.12	106.13	112.38
1	H	487	THR	N-CA-C	5.10	116.84	111.28
1	D	427	ALA	N-CA-C	5.10	116.59	108.79
1	A	203	THR	N-CA-C	-5.10	105.72	111.28
1	H	13	GLY	N-CA-C	-5.08	108.60	115.36
1	F	136	MET	N-CA-C	5.08	116.81	111.28
1	G	438	ARG	N-CA-C	-5.08	105.75	111.28
1	C	203	THR	N-CA-C	-5.07	105.75	111.28
1	D	64	ASP	N-CA-C	-5.07	105.75	111.28
1	D	426	THR	N-CA-C	5.07	116.88	111.36
1	C	350	LEU	N-CA-C	5.06	116.60	111.14
1	D	344	GLY	N-CA-C	-5.06	108.34	115.32
1	F	344	GLY	N-CA-C	-5.05	108.35	115.32
1	E	148	GLU	N-CA-C	5.05	116.78	111.28
1	C	53	LEU	N-CA-C	-5.04	105.79	111.28
1	B	131	ILE	N-CA-C	5.03	115.80	110.72
1	G	479	GLN	N-CA-C	-5.02	105.81	111.28
1	B	94	LYS	N-CA-C	-5.01	105.95	111.71
1	F	179	VAL	CB-CA-C	-5.00	107.44	114.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3344	0	3133	160	0
1	B	3344	0	3133	182	0
1	C	3344	0	3133	240	0
1	D	3344	0	3133	242	0
1	E	3344	0	3133	236	0
1	F	3344	0	3133	194	0
1	G	3344	0	3133	342	0
1	H	3344	0	3133	307	0
All	All	26752	0	25064	1876	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 36.

All (1876) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:237:LEU:CD1	1:G:239:LEU:HG	1.42	1.46
1:H:237:LEU:HD13	1:H:239:LEU:CG	1.57	1.32
1:B:237:LEU:CD1	1:B:239:LEU:HG	1.61	1.31
1:H:237:LEU:CD1	1:H:239:LEU:HG	1.64	1.28
1:C:233:TRP:CD1	1:C:235:GLY:H	1.52	1.26
1:G:415:TYR:CE2	1:G:417:PHE:CZ	2.22	1.26
1:F:400:ASP:O	1:F:403:ILE:HG23	1.34	1.25
1:H:99:LYS:HE3	1:H:135:ASP:OD2	1.36	1.24
1:B:243:ASP:O	1:B:247:ILE:HG13	1.33	1.23
1:F:436:ILE:HD11	1:F:484:ALA:CA	1.70	1.22
1:G:415:TYR:HE2	1:G:417:PHE:CZ	1.57	1.22
1:G:250:GLU:OE2	1:G:260:LEU:HD23	1.39	1.22
1:D:169:VAL:HG11	1:D:324:ILE:CD1	1.70	1.22
1:D:329:GLY:O	1:D:333:GLU:HG3	1.38	1.22
1:G:415:TYR:HE2	1:G:417:PHE:CE1	1.57	1.21
1:H:8:LEU:HD11	1:H:18:LEU:CD1	1.69	1.21
1:G:8:LEU:CD1	1:G:18:LEU:HD12	1.70	1.20
1:H:8:LEU:CD1	1:H:18:LEU:HD12	1.71	1.20
1:F:246:THR:HG21	1:F:260:LEU:HD21	1.20	1.20
1:H:237:LEU:CD1	1:H:239:LEU:CG	2.20	1.19
1:F:436:ILE:HD13	1:F:484:ALA:CB	1.72	1.18
1:C:219:GLU:O	1:C:223:ILE:HG13	1.44	1.17
1:F:436:ILE:CD1	1:F:484:ALA:CB	2.23	1.16
1:H:237:LEU:HD11	1:H:239:LEU:HD12	1.27	1.16
1:F:135:ASP:OD1	1:F:138:GLU:HG3	1.44	1.15
1:F:436:ILE:CD1	1:F:484:ALA:HB2	1.75	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:8:LEU:CD1	1:D:18:LEU:HD12	1.77	1.14
1:D:180:PRO:HG3	1:D:390:MET:HE2	1.27	1.14
1:F:329:GLY:O	1:F:333:GLU:HG3	1.45	1.14
1:D:237:LEU:HD11	1:D:239:LEU:HD12	1.29	1.14
1:G:215:PHE:C	1:G:220:ILE:HD11	1.73	1.14
1:A:175:ASN:HD22	1:A:191:LYS:HE2	1.06	1.13
1:C:180:PRO:HG3	1:C:390:MET:CE	1.78	1.13
1:H:329:GLY:O	1:H:333:GLU:HG3	1.49	1.12
1:D:8:LEU:HD11	1:D:18:LEU:HD12	1.22	1.12
1:G:216:SER:O	1:G:220:ILE:HG12	1.50	1.12
1:A:400:ASP:O	1:A:403:ILE:HG23	1.46	1.12
1:C:203:THR:O	1:C:207:VAL:HG23	1.50	1.11
1:D:424:TYR:O	1:D:492:ILE:HG23	1.48	1.11
1:F:237:LEU:HD13	1:F:239:LEU:HG	1.14	1.11
1:H:166:ILE:CD1	1:H:281:ILE:HG23	1.80	1.11
1:D:237:LEU:HD13	1:D:239:LEU:HG	1.20	1.10
1:C:180:PRO:HG3	1:C:390:MET:HE2	1.24	1.10
1:H:8:LEU:CD1	1:H:18:LEU:CD1	2.28	1.09
1:A:342:MET:HE1	1:A:405:PRO:HD2	1.30	1.09
1:C:8:LEU:HD11	1:C:18:LEU:HD22	1.31	1.09
1:G:8:LEU:HD11	1:G:18:LEU:HD12	1.20	1.09
1:H:161:MET:SD	1:H:276:TYR:HB2	1.91	1.09
1:D:113:VAL:HG21	1:D:149:THR:HG21	1.10	1.08
1:G:368:ALA:HB2	1:G:376:MET:CE	1.83	1.08
1:D:432:ALA:HB1	1:D:487:THR:HG21	1.35	1.08
1:H:166:ILE:HD13	1:H:281:ILE:HG23	1.34	1.07
1:A:243:ASP:O	1:A:247:ILE:HG13	1.51	1.07
1:G:237:LEU:CD1	1:G:239:LEU:CG	2.32	1.07
1:A:113:VAL:HG21	1:A:149:THR:CG2	1.84	1.07
1:E:8:LEU:HD11	1:E:18:LEU:HD12	1.35	1.06
1:G:415:TYR:CE2	1:G:417:PHE:CE1	2.38	1.06
1:E:192:THR:OG1	1:E:272:MET:HE1	1.55	1.06
1:H:466:LEU:HD13	1:H:490:ILE:HG21	1.35	1.06
1:C:237:LEU:HD13	1:C:239:LEU:HG	1.36	1.05
1:D:180:PRO:HG3	1:D:390:MET:CE	1.85	1.05
1:F:180:PRO:HG2	1:F:390:MET:HE2	1.33	1.05
1:C:164:HIS:CE1	1:C:265:ILE:HD13	1.91	1.05
1:C:237:LEU:HD11	1:C:239:LEU:HD12	1.35	1.05
1:H:424:TYR:O	1:H:492:ILE:HG23	1.56	1.05
1:B:237:LEU:CD1	1:B:239:LEU:CG	2.35	1.05
1:G:237:LEU:HD13	1:G:239:LEU:CG	1.86	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:436:ILE:HD11	1:B:484:ALA:HA	1.34	1.05
1:A:237:LEU:CD1	1:A:239:LEU:HG	1.87	1.05
1:D:135:ASP:HB3	1:D:138:GLU:HG3	1.37	1.04
1:G:135:ASP:OD1	1:G:138:GLU:HG3	1.56	1.04
1:E:180:PRO:HG3	1:E:390:MET:HE2	1.36	1.04
1:E:237:LEU:HD13	1:E:239:LEU:HG	1.37	1.04
1:B:432:ALA:HB1	1:B:487:THR:HG21	1.40	1.04
1:G:174:THR:O	1:G:178:VAL:HG23	1.56	1.04
1:A:342:MET:HE1	1:A:405:PRO:CD	1.88	1.03
1:D:9:ASP:O	1:H:51:SER:HB2	1.57	1.03
1:H:324:ILE:HD11	1:H:353:LYS:HD3	1.38	1.03
1:C:180:PRO:CG	1:C:390:MET:CE	2.35	1.03
1:G:8:LEU:CD1	1:G:18:LEU:CD1	2.36	1.03
1:B:360:ILE:O	1:B:364:MET:HG3	1.57	1.03
1:G:452:LEU:HD23	1:G:467:PHE:CB	1.88	1.03
1:H:237:LEU:CD1	1:H:239:LEU:CD1	2.36	1.03
1:G:473:HIS:HB2	1:G:476:ARG:HB2	1.41	1.02
1:H:279:ILE:HB	1:H:315:VAL:HG22	1.40	1.02
1:D:44:VAL:HG22	1:D:69:HIS:CE1	1.94	1.02
1:D:237:LEU:HD13	1:D:239:LEU:CG	1.89	1.02
1:H:152:MET:HE3	1:H:271:ALA:HA	1.42	1.02
1:A:237:LEU:HD13	1:A:239:LEU:HG	1.04	1.01
1:C:339:SER:O	1:C:343:THR:HG23	1.59	1.01
1:E:246:THR:HG21	1:E:260:LEU:HD21	1.41	1.01
1:G:8:LEU:HD13	1:G:18:LEU:CD1	1.91	1.01
1:D:432:ALA:HB1	1:D:487:THR:CG2	1.88	1.01
1:D:169:VAL:HG11	1:D:324:ILE:HD11	1.38	1.01
1:F:237:LEU:CD1	1:F:239:LEU:HG	1.89	1.01
1:A:113:VAL:CG2	1:A:149:THR:HG21	1.90	1.00
1:D:191:LYS:HE3	1:D:193:SER:OG	1.59	1.00
1:B:436:ILE:HD13	1:B:484:ALA:HB2	1.39	1.00
1:B:157:ARG:O	1:B:160:ILE:HD11	1.62	1.00
1:B:237:LEU:HD13	1:B:239:LEU:CG	1.92	1.00
1:C:134:LEU:HD22	1:C:138:GLU:HB3	1.42	0.99
1:C:180:PRO:CG	1:C:390:MET:HE2	1.91	0.99
1:F:436:ILE:CD1	1:F:484:ALA:CA	2.41	0.99
1:D:169:VAL:CG1	1:D:324:ILE:CD1	2.40	0.99
1:G:368:ALA:HB2	1:G:376:MET:HE3	1.43	0.98
1:H:117:LEU:HD22	1:H:121:GLU:HB3	1.45	0.98
1:H:179:VAL:HG21	1:H:231:LEU:HD21	1.45	0.98
1:A:113:VAL:HG21	1:A:149:THR:HG21	1.00	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:436:ILE:CD1	1:F:484:ALA:HA	1.91	0.98
1:G:219:GLU:O	1:G:223:ILE:HG13	1.65	0.97
1:F:326:HIS:HB3	1:F:452:LEU:O	1.65	0.97
1:F:436:ILE:HD11	1:F:484:ALA:HA	0.99	0.97
1:H:266:MET:HG3	1:H:305:LEU:HD23	1.42	0.97
1:A:237:LEU:HD13	1:A:239:LEU:CG	1.92	0.96
1:B:432:ALA:HB1	1:B:487:THR:CG2	1.95	0.96
1:H:183:ALA:HB1	1:H:389:LYS:CE	1.95	0.96
1:B:436:ILE:CD1	1:B:484:ALA:HA	1.95	0.96
1:E:192:THR:HG21	1:E:272:MET:HE2	1.46	0.96
1:H:220:ILE:O	1:H:224:VAL:HG23	1.64	0.96
1:H:237:LEU:CD1	1:H:239:LEU:HD12	1.94	0.96
1:A:157:ARG:O	1:A:160:ILE:HD11	1.65	0.95
1:C:237:LEU:CD1	1:C:239:LEU:HG	1.94	0.95
1:D:414:THR:HG22	1:D:470:HIS:HA	1.46	0.95
1:G:113:VAL:HG21	1:G:149:THR:HG21	1.46	0.95
1:B:436:ILE:HD13	1:B:484:ALA:CB	1.96	0.95
1:D:237:LEU:CD1	1:D:239:LEU:HD12	1.96	0.95
1:G:452:LEU:CD2	1:G:467:PHE:HB3	1.96	0.95
1:B:237:LEU:HD13	1:B:239:LEU:HG	0.97	0.95
1:C:237:LEU:CD1	1:C:239:LEU:CG	2.46	0.94
1:G:215:PHE:O	1:G:220:ILE:HD11	1.67	0.94
1:F:436:ILE:HD13	1:F:484:ALA:HB2	0.93	0.93
1:H:237:LEU:HD11	1:H:239:LEU:CD1	1.97	0.93
1:F:180:PRO:CG	1:F:390:MET:HE2	1.98	0.93
1:C:233:TRP:NE1	1:C:235:GLY:H	1.66	0.92
1:G:246:THR:HG21	1:G:260:LEU:HD21	1.52	0.92
1:H:179:VAL:HB	1:H:180:PRO:HD3	1.51	0.92
1:C:246:THR:HG21	1:C:260:LEU:HD21	1.51	0.92
1:F:151:ASP:O	1:F:239:LEU:HD23	1.68	0.92
1:B:469:ILE:HG22	1:B:477:LEU:CD1	1.99	0.92
1:C:212:ASP:O	1:C:215:PHE:HE2	1.52	0.92
1:E:117:LEU:HD22	1:E:121:GLU:HB3	1.47	0.91
1:C:8:LEU:CD1	1:C:18:LEU:HD22	2.00	0.91
1:G:237:LEU:HD13	1:G:239:LEU:HG	0.91	0.91
1:G:329:GLY:O	1:G:333:GLU:HG3	1.71	0.91
1:D:237:LEU:CD1	1:D:239:LEU:CG	2.49	0.91
1:E:189:ILE:HG23	1:E:189:ILE:O	1.69	0.91
1:G:179:VAL:HB	1:G:180:PRO:HD3	1.52	0.91
1:H:237:LEU:HD13	1:H:239:LEU:CD1	1.97	0.91
1:G:237:LEU:HD11	1:G:239:LEU:HG	1.49	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:TRP:CD1	1:C:235:GLY:N	2.38	0.90
1:A:175:ASN:ND2	1:A:191:LYS:HE2	1.86	0.90
1:F:180:PRO:HG2	1:F:390:MET:CE	2.01	0.90
1:G:187:LEU:HD21	1:G:367:VAL:HG23	1.52	0.90
1:G:35:VAL:CG1	1:G:48:VAL:HG23	2.02	0.90
1:G:452:LEU:HD23	1:G:467:PHE:HB2	1.52	0.90
1:A:175:ASN:HD22	1:A:191:LYS:CE	1.85	0.89
1:C:20:ASN:HD22	1:C:23:ASP:H	1.21	0.89
1:D:191:LYS:HE3	1:D:193:SER:HG	1.36	0.89
1:G:452:LEU:HD23	1:G:467:PHE:HB3	1.54	0.89
1:G:415:TYR:CE2	1:G:417:PHE:CE2	2.61	0.89
1:G:8:LEU:HD13	1:G:18:LEU:HD11	1.55	0.89
1:A:399:GLY:O	1:A:401:PRO:HD3	1.72	0.89
1:C:117:LEU:HD22	1:C:121:GLU:CB	2.03	0.89
1:C:237:LEU:HD11	1:C:239:LEU:CD1	2.02	0.89
1:B:478:ASP:O	1:B:482:VAL:HG23	1.72	0.89
1:D:237:LEU:CD1	1:D:239:LEU:HG	2.02	0.89
1:C:488:GLU:OE1	1:C:488:GLU:HA	1.70	0.88
1:H:183:ALA:HB1	1:H:389:LYS:HE3	1.55	0.88
1:D:9:ASP:OD2	1:H:52:ASN:CB	2.22	0.88
1:D:8:LEU:CD1	1:D:18:LEU:CD1	2.52	0.87
1:H:152:MET:CE	1:H:271:ALA:HA	2.03	0.87
1:A:117:LEU:HD22	1:A:121:GLU:HB3	1.55	0.87
1:C:360:ILE:O	1:C:364:MET:HG3	1.74	0.87
1:G:35:VAL:HG11	1:G:48:VAL:CG2	2.03	0.87
1:D:9:ASP:O	1:H:51:SER:CB	2.22	0.87
1:E:179:VAL:HB	1:E:180:PRO:HD3	1.56	0.87
1:H:237:LEU:HD13	1:H:239:LEU:HG	0.88	0.87
1:B:142:LEU:O	1:B:146:MET:HG3	1.74	0.87
1:A:261:MET:O	1:A:265:ILE:HG13	1.73	0.87
1:G:177:LEU:O	1:G:181:ILE:HD12	1.74	0.87
1:C:212:ASP:O	1:C:215:PHE:CE2	2.27	0.87
1:E:8:LEU:O	1:E:63:ARG:HG2	1.74	0.87
1:E:180:PRO:HG3	1:E:390:MET:CE	2.04	0.87
1:H:117:LEU:HD22	1:H:121:GLU:CB	2.05	0.87
1:D:44:VAL:CG2	1:D:69:HIS:CE1	2.58	0.86
1:G:177:LEU:O	1:G:181:ILE:CD1	2.23	0.86
1:G:166:ILE:CD1	1:G:281:ILE:HG23	2.06	0.86
1:D:237:LEU:HD11	1:D:239:LEU:CD1	2.06	0.85
1:F:246:THR:CG2	1:F:260:LEU:HD21	2.04	0.85
1:G:368:ALA:HB2	1:G:376:MET:HE1	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:180:PRO:HG3	1:H:390:MET:CE	2.07	0.85
1:D:237:LEU:CD1	1:D:239:LEU:CD1	2.54	0.85
1:G:179:VAL:HB	1:G:180:PRO:CD	2.04	0.85
1:A:18:LEU:HD23	1:A:51:SER:OG	1.77	0.85
1:E:180:PRO:CG	1:E:390:MET:HE2	2.07	0.85
1:E:214:SER:O	1:E:215:PHE:CD1	2.29	0.84
1:E:176:ILE:O	1:E:180:PRO:HD2	1.77	0.84
1:G:424:TYR:O	1:G:492:ILE:HG23	1.76	0.84
1:G:452:LEU:CD2	1:G:467:PHE:CB	2.53	0.84
1:B:178:VAL:O	1:B:182:VAL:HG23	1.77	0.84
1:D:113:VAL:HG21	1:D:149:THR:CG2	2.03	0.84
1:E:326:HIS:HB3	1:E:452:LEU:O	1.76	0.84
1:G:216:SER:C	1:G:220:ILE:HG12	2.03	0.84
1:H:127:THR:O	1:H:131:ILE:HG13	1.76	0.84
1:C:142:LEU:O	1:C:146:MET:HG3	1.78	0.84
1:E:18:LEU:HD23	1:E:49:ALA:HB3	1.60	0.84
1:F:360:ILE:O	1:F:364:MET:HG3	1.76	0.84
1:G:8:LEU:HD11	1:G:18:LEU:CD1	2.04	0.84
1:F:400:ASP:O	1:F:403:ILE:CG2	2.21	0.83
1:B:261:MET:O	1:B:265:ILE:HG13	1.79	0.83
1:G:99:LYS:HZ1	1:G:137:ASP:HB2	1.42	0.83
1:G:332:LEU:HD12	1:G:449:GLY:HA3	1.59	0.83
1:B:281:ILE:HD13	1:B:298:LEU:HD23	1.59	0.83
1:E:192:THR:HG21	1:E:272:MET:CE	2.08	0.83
1:H:319:TYR:CZ	1:H:321:GLY:HA3	2.13	0.83
1:D:424:TYR:C	1:D:492:ILE:HG23	2.01	0.83
1:H:8:LEU:CD1	1:H:18:LEU:HD11	2.09	0.83
1:H:466:LEU:HD13	1:H:490:ILE:CG2	2.07	0.83
1:E:400:ASP:O	1:E:403:ILE:HG23	1.77	0.83
1:G:166:ILE:HD13	1:G:281:ILE:HG23	1.57	0.83
1:E:37:ILE:HG12	1:E:79:VAL:HG22	1.58	0.83
1:F:8:LEU:CD1	1:F:18:LEU:HD13	2.09	0.83
1:H:415:TYR:HE2	1:H:417:PHE:CZ	1.97	0.83
1:B:237:LEU:HD11	1:B:239:LEU:CG	2.07	0.82
1:C:117:LEU:HD22	1:C:121:GLU:HB3	1.59	0.82
1:G:341:LEU:HD13	1:G:390:MET:HG2	1.59	0.82
1:H:161:MET:HE3	1:H:361:LEU:CD2	2.07	0.82
1:B:170:PRO:CG	1:B:430:ASN:HB3	2.08	0.82
1:G:170:PRO:HD2	1:G:430:ASN:OD1	1.80	0.82
1:E:114:ASP:O	1:E:115:ARG:HB2	1.77	0.82
1:G:400:ASP:HB3	1:G:403:ILE:HG23	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:35:VAL:CG1	1:H:48:VAL:HG21	2.10	0.82
1:B:173:LYS:HE3	1:B:333:GLU:HG2	1.61	0.82
