Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 03:25 AM EDT

PDB ID	:	7LZ4
Title	:	Crystal structure of A211D mutant of Protein Kinase A RIa subunit, a Carney Complex mutation
Authors	:	Del Rio, J.; Wu, J.; Taylor, S.S.
Deposited on	:	2021-03-08
Resolution	:	4.16 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:

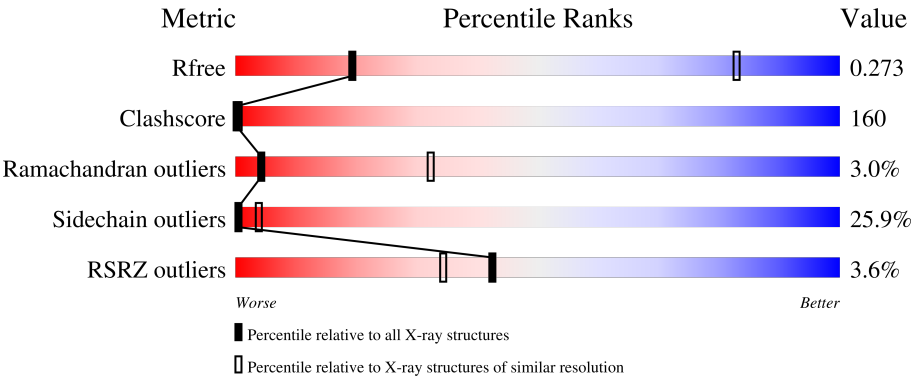
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.16 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1020 (4.54-3.76)
Clashscore	141614	1028 (4.52-3.80)
Ramachandran outliers	138981	1005 (4.54-3.78)
Sidechain outliers	138945	1024 (4.54-3.76)
RSRZ outliers	127900	1055 (4.62-3.70)

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 <=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	269	5% 14% 59% 21% 5%
1	B	269	4% 15% 55% 26% .
1	C	269	3% 13% 55% 25% 7%
1	D	269	4% 14% 58% 22% 5% .
1	E	269	4% 17% 59% 20% .

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Mol	Chain	Length	Quality of chain
1	F	269	3% 17% 55% 24%
1	G	269	4% 18% 51% 26%
1	H	269	3% 10% 60% 26%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CMP	A	401	-	-	X	-
2	CMP	A	402	-	-	X	-
2	CMP	B	401	-	-	X	-
2	CMP	B	402	-	-	X	-
2	CMP	C	401	-	-	X	-
2	CMP	C	402	-	-	X	-
2	CMP	D	401	-	-	X	-
2	CMP	D	402	-	-	X	-
2	CMP	E	401	-	-	X	-
2	CMP	E	402	-	-	X	-
2	CMP	F	401	-	-	X	-
2	CMP	F	402	-	-	X	-
2	CMP	G	401	-	-	X	-
2	CMP	G	402	-	-	X	-
2	CMP	H	401	-	-	X	-
2	CMP	H	402	-	-	X	-

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 17138 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.

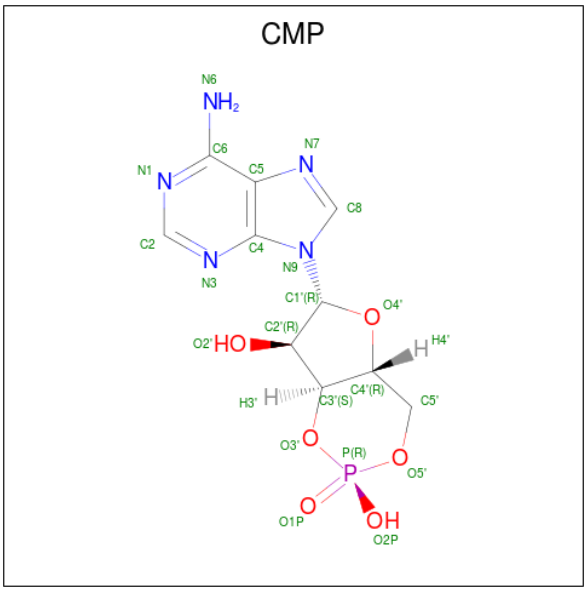
- Molecule 1 is a protein called cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	B	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	C	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	D	266	Total	C	N	O	S	0	0	0
			2086	1325	356	397	8			
1	E	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	F	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	G	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	H	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	211	ASP	ALA	engineered mutation	UNP P00514
B	211	ASP	ALA	engineered mutation	UNP P00514
C	211	ASP	ALA	engineered mutation	UNP P00514
D	211	ASP	ALA	engineered mutation	UNP P00514
E	211	ASP	ALA	engineered mutation	UNP P00514
F	211	ASP	ALA	engineered mutation	UNP P00514
G	211	ASP	ALA	engineered mutation	UNP P00514
H	211	ASP	ALA	engineered mutation	UNP P00514

- Molecule 2 is ADENOSINE-3',5'-CYCLIC-MONOPHOSPHATE (three-letter code: CMP) (formula: $C_{10}H_{12}N_5O_6P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	A	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	B	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	B	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	C	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	C	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	D	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	D	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	E	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	E	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	F	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	F	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	G	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	G	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

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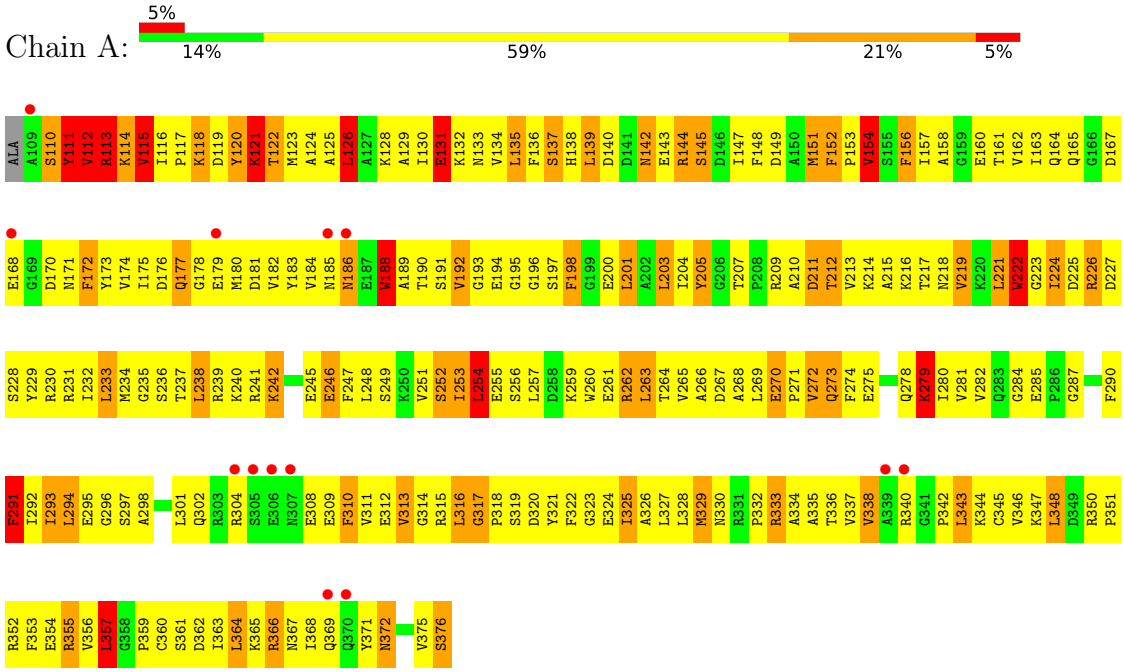
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	H	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	H	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

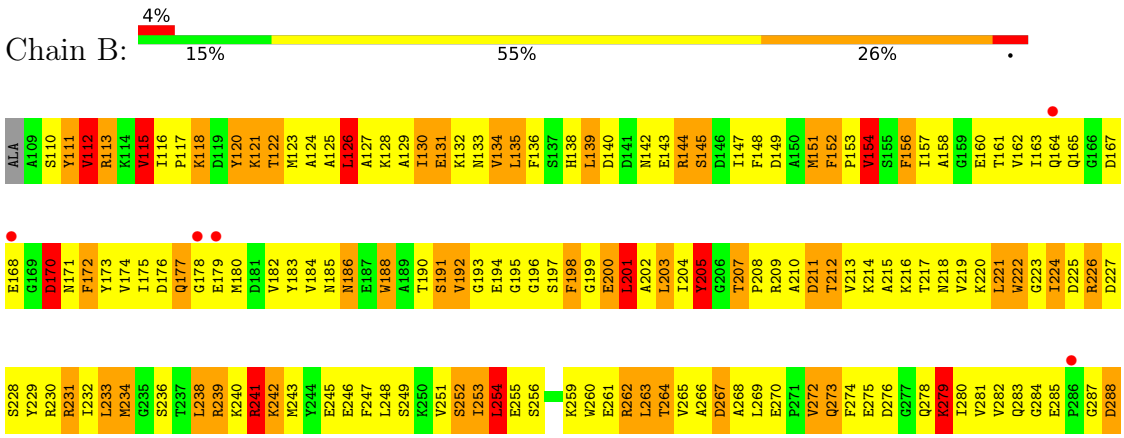
3 Residue-property plots (i)