1:D:415:TYR:CD2	1:D:481:ILE:HD13	2.14	0.82
1:G:250:GLU:OE2	1:G:260:LEU:CD2	2.24	0.82
1:B:469:ILE:CG2	1:B:477:LEU:CD1	2.57	0.82
1:A:448:ALA:HA	1:A:470:HIS:O	1.80	0.81
1:D:424:TYR:O	1:D:492:ILE:CG2	2.28	0.81
1:G:192:THR:HA	1:G:232:VAL:O	1.79	0.81
1:H:266:MET:HG3	1:H:305:LEU:CD2	2.11	0.81
1:B:469:ILE:CG2	1:B:477:LEU:HD12	2.11	0.81
1:D:200:ALA:O	1:D:443:PRO:HB3	1.80	0.81
1:D:59:VAL:HG11	1:D:79:VAL:HG21	1.63	0.81
1:A:400:ASP:HB2	1:A:403:ILE:HG22	1.63	0.81
1:C:20:ASN:ND2	1:C:22:GLU:H	1.78	0.81
1:E:445:ASP:HB3	1:E:472:GLU:OE1	1.79	0.81
1:D:414:THR:HG21	1:D:470:HIS:ND1	1.95	0.81
1:E:90:TYR:CD1	1:E:104:GLU:HG2	2.16	0.81
1:E:154:ASP:O	1:E:221:LYS:HD2	1.81	0.81
1:E:180:PRO:CG	1:E:390:MET:CE	2.57	0.81
1:G:166:ILE:HD12	1:G:289:VAL:HG23	1.63	0.81
1:E:400:ASP:HB3	1:E:403:ILE:CG2	2.11	0.80
1:H:327:THR:OG1	1:H:336:GLU:CD	2.24	0.80
1:G:211:ALA:HB1	1:G:397:GLN:CB	2.11	0.80
1:A:117:LEU:HD22	1:A:121:GLU:CB	2.10	0.80
1:D:278:LEU:HD12	1:D:314:GLU:O	1.81	0.80
1:E:117:LEU:HD23	1:E:121:GLU:HG2	1.63	0.80
1:C:237:LEU:CD1	1:C:239:LEU:HD12	2.11	0.80
1:D:203:THR:O	1:D:207:VAL:HG23	1.81	0.80
1:F:323:PRO:HD3	1:F:430:ASN:OD1	1.82	0.80
1:G:35:VAL:HG13	1:G:48:VAL:HG23	1.63	0.80
1:A:242:ALA:O	1:A:246:THR:HG23	1.79	0.80
1:H:356:GLY:O	1:H:360:ILE:HG13	1.81	0.80
1:H:414:THR:CG2	1:H:470:HIS:ND1	2.44	0.80
1:H:179:VAL:HB	1:H:180:PRO:CD	2.12	0.80
1:D:9:ASP:O	1:H:51:SER:CA	2.30	0.80
1:E:380:ILE:HG22	1:E:386:ALA:HB2	1.63	0.80
1:H:326:HIS:HB3	1:H:452:LEU:O	1.80	0.80
1:C:180:PRO:HG2	1:C:390:MET:CE	2.10	0.80
1:E:8:LEU:HD11	1:E:18:LEU:CD1	2.12	0.80
1:F:18:LEU:HD23	1:F:51:SER:OG	1.81	0.80
1:F:101:ARG:CG	1:F:104:GLU:OE1	2.30	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:ARG:O	1:B:160:ILE:CD1	2.30	0.79
1:A:237:LEU:CD1	1:A:239:LEU:CG	2.57	0.79
1:H:415:TYR:CE2	1:H:417:PHE:CE2	2.71	0.79
1:B:170:PRO:HG2	1:B:430:ASN:CG	2.08	0.79
1:E:29:LEU:HD21	1:E:81:PRO:HG3	1.62	0.79
1:F:151:ASP:O	1:F:239:LEU:CD2	2.29	0.79
1:F:237:LEU:HD13	1:F:239:LEU:CG	2.05	0.79
1:C:164:HIS:HE1	1:C:265:ILE:HD13	1.46	0.79
1:C:233:TRP:NE1	1:C:235:GLY:N	2.30	0.79
1:G:415:TYR:CD2	1:G:417:PHE:CE2	2.70	0.79
1:H:8:LEU:HD11	1:H:18:LEU:HD12	0.86	0.79
1:H:35:VAL:CG1	1:H:48:VAL:CG2	2.61	0.79
1:H:415:TYR:CE2	1:H:417:PHE:CZ	2.69	0.79
1:B:250:GLU:OE1	1:B:257:PRO:HD2	1.83	0.79
1:D:135:ASP:HB3	1:D:138:GLU:CG	2.12	0.79
1:D:169:VAL:CG1	1:D:324:ILE:HD13	2.10	0.79
1:D:176:ILE:O	1:D:180:PRO:HD2	1.82	0.79
1:E:342:MET:HE1	1:E:405:PRO:CD	2.13	0.79
1:G:183:ALA:HB1	1:G:389:LYS:HE3	1.64	0.79
1:G:331:ALA:O	1:G:335:ARG:HG3	1.82	0.79
1:B:151:ASP:O	1:B:239:LEU:HD23	1.83	0.79
1:B:170:PRO:HG2	1:B:430:ASN:CB	2.13	0.79
1:E:117:LEU:HD22	1:E:121:GLU:CB	2.13	0.79
1:E:319:TYR:CZ	1:E:321:GLY:HA3	2.17	0.79
1:F:243:ASP:O	1:F:247:ILE:HG13	1.83	0.79
1:F:101:ARG:CB	1:F:104:GLU:OE1	2.30	0.79
1:G:477:LEU:HD12	1:G:477:LEU:O	1.82	0.79
1:D:432:ALA:CB	1:D:487:THR:CG2	2.62	0.78
1:G:216:SER:O	1:G:220:ILE:CG1	2.30	0.78
1:G:351:ILE:O	1:G:355:THR:HG23	1.83	0.78
1:H:436:ILE:HG21	1:H:469:ILE:HD11	1.64	0.78
1:A:157:ARG:O	1:A:160:ILE:CD1	2.31	0.78
1:E:237:LEU:CD1	1:E:239:LEU:HG	2.13	0.78
1:H:183:ALA:HB1	1:H:389:LYS:HE2	1.64	0.78
1:E:8:LEU:CD1	1:E:18:LEU:HD12	2.12	0.78
1:H:180:PRO:HG3	1:H:390:MET:HE1	1.66	0.78
1:E:117:LEU:CD2	1:E:121:GLU:HG2	2.14	0.78
1:H:414:THR:HG21	1:H:470:HIS:ND1	1.98	0.78
1:D:227:VAL:O	1:D:389:LYS:HE3	1.83	0.78
1:E:4:LYS:HA	1:E:75:GLU:O	1.84	0.78
1:F:118:ARG:O	1:F:122:ILE:HG13	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:177:LEU:HD22	1:G:341:LEU:CD2	2.12	0.78
1:C:20:ASN:ND2	1:C:22:GLU:N	2.32	0.78
1:D:477:LEU:O	1:D:481:ILE:HG13	1.84	0.78
1:H:166:ILE:HD11	1:H:281:ILE:HG23	1.65	0.78
1:C:177:LEU:O	1:C:181:ILE:HG13	1.84	0.77
1:E:143:THR:OG1	1:E:263:ALA:HA	1.85	0.77
1:G:175:ASN:ND2	1:G:191:LYS:HE2	1.98	0.77
1:G:177:LEU:C	1:G:181:ILE:HD12	2.09	0.77
1:C:143:THR:OG1	1:C:263:ALA:HA	1.84	0.77
1:G:68:LEU:O	1:G:69:HIS:CG	2.37	0.77
1:G:187:LEU:HD21	1:G:367:VAL:CG2	2.15	0.77
1:D:10:MET:CB	1:H:51:SER:HB3	2.15	0.77
1:G:446:LYS:HD3	1:G:446:LYS:N	1.99	0.77
1:H:331:ALA:O	1:H:335:ARG:HG3	1.84	0.77
1:E:342:MET:HE1	1:E:405:PRO:HD2	1.66	0.77
1:D:9:ASP:O	1:H:51:SER:HA	1.85	0.77
1:G:415:TYR:HE2	1:G:417:PHE:CD1	2.02	0.77
1:D:114:ASP:OD2	1:D:116:LYS:HE3	1.85	0.77
1:E:415:TYR:HE2	1:E:417:PHE:CE2	2.03	0.77
1:G:44:VAL:HG22	1:G:69:HIS:CE1	2.21	0.77
1:E:155:ILE:HD13	1:E:224:VAL:HG11	1.65	0.76
1:G:99:LYS:NZ	1:G:137:ASP:HB2	2.00	0.76
1:G:210:PHE:CZ	1:G:338:LEU:HD21	2.20	0.76
1:C:233:TRP:HD1	1:C:234:GLY:N	1.84	0.76
1:E:217:LEU:HD21	1:E:237:LEU:HB2	1.67	0.76
1:F:179:VAL:HB	1:F:180:PRO:HD3	1.66	0.76
1:E:216:SER:O	1:E:220:ILE:HG13	1.86	0.76
1:G:415:TYR:HE2	1:G:417:PHE:CE2	2.01	0.76
1:C:176:ILE:O	1:C:180:PRO:HD2	1.85	0.76
1:A:400:ASP:O	1:A:403:ILE:CG2	2.30	0.76
1:C:134:LEU:CD2	1:C:138:GLU:HB3	2.15	0.76
1:C:233:TRP:CD1	1:C:234:GLY:N	2.53	0.76
1:G:30:HIS:HB2	1:G:33:ASP:OD2	1.85	0.76
1:H:191:LYS:HB3	1:H:231:LEU:HD23	1.66	0.76
1:D:129:LEU:HD22	1:D:134:LEU:HD21	1.68	0.76
1:F:8:LEU:HD11	1:F:18:LEU:HD13	1.68	0.76
1:G:35:VAL:CG1	1:G:48:VAL:CG2	2.62	0.76
1:G:175:ASN:HD22	1:G:191:LYS:HE2	1.50	0.76
1:H:483:LEU:O	1:H:487:THR:HG23	1.86	0.76
1:B:436:ILE:CD1	1:B:484:ALA:CA	2.63	0.76
1:C:35:VAL:HG13	1:C:48:VAL:CG2	2.16	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:466:LEU:HB3	1:F:490:ILE:CD1	2.14	0.76
1:H:278:LEU:HD12	1:H:314:GLU:O	1.86	0.76
1:C:35:VAL:CG1	1:C:48:VAL:CG2	2.64	0.76
1:C:237:LEU:CD1	1:C:239:LEU:CD1	2.64	0.76
1:F:436:ILE:HD11	1:F:484:ALA:CB	2.05	0.76
1:H:117:LEU:HD23	1:H:121:GLU:HG2	1.67	0.76
1:H:117:LEU:CD2	1:H:121:GLU:HG2	2.16	0.75
1:H:176:ILE:O	1:H:180:PRO:HD2	1.86	0.75
1:H:176:ILE:O	1:H:180:PRO:HG2	1.87	0.75
1:H:179:VAL:CG2	1:H:231:LEU:HD21	2.16	0.75
1:C:233:TRP:NE1	1:C:235:GLY:HA3	2.01	0.75
1:B:469:ILE:HG21	1:B:477:LEU:HD12	1.69	0.75
1:A:179:VAL:HB	1:A:180:PRO:HD3	1.68	0.75
1:C:173:LYS:HD2	1:C:336:GLU:OE1	1.87	0.75
1:E:394:ILE:HG22	1:E:399:GLY:HA3	1.68	0.75
1:G:176:ILE:O	1:G:180:PRO:HG2	1.86	0.75
1:H:99:LYS:CE	1:H:135:ASP:OD2	2.27	0.75
1:A:400:ASP:HB2	1:A:403:ILE:CG2	2.16	0.75
1:C:237:LEU:HD13	1:C:239:LEU:CG	2.11	0.74
1:D:329:GLY:O	1:D:333:GLU:CG	2.28	0.74
1:B:237:LEU:HD11	1:B:239:LEU:HD12	1.69	0.74
1:B:432:ALA:CB	1:B:487:THR:HG21	2.17	0.74
1:H:183:ALA:HB3	1:H:389:LYS:HG2	1.69	0.74
1:D:432:ALA:CB	1:D:487:THR:HG21	2.16	0.74
1:G:210:PHE:CD2	1:G:338:LEU:HD11	2.22	0.74
1:H:329:GLY:O	1:H:333:GLU:CG	2.34	0.74
1:D:18:LEU:HD23	1:D:49:ALA:HB3	1.67	0.74
1:E:243:ASP:O	1:E:247:ILE:HG13	1.88	0.74
1:G:394:ILE:HG22	1:G:399:GLY:HA3	1.70	0.74
1:H:166:ILE:CG1	1:H:282:PRO:HD2	2.18	0.74
1:C:179:VAL:HB	1:C:180:PRO:HD3	1.70	0.73
1:F:237:LEU:CD1	1:F:239:LEU:CG	2.63	0.73
1:F:35:VAL:HG13	1:F:48:VAL:HG23	1.71	0.73
1:G:35:VAL:HG11	1:G:48:VAL:HG23	1.68	0.73
1:C:233:TRP:CE2	1:C:235:GLY:HA3	2.23	0.73
1:D:212:ASP:O	1:D:215:PHE:HE2	1.71	0.73
1:B:52:ASN:CB	1:F:9:ASP:OD2	2.36	0.73
1:E:342:MET:CE	1:E:405:PRO:HG2	2.19	0.73
1:E:415:TYR:CE2	1:E:417:PHE:CE2	2.77	0.73
1:B:135:ASP:HB3	1:B:138:GLU:OE1	1.89	0.72
1:B:170:PRO:HD2	1:B:430:ASN:ND2	2.04	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:418:THR:HA	1:G:464:ASP:O	1.88	0.72
1:B:92:LYS:O	1:B:95:MET:HB3	1.89	0.72
1:B:237:LEU:HD11	1:B:239:LEU:CD1	2.18	0.72
1:A:99:LYS:HZ2	1:A:137:ASP:HB2	1.55	0.72
1:D:117:LEU:HD22	1:D:121:GLU:CB	2.19	0.72
1:E:192:THR:CG2	1:E:272:MET:CE	2.67	0.72
1:E:179:VAL:HG13	1:E:189:ILE:HG23	1.72	0.72
1:F:142:LEU:O	1:F:146:MET:HG3	1.89	0.72
1:H:180:PRO:CG	1:H:390:MET:CE	2.67	0.72
1:H:448:ALA:HA	1:H:470:HIS:O	1.90	0.72
1:C:196:ALA:HB2	1:C:201:ALA:C	2.14	0.72
1:F:477:LEU:O	1:F:481:ILE:HG13	1.89	0.72
1:G:166:ILE:HD12	1:G:289:VAL:CG2	2.19	0.72
1:G:368:ALA:CB	1:G:376:MET:HE3	2.19	0.72
1:C:117:LEU:CD2	1:C:121:GLU:CB	2.66	0.72
1:C:291:THR:OG1	1:C:294:GLU:HB2	1.90	0.72
1:H:35:VAL:HG13	1:H:48:VAL:CG2	2.19	0.72
1:H:146:MET:HE1	1:H:264:SER:HA	1.71	0.72
1:C:278:LEU:HD12	1:C:314:GLU:O	1.90	0.72
1:H:35:VAL:HG11	1:H:48:VAL:HG21	1.71	0.72
1:C:59:VAL:HG11	1:C:79:VAL:HG21	1.72	0.72
1:F:101:ARG:HG3	1:F:104:GLU:OE1	1.88	0.72
1:H:324:ILE:CD1	1:H:353:LYS:HD3	2.16	0.72
1:E:300:ARG:HD2	1:F:300:ARG:HD2	1.71	0.71
1:B:18:LEU:HD23	1:B:51:SER:CB	2.20	0.71
1:H:4:LYS:HA	1:H:75:GLU:O	1.90	0.71
1:A:54:VAL:HG11	1:A:58:GLU:O	1.91	0.71
1:A:203:THR:O	1:A:207:VAL:HG23	1.90	0.71
1:H:450:ILE:HG22	1:H:452:LEU:HD12	1.70	0.71
1:B:8:LEU:HD12	1:B:18:LEU:HD13	1.73	0.71
1:A:484:ALA:HA	1:A:487:THR:OG1	1.90	0.71
1:E:169:VAL:HG13	1:E:172:ASN:HB2	1.71	0.71
1:F:331:ALA:CB	1:F:446:LYS:O	2.37	0.71
1:D:114:ASP:O	1:D:115:ARG:HB2	1.90	0.71
1:G:488:GLU:N	1:G:489:PRO:HD3	2.05	0.71
1:H:424:TYR:O	1:H:492:ILE:CG2	2.37	0.71
1:B:436:ILE:HD13	1:B:484:ALA:CA	2.20	0.71
1:A:250:GLU:OE1	1:A:257:PRO:HD2	1.91	0.71
1:D:114:ASP:O	1:D:115:ARG:CB	2.38	0.71
1:D:155:ILE:CD1	1:D:224:VAL:HG11	2.21	0.71
1:E:114:ASP:O	1:E:115:ARG:CB	2.39	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:GLY:O	1:C:58:GLU:HB2	1.91	0.70
1:C:331:ALA:O	1:C:335:ARG:HG3	1.91	0.70
1:E:432:ALA:O	1:E:436:ILE:HG13	1.90	0.70
1:F:101:ARG:HB2	1:F:104:GLU:OE1	1.91	0.70
1:B:72:SER:O	1:B:75:GLU:HB2	1.91	0.70
1:D:117:LEU:HD22	1:D:121:GLU:HB3	1.72	0.70
1:C:326:HIS:HB3	1:C:452:LEU:O	1.92	0.70
1:H:265:ILE:HD12	1:H:302:PHE:HZ	1.56	0.70
1:G:415:TYR:CD2	1:G:417:PHE:CZ	2.78	0.70
1:C:172:ASN:OD1	1:C:353:LYS:NZ	2.25	0.70
1:E:177:LEU:HD22	1:E:341:LEU:HG	1.72	0.70
1:H:35:VAL:HG11	1:H:48:VAL:CG2	2.21	0.70
1:A:478:ASP:O	1:A:482:VAL:HG23	1.92	0.70
1:E:203:THR:O	1:E:207:VAL:HG23	1.91	0.70
1:G:332:LEU:CD1	1:G:449:GLY:HA3	2.21	0.70
1:B:179:VAL:HB	1:B:180:PRO:HD3	1.74	0.70
1:B:436:ILE:CD1	1:B:484:ALA:CB	2.69	0.70
1:H:424:TYR:C	1:H:492:ILE:HG23	2.15	0.70
1:G:185:ALA:HB1	1:G:367:VAL:HG11	1.74	0.70
1:H:135:ASP:OD1	1:H:138:GLU:HG3	1.92	0.70
1:E:155:ILE:HA	1:E:221:LYS:HE3	1.72	0.70
1:F:72:SER:O	1:F:75:GLU:HB2	1.92	0.70
1:F:180:PRO:CG	1:F:390:MET:CE	2.66	0.70
1:G:44:VAL:CG2	1:G:69:HIS:CG	2.75	0.69
1:B:432:ALA:CB	1:B:487:THR:CG2	2.69	0.69
1:A:192:THR:HA	1:A:232:VAL:O	1.93	0.69
1:C:3:ALA:HB1	1:C:57:GLY:O	1.91	0.69
1:D:67:ASP:OD1	1:D:68:LEU:N	2.25	0.69
1:D:175:ASN:O	1:D:179:VAL:HG23	1.92	0.69
1:G:240:ALA:N	1:G:241:PRO:CD	2.54	0.69
1:G:360:ILE:O	1:G:364:MET:HG3	1.92	0.69
1:F:187:LEU:HD21	1:F:367:VAL:HG23	1.74	0.69
1:H:179:VAL:HG21	1:H:231:LEU:CD2	2.22	0.69
1:F:172:ASN:OD1	1:F:324:ILE:HD13	1.90	0.69
1:G:108:ILE:O	1:G:112:ILE:HG13	1.92	0.69
1:G:159:PRO:HA	1:G:275:GLN:HE21	1.58	0.69
1:H:161:MET:CE	1:H:361:LEU:HD23	2.22	0.69
1:B:191:LYS:HE3	1:B:193:SER:OG	1.92	0.69
1:C:233:TRP:NE1	1:C:235:GLY:CA	2.55	0.69
1:G:179:VAL:HG21	1:G:231:LEU:HD21	1.75	0.69
1:G:215:PHE:CB	1:G:220:ILE:CD1	2.71	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:319:TYR:CE1	1:H:321:GLY:N	2.61	0.69
1:H:466:LEU:CD1	1:H:490:ILE:HG21	2.20	0.69
1:D:176:ILE:O	1:D:180:PRO:CG	2.41	0.69
1:F:177:LEU:HD22	1:F:341:LEU:HG	1.75	0.69
1:A:212:ASP:O	1:A:215:PHE:HE2	1.76	0.69
1:E:414:THR:HG22	1:E:470:HIS:ND1	2.08	0.69
1:B:176:ILE:O	1:B:180:PRO:HD2	1.92	0.69
1:A:54:VAL:HG13	1:A:58:GLU:HB2	1.75	0.69
1:A:342:MET:CE	1:A:405:PRO:CD	2.70	0.68
1:C:145:ALA:O	1:C:149:THR:HG23	1.93	0.68
1:D:176:ILE:O	1:D:180:PRO:CD	2.40	0.68
1:G:326:HIS:HB3	1:G:452:LEU:O	1.92	0.68
1:D:237:LEU:HD13	1:D:239:LEU:CD1	2.22	0.68
1:B:179:VAL:HB	1:B:180:PRO:CD	2.23	0.68
1:H:424:TYR:O	1:H:492:ILE:HA	1.93	0.68
1:C:180:PRO:HG3	1:C:390:MET:HE1	1.73	0.68
1:D:143:THR:OG1	1:D:263:ALA:HA	1.94	0.68
1:G:358:ALA:O	1:G:362:LEU:HG	1.92	0.68
1:G:400:ASP:HB3	1:G:403:ILE:CG2	2.22	0.68
1:H:319:TYR:OH	1:H:321:GLY:HA3	1.92	0.68
1:B:175:ASN:O	1:B:179:VAL:HG23	1.94	0.68
1:C:92:LYS:O	1:C:96:HIS:HD2	1.76	0.68
1:E:319:TYR:CE1	1:E:321:GLY:HA3	2.28	0.68
1:G:342:MET:CE	1:G:405:PRO:HG2	2.23	0.68
1:E:342:MET:HE2	1:E:405:PRO:HG2	1.76	0.68
1:G:166:ILE:CD1	1:G:289:VAL:HG21	2.24	0.68
1:G:176:ILE:HG22	1:G:390:MET:CE	2.23	0.68
1:B:192:THR:HA	1:B:232:VAL:O	1.94	0.67
1:A:108:ILE:O	1:A:112:ILE:HG13	1.93	0.67
1:C:483:LEU:O	1:C:487:THR:HG23	1.94	0.67
1:E:448:ALA:HA	1:E:470:HIS:O	1.94	0.67
1:F:135:ASP:OD1	1:F:138:GLU:CG	2.35	0.67
1:F:400:ASP:HB3	1:F:403:ILE:CG2	2.24	0.67
1:A:27:ALA:O	1:A:28:LYS:CB	2.40	0.67
1:A:351:ILE:O	1:A:355:THR:HG23	1.95	0.67
1:A:466:LEU:HB3	1:A:490:ILE:HD12	1.76	0.67
1:E:9:ASP:HA	1:E:63:ARG:HG3	1.75	0.67
1:B:166:ILE:HD11	1:B:281:ILE:HG23	1.76	0.67
1:A:471:ALA:HB3	1:A:477:LEU:HB2	1.74	0.67
1:C:135:ASP:OD1	1:C:138:GLU:HB2	1.94	0.67
1:G:166:ILE:CD1	1:G:289:VAL:CG2	2.72	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:35:VAL:HG13	1:C:48:VAL:HG23	1.75	0.67
1:C:109:VAL:O	1:C:113:VAL:HG23	1.94	0.67
1:D:8:LEU:HD13	1:D:18:LEU:CD1	2.24	0.67
1:E:15:TYR:CD2	1:E:65:VAL:HG22	2.29	0.67
1:E:155:ILE:HD13	1:E:224:VAL:HG21	1.76	0.67
1:G:72:SER:O	1:G:75:GLU:HB2	1.95	0.67
1:C:94:LYS:O	1:C:132:ASN:ND2	2.28	0.67
1:G:299:ALA:O	1:G:303:ILE:HG13	1.95	0.67
1:D:51:SER:HB3	1:H:10:MET:HB2	1.76	0.67
1:G:35:VAL:HG22	1:G:46:GLY:O	1.95	0.67
1:A:114:ASP:O	1:A:115:ARG:HB2	1.93	0.67
1:C:237:LEU:HD11	1:C:239:LEU:CG	2.18	0.67
1:D:219:GLU:O	1:D:223:ILE:HG13	1.95	0.67
1:A:166:ILE:HD11	1:A:281:ILE:HG23	1.77	0.66
1:G:177:LEU:O	1:G:181:ILE:CG1	2.42	0.66
1:C:323:PRO:HD3	1:C:430:ASN:OD1	1.95	0.66
1:C:391:LYS:HB3	1:C:401:PRO:HB3	1.75	0.66
1:E:179:VAL:HB	1:E:180:PRO:CD	2.24	0.66
1:H:170:PRO:HG3	1:H:434:THR:OG1	1.95	0.66
1:A:342:MET:CE	1:A:405:PRO:HG2	2.25	0.66
1:D:326:HIS:HB3	1:D:452:LEU:O	1.95	0.66
1:A:142:LEU:O	1:A:146:MET:HG3	1.96	0.66
1:E:400:ASP:O	1:E:403:ILE:HG12	1.96	0.66
1:F:331:ALA:HB2	1:F:446:LYS:O	1.94	0.66
1:H:151:ASP:O	1:H:239:LEU:HD23	1.96	0.66
1:D:448:ALA:HA	1:D:470:HIS:O	1.95	0.66
1:F:341:LEU:CD1	1:F:390:MET:HE3	2.26	0.66
1:H:319:TYR:CE1	1:H:321:GLY:HA3	2.31	0.66
1:H:424:TYR:N	1:H:492:ILE:HG23	2.10	0.66
1:F:176:ILE:O	1:F:180:PRO:HD2	1.94	0.66
1:C:35:VAL:CG1	1:C:48:VAL:HG21	2.26	0.66
1:C:134:LEU:HD22	1:C:138:GLU:CB	2.21	0.66
1:D:143:THR:HG21	1:D:309:LEU:HD11	1.78	0.66
1:G:341:LEU:HD11	1:G:390:MET:HE3	1.77	0.66
1:H:415:TYR:CD2	1:H:417:PHE:CE2	2.83	0.66
1:B:472:GLU:O	1:B:473:HIS:ND1	2.28	0.66
1:F:4:LYS:HA	1:F:75:GLU:O	1.96	0.66
1:F:145:ALA:O	1:F:149:THR:HG23	1.96	0.66
1:G:215:PHE:HB2	1:G:220:ILE:CD1	2.25	0.66
1:H:161:MET:CE	1:H:361:LEU:CD2	2.74	0.66
1:D:176:ILE:O	1:D:180:PRO:HG2	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:90:TYR:CE1	1:E:104:GLU:HG2	2.31	0.66
1:C:164:HIS:ND1	1:C:265:ILE:HD13	2.11	0.65
1:C:314:GLU:HG3	1:C:364:MET:HE3	1.78	0.65
1:F:220:ILE:O	1:F:224:VAL:HG23	1.96	0.65
1:G:400:ASP:CB	1:G:403:ILE:HG23	2.25	0.65
1:H:374:LYS:O	1:H:377:ALA:HB3	1.96	0.65
1:C:192:THR:HA	1:C:232:VAL:O	1.96	0.65
1:E:246:THR:CG2	1:E:260:LEU:HD21	2.23	0.65
1:H:177:LEU:HD22	1:H:341:LEU:HD21	1.79	0.65
1:F:121:GLU:OE1	1:F:121:GLU:N	2.30	0.65
1:F:255:ILE:HG13	1:F:255:ILE:O	1.96	0.65
1:B:170:PRO:CG	1:B:430:ASN:CB	2.72	0.65
1:B:471:ALA:HB3	1:B:477:LEU:HB2	1.79	0.65
1:A:67:ASP:OD1	1:A:68:LEU:N	2.28	0.65
1:C:9:ASP:OD1	1:C:63:ARG:NH1	2.30	0.65
1:C:24:ALA:CB	1:C:50:LEU:HD21	2.27	0.65
1:C:61:ILE:HG13	1:C:61:ILE:O	1.97	0.65
1:D:61:ILE:O	1:D:61:ILE:HG13	1.95	0.65
1:D:187:LEU:HD11	1:D:365:GLY:HA3	1.79	0.65
1:E:45:TYR:CE2	1:E:116:LYS:HE2	2.31	0.65
1:A:105:ILE:O	1:A:109:VAL:HG23	1.96	0.65
1:E:478:ASP:O	1:E:482:VAL:HG23	1.96	0.65
1:G:117:LEU:HD22	1:G:121:GLU:HB3	1.78	0.65
1:H:67:ASP:OD1	1:H:68:LEU:N	2.30	0.65
1:D:27:ALA:O	1:D:28:LYS:CB	2.45	0.65
1:D:169:VAL:HG12	1:D:324:ILE:HD13	1.79	0.65
1:E:59:VAL:HG13	1:E:59:VAL:O	1.97	0.65
1:H:224:VAL:O	1:H:228:GLY:N	2.28	0.65
1:B:170:PRO:CD	1:B:430:ASN:CG	2.70	0.65
1:C:214:SER:C	1:C:215:PHE:CD2	2.75	0.65
1:D:44:VAL:HG12	1:D:45:TYR:N	2.11	0.65
1:E:180:PRO:HG2	1:E:390:MET:CE	2.25	0.65
1:H:182:VAL:O	1:H:185:ALA:HB3	1.97	0.65
1:H:415:TYR:HE2	1:H:417:PHE:CE2	2.10	0.65
1:C:20:ASN:HD21	1:C:22:GLU:CB	2.10	0.65
1:D:135:ASP:OD1	1:D:136:MET:N	2.30	0.65
1:A:54:VAL:CG1	1:A:58:GLU:HB2	2.26	0.65
1:E:394:ILE:HG22	1:E:399:GLY:CA	2.27	0.65
1:G:177:LEU:O	1:G:181:ILE:HG13	1.96	0.65
1:A:94:LYS:O	1:A:94:LYS:HD3	1.97	0.64
1:E:280:ASP:C	1:E:280:ASP:OD1	2.39	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:5:ILE:N	1:F:75:GLU:O	2.27	0.64
1:G:444:GLU:OE1	1:G:444:GLU:N	2.30	0.64
1:E:192:THR:CG2	1:E:272:MET:HE1	2.27	0.64
1:G:390:MET:O	1:G:394:ILE:HG13	1.96	0.64
1:H:35:VAL:HG13	1:H:48:VAL:HG21	1.78	0.64
1:A:171:GLY:O	1:A:173:LYS:NZ	2.30	0.64
1:D:432:ALA:O	1:D:436:ILE:HG13	1.96	0.64
1:G:179:VAL:HG13	1:G:189:ILE:HG23	1.79	0.64
1:B:280:ASP:O	1:B:282:PRO:HD3	1.98	0.64
1:F:176:ILE:O	1:F:180:PRO:CD	2.45	0.64
1:A:20:ASN:OD1	1:A:21:GLU:N	2.30	0.64
1:D:94:LYS:O	1:D:94:LYS:HD3	1.98	0.64
1:E:217:LEU:CD2	1:E:237:LEU:HB2	2.28	0.64
1:G:67:ASP:OD1	1:G:68:LEU:N	2.30	0.64
1:B:173:LYS:HD2	1:B:336:GLU:OE1	1.98	0.64
1:C:176:ILE:O	1:C:180:PRO:CD	2.45	0.64
1:D:10:MET:HB2	1:H:51:SER:HB3	1.79	0.64
1:E:177:LEU:O	1:E:181:ILE:HG13	1.97	0.64
1:C:237:LEU:HD11	1:C:239:LEU:HB2	1.79	0.64
1:D:330:PRO:HG2	1:D:446:LYS:HA	1.80	0.64
1:G:432:ALA:O	1:G:436:ILE:HG13	1.98	0.64
1:C:67:ASP:OD1	1:C:68:LEU:N	2.30	0.64
1:C:233:TRP:HD1	1:C:234:GLY:H	1.46	0.64
1:E:155:ILE:HG21	1:E:224:VAL:CG1	2.27	0.64
1:C:17:VAL:HG21	1:C:37:ILE:HD11	1.79	0.63
1:F:101:ARG:N	1:F:104:GLU:OE1	2.30	0.63
1:F:164:HIS:HB3	1:F:279:ILE:HD13	1.80	0.63
1:H:319:TYR:CE1	1:H:321:GLY:CA	2.80	0.63
1:H:376:MET:O	1:H:380:ILE:HG13	1.98	0.63
1:A:477:LEU:O	1:A:481:ILE:HG13	1.98	0.63
1:F:466:LEU:HB3	1:F:490:ILE:HD12	1.80	0.63
1:H:38:GLU:HB3	1:H:43:ALA:HB2	1.79	0.63
1:B:258:THR:O	1:B:262:LEU:HG	1.98	0.63
1:H:175:ASN:HB3	1:H:191:LYS:HE2	1.81	0.63
1:H:180:PRO:HG3	1:H:390:MET:HE2	1.78	0.63
1:G:18:LEU:HD23	1:G:49:ALA:HB3	1.79	0.63
1:G:176:ILE:O	1:G:180:PRO:HD2	1.98	0.63
1:H:27:ALA:O	1:H:28:LYS:CB	2.46	0.63
1:G:183:ALA:O	1:G:186:GLY:N	2.30	0.63
1:A:72:SER:O	1:A:75:GLU:HB2	1.98	0.63
1:E:169:VAL:CG1	1:E:172:ASN:HB2	2.27	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:LEU:HD12	1:A:449:GLY:HA3	1.81	0.63
1:H:151:ASP:O	1:H:239:LEU:CD2	2.47	0.63
1:B:170:PRO:HG2	1:B:430:ASN:HB3	1.79	0.63
1:E:155:ILE:CD1	1:E:224:VAL:HG21	2.27	0.63
1:H:368:ALA:HB2	1:H:376:MET:CE	2.29	0.63
1:D:129:LEU:CD2	1:D:134:LEU:HD21	2.28	0.62
1:G:68:LEU:C	1:G:69:HIS:CG	2.76	0.62
1:H:211:ALA:HB1	1:H:397:GLN:CB	2.29	0.62
1:B:94:LYS:O	1:B:94:LYS:HD3	2.00	0.62
1:A:18:LEU:HD23	1:A:51:SER:CB	2.30	0.62
1:C:99:LYS:HE3	1:C:135:ASP:OD2	1.99	0.62
1:E:155:ILE:HD13	1:E:224:VAL:CG1	2.30	0.62
1:F:61:ILE:HG13	1:F:61:ILE:O	1.97	0.62
1:F:143:THR:HG21	1:F:309:LEU:HD11	1.82	0.62
1:G:121:GLU:OE1	1:G:121:GLU:N	2.30	0.62
1:B:135:ASP:CB	1:B:138:GLU:OE1	2.47	0.62
1:B:170:PRO:HD2	1:B:430:ASN:CG	2.24	0.62
1:D:426:THR:HG21	1:D:493:GLU:HB2	1.81	0.62
1:E:237:LEU:C	1:E:237:LEU:HD12	2.24	0.62
1:E:390:MET:O	1:E:394:ILE:HG13	1.99	0.62
1:F:179:VAL:HG13	1:F:189:ILE:HG23	1.79	0.62
1:H:237:LEU:CD1	1:H:239:LEU:CB	2.77	0.62
1:C:394:ILE:O	1:C:398:GLY:N	2.32	0.62
1:H:179:VAL:CB	1:H:180:PRO:HD3	2.29	0.62
1:A:250:GLU:CD	1:A:260:LEU:HD23	2.25	0.62
1:H:134:LEU:HD22	1:H:138:GLU:OE1	1.99	0.62
1:H:177:LEU:HD22	1:H:341:LEU:CD2	2.30	0.62
1:C:3:ALA:HB1	1:C:57:GLY:C	2.24	0.62
1:F:466:LEU:HB3	1:F:490:ILE:HD13	1.80	0.62
1:G:178:VAL:HG13	1:G:358:ALA:HB2	1.80	0.62
1:C:24:ALA:CB	1:C:50:LEU:CD2	2.78	0.62
1:C:164:HIS:HE1	1:C:265:ILE:CD1	2.10	0.62
1:G:99:LYS:NZ	1:G:135:ASP:OD2	2.30	0.62
1:H:216:SER:O	1:H:220:ILE:HG13	2.00	0.62
1:C:367:VAL:HG12	1:C:376:MET:SD	2.40	0.61
1:C:129:LEU:HD22	1:C:134:LEU:HG	1.83	0.61
1:A:99:LYS:NZ	1:A:137:ASP:HB2	2.14	0.61
1:C:466:LEU:HB3	1:C:490:ILE:HD13	1.82	0.61
1:D:182:VAL:O	1:D:185:ALA:HB3	2.00	0.61
1:D:414:THR:HG21	1:D:470:HIS:CE1	2.34	0.61
1:E:400:ASP:HB3	1:E:403:ILE:HG23	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:161:MET:HE3	1:H:361:LEU:HD23	1.81	0.61
1:A:227:VAL:O	1:A:389:LYS:HE3	2.01	0.61
1:H:414:THR:HG22	1:H:470:HIS:ND1	2.14	0.61
1:D:360:ILE:O	1:D:364:MET:HG3	2.00	0.61
1:F:319:TYR:CZ	1:F:321:GLY:HA3	2.35	0.61
1:F:448:ALA:HA	1:F:470:HIS:O	2.00	0.61
1:G:206:VAL:HG13	1:G:334:ALA:HB2	1.81	0.61
1:B:469:ILE:HG22	1:B:477:LEU:HD11	1.80	0.61
1:A:92:LYS:O	1:A:95:MET:HB3	2.01	0.61
1:F:177:LEU:O	1:F:181:ILE:HG13	2.00	0.61
1:H:374:LYS:O	1:H:378:LYS:N	2.30	0.61
1:B:170:PRO:CG	1:B:430:ASN:CG	2.73	0.61
1:C:117:LEU:HD22	1:C:121:GLU:HB2	1.79	0.61
1:C:200:ALA:O	1:C:443:PRO:HB3	2.00	0.61
1:D:10:MET:HA	1:H:50:LEU:O	2.01	0.61
1:D:177:LEU:HD23	1:D:341:LEU:HG	1.81	0.61
1:E:358:ALA:O	1:E:362:LEU:HG	2.00	0.61
1:H:166:ILE:HG13	1:H:282:PRO:HD2	1.83	0.61
1:H:423:GLY:HA3	1:H:492:ILE:CG2	2.30	0.61
1:A:6:ARG:HG3	1:A:73:GLU:OE2	2.01	0.61
1:D:445:ASP:CG	1:D:472:GLU:OE1	2.44	0.61
1:C:237:LEU:CD1	1:C:239:LEU:CB	2.78	0.61
1:F:240:ALA:N	1:F:241:PRO:HD3	2.16	0.61
1:F:329:GLY:O	1:F:333:GLU:CG	2.36	0.61
1:A:255:ILE:O	1:A:255:ILE:HG13	2.01	0.60
1:C:6:ARG:O	1:C:60:GLY:HA2	2.01	0.60
1:E:394:ILE:CG2	1:E:399:GLY:HA3	2.31	0.60
1:E:471:ALA:HB3	1:E:477:LEU:HB2	1.83	0.60
1:F:347:PRO:O	1:F:351:ILE:HG12	2.01	0.60
1:H:184:ALA:HB3	1:H:380:ILE:HG21	1.83	0.60
1:H:450:ILE:HG22	1:H:452:LEU:CD1	2.30	0.60
1:F:227:VAL:O	1:F:389:LYS:HE3	2.00	0.60
1:G:177:LEU:HD22	1:G:341:LEU:HD21	1.83	0.60
1:G:216:SER:O	1:G:220:ILE:N	2.30	0.60
1:H:61:ILE:HG13	1:H:61:ILE:O	1.99	0.60
1:D:59:VAL:HG11	1:D:79:VAL:CG2	2.31	0.60
1:E:143:THR:HG21	1:E:309:LEU:HD11	1.84	0.60
1:H:174:THR:HG21	1:H:357:LEU:HD12	1.81	0.60
1:B:223:ILE:O	1:B:227:VAL:N	2.33	0.60
1:D:19:ILE:CD1	1:D:29:LEU:HD12	2.30	0.60
1:G:467:PHE:HE1	1:G:469:ILE:HG13	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:176:ILE:O	1:H:180:PRO:CD	2.49	0.60
1:B:323:PRO:HG3	1:B:430:ASN:OD1	2.00	0.60
1:G:166:ILE:HD11	1:G:281:ILE:HG23	1.83	0.60
1:H:246:THR:HG21	1:H:260:LEU:HD21	1.84	0.60
1:D:135:ASP:OD1	1:D:137:ASP:N	2.30	0.60
1:E:192:THR:CB	1:E:272:MET:HE1	2.31	0.60
1:E:394:ILE:O	1:E:399:GLY:N	2.32	0.60
1:D:129:LEU:HD22	1:D:134:LEU:CD2	2.32	0.60
1:D:227:VAL:O	1:D:389:LYS:CE	2.49	0.60
1:E:122:ILE:HD13	1:E:245:ILE:HG22	1.84	0.60
1:E:155:ILE:HD13	1:E:224:VAL:CB	2.31	0.60
1:H:423:GLY:HA3	1:H:492:ILE:HG22	1.81	0.60
1:B:448:ALA:HA	1:B:470:HIS:O	2.02	0.60
1:C:92:LYS:O	1:C:96:HIS:CD2	2.55	0.60
1:H:184:ALA:CB	1:H:380:ILE:HG21	2.31	0.60
1:A:99:LYS:NZ	1:A:135:ASP:OD2	2.34	0.59
1:C:35:VAL:HG11	1:C:48:VAL:CG2	2.32	0.59
1:C:117:LEU:CD2	1:C:121:GLU:HB3	2.27	0.59
1:F:400:ASP:C	1:F:403:ILE:HG23	2.23	0.59
1:H:122:ILE:O	1:H:126:VAL:HG23	2.02	0.59
1:D:193:SER:CB	1:D:203:THR:CB	2.81	0.59
1:E:214:SER:O	1:E:215:PHE:HD1	1.82	0.59
1:G:38:GLU:HB3	1:G:43:ALA:HB2	1.84	0.59
1:A:400:ASP:C	1:A:403:ILE:HG23	2.24	0.59
1:G:239:LEU:C	1:G:241:PRO:HD3	2.27	0.59
1:G:341:LEU:HD11	1:G:390:MET:CE	2.32	0.59
1:B:338:LEU:HD22	1:B:387:TRP:HZ3	1.68	0.59
1:C:426:THR:HG21	1:C:493:GLU:CD	2.28	0.59
1:B:113:VAL:HG22	1:B:241:PRO:HG2	1.85	0.59
1:E:327:THR:OG1	1:E:336:GLU:OE1	2.20	0.59
1:F:35:VAL:CG1	1:F:48:VAL:CG2	2.81	0.59
1:H:37:ILE:O	1:H:43:ALA:HA	2.03	0.59
1:C:44:VAL:HG22	1:C:69:HIS:CE1	2.38	0.59
1:C:117:LEU:HD23	1:C:121:GLU:HG2	1.85	0.59
1:E:255:ILE:O	1:E:255:ILE:CG1	2.51	0.59