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

• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

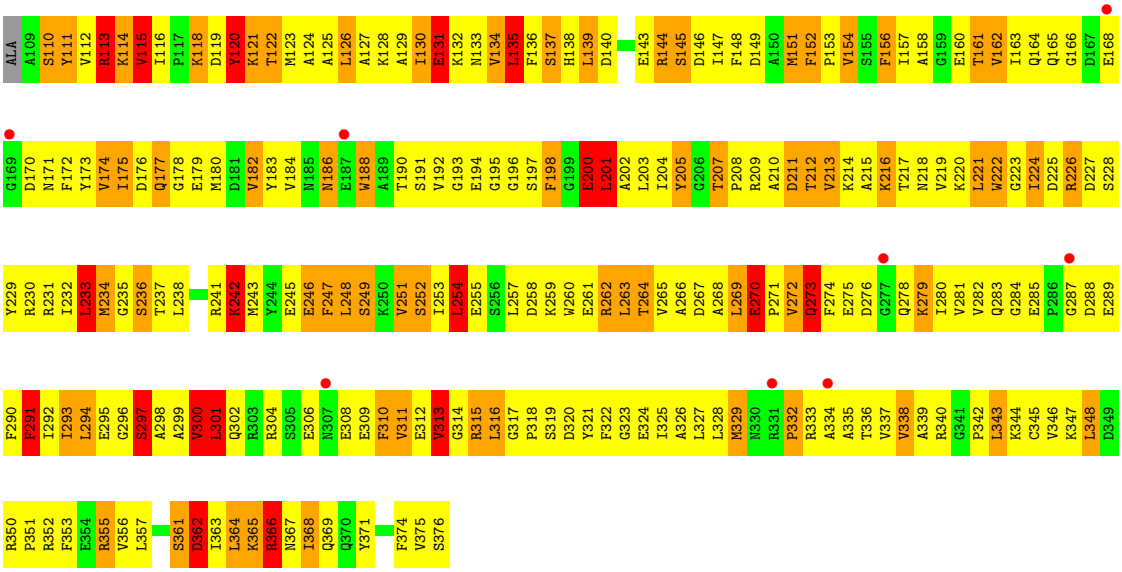


• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



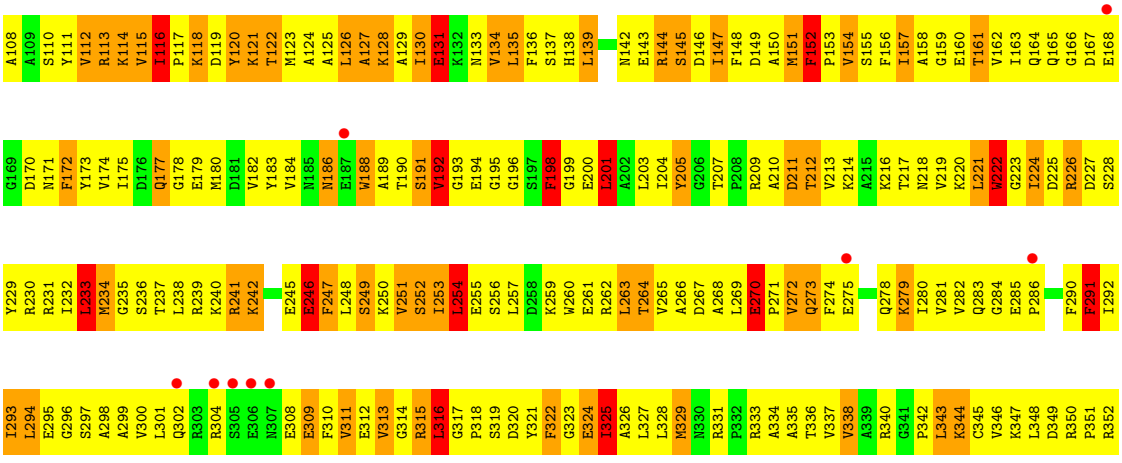
• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

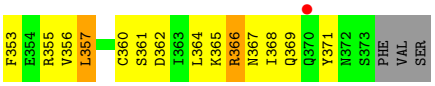
Chain C:



• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

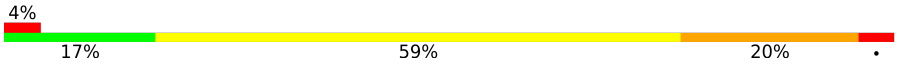
Chain D:

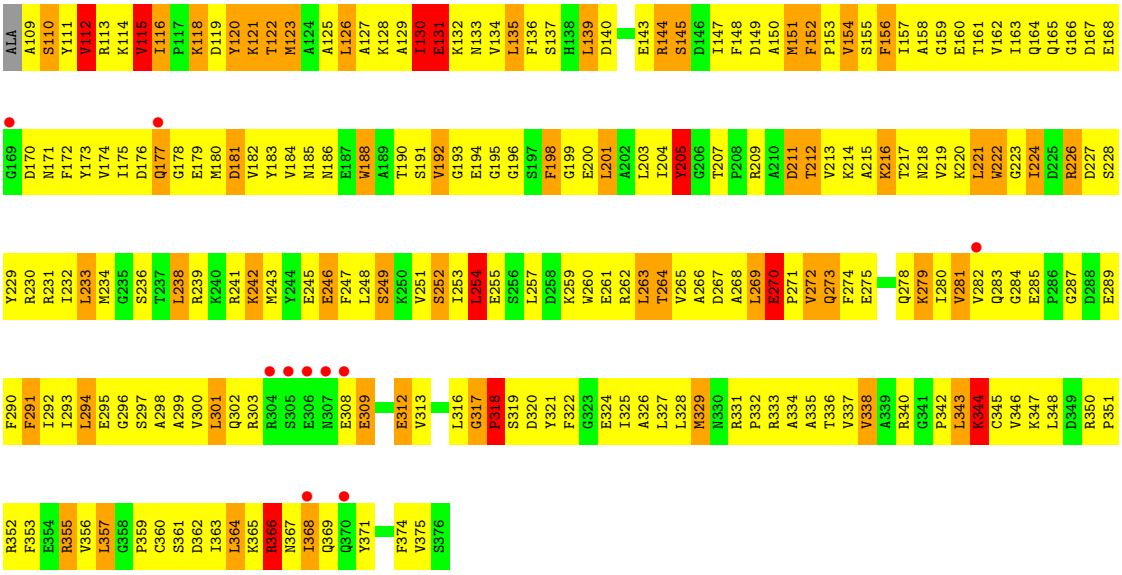




• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

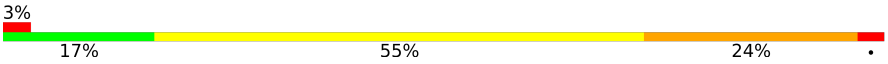
Chain E:

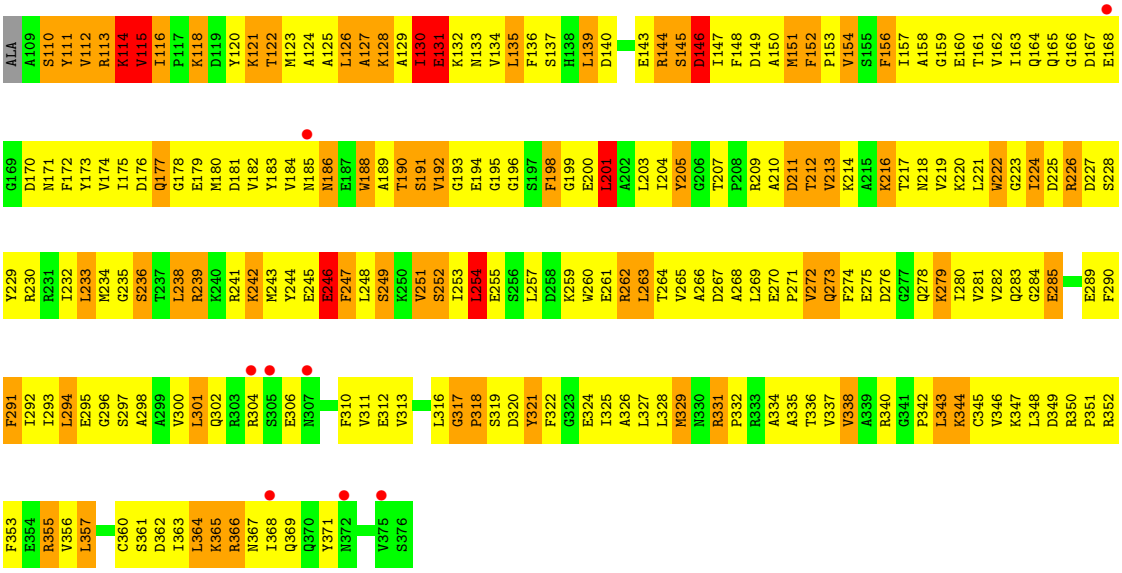




• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

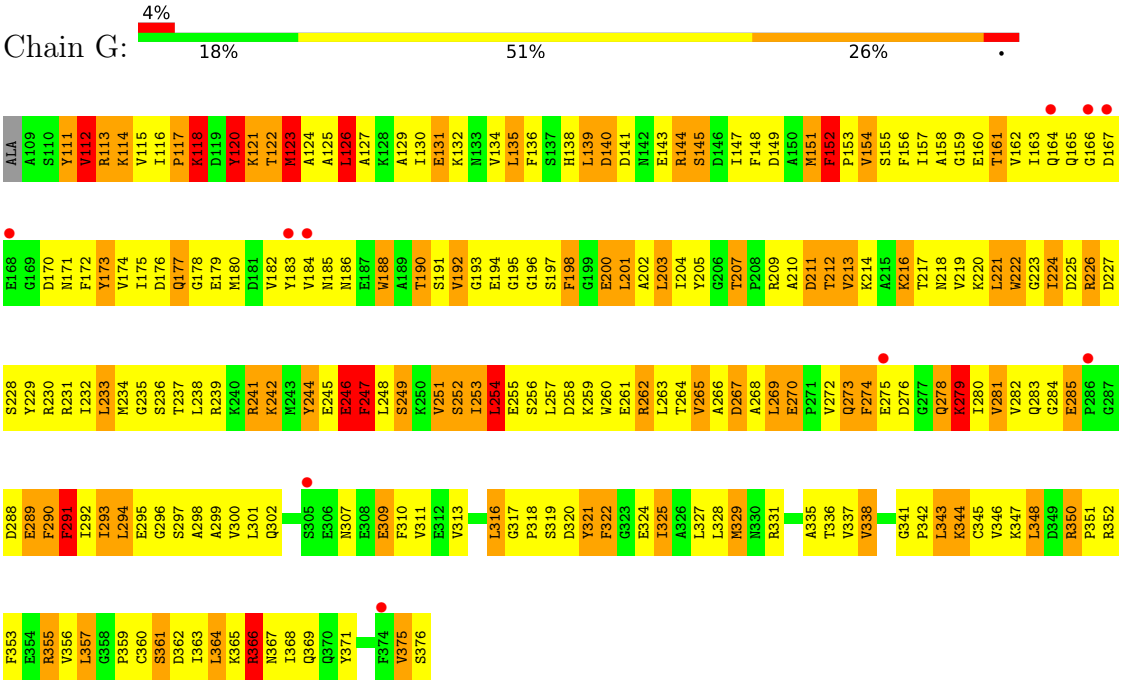
Chain F:





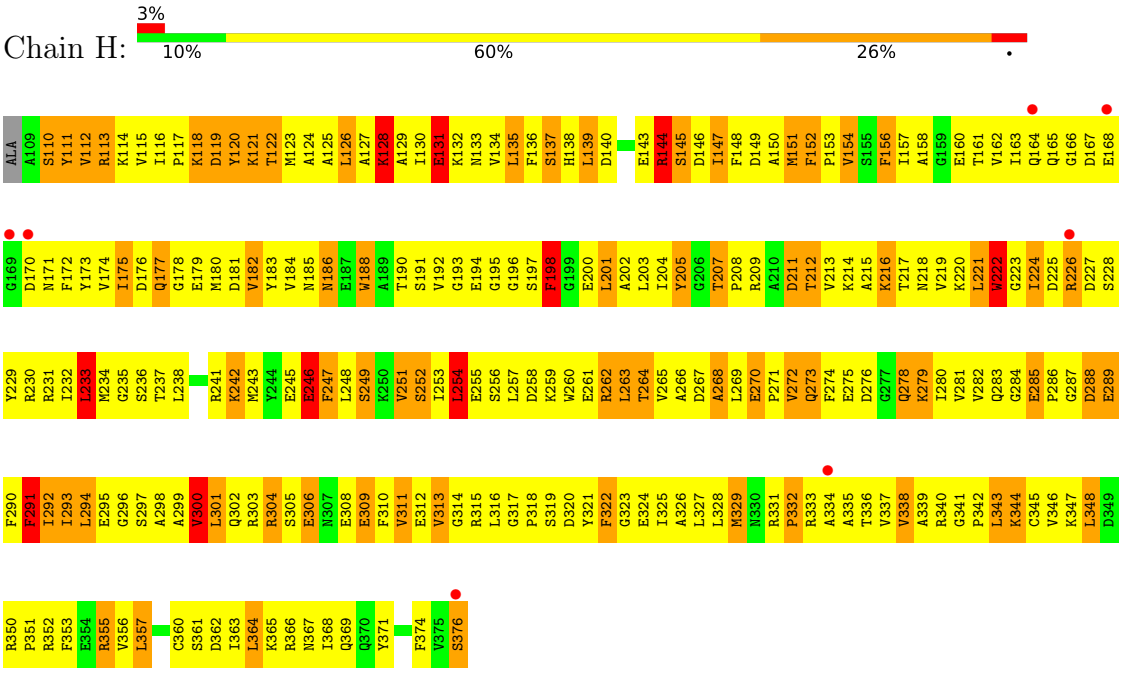
• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