1:F:117:LEU:HD22	1:F:121:GLU:HG2	1.83	0.59
1:F:341:LEU:HD11	1:F:390:MET:HE3	1.85	0.59
1:F:415:TYR:CD2	1:F:481:ILE:HD13	2.37	0.59
1:H:121:GLU:N	1:H:121:GLU:OE1	2.32	0.59
1:H:174:THR:O	1:H:178:VAL:HG23	2.03	0.59
1:B:332:LEU:HD12	1:B:449:GLY:HA3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:466:LEU:HB3	1:D:490:ILE:HD12	1.85	0.59
1:G:292:VAL:HG23	1:G:293:GLU:N	2.18	0.59
1:G:400:ASP:CG	1:G:403:ILE:HG23	2.26	0.59
1:C:237:LEU:CD1	1:C:239:LEU:HB2	2.32	0.59
1:E:38:GLU:HB3	1:E:43:ALA:HB2	1.85	0.59
1:G:206:VAL:HG13	1:G:334:ALA:CA	2.33	0.59
1:A:323:PRO:HD3	1:A:430:ASN:OD1	2.03	0.59
1:E:151:ASP:O	1:E:239:LEU:HD23	2.03	0.59
1:G:154:ASP:O	1:G:221:LYS:HE3	2.02	0.59
1:G:331:ALA:CB	1:G:446:LYS:O	2.51	0.59
1:A:54:VAL:HG13	1:A:58:GLU:CB	2.33	0.58
1:C:280:ASP:O	1:C:282:PRO:HD3	2.01	0.58
1:D:414:THR:CG2	1:D:470:HIS:ND1	2.64	0.58
1:G:454:VAL:HG22	1:G:466:LEU:O	2.03	0.58
1:D:169:VAL:HG11	1:D:324:ILE:HD13	1.68	0.58
1:F:87:SER:HA	1:F:90:TYR:CD2	2.37	0.58
1:G:113:VAL:CG2	1:G:149:THR:HG21	2.28	0.58
1:G:164:HIS:ND1	1:G:165:SER:N	2.50	0.58
1:G:179:VAL:CB	1:G:180:PRO:HD3	2.31	0.58
1:G:237:LEU:HD11	1:G:239:LEU:CG	2.13	0.58
1:C:180:PRO:CG	1:C:390:MET:HE1	2.30	0.58
1:D:256:ASP:OD1	1:D:261:MET:HB2	2.03	0.58
1:H:451:GLU:O	1:H:467:PHE:HB2	2.03	0.58
1:G:193:SER:O	1:G:233:TRP:HD1	1.85	0.58
1:G:461:LYS:O	1:G:464:ASP:CG	2.46	0.58
1:C:174:THR:HG23	1:C:354:ALA:HB2	1.85	0.58
1:B:391:LYS:HB3	1:B:401:PRO:HB3	1.85	0.58
1:H:176:ILE:O	1:H:180:PRO:CG	2.52	0.58
1:C:20:ASN:HD22	1:C:23:ASP:N	1.97	0.58
1:B:177:LEU:HD23	1:B:341:LEU:HD21	1.86	0.58
1:D:29:LEU:HD13	1:D:48:VAL:HG21	1.85	0.58
1:D:242:ALA:O	1:D:246:THR:HG23	2.03	0.58
1:G:176:ILE:HG22	1:G:390:MET:HE1	1.86	0.58
1:A:237:LEU:C	1:A:237:LEU:HD12	2.29	0.58
1:A:488:GLU:OE1	1:A:488:GLU:HA	2.04	0.58
1:D:400:ASP:O	1:D:403:ILE:HG22	2.02	0.58
1:D:432:ALA:HB1	1:D:487:THR:HG22	1.81	0.58
1:E:179:VAL:CB	1:E:180:PRO:HD3	2.31	0.58
1:F:219:GLU:O	1:F:223:ILE:HG13	2.04	0.58
1:B:208:GLU:HA	1:B:211:ALA:O	2.03	0.58
1:D:179:VAL:HB	1:D:180:PRO:CD	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4:LYS:CA	1:E:75:GLU:O	2.49	0.58
1:E:394:ILE:HG22	1:E:399:GLY:C	2.29	0.58
1:G:173:LYS:NZ	1:G:336:GLU:OE1	2.33	0.58
1:G:415:TYR:HD2	1:G:417:PHE:CE2	2.19	0.57
1:B:64:ASP:O	1:B:67:ASP:OD1	2.22	0.57
1:B:266:MET:HG3	1:B:305:LEU:HD23	1.85	0.57
1:C:426:THR:CG2	1:C:493:GLU:HB2	2.34	0.57
1:F:146:MET:HE1	1:F:243:ASP:HA	1.86	0.57
1:C:35:VAL:HG11	1:C:48:VAL:HG21	1.85	0.57
1:E:144:ILE:HG12	1:E:309:LEU:CD2	2.34	0.57
1:E:445:ASP:CB	1:E:472:GLU:OE1	2.51	0.57
1:A:191:LYS:HE3	1:A:193:SER:OG	2.05	0.57
1:E:104:GLU:O	1:E:108:ILE:HG13	2.04	0.57
1:E:292:VAL:HG23	1:E:293:GLU:N	2.20	0.57
1:H:164:HIS:ND1	1:H:165:SER:N	2.53	0.57
1:H:187:LEU:HD21	1:H:367:VAL:HG23	1.87	0.57
1:A:151:ASP:O	1:A:239:LEU:HD23	2.03	0.57
1:D:44:VAL:HG21	1:D:69:HIS:CD2	2.40	0.57
1:E:8:LEU:CD1	1:E:18:LEU:CD1	2.80	0.57
1:E:14:ARG:NH1	1:E:119:ASP:OD2	2.30	0.57
1:G:113:VAL:HG21	1:G:149:THR:CG2	2.27	0.57
1:G:326:HIS:CD2	1:G:452:LEU:O	2.56	0.57
1:B:278:LEU:HD12	1:B:314:GLU:O	2.05	0.57
1:E:38:GLU:HB3	1:E:43:ALA:CB	2.35	0.57
1:H:414:THR:HG22	1:H:470:HIS:HA	1.86	0.57
1:C:180:PRO:HG2	1:C:390:MET:HE3	1.85	0.57
1:C:258:THR:O	1:C:262:LEU:HG	2.05	0.57
1:F:72:SER:O	1:F:75:GLU:CB	2.53	0.57
1:B:59:VAL:HG11	1:B:79:VAL:HG21	1.87	0.56
1:H:183:ALA:CB	1:H:389:LYS:HG2	2.34	0.56
1:H:415:TYR:HE2	1:H:417:PHE:CE1	2.23	0.56
1:A:173:LYS:HD2	1:A:336:GLU:OE1	2.05	0.56
1:D:66:LEU:O	1:D:69:HIS:O	2.22	0.56
1:G:44:VAL:HG22	1:G:69:HIS:CG	2.39	0.56
1:G:44:VAL:HG21	1:G:69:HIS:CG	2.40	0.56
1:G:331:ALA:HB3	1:G:446:LYS:O	2.04	0.56
1:B:14:ARG:HG3	1:B:16:THR:HG23	1.86	0.56
1:A:220:ILE:HD11	1:A:232:VAL:HG21	1.88	0.56
1:C:20:ASN:HD21	1:C:22:GLU:H	1.53	0.56
1:D:44:VAL:HG22	1:D:69:HIS:NE2	2.19	0.56
1:D:104:GLU:O	1:D:108:ILE:HG13	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:163:VAL:O	1:D:163:VAL:HG13	2.05	0.56
1:E:156:ASP:H	1:E:221:LYS:HE3	1.71	0.56
1:E:368:ALA:HB1	1:E:372:THR:OG1	2.04	0.56
1:F:35:VAL:HG13	1:F:48:VAL:CG2	2.35	0.56
1:G:280:ASP:O	1:G:282:PRO:HD3	2.05	0.56
1:H:6:ARG:HG3	1:H:73:GLU:OE2	2.05	0.56
1:H:335:ARG:HG2	1:H:408:ILE:HB	1.87	0.56
1:H:400:ASP:O	1:H:403:ILE:HG23	2.06	0.56
1:H:424:TYR:N	1:H:492:ILE:CG2	2.68	0.56
1:B:469:ILE:CG2	1:B:477:LEU:HD11	2.35	0.56
1:G:72:SER:O	1:G:75:GLU:CB	2.53	0.56
1:G:327:THR:HG23	1:G:336:GLU:OE2	2.05	0.56
1:B:151:ASP:O	1:B:239:LEU:CD2	2.54	0.56
1:B:237:LEU:HD12	1:B:237:LEU:C	2.30	0.56
1:B:400:ASP:O	1:B:403:ILE:HG23	2.05	0.56
1:D:129:LEU:HD13	1:D:134:LEU:HD11	1.87	0.56
1:D:177:LEU:CD2	1:D:341:LEU:HG	2.35	0.56
1:F:400:ASP:HB3	1:F:403:ILE:HG22	1.86	0.56
1:G:8:LEU:HD13	1:G:18:LEU:HD12	1.59	0.56
1:H:35:VAL:HG13	1:H:48:VAL:HG23	1.87	0.56
1:H:166:ILE:HG12	1:H:281:ILE:HA	1.87	0.56
1:H:353:LYS:O	1:H:357:LEU:HG	2.06	0.56
1:A:176:ILE:O	1:A:180:PRO:CD	2.54	0.56
1:A:342:MET:HE2	1:A:405:PRO:HG2	1.86	0.56
1:C:121:GLU:OE1	1:C:121:GLU:N	2.30	0.56
1:C:289:VAL:HG11	1:C:295:ALA:HB2	1.86	0.56
1:E:8:LEU:O	1:E:63:ARG:CG	2.52	0.56
1:F:487:THR:O	1:F:488:GLU:C	2.47	0.56
1:G:321:GLY:O	1:G:430:ASN:ND2	2.39	0.56
1:B:341:LEU:O	1:B:387:TRP:HB2	2.06	0.56
1:A:342:MET:CE	1:A:405:PRO:HD2	2.21	0.56
1:E:161:MET:HG2	1:E:188:THR:O	2.06	0.56
1:E:189:ILE:O	1:E:189:ILE:CG2	2.43	0.56
1:G:189:ILE:HG23	1:G:189:ILE:O	2.06	0.56
1:H:414:THR:HG21	1:H:470:HIS:CE1	2.40	0.56
1:A:250:GLU:OE1	1:A:260:LEU:HD23	2.06	0.56
1:C:166:ILE:CG1	1:C:282:PRO:HD2	2.36	0.56
1:E:18:LEU:HD22	1:E:51:SER:OG	2.05	0.56
1:F:331:ALA:HB3	1:F:446:LYS:O	2.06	0.56
1:H:180:PRO:CG	1:H:390:MET:HE2	2.34	0.56
1:H:241:PRO:O	1:H:245:ILE:HG13	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:44:VAL:CG1	1:D:45:TYR:N	2.69	0.55
1:D:181:ILE:HD11	1:D:381:LEU:HD13	1.88	0.55
1:G:24:ALA:O	1:G:28:LYS:N	2.35	0.55
1:C:299:ALA:O	1:C:303:ILE:HG13	2.06	0.55
1:F:189:ILE:HG23	1:F:189:ILE:O	2.06	0.55
1:G:170:PRO:HG3	1:G:434:THR:OG1	2.06	0.55
1:G:183:ALA:O	1:G:186:GLY:HA2	2.06	0.55
1:H:166:ILE:CD1	1:H:281:ILE:CG2	2.71	0.55
1:E:92:LYS:O	1:E:95:MET:HB3	2.06	0.55
1:G:177:LEU:HD22	1:G:341:LEU:HD23	1.88	0.55
1:G:413:LYS:C	1:G:414:THR:CG2	2.78	0.55
1:G:423:GLY:HA3	1:G:492:ILE:CG2	2.36	0.55
1:H:135:ASP:OD1	1:H:138:GLU:CG	2.54	0.55
1:H:189:ILE:HG23	1:H:189:ILE:O	2.07	0.55
1:H:206:VAL:CG1	1:H:334:ALA:HB2	2.36	0.55
1:B:242:ALA:O	1:B:246:THR:HG23	2.07	0.55
1:D:356:GLY:O	1:D:360:ILE:HG13	2.06	0.55
1:E:183:ALA:HB1	1:E:389:LYS:HE3	1.89	0.55
1:G:68:LEU:O	1:G:69:HIS:CD2	2.59	0.55
1:G:166:ILE:CG1	1:G:282:PRO:HD2	2.37	0.55
1:B:179:VAL:HG21	1:B:231:LEU:HD21	1.88	0.55
1:C:237:LEU:HD11	1:C:239:LEU:CB	2.36	0.55
1:E:192:THR:HA	1:E:232:VAL:O	2.06	0.55
1:F:191:LYS:HE3	1:F:193:SER:OG	2.06	0.55
1:F:237:LEU:C	1:F:237:LEU:HD12	2.32	0.55
1:G:223:ILE:HG23	1:G:396:ALA:HB1	1.89	0.55
1:B:237:LEU:CD1	1:B:239:LEU:CB	2.84	0.55
1:B:418:THR:HG22	1:B:465:PRO:HA	1.87	0.55
1:G:44:VAL:HG22	1:G:69:HIS:ND1	2.21	0.55
1:G:126:VAL:CG2	1:G:246:THR:HG23	2.37	0.55
1:B:12:SER:CB	1:B:16:THR:HG21	2.37	0.55
1:B:185:ALA:HB1	1:B:367:VAL:HG11	1.88	0.55
1:E:35:VAL:CG1	1:E:48:VAL:CG2	2.84	0.55
1:G:174:THR:O	1:G:178:VAL:CG2	2.44	0.55
1:B:114:ASP:O	1:B:115:ARG:HB2	2.06	0.55
1:E:253:LEU:O	1:E:255:ILE:HG23	2.07	0.55
1:B:170:PRO:HB2	1:B:323:PRO:HB3	1.89	0.55
1:A:331:ALA:CB	1:A:446:LYS:O	2.55	0.55
1:C:166:ILE:HG12	1:C:282:PRO:HD2	1.87	0.55
1:E:134:LEU:HD22	1:E:138:GLU:HB3	1.89	0.55
1:A:342:MET:CE	1:A:405:PRO:CG	2.85	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:160:ILE:CG2	1:D:274:SER:HA	2.37	0.55
1:B:105:ILE:O	1:B:109:VAL:HG23	2.06	0.54
1:D:10:MET:HA	1:H:51:SER:CB	2.37	0.54
1:D:29:LEU:HD21	1:D:81:PRO:HG3	1.88	0.54
1:E:35:VAL:HG13	1:E:48:VAL:HG23	1.88	0.54
1:E:319:TYR:CE1	1:E:321:GLY:CA	2.90	0.54
1:G:170:PRO:CD	1:G:430:ASN:OD1	2.55	0.54
1:H:291:THR:OG1	1:H:294:GLU:HB2	2.06	0.54
1:B:189:ILE:HG23	1:B:189:ILE:O	2.07	0.54
1:C:189:ILE:O	1:C:189:ILE:HG23	2.07	0.54
1:F:61:ILE:O	1:F:61:ILE:CG1	2.55	0.54
1:F:212:ASP:O	1:F:215:PHE:CE2	2.60	0.54
1:G:68:LEU:C	1:G:69:HIS:CD2	2.85	0.54
1:C:173:LYS:CD	1:C:336:GLU:OE1	2.54	0.54
1:G:341:LEU:CD1	1:G:390:MET:HE3	2.37	0.54
1:G:423:GLY:HA3	1:G:492:ILE:HG21	1.88	0.54
1:B:18:LEU:N	1:B:60:GLY:O	2.34	0.54
1:C:246:THR:CG2	1:C:260:LEU:HD21	2.34	0.54
1:C:400:ASP:OD1	1:C:402:ASN:N	2.33	0.54
1:D:445:ASP:HB3	1:D:472:GLU:OE1	2.07	0.54
1:H:175:ASN:HD22	1:H:191:LYS:HE2	1.71	0.54
1:F:400:ASP:OD1	1:F:402:ASN:N	2.39	0.54
1:G:255:ILE:CG1	1:G:255:ILE:O	2.56	0.54
1:D:11:PHE:N	1:H:50:LEU:O	2.40	0.54
1:D:155:ILE:HD13	1:D:224:VAL:HG11	1.90	0.54
1:G:341:LEU:O	1:G:387:TRP:HB2	2.08	0.54
1:A:360:ILE:O	1:A:364:MET:HG3	2.07	0.54
1:C:426:THR:HG21	1:C:493:GLU:HB2	1.90	0.54
1:C:467:PHE:CD2	1:C:490:ILE:HD12	2.43	0.54
1:G:159:PRO:HA	1:G:275:GLN:NE2	2.22	0.54
1:B:220:ILE:HD11	1:B:232:VAL:HG11	1.88	0.54
1:B:469:ILE:HG21	1:B:477:LEU:CD1	2.34	0.54
1:C:233:TRP:CD1	1:C:233:TRP:C	2.82	0.54
1:D:151:ASP:O	1:D:239:LEU:HD23	2.08	0.54
1:D:180:PRO:CG	1:D:390:MET:HE2	2.18	0.54
1:G:169:VAL:O	1:G:169:VAL:HG13	2.08	0.54
1:G:255:ILE:O	1:G:255:ILE:HG13	2.07	0.54
1:G:424:TYR:HA	1:G:458:GLU:O	2.07	0.54
1:B:432:ALA:HB1	1:B:487:THR:HG22	1.83	0.54
1:C:3:ALA:HB3	1:C:59:VAL:HG13	1.90	0.54
1:D:237:LEU:CD1	1:D:239:LEU:CB	2.85	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:224:VAL:O	1:E:228:GLY:N	2.41	0.54
1:F:111:ASP:HB3	1:F:117:LEU:HG	1.90	0.54
1:G:413:LYS:O	1:G:414:THR:HG22	2.07	0.54
1:C:283:THR:HA	1:C:289:VAL:O	2.08	0.53
1:D:189:ILE:HG23	1:D:189:ILE:O	2.08	0.53
1:E:44:VAL:HG22	1:E:69:HIS:CE1	2.43	0.53
1:E:54:VAL:O	1:E:54:VAL:HG13	2.08	0.53
1:F:90:TYR:CD1	1:F:104:GLU:HG2	2.43	0.53
1:G:166:ILE:HG12	1:G:282:PRO:HD2	1.90	0.53
1:H:166:ILE:HG12	1:H:282:PRO:CD	2.38	0.53
1:A:483:LEU:O	1:A:487:THR:HG23	2.09	0.53
1:C:171:GLY:O	1:C:173:LYS:NZ	2.41	0.53
1:F:202:GLY:H	1:F:205:ASP:HB2	1.71	0.53
1:G:176:ILE:O	1:G:180:PRO:CG	2.56	0.53
1:G:418:THR:HB	1:G:463:GLY:C	2.33	0.53
1:H:188:THR:HG23	1:H:228:GLY:O	2.08	0.53
1:A:121:GLU:CD	1:A:121:GLU:H	2.16	0.53
1:C:241:PRO:O	1:C:245:ILE:HG13	2.08	0.53
1:E:329:GLY:O	1:E:333:GLU:HG3	2.08	0.53
1:G:183:ALA:O	1:G:186:GLY:CA	2.56	0.53
1:H:305:LEU:HG	1:H:309:LEU:HD12	1.91	0.53
1:C:26:GLU:O	1:G:476:ARG:NH2	2.41	0.53
1:G:176:ILE:CG2	1:G:390:MET:HE1	2.39	0.53
1:H:394:ILE:O	1:H:397:GLN:CB	2.56	0.53
1:C:143:THR:HG21	1:C:309:LEU:HD11	1.91	0.53
1:C:305:LEU:HD12	1:C:305:LEU:O	2.08	0.53
1:D:436:ILE:O	1:D:439:ALA:HB3	2.08	0.53
1:F:67:ASP:OD1	1:F:68:LEU:N	2.41	0.53
1:F:192:THR:HG22	1:F:232:VAL:HG23	1.90	0.53
1:H:175:ASN:ND2	1:H:191:LYS:HE2	2.24	0.53
1:B:161:MET:O	1:B:189:ILE:HG13	2.09	0.53
1:B:173:LYS:CE	1:B:333:GLU:HG2	2.35	0.53
1:B:281:ILE:CD1	1:B:298:LEU:HD23	2.35	0.53
1:A:212:ASP:O	1:A:215:PHE:CE2	2.59	0.53
1:D:44:VAL:HG21	1:D:69:HIS:CG	2.44	0.53
1:G:59:VAL:O	1:G:59:VAL:HG13	2.08	0.53
1:B:170:PRO:CD	1:B:430:ASN:ND2	2.72	0.53
1:E:169:VAL:HG13	1:E:169:VAL:O	2.08	0.53
1:G:341:LEU:CD1	1:G:390:MET:HG2	2.33	0.53
1:G:416:THR:HG22	1:G:417:PHE:N	2.22	0.53
1:H:227:VAL:O	1:H:389:LYS:NZ	2.28	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:391:LYS:HD2	1:H:401:PRO:HB3	1.90	0.53
1:B:212:ASP:O	1:B:215:PHE:HE2	1.91	0.53
1:B:426:THR:HG21	1:B:493:GLU:HB2	1.91	0.53
1:E:224:VAL:O	1:E:228:GLY:CA	2.57	0.53
1:F:319:TYR:CE1	1:F:321:GLY:HA3	2.44	0.53
1:H:166:ILE:HG12	1:H:282:PRO:HD2	1.87	0.53
1:H:240:ALA:N	1:H:241:PRO:CD	2.72	0.53
1:C:173:LYS:CE	1:C:336:GLU:OE1	2.56	0.52
1:D:135:ASP:OD1	1:D:135:ASP:C	2.51	0.52
1:E:122:ILE:CD1	1:E:245:ILE:HG22	2.40	0.52