Chain G:



• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	176.79Å 176.79Å 345.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.25 – 4.16 48.25 – 4.15	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.25-4.16) 99.4 (48.25-4.15)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.69 (at 4.14Å)	Xtriage
Refinement program	PHENIX 1.7_650	Depositor
R, R_{free}	0.221 , 0.270 0.225 , 0.273	Depositor DCC
R_{free} test set	1526 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	125.7	Xtriage
Anisotropy	0.440	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 97.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.418 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	17138	wwPDB-VP
Average B, all atoms (Å^2)	135.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

Bond lengths and bond angles in the following residue types are not validated in this section: CMP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	1.35	15/2138 (0.7%)	1.60	33/2887 (1.1%)
1	B	1.31	13/2138 (0.6%)	1.55	31/2887 (1.1%)
1	C	1.27	5/2138 (0.2%)	1.61	34/2887 (1.2%)
1	D	1.33	20/2124 (0.9%)	1.44	27/2869 (0.9%)
1	E	1.12	8/2138 (0.4%)	1.39	19/2887 (0.7%)
1	F	1.26	14/2138 (0.7%)	1.48	27/2887 (0.9%)
1	G	1.60	32/2138 (1.5%)	1.82	58/2887 (2.0%)
1	H	1.27	12/2138 (0.6%)	1.56	33/2887 (1.1%)
All	All	1.32	119/17090 (0.7%)	1.56	262/23078 (1.1%)

All (119) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	131	GLU	CB-CG	-16.50	1.20	1.52
1	D	152	PHE	CE1-CZ	-12.97	1.12	1.37
1	A	112	VAL	CA-CB	12.67	1.81	1.54
1	G	289	GLU	CB-CG	-12.20	1.28	1.52
1	B	241	ARG	CZ-NH1	11.78	1.48	1.33
1	G	131	GLU	CG-CD	-11.69	1.34	1.51
1	D	152	PHE	CG-CD2	-11.31	1.21	1.38
1	D	152	PHE	CE2-CZ	-11.15	1.16	1.37
1	F	318	PRO	CG-CD	10.83	1.86	1.50
1	G	121	LYS	CB-CG	-10.71	1.23	1.52
1	D	152	PHE	CG-CD1	-10.15	1.23	1.38
1	F	285	GLU	CG-CD	-10.13	1.36	1.51
1	A	112	VAL	CB-CG2	9.80	1.73	1.52
1	G	270	GLU	CB-CG	-9.60	1.33	1.52
1	B	241	ARG	CB-CG	-9.46	1.26	1.52
1	F	285	GLU	CD-OE1	-9.18	1.15	1.25
1	H	288	ASP	CB-CG	-9.14	1.32	1.51
1	D	131	GLU	CB-CG	-8.91	1.35	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	112	VAL	CA-C	8.38	1.74	1.52
1	F	192	VAL	CA-CB	-8.28	1.37	1.54
1	A	131	GLU	CB-CG	-7.70	1.37	1.52
1	F	131	GLU	CG-CD	-7.66	1.40	1.51
1	F	131	GLU	CB-CG	-7.55	1.37	1.52
1	G	279	LYS	CD-CE	-7.35	1.32	1.51
1	G	152	PHE	CG-CD2	-7.30	1.27	1.38
1	E	318	PRO	N-CA	7.25	1.59	1.47
1	F	317	GLY	C-O	-7.25	1.12	1.23
1	B	241	ARG	CZ-NH2	7.16	1.42	1.33
1	H	278	GLN	CB-CG	-7.14	1.33	1.52
1	G	152	PHE	CG-CD1	-7.13	1.28	1.38
1	B	289	GLU	CB-CG	-7.12	1.38	1.52
1	G	285	GLU	CG-CD	-7.11	1.41	1.51
1	F	331	ARG	CB-CG	-6.94	1.33	1.52
1	E	192	VAL	CA-CB	-6.93	1.40	1.54
1	G	322	PHE	CB-CG	-6.89	1.39	1.51
1	A	372	ASN	CG-ND2	-6.86	1.15	1.32
1	A	115	VAL	CA-CB	-6.77	1.40	1.54
1	H	288	ASP	CG-OD1	-6.71	1.09	1.25
1	G	241	ARG	CB-CG	-6.67	1.34	1.52
1	D	108	ALA	CA-CB	6.64	1.66	1.52
1	D	114	LYS	N-CA	6.63	1.59	1.46
1	E	131	GLU	CB-CG	-6.57	1.39	1.52
1	G	291	PHE	CB-CG	-6.55	1.40	1.51
1	A	131	GLU	CG-CD	-6.51	1.42	1.51
1	G	285	GLU	CD-OE1	-6.48	1.18	1.25
1	G	246	GLU	CB-CG	-6.47	1.39	1.52
1	G	152	PHE	CE2-CZ	-6.46	1.25	1.37
1	G	270	GLU	CG-CD	-6.45	1.42	1.51
1	G	291	PHE	CG-CD1	-6.38	1.29	1.38
1	F	318	PRO	N-CD	-6.36	1.39	1.47
1	E	318	PRO	N-CD	6.33	1.56	1.47
1	D	115	VAL	CB-CG2	-6.25	1.39	1.52
1	G	131	GLU	N-CA	6.23	1.58	1.46
1	F	246	GLU	CB-CG	-6.09	1.40	1.52
1	H	291	PHE	CB-CG	-6.01	1.41	1.51
1	F	115	VAL	CB-CG2	6.00	1.65	1.52
1	G	278	GLN	CB-CG	-5.96	1.36	1.52
1	B	113	ARG	CA-C	5.93	1.68	1.52
1	A	188	TRP	CB-CG	5.92	1.60	1.50
1	C	291	PHE	CE2-CZ	-5.91	1.26	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	291	PHE	CD2-CE2	5.88	1.50	1.39
1	D	131	GLU	CG-CD	-5.84	1.43	1.51
1	G	152	PHE	CE1-CZ	-5.79	1.26	1.37
1	D	270	GLU	CG-CD	-5.78	1.43	1.51
1	B	154	VAL	CA-CB	-5.72	1.42	1.54
1	F	317	GLY	CA-C	5.72	1.61	1.51
1	H	322	PHE	CB-CG	-5.71	1.41	1.51
1	D	241	ARG	CG-CD	-5.71	1.37	1.51
1	H	278	GLN	CD-OE1	-5.65	1.11	1.24
1	D	291	PHE	CB-CG	-5.63	1.41	1.51
1	H	268	ALA	CA-CB	-5.61	1.40	1.52
1	H	111	TYR	CD2-CE2	-5.59	1.30	1.39
1	D	246	GLU	CB-CG	-5.58	1.41	1.52
1	G	192	VAL	CB-CG2	-5.55	1.41	1.52
1	B	115	VAL	CA-CB	-5.55	1.43	1.54
1	D	270	GLU	CB-CG	-5.55	1.41	1.52
1	H	146	ASP	CB-CG	5.51	1.63	1.51
1	E	205	TYR	CD1-CE1	5.45	1.47	1.39
1	G	267	ASP	CB-CG	5.44	1.63	1.51
1	D	222	TRP	CB-CG	-5.40	1.40	1.50
1	G	297	SER	CB-OG	-5.39	1.35	1.42
1	A	154	VAL	CA-CB	-5.38	1.43	1.54
1	H	322	PHE	CD2-CE2	-5.38	1.28	1.39
1	G	361	SER	N-CA	5.37	1.57	1.46
1	F	213	VAL	CB-CG2	-5.36	1.41	1.52
1	A	291	PHE	CB-CG	-5.33	1.42	1.51
1	G	278	GLN	CG-CD	-5.33	1.38	1.51
1	D	115	VAL	N-CA	5.32	1.56	1.46
1	G	192	VAL	CA-CB	-5.32	1.43	1.54
1	C	270	GLU	CB-CG	-5.31	1.42	1.52
1	G	290	PHE	CB-CG	-5.31	1.42	1.51
1	E	318	PRO	CG-CD	5.29	1.68	1.50
1	D	127	ALA	CA-CB	-5.28	1.41	1.52
1	C	291	PHE	CB-CG	-5.27	1.42	1.51
1	F	127	ALA	CA-CB	-5.26	1.41	1.52
1	H	278	GLN	CD-NE2	-5.26	1.19	1.32
1	A	222	TRP	CB-CG	-5.25	1.40	1.50
1	E	131	GLU	CG-CD	-5.25	1.44	1.51
1	G	331	ARG	CZ-NH2	5.24	1.39	1.33
1	B	322	PHE	CE2-CZ	5.23	1.47	1.37
1	B	291	PHE	CE1-CZ	5.19	1.47	1.37
1	D	192	VAL	CA-CB	-5.19	1.43	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	291	PHE	CG-CD1	-5.17	1.30	1.38
1	C	279	LYS	CE-NZ	-5.14	1.36	1.49
1	E	318	PRO	CA-CB	5.14	1.63	1.53
1	G	281	VAL	CB-CG2	-5.10	1.42	1.52
1	H	222	TRP	CB-CG	-5.10	1.41	1.50
1	B	267	ASP	CB-CG	5.10	1.62	1.51
1	A	113	ARG	N-CA	5.08	1.56	1.46
1	D	322	PHE	CE2-CZ	-5.08	1.27	1.37
1	C	291	PHE	CG-CD1	-5.07	1.31	1.38
1	B	205	TYR	CZ-OH	5.07	1.46	1.37
1	A	142	ASN	CG-ND2	-5.05	1.20	1.32
1	D	291	PHE	CG-CD1	-5.04	1.31	1.38
1	A	279	LYS	CB-CG	-5.04	1.39	1.52
1	A	354	GLU	CG-CD	-5.03	1.44	1.51
1	G	141	ASP	C-N	5.02	1.45	1.34
1	G	213	VAL	CB-CG1	-5.02	1.42	1.52
1	G	278	GLN	CD-NE2	-5.00	1.20	1.32

All (262) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	288	ASP	CB-CG-OD1	-22.79	97.79	118.30
1	A	357	LEU	CB-CG-CD1	-21.79	73.97	111.00
1	H	288	ASP	CB-CG-OD2	21.11	137.30	118.30
1	C	279	LYS	CD-CE-NZ	-19.95	65.81	111.70
1	G	121	LYS	CA-CB-CG	17.60	152.12	113.40
1	C	242	LYS	CD-CE-NZ	-14.44	78.50	111.70
1	B	201	LEU	CA-CB-CG	-12.67	86.17	115.30
1	G	121	LYS	CB-CA-C	-12.20	86.00	110.40
1	A	316	LEU	CA-CB-CG	-11.76	88.25	115.30
1	C	254	LEU	CA-CB-CG	-11.64	88.54	115.30
1	H	254	LEU	CA-CB-CG	-11.44	88.98	115.30
1	B	254	LEU	CA-CB-CG	-11.33	89.23	115.30
1	C	115	VAL	CB-CA-C	-11.33	89.87	111.40
1	G	254	LEU	CA-CB-CG	-11.07	89.84	115.30
1	A	254	LEU	CA-CB-CG	-10.81	90.44	115.30
1	B	115	VAL	CB-CA-C	-10.75	90.98	111.40
1	F	285	GLU	CG-CD-OE1	-10.64	97.02	118.30
1	G	357	LEU	CB-CG-CD1	-10.55	93.06	111.00
1	E	254	LEU	CA-CB-CG	-10.39	91.40	115.30
1	F	130	ILE	CG1-CB-CG2	-10.26	88.83	111.40
1	B	241	ARG	NE-CZ-NH2	-9.96	115.32	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	201	LEU	CA-CB-CG	-9.90	92.52	115.30
1	C	366	ARG	NE-CZ-NH2	9.73	125.17	120.30
1	A	115	VAL	CB-CA-C	-9.73	92.92	111.40
1	B	279	LYS	N-CA-CB	-9.72	93.10	110.60
1	C	366	ARG	NE-CZ-NH1	-9.64	115.48	120.30
1	F	285	GLU	CG-CD-OE2	9.46	137.21	118.30
1	H	201	LEU	CA-CB-CG	-9.34	93.82	115.30
1	A	279	LYS	CG-CD-CE	-9.18	84.35	111.90
1	F	201	LEU	CA-CB-CG	-9.06	94.46	115.30
1	F	254	LEU	CA-CB-CG	-9.04	94.51	115.30
1	G	221	LEU	CB-CG-CD2	-8.96	95.77	111.00
1	G	289	GLU	CA-CB-CG	8.96	133.12	113.40
1	H	278	GLN	CB-CA-C	-8.85	92.69	110.40
1	G	131	GLU	CA-CB-CG	8.81	132.78	113.40
1	G	316	LEU	CB-CG-CD1	-8.61	96.36	111.00
1	B	279	LYS	CD-CE-NZ	-8.57	91.98	111.70
1	F	331	ARG	CB-CA-C	-8.44	93.53	110.40
1	G	201	LEU	CA-CB-CG	-8.26	96.31	115.30
1	C	201	LEU	CA-CB-CG	-8.24	96.35	115.30
1	D	246	GLU	CB-CA-C	-8.22	93.95	110.40
1	B	279	LYS	CB-CG-CD	-8.17	90.36	111.60
1	A	121	LYS	CD-CE-NZ	8.14	130.43	111.70
1	D	113	ARG	NE-CZ-NH2	-8.13	116.24	120.30
1	E	201	LEU	CA-CB-CG	-8.07	96.75	115.30
1	H	128	LYS	CD-CE-NZ	8.00	130.10	111.70
1	G	173	TYR	CB-CG-CD2	-7.92	116.25	121.00
1	D	221	LEU	CB-CG-CD2	-7.91	97.56	111.00
1	F	355	ARG	NE-CZ-NH1	-7.89	116.36	120.30
1	A	279	LYS	CB-CG-CD	7.86	132.03	111.60
1	D	263	LEU	CA-CB-CG	-7.78	97.40	115.30
1	D	263	LEU	CB-CG-CD2	-7.77	97.79	111.00
1	E	366	ARG	NE-CZ-NH2	7.73	124.17	120.30
1	G	173	TYR	CB-CG-CD1	7.72	125.63	121.00
1	E	317	GLY	C-N-CD	-7.63	103.81	120.60
1	F	110	SER	N-CA-C	-7.59	90.52	111.00
1	H	294	LEU	CB-CG-CD1	-7.58	98.12	111.00
1	B	241	ARG	NH1-CZ-NH2	7.54	127.70	119.40
1	E	366	ARG	NE-CZ-NH1	-7.53	116.54	120.30
1	C	114	LYS	CD-CE-NZ	7.51	128.99	111.70
1	B	263	LEU	CA-CB-CG	-7.51	98.03	115.30
1	C	200	GLU	CA-CB-CG	7.48	129.86	113.40
1	F	146	ASP	CB-CG-OD2	7.43	124.99	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	216	LYS	N-CA-C	-7.38	91.07	111.00
1	D	270	GLU	CB-CA-C	7.30	125.00	110.40
1	G	366	ARG	NE-CZ-NH1	-7.21	116.69	120.30
1	F	263	LEU	CA-CB-CG	-7.21	98.73	115.30
1	F	365	LYS	CD-CE-NZ	-7.20	95.14	111.70
1	A	203	LEU	CB-CG-CD1	-7.19	98.77	111.00
1	B	355	ARG	NE-CZ-NH1	-7.17	116.72	120.30
1	B	288	ASP	CB-CG-OD1	-7.16	111.85	118.30
1	G	344	LYS	CD-CE-NZ	7.16	128.17	111.70
1	G	244	TYR	CB-CG-CD1	-7.16	116.71	121.00
1	E	118	LYS	N-CA-C	7.09	130.13	111.00
1	B	203	LEU	CB-CG-CD1	-7.06	99.00	111.00
1	D	343	LEU	CA-CB-CG	-7.06	99.06	115.30
1	G	288	ASP	CB-CG-OD1	-7.04	111.97	118.30
1	G	361	SER	N-CA-CB	-7.02	99.97	110.50
1	A	113	ARG	N-CA-C	7.00	129.91	111.00
1	G	192	VAL	CG1-CB-CG2	6.97	122.06	110.90
1	C	300	VAL	CB-CA-C	6.96	124.62	111.40
1	G	321	TYR	CB-CG-CD1	-6.91	116.85	121.00
1	D	201	LEU	CA-CB-CG	-6.90	99.42	115.30
1	C	175	ILE	CG1-CB-CG2	-6.87	96.29	111.40
1	H	118	LYS	N-CA-C	6.85	129.48	111.00
1	C	118	LYS	N-CA-C	6.82	129.41	111.00
1	G	270	GLU	CA-CB-CG	6.80	128.36	113.40
1	F	114	LYS	CD-CE-NZ	6.80	127.33	111.70
1	G	140	ASP	N-CA-CB	6.78	122.81	110.60
1	C	273	GLN	CB-CA-C	-6.78	96.84	110.40
1	E	357	LEU	CB-CG-CD1	-6.78	99.48	111.00
1	E	355	ARG	NE-CZ-NH1	-6.77	116.91	120.30
1	A	112	VAL	CA-CB-CG2	6.74	121.01	110.90
1	G	288	ASP	CB-CG-OD2	6.73	124.36	118.30
1	A	314	GLY	N-CA-C	6.70	129.84	113.10
1	B	241	ARG	NE-CZ-NH1	-6.69	116.95	120.30
1	G	115	VAL	N-CA-C	6.69	129.07	111.00
1	H	221	LEU	CA-CB-CG	-6.59	100.13	115.30
1	E	343	LEU	CA-CB-CG	-6.58	100.16	115.30
1	A	343	LEU	CA-CB-CG	-6.58	100.17	115.30
1	G	201	LEU	CB-CG-CD2	-6.52	99.92	111.00
1	D	115	VAL	CB-CA-C	-6.48	99.08	111.40
1	B	241	ARG	N-CA-CB	-6.48	98.93	110.60
1	D	114	LYS	N-CA-C	6.45	128.42	111.00
1	A	263	LEU	CA-CB-CG	-6.45	100.47	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	115	VAL	CB-CA-C	-6.44	99.17	111.40
1	H	343	LEU	CB-CA-C	6.44	122.43	110.20
1	C	233	LEU	CA-CB-CG	-6.43	100.51	115.30
1	G	279	LYS	CD-CE-NZ	-6.42	96.92	111.70
1	B	357	LEU	CB-CG-CD2	6.42	121.92	111.00
1	A	317	GLY	N-CA-C	-6.42	97.06	113.10
1	F	343	LEU	CA-CB-CG	-6.40	100.59	115.30
1	G	141	ASP	CB-CG-OD1	-6.39	112.55	118.30
1	G	121	LYS	CB-CG-CD	-6.35	95.08	111.60
1	B	192	VAL	CB-CA-C	-6.35	99.33	111.40
1	A	172	PHE	N-CA-C	-6.35	93.87	111.00
1	E	115	VAL	CB-CA-C	-6.30	99.42	111.40
1	B	170	ASP	CB-CG-OD1	-6.27	112.66	118.30
1	D	357	LEU	CB-CG-CD1	-6.25	100.37	111.00
1	F	331	ARG	CA-CB-CG	6.24	127.12	113.40
1	A	115	VAL	CG1-CB-CG2	6.24	120.88	110.90
1	E	221	LEU	CA-CB-CG	-6.23	100.97	115.30
1	C	242	LYS	CA-CB-CG	-6.20	99.77	113.40
1	D	113	ARG	CB-CA-C	-6.17	98.06	110.40
1	G	131	GLU	CB-CA-C	-6.17	98.06	110.40
1	G	366	ARG	NE-CZ-NH2	6.14	123.37	120.30
1	D	115	VAL	N-CA-C	6.11	127.51	111.00
1	A	118	LYS	N-CA-C	6.11	127.49	111.00
1	C	297	SER	CB-CA-C	6.11	121.70	110.10
1	G	355	ARG	NE-CZ-NH1	-6.10	117.25	120.30
1	H	201	LEU	CB-CG-CD2	-6.10	100.63	111.00
1	B	221	LEU	CA-CB-CG	-6.09	101.29	115.30
1	H	263	LEU	CA-CB-CG	-6.07	101.35	115.30
1	D	152	PHE	CB-CG-CD2	6.06	125.04	120.80
1	G	267	ASP	CB-CG-OD1	6.06	123.75	118.30
1	F	118	LYS	N-CA-C	6.03	127.29	111.00