1:H:157:ARG:O	1:H:160:ILE:HD11	2.09	0.52
1:D:155:ILE:HD12	1:D:224:VAL:HG11	1.90	0.52
1:G:237:LEU:CD1	1:G:239:LEU:CB	2.86	0.52
1:G:355:THR:O	1:G:359:GLY:N	2.35	0.52
1:H:44:VAL:HG22	1:H:45:TYR:N	2.24	0.52
1:B:102:LYS:O	1:B:106:GLU:HG3	2.09	0.52
1:C:59:VAL:O	1:C:59:VAL:HG23	2.07	0.52
1:G:179:VAL:HG21	1:G:231:LEU:CD2	2.39	0.52
1:G:215:PHE:C	1:G:220:ILE:CD1	2.65	0.52
1:H:188:THR:HA	1:H:228:GLY:O	2.10	0.52
1:D:335:ARG:O	1:D:339:SER:OG	2.22	0.52
1:E:155:ILE:HA	1:E:221:LYS:CE	2.38	0.52
1:F:423:GLY:HA3	1:F:492:ILE:HG23	1.91	0.52
1:G:27:ALA:O	1:G:28:LYS:CB	2.56	0.52
1:B:166:ILE:CD1	1:B:281:ILE:HG23	2.37	0.52
1:D:135:ASP:HB3	1:D:138:GLU:OE1	2.10	0.52
1:E:18:LEU:N	1:E:60:GLY:O	2.34	0.52
1:G:29:LEU:HD13	1:G:48:VAL:HG21	1.91	0.52
1:G:446:LYS:N	1:G:446:LYS:CD	2.65	0.52
1:A:18:LEU:N	1:A:60:GLY:O	2.29	0.52
1:G:224:VAL:O	1:G:228:GLY:N	2.38	0.52
1:G:327:THR:OG1	1:G:336:GLU:OE1	2.27	0.52
1:C:400:ASP:OD1	1:C:402:ASN:HB2	2.10	0.52
1:E:35:VAL:HG13	1:E:48:VAL:CG2	2.40	0.52
1:E:94:LYS:HB2	1:E:100:LEU:HD11	1.92	0.52
1:G:319:TYR:CZ	1:G:321:GLY:HA3	2.44	0.52
1:G:461:LYS:N	1:G:464:ASP:OD2	2.38	0.52
1:A:166:ILE:CD1	1:A:281:ILE:HG23	2.39	0.52
1:A:426:THR:HG21	1:A:493:GLU:HB2	1.92	0.52
1:D:178:VAL:O	1:D:182:VAL:HG23	2.09	0.52
1:F:425:VAL:O	1:F:425:VAL:HG12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:246:THR:CG2	1:G:260:LEU:HD21	2.32	0.52
1:G:363:GLU:HG3	1:G:373:GLY:HA3	1.92	0.52
1:G:423:GLY:O	1:G:460:VAL:N	2.35	0.52
1:H:210:PHE:CD2	1:H:338:LEU:HD11	2.44	0.52
1:D:3:ALA:HB3	1:D:59:VAL:HG13	1.92	0.52
1:E:155:ILE:HD13	1:E:224:VAL:CG2	2.38	0.52
1:G:452:LEU:CD2	1:G:467:PHE:HB2	2.27	0.52
1:B:101:ARG:HB2	1:B:104:GLU:HG3	1.92	0.52
1:A:44:VAL:HG22	1:A:45:TYR:N	2.25	0.52
1:C:292:VAL:HG23	1:C:293:GLU:N	2.25	0.52
1:D:5:ILE:HA	1:D:59:VAL:HG23	1.92	0.52
1:D:192:THR:HA	1:D:232:VAL:O	2.10	0.52
1:D:253:LEU:O	1:D:255:ILE:HG23	2.09	0.52
1:E:59:VAL:O	1:E:59:VAL:CG1	2.58	0.52
1:G:178:VAL:HA	1:G:181:ILE:HD12	1.91	0.52
1:G:477:LEU:HD12	1:G:477:LEU:C	2.33	0.52
1:A:189:ILE:HG23	1:A:189:ILE:O	2.10	0.51
1:C:117:LEU:CD2	1:C:121:GLU:HG2	2.39	0.51
1:C:296:ARG:O	1:C:300:ARG:HG3	2.10	0.51
1:E:54:VAL:O	1:E:54:VAL:CG1	2.58	0.51
1:F:171:GLY:O	1:F:173:LYS:NZ	2.34	0.51
1:G:95:MET:HE2	1:G:124:SER:OG	2.11	0.51
1:G:488:GLU:N	1:G:489:PRO:CD	2.73	0.51
1:H:163:VAL:HB	1:H:361:LEU:HD11	1.92	0.51
1:H:233:TRP:CE2	1:H:235:GLY:HA3	2.45	0.51
1:A:32:ASP:N	1:A:48:VAL:O	2.25	0.51
1:D:237:LEU:CD1	1:D:239:LEU:HB2	2.41	0.51
1:G:112:ILE:HG23	1:G:122:ILE:HD11	1.92	0.51
1:B:331:ALA:CB	1:B:446:LYS:O	2.59	0.51
1:C:59:VAL:HG11	1:C:79:VAL:CG2	2.38	0.51
1:C:169:VAL:HG21	1:C:282:PRO:HB3	1.92	0.51
1:E:144:ILE:CG1	1:E:309:LEU:CD2	2.87	0.51
1:E:278:LEU:HD13	1:E:360:ILE:CG2	2.40	0.51
1:A:237:LEU:CD1	1:A:239:LEU:CB	2.88	0.51
1:D:187:LEU:CD1	1:D:365:GLY:HA3	2.41	0.51
1:F:87:SER:HA	1:F:90:TYR:HD2	1.75	0.51
1:F:129:LEU:HD22	1:F:134:LEU:HG	1.92	0.51
1:F:169:VAL:HG21	1:F:282:PRO:HB3	1.91	0.51
1:H:166:ILE:HD13	1:H:281:ILE:CG2	2.24	0.51
1:A:114:ASP:O	1:A:115:ARG:CB	2.56	0.51
1:C:102:LYS:O	1:C:106:GLU:HG3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:400:ASP:O	1:E:403:ILE:CG2	2.52	0.51
1:G:143:THR:OG1	1:G:263:ALA:HA	2.10	0.51
1:G:206:VAL:HG13	1:G:334:ALA:CB	2.40	0.51
1:G:215:PHE:CB	1:G:220:ILE:HD11	2.41	0.51
1:G:354:ALA:O	1:G:358:ALA:CB	2.59	0.51
1:H:100:LEU:N	1:H:138:GLU:OE2	2.38	0.51
1:H:117:LEU:CD2	1:H:121:GLU:CG	2.88	0.51
1:H:206:VAL:HG13	1:H:334:ALA:HB2	1.91	0.51
1:H:305:LEU:HG	1:H:309:LEU:CD1	2.40	0.51
1:A:20:ASN:OD1	1:A:20:ASN:C	2.54	0.51
1:C:432:ALA:O	1:C:436:ILE:HG13	2.10	0.51
1:D:212:ASP:O	1:D:215:PHE:CE2	2.60	0.51
1:D:394:ILE:HG23	1:D:399:GLY:HA3	1.92	0.51
1:E:155:ILE:O	1:E:156:ASP:C	2.48	0.51
1:G:164:HIS:CD2	1:G:265:ILE:HG23	2.45	0.51
1:G:327:THR:OG1	1:G:336:GLU:CD	2.53	0.51
1:H:61:ILE:O	1:H:61:ILE:CG1	2.58	0.51
1:H:292:VAL:HG23	1:H:293:GLU:N	2.25	0.51
1:B:17:VAL:HA	1:B:60:GLY:O	2.10	0.51
1:A:237:LEU:CD1	1:A:239:LEU:HB2	2.41	0.51
1:D:8:LEU:HD13	1:D:18:LEU:HD11	1.91	0.51
1:H:360:ILE:HG22	1:H:364:MET:SD	2.51	0.51
1:C:329:GLY:N	1:C:333:GLU:OE2	2.37	0.51
1:E:176:ILE:O	1:E:180:PRO:CD	2.54	0.51
1:E:180:PRO:HG2	1:E:390:MET:HE3	1.93	0.51
1:F:94:LYS:O	1:F:94:LYS:HD3	2.11	0.51
1:F:227:VAL:O	1:F:389:LYS:CE	2.58	0.51
1:F:436:ILE:CG2	1:F:450:ILE:HD11	2.41	0.51
1:G:55:GLY:O	1:G:58:GLU:HB2	2.10	0.51
1:G:334:ALA:O	1:G:338:LEU:HG	2.11	0.51
1:H:30:HIS:N	1:H:33:ASP:OD2	2.43	0.51
1:H:426:THR:HG21	1:H:493:GLU:HB2	1.91	0.51
1:C:20:ASN:ND2	1:C:22:GLU:CB	2.73	0.51
1:C:415:TYR:CD2	1:C:481:ILE:HD13	2.46	0.51
1:D:324:ILE:N	1:D:324:ILE:HD12	2.26	0.51
1:D:445:ASP:CB	1:D:472:GLU:OE1	2.59	0.51
1:E:117:LEU:CD2	1:E:121:GLU:CG	2.88	0.51
1:G:215:PHE:CA	1:G:220:ILE:HD11	2.40	0.51
1:B:134:LEU:HD22	1:B:138:GLU:HB3	1.93	0.51
1:C:173:LYS:NZ	1:C:336:GLU:OE1	2.43	0.51
1:C:418:THR:HA	1:C:464:ASP:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:461:LYS:N	1:D:464:ASP:OD2	2.44	0.51
1:E:292:VAL:CG2	1:E:293:GLU:N	2.74	0.51
1:H:368:ALA:HB2	1:H:376:MET:SD	2.51	0.51
1:C:191:LYS:HE3	1:C:193:SER:OG	2.11	0.50
1:D:129:LEU:HD12	1:D:260:LEU:HD22	1.92	0.50
1:D:237:LEU:C	1:D:237:LEU:HD12	2.37	0.50
1:E:18:LEU:CD2	1:E:49:ALA:HB3	2.38	0.50
1:E:154:ASP:O	1:E:221:LYS:CD	2.56	0.50
1:G:164:HIS:O	1:G:280:ASP:N	2.38	0.50
1:G:165:SER:HB2	1:G:280:ASP:HB3	1.91	0.50
1:G:220:ILE:O	1:G:224:VAL:HG23	2.11	0.50
1:H:166:ILE:HD11	1:H:281:ILE:CG2	2.36	0.50
1:H:477:LEU:HD12	1:H:477:LEU:O	2.11	0.50
1:B:32:ASP:N	1:B:48:VAL:O	2.32	0.50
1:A:177:LEU:HD22	1:A:341:LEU:HG	1.92	0.50
1:A:196:ALA:HB2	1:A:201:ALA:C	2.36	0.50
1:A:399:GLY:O	1:A:401:PRO:CD	2.55	0.50
1:C:448:ALA:HA	1:C:470:HIS:O	2.11	0.50
1:E:332:LEU:HD12	1:E:449:GLY:HA3	1.93	0.50
1:F:183:ALA:O	1:F:186:GLY:N	2.43	0.50
1:H:8:LEU:HD13	1:H:18:LEU:HD11	1.90	0.50
1:H:118:ARG:O	1:H:122:ILE:HG13	2.11	0.50
1:B:390:MET:O	1:B:394:ILE:HG13	2.10	0.50
1:F:35:VAL:HG11	1:F:48:VAL:CG2	2.41	0.50
1:F:227:VAL:O	1:F:389:LYS:NZ	2.43	0.50
1:G:127:THR:O	1:G:131:ILE:HG13	2.11	0.50
1:G:177:LEU:CD2	1:G:341:LEU:HD21	2.41	0.50
1:G:415:TYR:CE2	1:G:417:PHE:CD1	2.87	0.50
1:G:447:GLY:HA3	1:G:472:GLU:OE2	2.12	0.50
1:A:54:VAL:CG1	1:A:58:GLU:O	2.59	0.50
1:A:400:ASP:CB	1:A:403:ILE:CG2	2.87	0.50
1:D:10:MET:CB	1:H:51:SER:CB	2.87	0.50
1:G:9:ASP:C	1:G:9:ASP:OD1	2.55	0.50
1:D:163:VAL:O	1:D:163:VAL:CG1	2.59	0.50
1:E:154:ASP:O	1:E:221:LYS:NZ	2.41	0.50
1:E:164:HIS:HB3	1:E:279:ILE:HD13	1.92	0.50
1:G:250:GLU:OE1	1:G:256:ASP:OD1	2.30	0.50
1:G:474:GLU:O	1:G:478:ASP:OD1	2.30	0.50
1:B:332:LEU:CD1	1:B:449:GLY:HA3	2.41	0.50
1:A:165:SER:C	1:A:167:GLY:N	2.70	0.50
1:C:66:LEU:O	1:C:69:HIS:O	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:9:ASP:C	1:H:51:SER:HB2	2.33	0.50
1:E:127:THR:O	1:E:131:ILE:HG13	2.11	0.50
1:F:32:ASP:O	1:F:32:ASP:OD1	2.30	0.50
1:H:164:HIS:NE2	1:H:265:ILE:HG23	2.27	0.50
1:B:12:SER:CB	1:B:16:THR:CG2	2.89	0.50
1:B:326:HIS:HB3	1:B:452:LEU:O	2.11	0.50
1:A:483:LEU:O	1:A:487:THR:OG1	2.30	0.50
1:C:170:PRO:HB2	1:C:323:PRO:HB3	1.94	0.50
1:C:332:LEU:HD12	1:C:449:GLY:HA3	1.94	0.50
1:E:61:ILE:O	1:E:61:ILE:HG13	2.11	0.50
1:E:173:LYS:CE	1:E:333:GLU:HG2	2.41	0.50
1:F:330:PRO:HG2	1:F:446:LYS:HA	1.92	0.50
1:G:191:LYS:HB3	1:G:231:LEU:HD23	1.93	0.50
1:G:323:PRO:HD3	1:G:430:ASN:OD1	2.10	0.50
1:H:54:VAL:HG11	1:H:58:GLU:O	2.12	0.50
1:H:117:LEU:CD2	1:H:121:GLU:CB	2.86	0.50
1:H:328:VAL:HG12	1:H:329:GLY:N	2.26	0.50
1:H:391:LYS:HD2	1:H:401:PRO:CB	2.42	0.50
1:B:9:ASP:O	1:B:9:ASP:OD1	2.30	0.50
1:A:192:THR:O	1:A:192:THR:OG1	2.30	0.50
1:C:24:ALA:HB1	1:C:50:LEU:HD21	1.94	0.50
1:G:117:LEU:HD22	1:G:121:GLU:CB	2.42	0.50
1:G:342:MET:HE2	1:G:405:PRO:HG2	1.92	0.50
1:H:66:LEU:O	1:H:69:HIS:O	2.30	0.50
1:B:134:LEU:HD22	1:B:138:GLU:CB	2.42	0.50
1:B:176:ILE:HG23	1:B:390:MET:HE1	1.93	0.50
1:C:174:THR:CG2	1:C:354:ALA:HB2	2.42	0.50
1:E:224:VAL:O	1:E:228:GLY:HA2	2.11	0.50
1:H:255:ILE:HG13	1:H:255:ILE:O	2.11	0.50
1:B:92:LYS:O	1:B:95:MET:CB	2.59	0.49
1:A:379:GLU:O	1:A:383:SER:CB	2.60	0.49
1:E:202:GLY:O	1:E:206:VAL:HG23	2.12	0.49
1:F:215:PHE:CD2	1:F:232:VAL:HG12	2.46	0.49
1:G:99:LYS:HD2	1:G:135:ASP:OD2	2.12	0.49
1:G:206:VAL:CG1	1:G:334:ALA:HA	2.42	0.49
1:C:419:ALA:N	1:C:464:ASP:O	2.42	0.49
1:B:477:LEU:O	1:B:481:ILE:HG13	2.12	0.49
1:A:224:VAL:O	1:A:228:GLY:N	2.44	0.49
1:C:104:GLU:O	1:C:108:ILE:HG13	2.12	0.49
1:D:114:ASP:C	1:D:115:ARG:HG2	2.36	0.49
1:D:169:VAL:CG1	1:D:324:ILE:HD12	2.39	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:191:LYS:CE	1:D:193:SER:OG	2.48	0.49
1:E:9:ASP:O	1:E:9:ASP:OD1	2.30	0.49
1:G:177:LEU:C	1:G:181:ILE:CD1	2.78	0.49
1:D:35:VAL:HG13	1:D:48:VAL:HG23	1.93	0.49
1:D:72:SER:O	1:D:75:GLU:CB	2.60	0.49
1:G:233:TRP:CD1	1:G:235:GLY:H	2.30	0.49
1:H:374:LYS:HA	1:H:377:ALA:HB3	1.93	0.49
1:A:9:ASP:OD1	1:A:9:ASP:O	2.30	0.49
1:C:335:ARG:HG2	1:C:408:ILE:HB	1.94	0.49
1:D:461:LYS:O	1:D:464:ASP:OD2	2.30	0.49
1:F:280:ASP:O	1:F:282:PRO:HD3	2.11	0.49
1:G:44:VAL:HG22	1:G:69:HIS:CD2	2.48	0.49
1:H:64:ASP:O	1:H:67:ASP:OD1	2.30	0.49
1:D:296:ARG:O	1:D:300:ARG:HG3	2.12	0.49
1:F:368:ALA:HB2	1:F:376:MET:SD	2.51	0.49
1:G:233:TRP:CE2	1:G:235:GLY:HA3	2.48	0.49
1:H:129:LEU:O	1:H:133:GLY:N	2.43	0.49
1:G:176:ILE:O	1:G:180:PRO:CD	2.61	0.49
1:G:477:LEU:O	1:G:481:ILE:HG13	2.11	0.49
1:H:179:VAL:CB	1:H:180:PRO:CD	2.80	0.49
1:H:309:LEU:CB	1:H:311:GLN:OE1	2.61	0.49
1:A:129:LEU:HD12	1:A:260:LEU:HD13	1.95	0.49
1:A:151:ASP:HB3	1:A:217:LEU:CD1	2.42	0.49
1:A:369:PRO:O	1:A:372:THR:OG1	2.28	0.49
1:C:177:LEU:HD23	1:C:341:LEU:HG	1.95	0.49
1:D:170:PRO:HD2	1:D:430:ASN:ND2	2.28	0.49
1:D:280:ASP:O	1:D:282:PRO:HD3	2.12	0.49
1:G:100:LEU:HB3	1:G:105:ILE:HG13	1.94	0.49
1:H:35:VAL:HG22	1:H:46:GLY:O	2.13	0.49
1:A:54:VAL:HG11	1:A:58:GLU:C	2.37	0.49
1:A:220:ILE:CD1	1:A:232:VAL:HG21	2.41	0.49
1:C:134:LEU:HD23	1:C:138:GLU:CD	2.38	0.49
1:C:471:ALA:HB3	1:C:477:LEU:HB2	1.94	0.49
1:D:114:ASP:O	1:D:115:ARG:CG	2.60	0.49
1:D:394:ILE:HG22	1:D:399:GLY:C	2.37	0.49
1:E:184:ALA:C	1:E:186:GLY:N	2.71	0.49
1:E:414:THR:HA	1:E:469:ILE:O	2.13	0.49
1:G:129:LEU:HD22	1:G:134:LEU:HG	1.95	0.49
1:G:394:ILE:HG22	1:G:399:GLY:CA	2.41	0.49
1:H:202:GLY:O	1:H:206:VAL:HG23	2.12	0.49
1:B:16:THR:OG1	1:B:62:SER:HB3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:ILE:HD11	1:F:95:MET:HG3	1.95	0.49
1:A:176:ILE:O	1:A:180:PRO:HD2	2.13	0.49
1:A:484:ALA:CA	1:A:487:THR:OG1	2.59	0.49
1:C:135:ASP:O	1:C:139:ILE:HG13	2.13	0.49
1:D:26:GLU:O	1:H:476:ARG:NH2	2.45	0.49
1:E:342:MET:HE1	1:E:405:PRO:CG	2.42	0.49
1:F:114:ASP:O	1:F:115:ARG:HB2	2.11	0.49
1:G:9:ASP:OD1	1:G:9:ASP:O	2.30	0.49
1:H:180:PRO:CG	1:H:390:MET:HE1	2.35	0.49
1:B:170:PRO:HG2	1:B:430:ASN:OD1	2.13	0.48
1:A:135:ASP:O	1:A:139:ILE:HG13	2.13	0.48
1:E:330:PRO:HG2	1:E:446:LYS:HA	1.94	0.48
1:E:359:GLY:O	1:E:363:GLU:HG3	2.13	0.48
1:F:243:ASP:O	1:F:247:ILE:CG1	2.58	0.48
1:G:114:ASP:O	1:G:115:ARG:HB2	2.13	0.48
1:H:54:VAL:CG1	1:H:58:GLU:O	2.61	0.48
1:H:253:LEU:O	1:H:254:SER:CB	2.61	0.48
1:H:436:ILE:CG2	1:H:469:ILE:HD11	2.38	0.48
1:B:203:THR:O	1:B:207:VAL:HG23	2.12	0.48
1:D:183:ALA:HB2	1:D:229:ALA:HB2	1.95	0.48
1:D:190:PRO:HB3	1:D:224:VAL:HG21	1.95	0.48
1:F:175:ASN:ND2	1:F:191:LYS:HE2	2.28	0.48
1:G:416:THR:CG2	1:G:417:PHE:N	2.75	0.48
1:B:14:ARG:CG	1:B:16:THR:HG23	2.43	0.48
1:A:72:SER:O	1:A:75:GLU:CB	2.62	0.48
1:C:161:MET:O	1:C:189:ILE:HG13	2.13	0.48
1:C:246:THR:O	1:C:250:GLU:HG3	2.13	0.48
1:D:43:ALA:O	1:D:44:VAL:HG23	2.14	0.48
1:E:483:LEU:O	1:E:487:THR:OG1	2.24	0.48
1:F:17:VAL:HA	1:F:60:GLY:O	2.13	0.48