1	G	120	TYR	C-N-CA	-6.03	106.64	121.70
1	E	216	LYS	N-CA-C	-6.01	94.78	111.00
1	B	238	LEU	CA-CB-CG	-6.00	101.49	115.30
1	G	291	PHE	CB-CG-CD1	-6.00	116.60	120.80
1	G	239	ARG	CB-CG-CD	-5.97	96.08	111.60
1	G	265	VAL	CG1-CB-CG2	5.96	120.43	110.90
1	A	221	LEU	CA-CB-CG	-5.95	101.61	115.30
1	C	135	LEU	CB-CG-CD1	5.95	121.12	111.00
1	F	239	ARG	CG-CD-NE	5.94	124.28	111.80
1	H	300	VAL	CB-CA-C	5.94	122.69	111.40
1	H	289	GLU	CB-CA-C	-5.91	98.59	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	246	GLU	N-CA-CB	5.89	121.21	110.60
1	H	175	ILE	CG1-CB-CG2	-5.89	98.44	111.40
1	G	131	GLU	OE1-CD-OE2	5.88	130.36	123.30
1	H	288	ASP	N-CA-CB	-5.87	100.03	110.60
1	A	192	VAL	CB-CA-C	-5.84	100.30	111.40
1	B	172	PHE	N-CA-C	-5.84	95.23	111.00
1	G	113	ARG	N-CA-C	5.82	126.71	111.00
1	C	174	VAL	N-CA-C	-5.82	95.29	111.00
1	F	357	LEU	CB-CG-CD1	-5.80	101.14	111.00
1	F	114	LYS	CA-CB-CG	-5.79	100.67	113.40
1	C	343	LEU	CB-CA-C	5.78	121.19	110.20
1	G	244	TYR	CB-CG-CD2	5.78	124.47	121.00
1	E	344	LYS	CD-CE-NZ	5.76	124.95	111.70
1	D	254	LEU	CB-CG-CD2	5.75	120.77	111.00
1	B	239	ARG	CG-CD-NE	5.75	123.87	111.80
1	G	279	LYS	N-CA-CB	-5.74	100.28	110.60
1	C	270	GLU	N-CA-CB	5.72	120.90	110.60
1	B	288	ASP	CB-CG-OD2	5.71	123.44	118.30
1	G	131	GLU	CB-CG-CD	-5.70	98.82	114.20
1	D	118	LYS	N-CA-C	5.69	126.37	111.00
1	B	118	LYS	N-CA-C	5.69	126.35	111.00
1	B	343	LEU	CA-CB-CG	-5.68	102.24	115.30
1	E	263	LEU	CA-CB-CG	-5.67	102.25	115.30
1	C	348	LEU	N-CA-C	-5.67	95.69	111.00
1	D	131	GLU	N-CA-C	5.67	126.31	111.00
1	D	116	ILE	C-N-CD	-5.67	108.13	120.60
1	C	362	ASP	N-CA-C	5.65	126.27	111.00
1	G	114	LYS	CD-CE-NZ	5.65	124.70	111.70
1	G	357	LEU	CB-CG-CD2	5.65	120.60	111.00
1	F	114	LYS	CB-CA-C	-5.64	99.12	110.40
1	G	343	LEU	CA-CB-CG	-5.62	102.38	115.30
1	C	270	GLU	CA-CB-CG	5.61	125.73	113.40
1	B	314	GLY	N-CA-C	5.60	127.11	113.10
1	B	115	VAL	CG1-CB-CG2	5.60	119.86	110.90
1	F	263	LEU	CB-CG-CD2	-5.60	101.48	111.00
1	H	111	TYR	CB-CG-CD1	5.58	124.35	121.00
1	E	130	ILE	CG1-CB-CG2	-5.58	99.13	111.40
1	E	181	ASP	CB-CG-OD2	5.57	123.32	118.30
1	G	141	ASP	CB-CG-OD2	5.57	123.31	118.30
1	G	126	LEU	CB-CG-CD1	5.57	120.46	111.00
1	A	238	LEU	CB-CG-CD1	5.56	120.45	111.00
1	D	233	LEU	CA-CB-CG	-5.56	102.52	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	285	GLU	CB-CG-CD	-5.55	99.22	114.20
1	G	274	PHE	CB-CG-CD2	-5.54	116.92	120.80
1	G	200	GLU	CA-CB-CG	5.53	125.58	113.40
1	G	239	ARG	CG-CD-NE	5.53	123.41	111.80
1	A	219	VAL	CB-CA-C	-5.53	100.90	111.40
1	G	348	LEU	N-CA-C	-5.52	96.10	111.00
1	C	120	TYR	CB-CA-C	-5.51	99.38	110.40
1	C	355	ARG	NE-CZ-NH1	-5.48	117.56	120.30
1	C	366	ARG	N-CA-CB	-5.48	100.74	110.60
1	G	120	TYR	CB-CG-CD1	-5.48	117.72	121.00
1	A	131	GLU	N-CA-C	5.45	125.71	111.00
1	A	279	LYS	CD-CE-NZ	-5.45	99.17	111.70
1	H	147	ILE	CB-CG1-CD1	-5.43	98.69	113.90
1	D	316	LEU	CB-CG-CD1	5.42	120.22	111.00
1	C	301	LEU	CA-CB-CG	5.40	127.73	115.30
1	E	270	GLU	N-CA-CB	5.38	120.28	110.60
1	G	190	THR	N-CA-CB	5.37	120.50	110.30
1	G	111	TYR	CB-CG-CD1	-5.37	117.78	121.00
1	D	113	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	G	203	LEU	CB-CG-CD1	-5.35	101.91	111.00
1	C	216	LYS	N-CA-C	-5.35	96.56	111.00
1	H	355	ARG	NE-CZ-NH1	-5.35	117.63	120.30
1	D	172	PHE	N-CA-C	-5.34	96.57	111.00
1	H	344	LYS	CB-CA-C	-5.33	99.74	110.40
1	G	140	ASP	N-CA-C	-5.33	96.62	111.00
1	H	300	VAL	N-CA-C	-5.32	96.62	111.00
1	A	112	VAL	O-C-N	-5.32	114.19	122.70
1	F	216	LYS	CD-CE-NZ	5.31	123.92	111.70
1	D	198	PHE	CB-CG-CD1	-5.30	117.09	120.80
1	A	126	LEU	CB-CG-CD1	5.30	120.01	111.00
1	G	118	LYS	N-CA-C	5.29	125.28	111.00
1	A	110	SER	N-CA-C	5.29	125.28	111.00
1	D	152	PHE	CD1-CG-CD2	-5.28	111.43	118.30
1	A	112	VAL	CB-CA-C	5.28	121.42	111.40
1	H	357	LEU	CB-CG-CD1	-5.25	102.08	111.00
1	E	238	LEU	CA-CB-CG	-5.24	103.25	115.30
1	H	111	TYR	CB-CG-CD2	-5.23	117.86	121.00
1	B	170	ASP	CB-CG-OD2	5.22	123.00	118.30
1	D	246	GLU	CA-CB-CG	5.22	124.88	113.40
1	A	357	LEU	CB-CA-C	5.20	120.08	110.20
1	A	238	LEU	CA-CB-CG	-5.19	103.36	115.30
1	C	182	VAL	CB-CA-C	-5.19	101.53	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	267	ASP	CB-CG-OD1	5.19	122.97	118.30
1	G	123	MET	CB-CG-SD	-5.18	96.87	112.40
1	H	246	GLU	CB-CA-C	-5.16	100.07	110.40
1	C	221	LEU	CA-CB-CG	-5.16	103.43	115.30
1	D	170	ASP	CB-CG-OD1	-5.15	113.67	118.30
1	C	310	PHE	N-CA-C	5.15	124.90	111.00
1	H	357	LEU	CA-CB-CG	-5.14	103.47	115.30
1	H	348	LEU	N-CA-C	-5.14	97.12	111.00
1	A	113	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	H	131	GLU	CB-CA-C	-5.12	100.16	110.40
1	B	126	LEU	CB-CG-CD1	5.09	119.66	111.00
1	H	233	LEU	CA-CB-CG	-5.09	103.59	115.30
1	B	138	HIS	N-CA-C	5.08	124.73	111.00
1	H	111	TYR	OH-CZ-CE2	-5.08	106.39	120.10
1	F	114	LYS	N-CA-C	5.08	124.71	111.00
1	A	333	ARG	NE-CZ-NH2	-5.07	117.76	120.30
1	D	130	ILE	CG1-CB-CG2	-5.07	100.25	111.40
1	H	182	VAL	CB-CA-C	-5.07	101.77	111.40
1	H	216	LYS	N-CA-C	-5.06	97.33	111.00
1	C	113	ARG	N-CA-C	5.06	124.66	111.00
1	B	239	ARG	CB-CG-CD	-5.06	98.45	111.60
1	C	313	VAL	CB-CA-C	-5.05	101.81	111.40
1	F	344	LYS	CD-CE-NZ	5.04	123.30	111.70
1	A	355	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	C	270	GLU	CB-CA-C	-5.04	100.33	110.40
1	H	144	ARG	NE-CZ-NH1	5.03	122.81	120.30
1	H	198	PHE	CB-CG-CD1	-5.03	117.28	120.80
1	F	238	LEU	CA-CB-CG	-5.02	103.75	115.30
1	E	201	LEU	CB-CG-CD1	5.02	119.53	111.00
1	G	253	ILE	CG1-CB-CG2	-5.02	100.36	111.40
1	F	111	TYR	CB-CA-C	-5.00	100.40	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	2100	0	2069	737	0
1	B	2100	0	2071	708	0
1	C	2100	0	2069	789	0
1	D	2086	0	2060	702	0
1	E	2100	0	2071	683	0
1	F	2100	0	2071	684	0
1	G	2100	0	2071	605	0
1	H	2100	0	2071	748	0
2	A	44	0	22	40	0
2	B	44	0	22	55	0
2	C	44	0	22	36	0
2	D	44	0	22	37	0
2	E	44	0	22	35	0
2	F	44	0	22	29	0
2	G	44	0	22	30	0
2	H	44	0	22	38	0
All	All	17138	0	16729	5432	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 160.

All (5432) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:VAL:CA	1:A:112:VAL:CB	1.81	1.53
1:A:112:VAL:CA	1:A:112:VAL:C	1.74	1.50
2:C:402:CMP:H2	2:C:402:CMP:C2	0.97	1.50
2:A:401:CMP:H2	2:A:401:CMP:C2	0.97	1.49
2:A:402:CMP:H2	2:A:402:CMP:C2	0.97	1.49
2:E:401:CMP:H2	2:E:401:CMP:C2	0.97	1.49
2:G:402:CMP:C2	2:G:402:CMP:H2	0.97	1.49
2:H:402:CMP:H2	2:H:402:CMP:C2	0.97	1.49
2:D:401:CMP:H2	2:D:401:CMP:C2	0.97	1.48
2:H:401:CMP:H2	2:H:401:CMP:C2	0.97	1.48
2:D:402:CMP:H2	2:D:402:CMP:C2	0.97	1.48
2:B:401:CMP:H2	2:B:401:CMP:C2	0.97	1.48
2:C:401:CMP:H2	2:C:401:CMP:C2	0.97	1.48
2:B:402:CMP:H2	2:B:402:CMP:C2	0.97	1.48
2:F:401:CMP:H2	2:F:401:CMP:C2	0.97	1.48
2:E:402:CMP:H2	2:E:402:CMP:C2	0.97	1.48
2:G:401:CMP:C2	2:G:401:CMP:H2	0.97	1.47
2:F:402:CMP:H2	2:F:402:CMP:C2	0.97	1.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:273:GLN:HE21	1:G:273:GLN:N	1.06	1.42
1:C:273:GLN:HE21	1:C:273:GLN:N	1.14	1.40
1:F:318:PRO:CG	1:F:318:PRO:CD	1.86	1.36
1:A:165:GLN:N	1:A:212:THR:HG23	1.41	1.30
1:B:165:GLN:N	1:B:212:THR:HG23	1.48	1.28
1:C:156:PHE:CE2	1:C:162:VAL:HG12	1.67	1.28
1:H:294:LEU:HD12	1:H:295:GLU:N	1.46	1.28
1:C:280:ILE:CD1	1:C:322:PHE:HE2	1.47	1.27
1:H:302:GLN:HE22	1:H:374:PHE:CB	1.48	1.26
1:D:165:GLN:N	1:D:212:THR:HG23	1.52	1.25
1:G:273:GLN:N	1:G:273:GLN:NE2	1.80	1.25
1:H:175:ILE:O	1:H:175:ILE:HD12	1.29	1.24
1:E:111:TYR:CE2	1:H:111:TYR:HE2	1.56	1.24
1:B:313:VAL:HG21	2:B:402:CMP:N6	1.50	1.24
1:A:175:ILE:HD12	1:A:175:ILE:O	1.37	1.23
1:E:273:GLN:N	1:E:273:GLN:HE21	1.33	1.23
1:B:175:ILE:HD12	1:B:175:ILE:O	1.36	1.22
1:H:280:ILE:CD1	1:H:322:PHE:HE2	1.51	1.22
1:F:157:ILE:HD12	1:H:243:MET:CE	1.69	1.21
1:H:284:GLY:O	1:H:332:PRO:HB3	1.41	1.21
1:A:273:GLN:N	1:A:273:GLN:HE21	1.35	1.20
1:G:165:GLN:N	1:G:212:THR:HG23	1.56	1.20
1:E:182:VAL:HG22	1:E:190:THR:O	1.39	1.20
1:H:156:PHE:CE2	1:H:162:VAL:HG12	1.76	1.20
1:F:175:ILE:HD12	1:F:175:ILE:O	1.42	1.20
1:C:280:ILE:HD13	1:C:322:PHE:CE2	1.77	1.19
1:D:156:PHE:CD2	1:D:162:VAL:HG12	1.76	1.19
1:E:156:PHE:CD2	1:E:162:VAL:HG12	1.77	1.19
1:A:165:GLN:H	1:A:212:THR:CG2	1.55	1.19
1:G:265:VAL:HG12	1:G:269:LEU:HD11	1.20	1.19
1:E:165:GLN:N	1:E:212:THR:HG23	1.55	1.18
1:F:182:VAL:HG22	1:F:190:THR:O	1.39	1.18
1:C:196:GLY:HA2	1:C:355:ARG:NH2	1.57	1.18
1:G:273:GLN:NE2	1:G:273:GLN:H	1.35	1.18
1:H:156:PHE:CD2	1:H:162:VAL:HG12	1.78	1.18
1:B:273:GLN:N	1:B:273:GLN:NE2	1.92	1.18
1:C:243:MET:CE	1:E:157:ILE:HD12	1.73	1.18
1:D:126:LEU:HD12	1:D:126:LEU:O	1.42	1.18
1:G:293:ILE:HG13	1:G:345:CYS:SG	1.83	1.18
1:B:273:GLN:NE2	1:B:273:GLN:H	1.40	1.17
1:E:196:GLY:HA2	1:E:355:ARG:NH2	1.56	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:175:ILE:HD12	1:G:175:ILE:O	1.40	1.17
1:C:178:GLY:HA3	1:C:219:VAL:HG12	1.22	1.17
1:E:265:VAL:CG1	1:E:269:LEU:HD21	1.73	1.17
1:C:249:SER:CA	1:C:262:ARG:HH22	1.58	1.17
1:D:175:ILE:HD12	1:D:175:ILE:O	1.42	1.17
1:E:112:VAL:HG12	1:E:231:ARG:CZ	1.72	1.17
1:E:156:PHE:CE2	1:E:162:VAL:HG12	1.79	1.17
1:C:279:LYS:HE2	1:C:336:THR:HG23	1.23	1.17
1:E:300:VAL:HG21	2:E:402:CMP:H8	1.25	1.17
1:C:273:GLN:N	1:C:273:GLN:NE2	1.93	1.16
1:A:182:VAL:HG22	1:A:190:THR:O	1.43	1.16
1:C:284:GLY:C	1:C:332:PRO:HB3	1.65	1.16
1:C:284:GLY:O	1:C:332:PRO:HB3	1.45	1.16
1:G:293:ILE:HD11	1:G:343:LEU:CD1	1.76	1.16
1:A:301:LEU:HB3	1:A:310:PHE:HE2	1.02	1.16
1:C:157:ILE:HD12	1:C:157:ILE:O	1.46	1.16
1:F:251:VAL:CG1	1:F:254:LEU:HD21	1.75	1.16
1:C:265:VAL:O	1:C:269:LEU:HG	1.44	1.16
1:G:265:VAL:HG13	1:G:269:LEU:HD21	1.20	1.15
1:D:279:LYS:HB2	1:D:279:LYS:NZ	1.33	1.15
1:D:353:PHE:CE1	1:D:357:LEU:HD22	1.82	1.15
1:D:251:VAL:HG13	1:D:254:LEU:HD11	1.16	1.15
1:C:113:ARG:HG3	1:F:112:VAL:HG11	1.28	1.14
1:F:165:GLN:N	1:F:212:THR:HG23	1.60	1.14
1:C:182:VAL:HG22	1:C:190:THR:O	1.47	1.14
1:G:265:VAL:O	1:G:269:LEU:HG	1.42	1.14
1:E:111:TYR:HE2	1:H:112:VAL:HG12	1.10	1.14
1:H:272:VAL:HA	1:H:273:GLN:NE2	1.63	1.14
1:D:301:LEU:HD21	1:D:310:PHE:HB3	1.17	1.14
1:H:111:TYR:CD2	1:H:112:VAL:N	2.14	1.14
1:A:115:VAL:CG2	1:D:112:VAL:HG23	1.79	1.13
1:C:113:ARG:HG3	1:F:112:VAL:CG1	1.79	1.13
1:C:266:ALA:HA	1:C:269:LEU:HD12	1.13	1.12
1:F:156:PHE:CD2	1:F:162:VAL:HG12	1.84	1.13
1:A:178:GLY:HA3	1:A:219:VAL:HG12	1.24	1.12
1:A:230:ARG:NH1	1:A:234:MET:HE1	1.63	1.12
1:E:175:ILE:HD12	1:E:175:ILE:O	1.47	1.12
1:C:175:ILE:HD12	1:C:175:ILE:O	1.48	1.12
1:C:285:GLU:O	1:C:332:PRO:HA	1.49	1.12
1:C:294:LEU:HD13	1:C:344:LYS:O	1.44	1.12
1:C:356:VAL:HG23	1:C:357:LEU:HD13	1.29	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:259:LYS:O	1:D:262:ARG:HG2	1.45	1.12
1:C:272:VAL:C	1:C:273:GLN:HE21	1.52	1.12
1:B:158:ALA:HB2	1:B:217:THR:C	1.70	1.11
1:D:165:GLN:H	1:D:212:THR:CG2	1.63	1.11
1:G:294:LEU:HD12	1:G:294:LEU:N	1.62	1.11
1:B:269:LEU:HB3	1:B:346:VAL:CG2	1.81	1.11
1:C:294:LEU:HD11	1:C:345:CYS:HA	1.21	1.11
1:C:294:LEU:HD12	1:C:294:LEU:N	1.61	1.11
1:F:162:VAL:HG23	1:F:163:ILE:HG13	1.19	1.11
1:C:115:VAL:HG23	1:F:110:SER:HB2	1.29	1.11
1:D:251:VAL:CG1	1:D:254:LEU:HD11	1.81	1.11
1:E:279:LYS:HB2	1:E:279:LYS:NZ	1.45	1.11
1:C:280:ILE:HD13	1:C:322:PHE:HE2	1.08	1.11
1:H:165:GLN:N	1:H:212:THR:HG23	1.65	1.11
1:A:325:ILE:HD11	2:A:402:CMP:O2P	1.49	1.10
1:B:294:LEU:HD11	1:B:345:CYS:HA	1.30	1.10
1:D:294:LEU:HD11	1:D:345:CYS:HA	1.28	1.10
1:D:293:ILE:HD11	1:D:343:LEU:HD11	1.21	1.10
1:D:156:PHE:CE2	1:D:162:VAL:HG12	1.86	1.10
1:F:279:LYS:HB2	1:F:279:LYS:HZ3	1.11	1.10
1:B:165:GLN:H	1:B:212:THR:CG2	1.63	1.10
1:C:165:GLN:N	1:C:212:THR:HG23	1.66	1.10
1:D:294:LEU:HD12	1:D:294:LEU:H	1.12	1.10
1:F:156:PHE:CE2	1:F:162:VAL:HG12	1.86	1.10
1:G:266:ALA:HA	1:G:269:LEU:HD12	1.14	1.10
1:E:265:VAL:O	1:E:269:LEU:HG	1.50	1.10
1:G:182:VAL:HG22	1:G:190:THR:O	1.51	1.10
1:C:249:SER:HA	1:C:262:ARG:HH22	1.11	1.09
1:F:196:GLY:HA2	1:F:355:ARG:NH2	1.67	1.09
1:G:265:VAL:CG1	1:G:269:LEU:HD21	1.82	1.09
1:A:113:ARG:NE	1:D:113:ARG:HB3	1.66	1.09
1:C:274:PHE:HD2	1:C:343:LEU:HD23	1.12	1.09
1:D:233:LEU:H	1:D:233:LEU:HD12	1.15	1.09
1:D:324:GLU:OE2	1:D:371:TYR:HE2	1.35	1.09
1:G:126:LEU:HD12	1:G:126:LEU:O	1.49	1.09