1:F:400:ASP:C	1:F:400:ASP:OD1	2.56	0.48
1:G:12:SER:CB	1:G:16:THR:OG1	2.61	0.48
1:G:163:VAL:HG23	1:G:278:LEU:HD23	1.94	0.48
1:H:95:MET:HE2	1:H:124:SER:OG	2.13	0.48
1:H:102:LYS:O	1:H:106:GLU:HG3	2.13	0.48
1:B:176:ILE:O	1:B:180:PRO:CD	2.60	0.48
1:A:400:ASP:CB	1:A:403:ILE:HG22	2.38	0.48
1:D:169:VAL:HG21	1:D:282:PRO:HB3	1.94	0.48
1:E:405:PRO:O	1:E:408:ILE:HG13	2.12	0.48
1:G:177:LEU:CD2	1:G:341:LEU:CD2	2.88	0.48
1:H:14:ARG:HB3	1:H:14:ARG:NH1	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:160:ILE:CG2	1:H:274:SER:HA	2.43	0.48
1:B:9:ASP:OD1	1:B:9:ASP:C	2.56	0.48
1:D:43:ALA:C	1:D:44:VAL:HG23	2.38	0.48
1:E:360:ILE:O	1:E:364:MET:HG3	2.13	0.48
1:F:492:ILE:O	1:F:493:GLU:HG3	2.13	0.48
1:H:258:THR:O	1:H:262:LEU:HG	2.14	0.48
1:A:170:PRO:CG	1:A:430:ASN:HB3	2.44	0.48
1:D:169:VAL:HG12	1:D:324:ILE:CD1	2.36	0.48
1:F:37:ILE:HG12	1:F:79:VAL:HG22	1.96	0.48
1:G:32:ASP:O	1:G:118:ARG:NH1	2.22	0.48
1:A:134:LEU:HD22	1:A:138:GLU:HB3	1.95	0.48
1:A:200:ALA:HB2	1:A:434:THR:HG23	1.95	0.48
1:D:51:SER:HB2	1:H:9:ASP:O	2.13	0.48
1:E:121:GLU:OE1	1:E:121:GLU:N	2.41	0.48
1:E:342:MET:CE	1:E:405:PRO:CG	2.91	0.48
1:F:54:VAL:CG1	1:F:58:GLU:HB2	2.43	0.48
1:H:99:LYS:HG3	1:H:138:GLU:OE2	2.14	0.48
1:B:358:ALA:O	1:B:362:LEU:HG	2.13	0.48
1:C:39:ALA:HB2	1:C:77:VAL:CB	2.44	0.48
1:C:202:GLY:O	1:C:206:VAL:HG23	2.14	0.48
1:D:319:TYR:CZ	1:D:321:GLY:HA3	2.48	0.48
1:B:176:ILE:HG23	1:B:390:MET:CE	2.43	0.48
1:D:59:VAL:CG1	1:D:79:VAL:HG21	2.41	0.48
1:E:363:GLU:OE1	1:E:370:ALA:HA	2.13	0.48
1:G:73:GLU:HG3	1:G:74:GLY:N	2.28	0.48
1:H:175:ASN:CB	1:H:191:LYS:HE2	2.42	0.48
1:D:44:VAL:CG2	1:D:69:HIS:ND1	2.76	0.48
1:D:101:ARG:HB2	1:D:104:GLU:OE1	2.14	0.48
1:H:163:VAL:HG13	1:H:163:VAL:O	2.13	0.48
1:H:339:SER:O	1:H:343:THR:HG23	2.14	0.48
1:B:483:LEU:O	1:B:487:THR:OG1	2.30	0.47
1:C:114:ASP:O	1:C:115:ARG:HB2	2.14	0.47
1:C:164:HIS:CE1	1:C:265:ILE:CD1	2.78	0.47
1:D:135:ASP:CB	1:D:138:GLU:OE1	2.61	0.47
1:E:174:THR:O	1:E:178:VAL:HG23	2.14	0.47
1:F:31:PRO:O	1:F:32:ASP:HB3	2.14	0.47
1:G:388:GLU:O	1:G:391:LYS:HB2	2.14	0.47
1:G:473:HIS:HB2	1:G:476:ARG:CB	2.27	0.47
1:H:114:ASP:O	1:H:115:ARG:HB2	2.14	0.47
1:C:169:VAL:CG2	1:C:282:PRO:HB3	2.44	0.47
1:D:109:VAL:O	1:D:113:VAL:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:156:ASP:N	1:E:221:LYS:HE3	2.28	0.47
1:G:159:PRO:CA	1:G:275:GLN:HE21	2.27	0.47
1:G:163:VAL:O	1:G:163:VAL:CG1	2.62	0.47
1:B:31:PRO:HG3	1:B:50:LEU:HG	1.95	0.47
1:B:220:ILE:CD1	1:B:232:VAL:HG11	2.45	0.47
1:C:203:THR:O	1:C:207:VAL:CG2	2.41	0.47
1:C:253:LEU:O	1:C:255:ILE:HG23	2.14	0.47
1:D:10:MET:HA	1:H:51:SER:HB3	1.96	0.47
1:D:161:MET:O	1:D:189:ILE:HG13	2.13	0.47
1:F:54:VAL:HG13	1:F:58:GLU:HB2	1.95	0.47
1:F:166:ILE:CD1	1:F:281:ILE:HG23	2.45	0.47
1:G:183:ALA:C	1:G:186:GLY:H	2.22	0.47
1:H:328:VAL:O	1:H:332:LEU:HD12	2.14	0.47
1:H:369:PRO:O	1:H:372:THR:OG1	2.30	0.47
1:H:414:THR:HA	1:H:469:ILE:O	2.14	0.47
1:B:94:LYS:HD3	1:B:94:LYS:C	2.39	0.47
1:B:437:ALA:HB2	1:B:450:ILE:HD12	1.97	0.47
1:A:163:VAL:HB	1:A:361:LEU:HD11	1.96	0.47
1:D:185:ALA:CB	1:D:362:LEU:HD21	2.45	0.47
1:G:126:VAL:HG21	1:G:246:THR:HG23	1.95	0.47
1:B:54:VAL:HG13	1:B:54:VAL:O	2.14	0.47
1:D:233:TRP:CD1	1:D:235:GLY:H	2.32	0.47
1:D:375:LYS:O	1:D:379:GLU:HG3	2.15	0.47
1:F:183:ALA:HB3	1:F:389:LYS:HG2	1.97	0.47
1:F:490:ILE:HG22	1:F:492:ILE:CD1	2.44	0.47
1:G:175:ASN:HD22	1:G:191:LYS:CE	2.22	0.47
1:E:179:VAL:CB	1:E:180:PRO:CD	2.89	0.47
1:F:276:TYR:HB3	1:F:364:MET:HE2	1.97	0.47
1:G:240:ALA:N	1:G:241:PRO:HD3	2.29	0.47
1:G:492:ILE:HG22	1:G:493:GLU:N	2.29	0.47
1:H:215:PHE:HD2	1:H:232:VAL:HG11	1.80	0.47
1:H:328:VAL:O	1:H:332:LEU:HB2	2.15	0.47
1:B:135:ASP:OD1	1:B:136:MET:N	2.48	0.47
1:B:471:ALA:CB	1:B:477:LEU:HB2	2.44	0.47
1:A:331:ALA:HB2	1:A:446:LYS:O	2.15	0.47
1:D:418:THR:HA	1:D:464:ASP:O	2.15	0.47
1:E:92:LYS:O	1:E:95:MET:CB	2.62	0.47
1:E:117:LEU:HD22	1:E:121:GLU:CG	2.44	0.47
1:E:169:VAL:CG1	1:E:169:VAL:O	2.63	0.47
1:E:314:GLU:OE1	1:E:364:MET:SD	2.72	0.47
1:F:418:THR:HA	1:F:465:PRO:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:211:ALA:HB2	1:G:394:ILE:HG23	1.96	0.47
1:H:265:ILE:HD12	1:H:302:PHE:CZ	2.44	0.47
1:A:11:PHE:HD1	1:A:64:ASP:OD1	1.96	0.47
1:A:237:LEU:HD12	1:A:237:LEU:O	2.15	0.47
1:A:255:ILE:O	1:A:255:ILE:CG1	2.62	0.47
1:D:179:VAL:HB	1:D:180:PRO:HD3	1.97	0.47
1:D:237:LEU:HD11	1:D:239:LEU:HB2	1.96	0.47
1:E:192:THR:OG1	1:E:192:THR:O	2.30	0.47
1:G:166:ILE:CD1	1:G:289:VAL:HG23	2.37	0.47
1:H:152:MET:HE2	1:H:271:ALA:HA	1.95	0.47
1:B:170:PRO:HG3	1:B:430:ASN:HB3	1.91	0.47
1:A:237:LEU:HD11	1:A:239:LEU:HB2	1.96	0.47
1:D:135:ASP:HB3	1:D:138:GLU:CD	2.40	0.47
1:D:335:ARG:HG2	1:D:408:ILE:HB	1.97	0.47
1:E:44:VAL:HG12	1:E:45:TYR:N	2.29	0.47
1:B:489:PRO:C	1:B:490:ILE:HD12	2.40	0.47
1:D:172:ASN:C	1:D:174:THR:H	2.22	0.47
1:D:394:ILE:CG2	1:D:399:GLY:C	2.88	0.47
1:E:144:ILE:HD11	1:E:309:LEU:HD23	1.96	0.47
1:G:135:ASP:OD1	1:G:138:GLU:CG	2.45	0.47
1:G:341:LEU:CD1	1:G:390:MET:CE	2.92	0.47
1:G:492:ILE:O	1:G:493:GLU:HG3	2.14	0.47
1:D:10:MET:CA	1:H:51:SER:HB3	2.43	0.46
1:F:214:SER:O	1:F:215:PHE:CG	2.68	0.46
1:G:488:GLU:OE1	1:G:488:GLU:HA	2.15	0.46
1:H:164:HIS:CD2	1:H:265:ILE:HG23	2.51	0.46
1:H:191:LYS:N	1:H:230:CYS:O	2.40	0.46
1:A:172:ASN:OD1	1:A:174:THR:HB	2.15	0.46
1:C:208:GLU:HA	1:C:211:ALA:O	2.15	0.46
1:D:10:MET:CA	1:H:51:SER:CB	2.93	0.46
1:D:44:VAL:CG2	1:D:69:HIS:NE2	2.77	0.46
1:F:35:VAL:CG1	1:F:48:VAL:HG23	2.38	0.46
1:F:220:ILE:CD1	1:F:232:VAL:HG21	2.45	0.46
1:G:44:VAL:CG2	1:G:69:HIS:CD2	2.98	0.46
1:G:448:ALA:HA	1:G:470:HIS:O	2.15	0.46
1:H:90:TYR:N	1:H:90:TYR:CD1	2.79	0.46
1:A:224:VAL:O	1:A:228:GLY:HA2	2.15	0.46
1:C:179:VAL:CB	1:C:180:PRO:HD3	2.43	0.46
1:C:261:MET:HE1	1:C:298:LEU:HD21	1.96	0.46
1:E:219:GLU:O	1:E:223:ILE:HG13	2.13	0.46
1:E:342:MET:HE1	1:E:405:PRO:HG2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:237:LEU:CD1	1:H:239:LEU:HB2	2.44	0.46
1:C:135:ASP:OD1	1:C:138:GLU:CB	2.62	0.46
1:C:415:TYR:HE2	1:C:417:PHE:CE2	2.33	0.46
1:D:152:MET:HE3	1:D:271:ALA:HA	1.97	0.46
1:H:237:LEU:HD11	1:H:239:LEU:CG	2.23	0.46
1:H:327:THR:OG1	1:H:336:GLU:OE1	2.33	0.46
1:A:135:ASP:OD1	1:A:136:MET:N	2.49	0.46
1:A:224:VAL:O	1:A:228:GLY:CA	2.64	0.46
1:C:108:ILE:O	1:C:112:ILE:HG13	2.15	0.46
1:E:280:ASP:OD1	1:E:281:ILE:N	2.48	0.46
1:E:351:ILE:HD12	1:E:381:LEU:HD21	1.97	0.46
1:F:28:LYS:O	1:F:30:HIS:CD2	2.68	0.46
1:G:445:ASP:HB3	1:G:472:GLU:OE1	2.15	0.46
1:H:14:ARG:HB3	1:H:14:ARG:CZ	2.45	0.46
1:C:72:SER:O	1:C:75:GLU:CB	2.63	0.46
1:F:127:THR:O	1:F:131:ILE:HG13	2.15	0.46
1:E:31:PRO:O	1:E:32:ASP:CB	2.64	0.46
1:E:300:ARG:HE	1:F:300:ARG:HE	1.63	0.46
1:E:400:ASP:CB	1:E:403:ILE:HG23	2.45	0.46
1:G:327:THR:HG1	1:G:336:GLU:CD	2.23	0.46
1:H:8:LEU:HD13	1:H:18:LEU:CD1	2.37	0.46
1:H:117:LEU:HD22	1:H:121:GLU:CG	2.45	0.46
1:H:461:LYS:N	1:H:464:ASP:OD2	2.48	0.46
1:A:151:ASP:O	1:A:239:LEU:CD2	2.64	0.46
1:C:175:ASN:ND2	1:C:191:LYS:HE2	2.31	0.46
1:C:327:THR:OG1	1:C:336:GLU:CD	2.58	0.46
1:E:35:VAL:HG11	1:E:48:VAL:CG2	2.45	0.46
1:E:161:MET:CG	1:E:188:THR:O	2.63	0.46
1:G:418:THR:CA	1:G:464:ASP:O	2.60	0.46
1:B:237:LEU:HD11	1:B:239:LEU:CB	2.45	0.46
1:C:3:ALA:CB	1:C:57:GLY:O	2.60	0.46
1:E:492:ILE:O	1:E:493:GLU:HG3	2.15	0.46
1:F:18:LEU:HA	1:F:49:ALA:O	2.16	0.46
1:F:30:HIS:O	1:F:33:ASP:HB2	2.16	0.46
1:G:19:ILE:HD12	1:G:48:VAL:HG22	1.97	0.46
1:G:61:ILE:O	1:G:61:ILE:CG1	2.64	0.46
1:G:174:THR:HG21	1:G:353:LYS:HG2	1.98	0.46
1:G:215:PHE:HB3	1:G:220:ILE:HD13	1.97	0.46
1:G:342:MET:SD	1:G:405:PRO:HG2	2.56	0.46
1:H:415:TYR:HD2	1:H:417:PHE:CE2	2.34	0.46
1:A:95:MET:CE	1:A:124:SER:OG	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:GLY:O	1:A:206:VAL:HG23	2.15	0.46
1:C:44:VAL:HG12	1:C:45:TYR:N	2.30	0.46
1:C:329:GLY:O	1:C:333:GLU:HG3	2.16	0.46
1:D:101:ARG:N	1:D:104:GLU:OE1	2.30	0.46
1:E:179:VAL:HG13	1:E:189:ILE:CG2	2.41	0.46
1:F:44:VAL:HG22	1:F:69:HIS:CG	2.51	0.46
1:F:175:ASN:O	1:F:179:VAL:HG23	2.16	0.46
1:F:233:TRP:CD1	1:F:235:GLY:H	2.33	0.46
1:G:253:LEU:O	1:G:254:SER:CB	2.62	0.46
1:A:59:VAL:O	1:A:59:VAL:HG13	2.17	0.45
1:C:11:PHE:HD1	1:C:64:ASP:OD1	1.98	0.45
1:C:24:ALA:HB2	1:C:50:LEU:CD2	2.46	0.45
1:G:354:ALA:O	1:G:358:ALA:HB2	2.16	0.45
1:B:117:LEU:HD22	1:B:121:GLU:HB3	1.97	0.45
1:C:117:LEU:CD2	1:C:121:GLU:CG	2.94	0.45
1:C:272:MET:HE3	1:C:272:MET:HB3	1.67	0.45
1:E:278:LEU:CD1	1:E:360:ILE:HG21	2.46	0.45
1:F:17:VAL:HG11	1:F:37:ILE:HD11	1.96	0.45
1:G:163:VAL:O	1:G:163:VAL:HG13	2.15	0.45
1:H:261:MET:O	1:H:265:ILE:HG13	2.16	0.45
1:B:408:ILE:HA	1:B:409:PRO:HD3	1.71	0.45
1:A:10:MET:O	1:A:62:SER:HB2	2.15	0.45
1:A:165:SER:C	1:A:167:GLY:H	2.25	0.45
1:C:48:VAL:HG12	1:C:49:ALA:N	2.31	0.45
1:E:161:MET:HE3	1:E:361:LEU:HD22	1.99	0.45
1:E:278:LEU:HD13	1:E:360:ILE:HG21	1.98	0.45
1:F:172:ASN:OD1	1:F:324:ILE:CD1	2.63	0.45
1:F:342:MET:HE1	1:F:405:PRO:HD2	1.98	0.45
1:G:180:PRO:HG2	1:G:390:MET:HE2	1.98	0.45
1:H:179:VAL:HG13	1:H:189:ILE:HG23	1.99	0.45
1:H:417:PHE:HZ	1:H:481:ILE:HG23	1.82	0.45
1:C:3:ALA:HB1	1:C:58:GLU:HA	1.98	0.45
1:C:91:ILE:HD13	1:C:125:PHE:HB2	1.99	0.45
1:C:135:ASP:OD1	1:C:135:ASP:C	2.59	0.45
1:D:180:PRO:HG3	1:D:390:MET:HE1	1.89	0.45
1:E:91:ILE:HD13	1:E:125:PHE:HB2	1.99	0.45
1:E:339:SER:O	1:E:343:THR:OG1	2.23	0.45
1:F:174:THR:HG23	1:F:354:ALA:HB2	1.99	0.45
1:F:182:VAL:HG13	1:F:187:LEU:HD12	1.98	0.45
1:D:207:VAL:HG11	1:D:231:LEU:O	2.17	0.45
1:G:179:VAL:CG2	1:G:231:LEU:HD21	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:174:THR:CG2	1:H:357:LEU:HD12	2.46	0.45
1:B:237:LEU:HD11	1:B:239:LEU:HB2	1.99	0.45
1:C:17:VAL:HG21	1:C:37:ILE:CD1	2.45	0.45
1:D:166:ILE:CG1	1:D:282:PRO:HD2	2.47	0.45
1:E:379:GLU:O	1:E:383:SER:CB	2.64	0.45
1:G:368:ALA:CB	1:G:376:MET:CE	2.73	0.45
1:G:414:THR:HA	1:G:469:ILE:O	2.17	0.45
1:H:92:LYS:O	1:H:95:MET:HB3	2.16	0.45
1:H:179:VAL:CB	1:H:231:LEU:HD21	2.47	0.45
1:H:196:ALA:HB3	1:H:443:PRO:HG3	1.97	0.45
1:H:322:GLN:CB	1:H:323:PRO:CD	2.95	0.45
1:E:24:ALA:O	1:E:28:LYS:N	2.50	0.45
1:F:44:VAL:CG2	1:F:69:HIS:CG	2.99	0.45
1:F:278:LEU:CD1	1:F:360:ILE:HG21	2.47	0.45
1:G:177:LEU:HB3	1:G:181:ILE:HD11	1.98	0.45
1:H:237:LEU:C	1:H:237:LEU:HD12	2.42	0.45
1:B:125:PHE:O	1:B:129:LEU:HG	2.17	0.45
1:C:117:LEU:HD23	1:C:121:GLU:CG	2.46	0.45
1:C:134:LEU:CD2	1:C:138:GLU:CB	2.90	0.45
1:D:43:ALA:O	1:D:44:VAL:CG2	2.64	0.45
1:D:50:LEU:O	1:H:10:MET:HA	2.17	0.45
1:D:84:THR:HG23	1:D:85:PRO:HD2	1.98	0.45
1:E:92:LYS:HA	1:E:95:MET:HB2	1.98	0.45
1:F:175:ASN:CB	1:F:191:LYS:HE2	2.47	0.45
1:F:212:ASP:O	1:F:215:PHE:HE2	1.99	0.45
1:H:189:ILE:O	1:H:229:ALA:HB1	2.17	0.45
1:A:283:THR:HA	1:A:289:VAL:O	2.17	0.45
1:D:202:GLY:O	1:D:206:VAL:HG23	2.17	0.45
1:H:450:ILE:CG2	1:H:452:LEU:CD1	2.95	0.45
1:D:35:VAL:CG1	1:D:48:VAL:HG23	2.47	0.45
1:E:173:LYS:HE3	1:E:333:GLU:HG2	1.98	0.45
1:E:388:GLU:HA	1:E:391:LYS:HE2	1.99	0.45
1:C:220:ILE:HD11	1:C:232:VAL:HG21	1.98	0.44
1:E:135:ASP:C	1:E:135:ASP:OD1	2.60	0.44
1:E:202:GLY:H	1:E:205:ASP:HB2	1.82	0.44
1:G:216:SER:O	1:G:220:ILE:CD1	2.65	0.44
1:G:241:PRO:O	1:G:245:ILE:HG13	2.16	0.44
1:G:330:PRO:HG2	1:G:446:LYS:HA	2.00	0.44
1:D:155:ILE:HD13	1:D:224:VAL:CG1	2.46	0.44
1:D:327:THR:OG1	1:D:336:GLU:CD	2.60	0.44
1:D:368:ALA:HB2	1:D:376:MET:CE	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:255:ILE:O	1:E:255:ILE:HG13	2.16	0.44
1:G:169:VAL:HG13	1:G:172:ASN:HB2	2.00	0.44
1:H:161:MET:HB3	1:H:361:LEU:HD22	1.98	0.44
1:H:164:HIS:CE1	1:H:165:SER:O	2.70	0.44
1:H:391:LYS:HD3	1:H:401:PRO:O	2.17	0.44
1:F:1:MET:O	1:F:79:VAL:N	2.47	0.44
1:A:439:ALA:C	1:A:441:GLY:H	2.26	0.44