1:G:294:LEU:HD11	1:G:345:CYS:HA	1.33	1.09
1:E:162:VAL:HG23	1:E:163:ILE:HG13	1.32	1.09
1:F:273:GLN:N	1:F:273:GLN:HE21	1.50	1.09
1:E:324:GLU:O	1:E:328:LEU:HD12	1.52	1.09
1:H:182:VAL:HG22	1:H:190:THR:O	1.51	1.09
1:A:115:VAL:HG21	1:D:112:VAL:HG23	1.24	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:LEU:HD13	1:B:344:LYS:O	1.51	1.09
1:F:280:ILE:CD1	1:F:322:PHE:HE2	1.65	1.09
1:A:156:PHE:CD2	1:A:162:VAL:HG12	1.88	1.08
1:B:324:GLU:O	1:B:328:LEU:HD12	1.51	1.08
1:D:279:LYS:HZ3	1:D:279:LYS:CB	1.65	1.08
1:D:356:VAL:HG23	1:D:357:LEU:HD12	1.30	1.08
1:D:365:LYS:O	1:D:368:ILE:HG13	1.53	1.08
1:F:114:LYS:HZ2	1:F:115:VAL:HG22	1.07	1.08
1:F:229:TYR:CD1	1:F:233:LEU:HD13	1.88	1.08
1:H:260:TRP:HE1	2:H:401:CMP:H2'	1.13	1.08
1:A:190:THR:HG22	1:A:191:SER:H	1.15	1.08
1:E:251:VAL:HG13	1:E:254:LEU:HD21	1.28	1.08
1:B:229:TYR:CD1	1:B:233:LEU:HD13	1.88	1.08
1:D:182:VAL:HG22	1:D:190:THR:O	1.51	1.08
1:D:253:ILE:HG13	1:D:254:LEU:HD13	1.35	1.08
1:E:293:ILE:HD13	1:E:317:GLY:O	1.54	1.08
1:G:365:LYS:O	1:G:368:ILE:HG13	1.54	1.08
1:A:116:ILE:O	1:A:118:LYS:HG3	1.50	1.08
1:B:161:THR:HA	1:B:214:LYS:HD2	1.30	1.08
1:G:165:GLN:H	1:G:212:THR:CG2	1.67	1.08
1:H:178:GLY:HA3	1:H:219:VAL:HG12	1.31	1.08
1:A:269:LEU:HD22	1:A:346:VAL:HG21	1.36	1.07
1:E:112:VAL:HG12	1:E:231:ARG:NE	1.68	1.07
1:E:294:LEU:N	1:E:294:LEU:HD12	1.57	1.07
1:G:294:LEU:CD1	1:G:345:CYS:HA	1.84	1.07
1:A:126:LEU:HD12	1:A:126:LEU:O	1.51	1.07
1:A:294:LEU:CD1	1:A:345:CYS:HA	1.85	1.07
1:B:294:LEU:H	1:B:294:LEU:HD12	1.13	1.07
1:C:265:VAL:HG12	1:C:269:LEU:HD11	1.12	1.07
1:G:279:LYS:HZ3	1:G:279:LYS:HB2	0.93	1.07
1:G:293:ILE:HD11	1:G:343:LEU:HD11	1.08	1.07
1:H:228:SER:O	1:H:232:ILE:HG22	1.54	1.07
1:H:273:GLN:HB3	1:H:344:LYS:HA	1.36	1.07
1:H:356:VAL:HG23	1:H:357:LEU:HD13	1.32	1.07
1:D:251:VAL:HG23	1:D:319:SER:O	1.55	1.07
1:E:175:ILE:HD11	1:E:196:GLY:H	1.17	1.07
1:G:279:LYS:HB2	1:G:279:LYS:NZ	1.53	1.07
1:B:175:ILE:HA	1:B:221:LEU:CD2	1.85	1.07
1:D:134:VAL:HG11	1:D:268:ALA:HA	1.36	1.07
1:D:273:GLN:HE21	1:D:273:GLN:N	1.51	1.07
1:C:134:VAL:HG11	1:C:268:ALA:HA	1.33	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:294:LEU:CD1	1:D:345:CYS:HA	1.85	1.07
1:E:226:ARG:HH11	1:E:226:ARG:HG3	1.18	1.07
1:E:294:LEU:CD1	1:E:345:CYS:HA	1.85	1.07
1:F:255:GLU:OE1	1:F:255:GLU:HA	1.53	1.07
1:A:294:LEU:HD11	1:A:345:CYS:HA	1.34	1.06
1:F:226:ARG:HH11	1:F:226:ARG:HG3	1.15	1.06
1:H:134:VAL:HG11	1:H:268:ALA:HA	1.36	1.06
1:B:196:GLY:HA2	1:B:355:ARG:NH2	1.70	1.06
1:D:298:ALA:HB1	1:D:338:VAL:O	1.56	1.06
1:F:126:LEU:HD12	1:F:126:LEU:O	1.56	1.06
1:H:165:GLN:H	1:H:212:THR:HG23	0.93	1.06
1:A:175:ILE:HA	1:A:221:LEU:CD2	1.85	1.06
1:H:157:ILE:HD12	1:H:157:ILE:O	1.56	1.06
1:A:273:GLN:N	1:A:273:GLN:NE2	2.01	1.06
1:C:229:TYR:HD1	1:C:233:LEU:CD1	1.69	1.06
1:E:165:GLN:H	1:E:212:THR:CG2	1.68	1.06
1:H:280:ILE:CD1	1:H:322:PHE:CE2	2.39	1.06
1:B:116:ILE:O	1:B:118:LYS:HG3	1.55	1.06
1:C:111:TYR:HE1	1:F:111:TYR:CE2	1.75	1.05
1:C:294:LEU:CD1	1:C:345:CYS:HA	1.84	1.05
1:F:294:LEU:HD12	1:F:294:LEU:N	1.70	1.05
1:F:324:GLU:O	1:F:328:LEU:HD12	1.55	1.05
1:G:226:ARG:HG3	1:G:226:ARG:HH11	1.15	1.05
1:C:111:TYR:CE1	1:F:111:TYR:CE2	2.44	1.05
1:D:200:GLU:HG2	1:D:201:LEU:H	1.15	1.05
1:C:278:GLN:HG3	1:C:279:LYS:N	1.66	1.05
1:D:291:PHE:CE1	1:D:347:LYS:NZ	2.25	1.05
1:H:279:LYS:NZ	1:H:336:THR:HG23	1.72	1.05
1:F:289:GLU:HG3	1:F:347:LYS:NZ	1.69	1.04
1:A:114:LYS:HG3	1:A:115:VAL:H	1.22	1.04
1:G:294:LEU:HD12	1:G:294:LEU:H	0.99	1.04
1:A:371:TYR:CE1	2:A:402:CMP:C8	2.41	1.04
1:C:243:MET:HE3	1:E:157:ILE:HD12	1.37	1.04
1:C:272:VAL:HA	1:C:273:GLN:NE2	1.72	1.04
1:F:251:VAL:HG12	1:F:254:LEU:CD2	1.88	1.04
1:C:113:ARG:HD2	1:F:112:VAL:HB	1.37	1.04
1:D:190:THR:HG22	1:D:191:SER:H	1.21	1.04
1:D:279:LYS:NZ	1:D:279:LYS:CB	2.06	1.04
1:D:324:GLU:HG2	1:D:325:ILE:N	1.70	1.04
1:D:356:VAL:HG23	1:D:357:LEU:CD1	1.86	1.04
1:G:161:THR:HA	1:G:214:LYS:HD2	1.40	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:233:LEU:H	1:G:233:LEU:HD12	1.22	1.04
1:H:272:VAL:CA	1:H:273:GLN:NE2	2.21	1.04
1:A:262:ARG:O	1:A:265:VAL:HB	1.56	1.04
1:C:275:GLU:O	1:C:278:GLN:HB3	1.56	1.04
1:F:289:GLU:HG3	1:F:347:LYS:HZ3	1.16	1.04
1:A:294:LEU:H	1:A:294:LEU:HD12	1.13	1.03
1:B:182:VAL:HG22	1:B:190:THR:O	1.56	1.03
1:C:156:PHE:CD2	1:C:162:VAL:HG12	1.91	1.03
1:C:281:VAL:HG11	1:C:333:ARG:HD2	1.35	1.03
1:D:293:ILE:HG13	1:D:345:CYS:SG	1.98	1.03
1:D:294:LEU:HD12	1:D:294:LEU:N	1.68	1.03
1:A:365:LYS:O	1:A:368:ILE:HG13	1.58	1.03
1:B:153:PRO:HB3	1:B:222:TRP:CZ3	1.92	1.03
1:B:356:VAL:HG23	1:B:357:LEU:HD13	1.34	1.03
1:G:302:GLN:CG	1:G:313:VAL:HG11	1.87	1.03
1:H:280:ILE:HD13	1:H:322:PHE:CE2	1.92	1.03
1:A:198:PHE:HD1	1:A:198:PHE:C	1.57	1.03
1:F:112:VAL:HG13	1:F:113:ARG:H	1.24	1.03
1:F:172:PHE:HB3	1:F:224:ILE:HD11	1.40	1.03
1:B:280:ILE:CD1	1:B:322:PHE:HE2	1.72	1.03
1:C:113:ARG:CG	1:F:112:VAL:HG11	1.88	1.03
1:C:269:LEU:HB3	1:C:346:VAL:CG2	1.89	1.03
1:D:293:ILE:HD11	1:D:343:LEU:CD1	1.88	1.03
1:G:251:VAL:HG13	1:G:254:LEU:HD21	1.37	1.03
1:H:251:VAL:O	1:H:254:LEU:HD11	1.57	1.03
1:B:251:VAL:HG13	1:B:254:LEU:HD21	1.35	1.03
1:E:266:ALA:HA	1:E:269:LEU:HD12	1.33	1.03
1:F:175:ILE:HD11	1:F:196:GLY:H	1.21	1.03
1:G:190:THR:HG22	1:G:191:SER:H	1.23	1.03
1:A:115:VAL:HG21	1:D:112:VAL:H	1.20	1.02
1:E:299:ALA:HB1	1:E:312:GLU:OE2	1.56	1.02
1:F:157:ILE:HD12	1:H:243:MET:HE1	1.41	1.02
1:G:266:ALA:HA	1:G:269:LEU:CD1	1.89	1.02
1:C:165:GLN:H	1:C:212:THR:CG2	1.71	1.02
1:E:175:ILE:HA	1:E:221:LEU:CD2	1.90	1.02
1:E:265:VAL:HG13	1:E:269:LEU:HD21	1.36	1.02
1:E:325:ILE:HD11	2:E:402:CMP:O2P	1.59	1.02
1:H:279:LYS:NZ	1:H:279:LYS:HB2	1.75	1.02
1:A:113:ARG:HE	1:D:113:ARG:HB3	0.89	1.02
1:B:111:TYR:O	1:B:112:VAL:HG22	1.58	1.02
1:B:280:ILE:HD11	1:B:322:PHE:HE2	1.17	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:249:SER:HA	1:C:262:ARG:NH2	1.73	1.02
1:C:280:ILE:CD1	1:C:322:PHE:CE2	2.38	1.02
1:E:229:TYR:CD1	1:E:233:LEU:HD13	1.94	1.02
1:A:266:ALA:HA	1:A:269:LEU:HD12	1.37	1.02
1:B:280:ILE:CD1	1:B:322:PHE:CE2	2.43	1.02
1:B:294:LEU:HD12	1:B:294:LEU:N	1.73	1.02