1:C:233:TRP:CZ2	1:C:235:GLY:HA3	2.52	0.44
1:D:208:GLU:HA	1:D:211:ALA:O	2.18	0.44
1:E:184:ALA:C	1:E:186:GLY:H	2.24	0.44
1:F:255:ILE:O	1:F:255:ILE:CG1	2.65	0.44
1:F:332:LEU:HD12	1:F:449:GLY:HA3	1.99	0.44
1:G:206:VAL:HG13	1:G:334:ALA:HA	1.97	0.44
1:B:289:VAL:HG11	1:B:295:ALA:HA	1.99	0.44
1:A:54:VAL:CG1	1:A:58:GLU:CB	2.93	0.44
1:A:117:LEU:HD23	1:A:121:GLU:HG2	1.99	0.44
1:C:212:ASP:O	1:C:215:PHE:CZ	2.69	0.44
1:D:17:VAL:HA	1:D:60:GLY:O	2.17	0.44
1:D:35:VAL:CG1	1:D:48:VAL:CG2	2.96	0.44
1:D:240:ALA:N	1:D:241:PRO:CD	2.80	0.44
1:D:471:ALA:HB3	1:D:477:LEU:HB2	1.99	0.44
1:E:94:LYS:O	1:E:94:LYS:HD3	2.17	0.44
1:F:3:ALA:HB1	1:F:57:GLY:O	2.17	0.44
1:F:178:VAL:O	1:F:182:VAL:HG23	2.17	0.44
1:G:492:ILE:CG2	1:G:493:GLU:N	2.80	0.44
1:H:161:MET:SD	1:H:276:TYR:CB	2.84	0.44
1:H:161:MET:O	1:H:189:ILE:HG13	2.18	0.44
1:B:29:LEU:HD13	1:B:48:VAL:HG21	2.00	0.44
1:H:160:ILE:HB	1:H:275:GLN:H	1.81	0.44
1:B:237:LEU:CD1	1:B:239:LEU:CD1	2.86	0.44
1:C:72:SER:O	1:C:75:GLU:HB2	2.17	0.44
1:C:400:ASP:OD1	1:C:402:ASN:CB	2.66	0.44
1:E:220:ILE:O	1:E:224:VAL:HG23	2.18	0.44
1:G:102:LYS:O	1:G:106:GLU:HG3	2.18	0.44
1:G:164:HIS:O	1:G:279:ILE:HA	2.17	0.44
1:G:179:VAL:HB	1:G:180:PRO:HD2	1.95	0.44
1:G:240:ALA:N	1:G:241:PRO:HD2	2.30	0.44
1:G:298:LEU:HD12	1:G:298:LEU:HA	1.86	0.44
1:B:165:SER:C	1:B:167:GLY:N	2.72	0.44
1:A:266:MET:HG3	1:A:305:LEU:HD23	1.99	0.44
1:A:332:LEU:CD1	1:A:449:GLY:HA3	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:MET:O	1:C:62:SER:HB2	2.18	0.44
1:C:17:VAL:CG2	1:C:37:ILE:HD11	2.46	0.44
1:F:192:THR:HA	1:F:232:VAL:O	2.18	0.44
1:H:9:ASP:C	1:H:9:ASP:OD1	2.59	0.44
1:H:309:LEU:HB2	1:H:311:GLN:OE1	2.18	0.44
1:B:430:ASN:O	1:B:434:THR:HG22	2.17	0.44
1:A:117:LEU:CD2	1:A:121:GLU:HG2	2.47	0.44
1:D:67:ASP:OD1	1:D:67:ASP:C	2.60	0.44
1:E:151:ASP:O	1:E:239:LEU:CD2	2.66	0.44
1:F:9:ASP:OD1	1:F:63:ARG:NH1	2.51	0.44
1:H:146:MET:HE2	1:H:267:SER:CB	2.48	0.44
1:H:217:LEU:O	1:H:221:LYS:N	2.45	0.44
1:B:18:LEU:HD23	1:B:51:SER:HB3	1.96	0.43
1:B:146:MET:HE2	1:B:146:MET:HB3	1.81	0.43
1:C:196:ALA:HB2	1:C:202:GLY:N	2.33	0.43
1:C:445:ASP:HB3	1:C:472:GLU:OE1	2.18	0.43
1:D:48:VAL:CG1	1:D:49:ALA:N	2.79	0.43
1:D:266:MET:HG3	1:D:305:LEU:HD23	2.00	0.43
1:F:126:VAL:CG2	1:F:246:THR:HG23	2.48	0.43
1:F:450:ILE:HG22	1:F:452:LEU:CD1	2.48	0.43
1:G:179:VAL:CB	1:G:180:PRO:CD	2.75	0.43
1:G:270:TYR:HA	1:G:311:GLN:HE22	1.82	0.43
1:A:9:ASP:OD1	1:A:9:ASP:C	2.61	0.43
1:C:144:ILE:HD11	1:C:309:LEU:HD23	2.00	0.43
1:E:143:THR:HG1	1:E:263:ALA:HA	1.81	0.43
1:E:403:ILE:O	1:E:403:ILE:HG13	2.15	0.43
1:F:390:MET:O	1:F:394:ILE:HG13	2.18	0.43
1:G:176:ILE:CG2	1:G:390:MET:CE	2.94	0.43
1:H:38:GLU:CB	1:H:43:ALA:HB2	2.47	0.43
1:H:72:SER:O	1:H:75:GLU:HB2	2.18	0.43
1:B:200:ALA:O	1:B:443:PRO:HB3	2.18	0.43
1:A:489:PRO:HD2	1:A:490:ILE:H	1.83	0.43
1:E:239:LEU:CD1	1:E:272:MET:HE3	2.49	0.43
1:G:68:LEU:O	1:G:69:HIS:ND1	2.50	0.43
1:G:188:THR:HA	1:G:228:GLY:O	2.19	0.43
1:G:319:TYR:CE1	1:G:321:GLY:N	2.87	0.43
1:H:394:ILE:HA	1:H:397:GLN:CB	2.48	0.43
1:A:426:THR:CG2	1:A:493:GLU:HB2	2.48	0.43
1:C:20:ASN:ND2	1:C:22:GLU:CA	2.81	0.43
1:D:193:SER:HB3	1:D:203:THR:CB	2.47	0.43
1:E:262:LEU:HD11	1:E:301:ASP:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:240:ALA:N	1:F:241:PRO:CD	2.81	0.43
1:G:61:ILE:O	1:G:61:ILE:HG13	2.18	0.43
1:G:135:ASP:O	1:G:139:ILE:HG13	2.18	0.43
1:G:179:VAL:HG13	1:G:189:ILE:CG2	2.47	0.43
1:G:215:PHE:HB3	1:G:220:ILE:CD1	2.49	0.43
1:G:292:VAL:CG2	1:G:293:GLU:N	2.81	0.43
1:G:473:HIS:CD2	1:G:476:ARG:HG3	2.53	0.43
1:B:179:VAL:CB	1:B:180:PRO:CD	2.93	0.43
1:C:19:ILE:HG22	1:C:24:ALA:HB2	2.01	0.43
1:C:48:VAL:CG1	1:C:49:ALA:N	2.81	0.43
1:D:166:ILE:HG12	1:D:282:PRO:HD2	2.00	0.43
1:E:400:ASP:HA	1:E:401:PRO:HD2	1.80	0.43
1:E:404:LYS:HA	1:E:405:PRO:HD3	1.83	0.43
1:G:319:TYR:OH	1:G:321:GLY:HA3	2.19	0.43
1:B:14:ARG:HG3	1:B:16:THR:CG2	2.47	0.43
1:C:163:VAL:O	1:C:163:VAL:HG13	2.18	0.43
1:D:51:SER:HB2	1:D:53:LEU:HG	2.00	0.43
1:E:305:LEU:O	1:E:305:LEU:HD12	2.18	0.43
1:F:38:GLU:HB3	1:F:43:ALA:CB	2.48	0.43
1:B:220:ILE:HD13	1:B:220:ILE:HA	1.76	0.43
1:E:109:VAL:O	1:E:113:VAL:HG23	2.19	0.43
1:E:155:ILE:HG21	1:E:224:VAL:HG11	1.98	0.43
1:H:38:GLU:HB3	1:H:43:ALA:CB	2.45	0.43
1:D:339:SER:O	1:D:343:THR:OG1	2.36	0.43
1:D:492:ILE:N	1:D:492:ILE:HD12	2.33	0.43
1:F:8:LEU:HD11	1:F:18:LEU:HD22	2.01	0.43
1:G:270:TYR:HD2	1:G:311:GLN:NE2	2.16	0.43
1:G:455:LYS:O	1:G:458:GLU:HB2	2.19	0.43
1:H:237:LEU:HD11	1:H:239:LEU:HB2	2.00	0.43
1:A:223:ILE:HG23	1:A:396:ALA:HB1	2.01	0.43
1:A:403:ILE:O	1:A:403:ILE:HG13	2.16	0.43
1:A:423:GLY:O	1:A:460:VAL:N	2.34	0.43
1:C:166:ILE:HG13	1:C:167:GLY:N	2.32	0.43
1:C:224:VAL:O	1:C:228:GLY:N	2.50	0.43
1:C:303:ILE:HA	1:C:313:VAL:HB	2.01	0.43
1:D:400:ASP:O	1:D:403:ILE:CG2	2.66	0.43
1:E:415:TYR:CD2	1:E:417:PHE:CE2	3.07	0.43
1:H:30:HIS:HB2	1:H:33:ASP:OD2	2.19	0.43
1:B:54:VAL:HG22	1:B:58:GLU:HB2	2.00	0.43
1:A:423:GLY:HA3	1:A:492:ILE:CG2	2.48	0.43
1:C:44:VAL:HG22	1:C:69:HIS:ND1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:241:PRO:O	1:D:245:ILE:HG13	2.18	0.43
1:G:467:PHE:CE1	1:G:469:ILE:HG13	2.51	0.43
1:H:322:GLN:CB	1:H:323:PRO:HD2	2.48	0.43
1:B:10:MET:O	1:B:62:SER:HB2	2.19	0.42
1:B:432:ALA:O	1:B:436:ILE:HG13	2.18	0.42
1:A:489:PRO:CD	1:A:490:ILE:H	2.33	0.42
1:C:425:VAL:O	1:C:425:VAL:HG12	2.16	0.42
1:C:436:ILE:O	1:C:439:ALA:HB3	2.19	0.42
1:D:54:VAL:HG13	1:D:58:GLU:HB2	2.01	0.42
1:D:276:TYR:CD1	1:D:312:TYR:HB2	2.54	0.42
1:D:467:PHE:N	1:D:467:PHE:CD2	2.86	0.42
1:E:163:VAL:O	1:E:163:VAL:HG13	2.18	0.42
1:E:183:ALA:HB3	1:E:389:LYS:HG2	1.99	0.42
1:B:325:GLY:O	1:B:326:HIS:HD2	2.02	0.42
1:C:127:THR:O	1:C:131:ILE:HG13	2.19	0.42
1:C:445:ASP:OD1	1:C:445:ASP:N	2.50	0.42
1:E:15:TYR:N	1:E:15:TYR:CD1	2.87	0.42
1:E:454:VAL:HA	1:E:458:GLU:OE1	2.19	0.42
1:H:233:TRP:CZ2	1:H:235:GLY:HA3	2.54	0.42
1:B:103:VAL:HG23	1:B:104:GLU:N	2.34	0.42
1:B:117:LEU:HD22	1:B:121:GLU:CB	2.49	0.42
1:A:292:VAL:HG23	1:A:293:GLU:N	2.34	0.42
1:D:338:LEU:HD23	1:D:338:LEU:HA	1.83	0.42
1:E:126:VAL:CG2	1:E:246:THR:HG23	2.49	0.42
1:E:255:ILE:O	1:E:255:ILE:HG12	2.20	0.42
1:F:114:ASP:O	1:F:115:ARG:CB	2.67	0.42
1:F:450:ILE:HG22	1:F:452:LEU:HD12	2.00	0.42
1:F:488:GLU:N	1:F:489:PRO:CD	2.82	0.42
1:B:210:PHE:O	1:B:211:ALA:HB2	2.19	0.42
1:C:376:MET:O	1:C:380:ILE:HG13	2.19	0.42
1:F:283:THR:HA	1:F:289:VAL:O	2.19	0.42
1:A:6:ARG:O	1:A:60:GLY:HA2	2.20	0.42
1:A:487:THR:O	1:A:488:GLU:C	2.62	0.42
1:D:169:VAL:CG2	1:D:282:PRO:HB3	2.48	0.42
1:F:425:VAL:HG22	1:F:492:ILE:HD11	2.02	0.42
1:G:30:HIS:CB	1:G:33:ASP:OD2	2.62	0.42
1:G:59:VAL:O	1:G:59:VAL:CG1	2.67	0.42
1:G:415:TYR:CE2	1:G:417:PHE:CD2	3.06	0.42
1:H:55:GLY:O	1:H:58:GLU:HB2	2.19	0.42
1:H:94:LYS:HA	1:H:94:LYS:HD3	1.77	0.42
1:B:331:ALA:HB3	1:B:446:LYS:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:122:ILE:CD1	1:E:245:ILE:CG2	2.97	0.42
1:F:44:VAL:HG12	1:F:45:TYR:N	2.34	0.42
1:F:175:ASN:HB3	1:F:191:LYS:HE2	2.01	0.42
1:F:436:ILE:CD1	1:F:484:ALA:HB1	2.40	0.42
1:F:423:GLY:HA3	1:F:492:ILE:CG2	2.49	0.42
1:G:91:ILE:HG22	1:G:95:MET:HE3	2.01	0.42
1:G:331:ALA:HB2	1:G:446:LYS:O	2.19	0.42
1:H:161:MET:CE	1:H:276:TYR:HB2	2.50	0.42
1:H:450:ILE:HG23	1:H:467:PHE:HD1	1.84	0.42
1:A:179:VAL:HG13	1:A:189:ILE:HG23	2.01	0.42
1:C:185:ALA:CB	1:C:362:LEU:HD21	2.50	0.42
1:F:331:ALA:HB2	1:F:446:LYS:C	2.45	0.42
1:G:99:LYS:HG3	1:G:100:LEU:N	2.35	0.42
1:G:413:LYS:C	1:G:414:THR:HG23	2.44	0.42
1:A:371:GLY:HA2	1:C:300:ARG:HG2	2.02	0.42
1:F:64:ASP:O	1:F:67:ASP:OD1	2.37	0.42
1:G:31:PRO:O	1:G:32:ASP:CB	2.68	0.42
1:H:327:THR:OG1	1:H:336:GLU:OE2	2.36	0.42
1:H:450:ILE:CG2	1:H:452:LEU:HD12	2.44	0.42
1:C:68:LEU:C	1:C:69:HIS:CD2	2.97	0.42
1:D:12:SER:C	1:D:14:ARG:H	2.24	0.42
1:F:359:GLY:O	1:F:363:GLU:HG3	2.20	0.42
1:G:72:SER:OG	1:G:75:GLU:OE1	2.30	0.42
1:G:114:ASP:O	1:G:115:ARG:CB	2.68	0.42
1:G:415:TYR:CZ	1:G:417:PHE:CE1	3.03	0.42
1:H:32:ASP:O	1:H:118:ARG:NH1	2.45	0.42
1:H:94:LYS:HE3	1:H:134:LEU:CD2	2.50	0.42
1:B:390:MET:HG3	1:B:394:ILE:HD11	2.02	0.41
1:C:144:ILE:CG1	1:C:309:LEU:CD2	2.98	0.41
1:F:380:ILE:HG22	1:F:386:ALA:HB2	2.02	0.41
1:H:423:GLY:C	1:H:492:ILE:CG2	2.92	0.41
1:B:19:ILE:HG22	1:B:20:ASN:N	2.34	0.41
1:A:35:VAL:HG22	1:A:48:VAL:HG23	2.01	0.41
1:C:126:VAL:CG2	1:C:246:THR:HG23	2.50	0.41
1:C:243:ASP:O	1:C:247:ILE:HG13	2.20	0.41
1:E:3:ALA:O	1:E:77:VAL:O	2.38	0.41
1:F:163:VAL:O	1:F:163:VAL:CG1	2.66	0.41
1:G:30:HIS:N	1:G:33:ASP:OD2	2.52	0.41
1:G:436:ILE:O	1:G:439:ALA:HB3	2.20	0.41
1:H:99:LYS:CG	1:H:138:GLU:OE2	2.68	0.41
1:A:319:TYR:CZ	1:A:321:GLY:HA3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:237:LEU:HD13	1:C:239:LEU:CD1	2.44	0.41
1:D:24:ALA:O	1:D:28:LYS:N	2.48	0.41
1:D:68:LEU:HD23	1:D:68:LEU:HA	1.65	0.41
1:E:183:ALA:HB1	1:E:389:LYS:CE	2.50	0.41
1:G:326:HIS:HD2	1:G:452:LEU:O	2.00	0.41
1:H:44:VAL:CG2	1:H:45:TYR:N	2.83	0.41
1:H:424:TYR:O	1:H:492:ILE:CA	2.62	0.41
1:C:166:ILE:HG12	1:C:282:PRO:CD	2.50	0.41
1:C:400:ASP:CG	1:C:402:ASN:HB2	2.45	0.41
1:E:173:LYS:HE2	1:E:333:GLU:HG2	2.02	0.41
1:F:163:VAL:O	1:F:163:VAL:HG13	2.19	0.41
1:F:180:PRO:HG3	1:F:390:MET:CE	2.46	0.41
1:F:223:ILE:HG23	1:F:396:ALA:HB1	2.02	0.41
1:F:282:PRO:HA	1:F:318:THR:O	2.20	0.41
1:G:292:VAL:O	1:G:296:ARG:N	2.50	0.41
1:G:400:ASP:O	1:G:403:ILE:HG12	2.21	0.41
1:H:471:ALA:HB3	1:H:477:LEU:HB2	2.02	0.41
1:B:283:THR:HA	1:B:289:VAL:O	2.21	0.41
1:B:490:ILE:HD12	1:B:490:ILE:N	2.35	0.41
1:C:215:PHE:CD2	1:C:215:PHE:N	2.88	0.41
1:E:15:TYR:N	1:E:15:TYR:HD1	2.19	0.41
1:E:142:LEU:O	1:E:146:MET:HG3	2.21	0.41
1:H:328:VAL:CG1	1:H:329:GLY:N	2.83	0.41
1:B:352:GLU:OE1	1:B:352:GLU:HA	2.21	0.41
1:C:114:ASP:O	1:C:115:ARG:CB	2.69	0.41
1:C:139:ILE:CD1	1:C:259:GLY:HA2	2.50	0.41
1:C:182:VAL:O	1:C:185:ALA:HB3	2.21	0.41
1:C:467:PHE:CE2	1:C:490:ILE:HD12	2.54	0.41
1:D:173:LYS:HE2	1:D:333:GLU:HA	2.03	0.41
1:E:134:LEU:HD22	1:E:138:GLU:CB	2.50	0.41
1:E:161:MET:HE3	1:E:161:MET:HB3	1.70	0.41
1:E:400:ASP:C	1:E:403:ILE:HG23	2.43	0.41
1:G:403:ILE:O	1:G:403:ILE:CG1	2.68	0.41
1:B:8:LEU:CD1	1:B:18:LEU:HD22	2.50	0.41
1:B:127:THR:O	1:B:131:ILE:HG13	2.20	0.41
1:A:453:TYR:HE2	1:A:468:THR:HG1	1.63	0.41
1:C:19:ILE:CG2	1:C:24:ALA:HB2	2.50	0.41
1:D:339:SER:O	1:D:343:THR:HG23	2.21	0.41
1:E:31:PRO:O	1:E:32:ASP:HB3	2.21	0.41
1:F:59:VAL:O	1:F:59:VAL:HG13	2.21	0.41
1:F:338:LEU:HA	1:F:338:LEU:HD23	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:161:MET:HE2	1:H:361:LEU:HD23	2.00	0.41
1:H:164:HIS:HB3	1:H:279:ILE:CD1	2.50	0.41
1:B:72:SER:O	1:B:75:GLU:CB	2.65	0.41
1:B:207:VAL:HG11	1:B:231:LEU:O	2.21	0.41
1:B:424:TYR:O	1:B:492:ILE:HG23	2.20	0.41
1:C:3:ALA:CB	1:C:57:GLY:C	2.92	0.41
1:C:161:MET:CE	1:C:276:TYR:HB2	2.50	0.41
1:D:91:ILE:HD13	1:D:125:PHE:HB2	2.03	0.41
1:D:329:GLY:C	1:D:333:GLU:HG3	2.31	0.41
1:D:394:ILE:O	1:D:398:GLY:N	2.54	0.41
1:F:27:ALA:O	1:F:28:LYS:CB	2.67	0.41
1:F:388:GLU:O	1:F:392:GLU:HG3	2.21	0.41
1:B:151:ASP:HB3	1:B:217:LEU:CD1	2.51	0.41
1:B:151:ASP:HB3	1:B:217:LEU:HD11	2.03	0.41
1:B:173:LYS:CD	1:B:336:GLU:OE1	2.68	0.41
1:B:364:MET:HE2	1:B:364:MET:HB3	1.83	0.41
1:C:175:ASN:HD22	1:C:191:LYS:HE2	1.86	0.41
1:C:237:LEU:HD12	1:C:239:LEU:N	2.36	0.41
1:C:260:LEU:O	1:C:264:SER:HB2	2.21	0.41
1:C:477:LEU:O	1:C:481:ILE:HG13	2.20	0.41
1:D:35:VAL:HG11	1:D:48:VAL:CG2	2.51	0.41
1:D:120:ILE:HG13	1:H:119:ASP:HB3	2.03	0.41
1:D:289:VAL:HG11	1:D:295:ALA:HB2	2.03	0.41
1:D:400:ASP:HA	1:D:401:PRO:HD2	1.91	0.41
1:E:30:HIS:O	1:E:33:ASP:HB2	2.21	0.41
1:E:117:LEU:CD2	1:E:121:GLU:CB	2.93	0.41
1:E:237:LEU:CD1	1:E:239:LEU:CG	2.94	0.41
1:E:255:ILE:HG13	1:E:257:PRO:HD3	2.02	0.41
1:E:319:TYR:OH	1:E:321:GLY:HA3	2.20	0.41
1:F:8:LEU:HD13	1:F:10:MET:HE3	2.02	0.41
1:G:177:LEU:CD2	1:G:341:LEU:HG	2.51	0.41
1:G:394:ILE:O	1:G:398:GLY:N	2.54	0.41
1:H:250:GLU:OE1	1:H:256:ASP:OD1	2.39	0.41
1:H:344:GLY:HA2	1:H:381:LEU:HG	2.02	0.41
1:B:488:GLU:OE1	1:B:488:GLU:HA	2.21	0.41
1:D:118:ARG:N	1:D:121:GLU:OE1	2.54	0.41
1:G:224:VAL:O	1:G:228:GLY:CA	2.68	0.41
1:G:478:ASP:O	1:G:482:VAL:HG23	2.20	0.41
1:H:367:VAL:HG12	1:H:376:MET:SD	2.61	0.41
1:H:368:ALA:HA	1:H:369:PRO:HD3	1.86	0.41
1:H:461:LYS:CB	1:H:464:ASP:OD2	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:491:ARG:C	1:H:492:ILE:HG13	2.45	0.41
1:B:287:VAL:O	1:B:288:LYS:C	2.64	0.40
1:A:121:GLU:CD	1:A:121:GLU:N	2.80	0.40
1:E:84:THR:HA	1:E:85:PRO:HD3	1.92	0.40
1:G:19:ILE:HD13	1:G:29:LEU:HD12	2.03	0.40
1:G:237:LEU:CD1	1:G:239:LEU:HB2	2.51	0.40
1:G:471:ALA:CB	1:G:477:LEU:HB2	2.51	0.40
1:H:181:ILE:O	1:H:184:ALA:HB3	2.21	0.40
1:B:129:LEU:O	1:B:133:GLY:N	2.50	0.40
1:B:289:VAL:HG11	1:B:295:ALA:CA	2.51	0.40
1:A:173:LYS:H	1:A:173:LYS:HG2	1.70	0.40
1:A:390:MET:O	1:A:394:ILE:HG13	2.22	0.40
1:C:51:SER:HB2	1:G:9:ASP:O	2.20	0.40
1:C:185:ALA:HB2	1:C:362:LEU:HD21	2.04	0.40
1:D:94:LYS:HD3	1:D:94:LYS:C	2.46	0.40
1:D:220:ILE:HD11	1:D:232:VAL:HG21	2.03	0.40
1:F:180:PRO:HG3	1:F:390:MET:HE2	1.97	0.40
1:F:400:ASP:CB	1:F:403:ILE:CG2	2.97	0.40
1:H:154:ASP:O	1:H:221:LYS:HE3	2.21	0.40
1:H:190:PRO:HA	1:H:230:CYS:H	1.87	0.40
1:B:253:LEU:O	1:B:255:ILE:HG23	2.21	0.40
1:B:451:GLU:O	1:B:467:PHE:HA	2.21	0.40
1:D:142:LEU:O	1:D:146:MET:HG3	2.21	0.40
1:E:276:TYR:HB3	1:E:364:MET:HE2	2.03	0.40
1:F:414:THR:HA	1:F:469:ILE:O	2.22	0.40
1:G:37:ILE:O	1:G:43:ALA:HA	2.22	0.40
1:G:155:ILE:CG2	1:G:160:ILE:HD11	2.51	0.40
1:G:326:HIS:O	1:G:451:GLU:HA	2.21	0.40
1:H:170:PRO:HB2	1:H:323:PRO:HB3	2.04	0.40
1:H:237:LEU:HD12	1:H:237:LEU:O	2.22	0.40
1:A:19:ILE:HG22	1:A:20:ASN:N	2.36	0.40
1:D:190:PRO:HB3	1:D:224:VAL:CG2	2.51	0.40
1:D:276:TYR:CE1	1:D:312:TYR:CD2	3.09	0.40
1:E:67:ASP:OD1	1:E:67:ASP:N	2.52	0.40
1:E:389:LYS:O	1:E:393:ILE:HG13	2.21	0.40
1:F:389:LYS:O	1:F:393:ILE:HG13	2.21	0.40
1:G:94:LYS:O	1:G:94:LYS:HD3	2.21	0.40
1:G:166:ILE:HG12	1:G:282:PRO:CD	2.50	0.40
1:G:324:ILE:CD1	1:G:353:LYS:HD3	2.51	0.40
1:H:436:ILE:CG2	1:H:469:ILE:CD1	2.99	0.40
1:A:4:LYS:HA	1:A:75:GLU:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:72:SER:O	1:D:75:GLU:HB3	2.21	0.40
1:D:391:LYS:HB3	1:D:401:PRO:HB3	2.04	0.40
1:F:490:ILE:HG22	1:F:492:ILE:HD12	2.04	0.40
1:G:87:SER:HB3	1:G:111:ASP:OD2	2.21	0.40
1:H:206:VAL:HG12	1:H:334:ALA:HB2	2.03	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	491/513 (96%)	482 (98%)	9 (2%)	0	100	100
1	B	491/513 (96%)	485 (99%)	6 (1%)	0	100	100
1	C	491/513 (96%)	482 (98%)	8 (2%)	1 (0%)	43	70
1	D	491/513 (96%)	479 (98%)	12 (2%)	0	100	100
1	E	491/513 (96%)	484 (99%)	6 (1%)	1 (0%)	43	70
1	F	491/513 (96%)	481 (98%)	10 (2%)	0	100	100
1	G	491/513 (96%)	480 (98%)	11 (2%)	0	100	100
1	H	491/513 (96%)	482 (98%)	9 (2%)	0	100	100
All	All	3928/4104 (96%)	3855 (98%)	71 (2%)	2 (0%)	48	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	115	ARG
1	C	409	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	292/404 (72%)	288 (99%)	4 (1%)	59	72
1	B	292/404 (72%)	287 (98%)	5 (2%)	53	69
1	C	292/404 (72%)	281 (96%)	11 (4%)	29	55
1	D	292/404 (72%)	289 (99%)	3 (1%)	68	75
1	E	292/404 (72%)	287 (98%)	5 (2%)	53	69
1	F	292/404 (72%)	285 (98%)	7 (2%)	43	64
1	G	292/404 (72%)	284 (97%)	8 (3%)	39	61
1	H	292/404 (72%)	285 (98%)	7 (2%)	43	64
All	All	2336/3232 (72%)	2286 (98%)	50 (2%)	47	66

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	38	GLU
1	B	61	ILE
1	B	220	ILE
1	B	456	VAL
1	B	482	VAL
1	A	103	VAL
1	A	126	VAL
1	A	220	ILE
1	A	476	ARG
1	C	84	THR
1	C	113	VAL
1	C	155	ILE
1	C	207	VAL
1	C	247	ILE
1	C	280	ASP
1	C	294	GLU
1	C	379	GLU
1	C	445	ASP
1	C	488	GLU

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Mol	Chain	Res	Type
1	C	492	ILE
1	D	84	THR
1	D	232	VAL
1	D	452	LEU
1	E	69	HIS
1	E	143	THR
1	E	177	LEU
1	E	450	ILE
1	E	490	ILE
1	F	10	MET
1	F	177	LEU
1	F	247	ILE
1	F	258	THR
1	F	305	LEU
1	F	436	ILE
1	F	450	ILE
1	G	38	GLU
1	G	47	SER
1	G	131	ILE
1	G	178	VAL
1	G	194	SER
1	G	324	ILE
1	G	456	VAL
1	G	482	VAL
1	H	10	MET
1	H	54	VAL
1	H	69	HIS
1	H	131	ILE
1	H	169	VAL
1	H	324	ILE
1	H	327	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	275	GLN
1	B	326	HIS
1	A	30	HIS
1	A	175	ASN
1	A	275	GLN
1	A	470	HIS
1	C	20	ASN

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Mol	Chain	Res	Type
1	C	69	HIS
1	C	96	HIS
1	C	326	HIS
1	D	164	HIS
1	D	275	GLN
1	E	69	HIS
1	E	164	HIS
1	E	275	GLN
1	F	30	HIS
1	G	96	HIS
1	G	175	ASN
1	G	275	GLN
1	G	311	GLN
1	G	326	HIS
1	G	473	HIS
1	H	30	HIS
1	H	69	HIS
1	H	430	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	493/513 (96%)	0.31	18 (3%)	45	30	11, 41, 74, 100	0
1	B	493/513 (96%)	0.54	32 (6%)	25	17	6, 46, 85, 121	0
1	C	493/513 (96%)	0.56	29 (5%)	28	19	15, 47, 87, 124	0
1	D	493/513 (96%)	0.57	29 (5%)	28	19	19, 52, 87, 132	0
1	E	493/513 (96%)	0.67	36 (7%)	21	15	11, 52, 98, 145	0
1	F	493/513 (96%)	0.45	21 (4%)	40	26	16, 47, 80, 153	0
1	G	493/513 (96%)	1.08	89 (18%)	3	3	28, 76, 141, 252	0
1	H	493/513 (96%)	1.11	86 (17%)	4	4	26, 86, 148, 225	0
All	All	3944/4104 (96%)	0.66	340 (8%)	16	13	6, 53, 112, 252	0

All (340) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	493	GLU	5.8
1	H	448	ALA	5.7
1	E	156	ASP	5.3
1	G	448	ALA	5.0
1	G	471	ALA	4.9
1	A	258	THR	4.5
1	B	447	GLY	4.5
1	E	157	ARG	4.5
1	H	185	ALA	4.5
1	H	154	ASP	4.4
1	D	379	GLU	4.4
1	H	362	LEU	4.4
1	G	154	ASP	4.3
1	H	457	GLY	4.2
1	C	199	SER	4.2
1	E	453	TYR	4.2

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Mol	Chain	Res	Type	RSRZ
1	C	448	ALA	4.1
1	G	469	ILE	3.9
1	H	277	VAL	3.9
1	F	242	ALA	3.9
1	G	432	ALA	3.8
1	G	466	LEU	3.8
1	C	52	ASN	3.8
1	H	444	GLU	3.8
1	E	226	LYS	3.7
1	G	362	LEU	3.7
1	H	179	VAL	3.7
1	F	243	ASP	3.7
1	G	447	GLY	3.7
1	G	156	ASP	3.6
1	G	383	SER	3.6
1	H	267	SER	3.5
1	C	156	ASP	3.5
1	E	78	SER	3.5
1	D	412	ASP	3.5
1	H	429	ASP	3.5
1	G	404	LYS	3.5
1	G	214	SER	3.5
1	A	172	ASN	3.4
1	H	213	VAL	3.4
1	G	51	SER	3.4
1	G	333	GLU	3.4
1	E	493	GLU	3.3
1	E	314	GLU	3.3
1	G	337	ALA	3.3
1	B	156	ASP	3.3
1	H	231	LEU	3.3
1	H	341	LEU	3.3
1	G	213	VAL	3.2
1	G	157	ARG	3.2
1	B	212	ASP	3.2
1	H	454	VAL	3.2
1	C	421	THR	3.2
1	A	157	ARG	3.2
1	G	175	ASN	3.2
1	C	214	SER	3.2
1	H	214	SER	3.2
1	G	421	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	H	408	ILE	3.2
1	B	387	TRP	3.2
1	D	134	LEU	3.2
1	G	70	ASN	3.2
1	D	212	ASP	3.1
1	G	367	VAL	3.1
1	H	76	THR	3.1
1	H	361	LEU	3.1
1	E	397	GLN	3.1
1	G	412	ASP	3.1
1	H	271	ALA	3.0
1	H	456	VAL	3.0
1	D	51	SER	3.0
1	H	212	ASP	3.0
1	H	21	GLU	3.0
1	G	194	SER	3.0
1	H	254	SER	3.0
1	H	360	ILE	3.0
1	C	440	ALA	3.0
1	H	236	ALA	3.0
1	G	272	MET	3.0
1	B	157	ARG	3.0
1	D	14	ARG	3.0
1	F	214	SER	3.0
1	G	391	LYS	3.0
1	G	286	GLY	3.0
1	C	70	ASN	3.0
1	H	155	ILE	3.0
1	C	471	ALA	2.9
1	C	424	TYR	2.9
1	H	78	SER	2.9
1	D	280	ASP	2.9
1	E	218	ASP	2.9
1	B	322	GLN	2.9
1	E	236	ALA	2.9
1	E	447	GLY	2.9
1	G	429	ASP	2.9
1	G	438	ARG	2.9
1	G	184	ALA	2.9
1	H	358	ALA	2.9
1	H	379	GLU	2.9
1	E	225	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	G	396	ALA	2.9
1	G	342	MET	2.9
1	H	318	THR	2.9
1	A	457	GLY	2.9
1	E	70	ASN	2.8
1	E	214	SER	2.8
1	E	374	LYS	2.8
1	H	161	MET	2.8
1	B	420	ALA	2.8
1	D	454	VAL	2.8
1	D	445	ASP	2.8
1	H	232	VAL	2.8
1	H	427	ALA	2.8
1	C	216	SER	2.8
1	G	210	PHE	2.7
1	G	408	ILE	2.8
1	G	426	THR	2.8
1	G	329	GLY	2.7
1	B	52	ASN	2.7
1	C	2	LYS	2.7
1	C	402	ASN	2.7
1	G	459	LYS	2.7
1	D	448	ALA	2.7
1	G	322	GLN	2.7
1	H	292	VAL	2.7
1	C	441	GLY	2.7
1	H	156	ASP	2.7
1	H	176	ILE	2.7
1	G	1	MET	2.7
1	E	62	SER	2.7
1	H	272	MET	2.7
1	G	168	GLY	2.7
1	H	466	LEU	2.7
1	E	64	ASP	2.7
1	G	450	ILE	2.6
1	G	465	PRO	2.6
1	H	490	ILE	2.6
1	C	444	GLU	2.6
1	G	167	GLY	2.6
1	B	442	ALA	2.6
1	D	482	VAL	2.6
1	E	68	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	G	211	ALA	2.6
1	G	340	ALA	2.6
1	G	10	MET	2.6
1	G	409	PRO	2.6
1	H	168	GLY	2.6
1	G	68	LEU	2.6
1	G	424	TYR	2.6
1	D	403	ILE	2.6
1	G	41	LYS	2.6
1	H	181	ILE	2.6
1	B	256	ASP	2.6
1	C	154	ASP	2.6
1	C	130	GLU	2.6
1	A	39	ALA	2.6
1	B	424	TYR	2.6
1	G	71	PHE	2.6
1	B	208	GLU	2.6
1	A	216	SER	2.6
1	B	237	LEU	2.6
1	F	488	GLU	2.6
1	F	39	ALA	2.6
1	G	264	SER	2.5
1	B	476	ARG	2.5
1	G	135	ASP	2.5
1	D	236	ALA	2.5
1	H	184	ALA	2.5
1	A	322	GLN	2.5
1	G	338	LEU	2.5
1	G	468	THR	2.5
1	G	453	TYR	2.5
1	E	277	VAL	2.5
1	B	493	GLU	2.5
1	H	70	ASN	2.5
1	H	133	GLY	2.5
1	A	472	GLU	2.5
1	E	26	GLU	2.5
1	E	9	ASP	2.5
1	H	426	THR	2.5
1	B	14	ARG	2.4
1	H	359	GLY	2.4
1	C	123	SER	2.4
1	C	193	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	130	GLU	2.4
1	D	193	SER	2.4
1	G	474	GLU	2.4
1	A	52	ASN	2.4
1	E	256	ASP	2.4
1	H	180	PRO	2.4
1	B	326	HIS	2.4
1	E	48	VAL	2.4
1	B	448	ALA	2.4
1	A	72	SER	2.4
1	H	425	VAL	2.4
1	E	73	GLU	2.4
1	C	72	SER	2.4
1	H	193	SER	2.4
1	C	401	PRO	2.4
1	G	473	HIS	2.4
1	H	23	ASP	2.4
1	H	61	ILE	2.4
1	H	316	ALA	2.4
1	G	215	PHE	2.4
1	B	193	SER	2.4
1	H	87	SER	2.4
1	H	149	THR	2.3
1	H	203	THR	2.3
1	H	284	GLY	2.3
1	H	320	GLY	2.3
1	A	448	ALA	2.3
1	D	166	ILE	2.3
1	B	333	GLU	2.3
1	G	330	PRO	2.3
1	G	347	PRO	2.3
1	D	441	GLY	2.3
1	F	150	GLY	2.3
1	G	76	THR	2.3
1	H	228	GLY	2.3
1	H	268	LYS	2.3
1	H	211	ALA	2.3
1	H	415	TYR	2.3
1	D	400	ASP	2.3
1	B	472	GLU	2.3
1	C	224	VAL	2.3
1	H	315	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	254	SER	2.3
1	B	492	ILE	2.3
1	B	471	ALA	2.3
1	D	402	ASN	2.3
1	H	381	LEU	2.3
1	D	444	GLU	2.3
1	E	304	GLU	2.3
1	H	339	SER	2.3
1	D	154	ASP	2.3
1	E	154	ASP	2.3
1	F	462	GLU	2.3
1	F	74	GLY	2.3
1	H	377	ALA	2.3
1	E	267	SER	2.3
1	G	254	SER	2.3
1	G	476	ARG	2.3
1	H	178	VAL	2.3
1	E	155	ILE	2.2
1	G	344	GLY	2.2
1	F	322	GLN	2.2
1	G	444	GLU	2.2
1	D	199	SER	2.2
1	D	214	SER	2.2
1	F	193	SER	2.2
1	D	52	ASN	2.2
1	G	380	ILE	2.2
1	A	400	ASP	2.2
1	B	457	GLY	2.2
1	D	53	LEU	2.2
1	E	272	MET	2.2
1	F	154	ASP	2.2
1	G	440	ALA	2.2
1	H	167	GLY	2.2
1	F	78	SER	2.2
1	G	388	GLU	2.2
1	C	331	ALA	2.2
1	H	329	GLY	2.2
1	C	114	ASP	2.2
1	E	63	ARG	2.2
1	H	7	ILE	2.2
1	H	311	GLN	2.2
1	A	493	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	98	GLU	2.2
1	F	365	GLY	2.2
1	G	441	GLY	2.2
1	D	156	ASP	2.2
1	A	76	THR	2.1
1	F	203	THR	2.1
1	H	303	ILE	2.1
1	E	10	MET	2.1
1	H	342	MET	2.1
1	C	493	GLU	2.1
1	H	196	ALA	2.1
1	G	411	GLY	2.1
1	H	159	PRO	2.1
1	H	369	PRO	2.1
1	F	23	ASP	2.1
1	C	96	HIS	2.1
1	G	206	VAL	2.1
1	E	74	GLY	2.1
1	F	234	GLY	2.1
1	G	405	PRO	2.1
1	H	208	GLU	2.1
1	E	135	ASP	2.1
1	G	328	VAL	2.1
1	H	343	THR	2.1
1	G	331	ALA	2.1
1	G	479	GLN	2.1
1	G	480	ALA	2.1
1	H	39	ALA	2.1
1	G	170	PRO	2.1
1	G	208	GLU	2.1
1	H	215	PHE	2.1
1	D	230	CYS	2.1
1	H	177	LEU	2.1
1	B	450	ILE	2.1
1	B	272	MET	2.1
1	B	429	ASP	2.1
1	G	327	THR	2.1
1	H	364	MET	2.1
1	A	442	ALA	2.1
1	C	167	GLY	2.1
1	F	441	GLY	2.1
1	B	148	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	26	GLU	2.1
1	G	209	VAL	2.0
1	G	123	SER	2.0
1	H	72	SER	2.0
1	A	350	LEU	2.0
1	G	8	LEU	2.0
1	H	1	MET	2.0
1	A	420	ALA	2.0
1	E	243	ASP	2.0
1	E	301	ASP	2.0
1	G	205	ASP	2.0
1	G	487	THR	2.0
1	H	270	TYR	2.0
1	G	366	GLY	2.0
1	H	275	GLN	2.0
1	C	443	PRO	2.0
1	F	190	PRO	2.0
1	D	26	GLU	2.0
1	D	474	GLU	2.0
1	G	482	VAL	2.0
1	E	8	LEU	2.0
1	B	76	THR	2.0
1	B	135	ASP	2.0
1	F	9	ASP	2.0
1	G	99	LYS	2.0
1	G	179	VAL	2.0
1	G	335	ARG	2.0
1	B	403	ILE	2.0
1	C	403	ILE	2.0
1	H	492	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.