1:D:273:GLN:N	1:D:273:GLN:NE2	2.06	1.02
1:E:294:LEU:HD12	1:E:294:LEU:H	1.06	1.02
1:F:114:LYS:NZ	1:F:115:VAL:HG22	1.74	1.02
1:B:180:MET:HB2	1:B:192:VAL:HB	1.40	1.02
1:C:115:VAL:HA	1:C:149:ASP:HB3	1.39	1.02
1:C:226:ARG:HH11	1:C:226:ARG:HG3	1.19	1.02
1:E:273:GLN:N	1:E:273:GLN:NE2	2.06	1.02
1:H:114:LYS:NZ	1:H:115:VAL:H	1.55	1.02
1:H:226:ARG:HH11	1:H:226:ARG:HG3	1.22	1.02
1:H:229:TYR:CD1	1:H:233:LEU:HD13	1.95	1.02
1:A:114:LYS:CG	1:A:115:VAL:H	1.72	1.01
1:B:126:LEU:HD12	1:B:126:LEU:O	1.59	1.01
1:B:172:PHE:HB3	1:B:224:ILE:HD11	1.40	1.01
1:E:111:TYR:CE2	1:H:111:TYR:CE2	2.47	1.01
1:H:161:THR:HA	1:H:214:LYS:HD2	1.42	1.01
1:A:301:LEU:HB3	1:A:310:PHE:CE2	1.94	1.01
1:E:348:LEU:HD21	1:E:356:VAL:HG21	1.43	1.01
1:H:251:VAL:HG13	1:H:254:LEU:HD21	1.38	1.01
1:A:229:TYR:CD1	1:A:233:LEU:HD13	1.95	1.01
1:C:229:TYR:CD1	1:C:233:LEU:CD1	2.43	1.01
1:D:162:VAL:HG23	1:D:163:ILE:HG13	1.39	1.01
1:D:260:TRP:HE1	2:D:401:CMP:H2'	1.23	1.01
1:F:165:GLN:H	1:F:212:THR:HG23	0.84	1.01
1:G:162:VAL:HG23	1:G:163:ILE:HG13	1.40	1.01
1:H:112:VAL:HG13	1:H:113:ARG:H	1.25	1.01
1:C:279:LYS:HE2	1:C:336:THR:CG2	1.90	1.01
1:D:135:LEU:HD12	1:D:136:PHE:H	1.25	1.01
1:B:156:PHE:CD2	1:B:162:VAL:HG12	1.95	1.00
1:B:190:THR:HG22	1:B:191:SER:H	1.24	1.00
1:C:165:GLN:H	1:C:212:THR:HG23	0.86	1.00
1:C:175:ILE:HA	1:C:221:LEU:CD2	1.91	1.00
1:E:294:LEU:HD11	1:E:345:CYS:HA	1.43	1.00
1:F:260:TRP:HE1	2:F:401:CMP:H2'	1.26	1.00
1:G:211:ASP:CG	2:G:401:CMP:H5'1	1.81	1.00
1:H:165:GLN:H	1:H:212:THR:CG2	1.74	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:272:VAL:HA	1:H:273:GLN:HE22	1.13	1.00
1:A:115:VAL:CB	1:D:112:VAL:HG23	1.90	1.00
1:A:260:TRP:CE2	2:A:401:CMP:C8	2.43	1.00
1:H:190:THR:HG22	1:H:191:SER:H	1.25	1.00
1:H:274:PHE:HD2	1:H:343:LEU:HD23	1.22	1.00
1:A:161:THR:HA	1:A:214:LYS:HD2	1.44	1.00
1:A:371:TYR:HE1	2:A:402:CMP:C8	1.74	1.00
1:B:269:LEU:HB3	1:B:346:VAL:HG21	1.38	1.00
1:F:165:GLN:H	1:F:212:THR:CG2	1.75	1.00
1:G:196:GLY:HA2	1:G:355:ARG:NH2	1.76	1.00
1:G:302:GLN:HG3	1:G:313:VAL:CG1	1.92	1.00
1:H:249:SER:CA	1:H:262:ARG:HH22	1.74	1.00
1:C:266:ALA:HA	1:C:269:LEU:CD1	1.92	1.00
1:F:233:LEU:HD12	1:F:233:LEU:H	1.26	1.00
1:B:139:LEU:HD12	1:B:139:LEU:H	1.26	1.00
1:C:139:LEU:H	1:C:139:LEU:HD12	1.24	1.00
1:E:126:LEU:O	1:E:126:LEU:HD12	1.60	1.00
1:E:265:VAL:HG12	1:E:269:LEU:HD11	1.41	1.00
1:E:280:ILE:CD1	1:E:322:PHE:HE2	1.75	1.00
1:G:229:TYR:CD1	1:G:233:LEU:HD13	1.96	1.00
1:C:282:VAL:O	1:C:285:GLU:HG2	1.62	1.00
1:D:229:TYR:CD1	1:D:233:LEU:HD13	1.97	1.00
1:E:279:LYS:NZ	1:E:279:LYS:CB	2.21	1.00
1:A:255:GLU:OE1	1:A:255:GLU:HA	1.56	1.00
1:G:279:LYS:HZ3	1:G:279:LYS:CB	1.72	1.00
1:B:294:LEU:CD1	1:B:345:CYS:HA	1.91	0.99
1:C:293:ILE:HD11	1:C:343:LEU:HD11	1.43	0.99
1:G:251:VAL:CG1	1:G:254:LEU:HD21	1.92	0.99
1:H:300:VAL:O	1:H:301:LEU:HD23	1.61	0.99
1:F:280:ILE:CD1	1:F:322:PHE:CE2	2.45	0.99
1:H:226:ARG:HG3	1:H:226:ARG:NH1	1.75	0.99
1:A:357:LEU:N	1:A:357:LEU:HD12	1.55	0.99
1:H:182:VAL:HG23	1:H:182:VAL:O	1.61	0.99
1:A:113:ARG:HE	1:D:113:ARG:CB	1.73	0.99
1:A:269:LEU:HB3	1:A:346:VAL:CG2	1.93	0.99
1:D:371:TYR:CE1	2:D:402:CMP:N7	2.30	0.99
1:A:233:LEU:H	1:A:233:LEU:HD12	1.26	0.99
1:C:158:ALA:HB2	1:C:217:THR:C	1.83	0.99
1:A:294:LEU:HD12	1:A:294:LEU:N	1.75	0.99
1:B:226:ARG:HG3	1:B:226:ARG:HH11	1.27	0.99
1:E:282:VAL:O	1:E:285:GLU:HG2	1.63	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:293:ILE:CD1	1:G:343:LEU:HD11	1.92	0.99
1:A:175:ILE:HD13	1:A:194:GLU:HA	1.45	0.99
1:C:110:SER:HB3	1:F:114:LYS:HE2	1.40	0.99
1:D:247:PHE:HE1	1:D:294:LEU:HA	1.27	0.99
1:G:356:VAL:HG23	1:G:357:LEU:CD1	1.93	0.98
1:A:172:PHE:HB3	1:A:224:ILE:HD11	1.44	0.98
1:E:111:TYR:CE2	1:H:112:VAL:HG12	1.98	0.98
1:A:135:LEU:HD12	1:A:136:PHE:H	1.24	0.98
1:E:111:TYR:HE2	1:H:112:VAL:CG1	1.76	0.98
1:A:157:ILE:O	1:A:157:ILE:HD12	1.64	0.98
1:C:265:VAL:HG13	1:C:269:LEU:HD21	1.45	0.98
1:E:365:LYS:O	1:E:368:ILE:HG13	1.63	0.98
1:H:269:LEU:HB3	1:H:346:VAL:HG21	1.45	0.98
1:D:259:LYS:HG3	1:D:260:TRP:N	1.79	0.98
1:C:273:GLN:HB3	1:C:343:LEU:O	1.63	0.98
1:H:154:VAL:HG12	1:H:221:LEU:HB2	1.45	0.98
1:A:251:VAL:HG23	1:A:319:SER:O	1.63	0.98
1:B:200:GLU:HG2	1:B:201:LEU:H	1.29	0.98
1:C:229:TYR:CD1	1:C:233:LEU:HD13	1.98	0.98
1:D:226:ARG:HH11	1:D:226:ARG:HG3	1.23	0.98
1:H:196:GLY:HA2	1:H:355:ARG:NH2	1.77	0.98
1:D:247:PHE:CE1	1:D:294:LEU:HA	1.98	0.98
1:H:229:TYR:CD1	1:H:233:LEU:CD1	2.47	0.98
1:B:233:LEU:H	1:B:233:LEU:HD12	1.26	0.97
1:E:251:VAL:HG23	1:E:319:SER:O	1.63	0.97
1:A:135:LEU:HD12	1:A:136:PHE:N	1.80	0.97
1:A:293:ILE:HD11	1:A:343:LEU:HD11	1.42	0.97
1:A:230:ARG:NH1	1:A:234:MET:CE	2.26	0.97
1:C:281:VAL:CG1	1:C:333:ARG:HD2	1.93	0.97
1:D:301:LEU:HD23	1:D:310:PHE:HD1	1.28	0.97
1:B:260:TRP:HE1	2:B:401:CMP:H2'	1.29	0.97
1:H:229:TYR:HD1	1:H:233:LEU:CD1	1.77	0.97
1:H:284:GLY:C	1:H:332:PRO:HB3	1.85	0.97
1:C:204:ILE:HG22	1:C:205:TYR:CD2	2.00	0.97
1:F:293:ILE:HD11	1:F:343:LEU:HD11	1.47	0.97
1:A:198:PHE:HD1	1:A:198:PHE:O	1.46	0.97
1:H:253:ILE:HG13	1:H:254:LEU:H	1.30	0.96
1:A:139:LEU:H	1:A:139:LEU:HD12	1.28	0.96
1:A:226:ARG:HH11	1:A:226:ARG:HG3	1.28	0.96
1:G:148:PHE:CD1	1:H:120:TYR:CE1	2.52	0.96
1:B:229:TYR:HD1	1:B:233:LEU:HD13	1.27	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:294:LEU:HD12	1:C:294:LEU:H	1.16	0.96
1:D:182:VAL:HG12	1:D:213:VAL:HG22	1.43	0.96
1:F:157:ILE:HD12	1:H:243:MET:HE3	1.40	0.96
1:A:153:PRO:HB3	1:A:222:TRP:CZ3	2.01	0.96
1:A:259:LYS:HG3	1:A:260:TRP:N	1.78	0.96
1:C:265:VAL:HG12	1:C:269:LEU:CD1	1.93	0.96
1:E:178:GLY:HA3	1:E:219:VAL:HG12	1.45	0.96
1:B:259:LYS:HG3	1:B:260:TRP:N	1.80	0.96
1:B:260:TRP:CE2	2:B:401:CMP:C8	2.48	0.96
1:C:283:GLN:HA	1:C:333:ARG:O	1.66	0.96
1:G:172:PHE:HB3	1:G:224:ILE:HD11	1.46	0.96
1:G:247:PHE:HE1	1:G:294:LEU:HA	1.29	0.96
1:A:198:PHE:C	1:A:198:PHE:CD1	2.32	0.96
1:E:249:SER:N	1:E:262:ARG:HH22	1.61	0.96
1:A:247:PHE:HE1	1:A:294:LEU:HA	1.28	0.96
1:B:273:GLN:N	1:B:273:GLN:HE21	1.53	0.96
1:C:156:PHE:HE2	1:C:162:VAL:HG12	1.19	0.96
1:C:230:ARG:HG2	1:C:234:MET:HE1	1.46	0.96
1:C:324:GLU:O	1:C:328:LEU:HD12	1.65	0.96
1:D:172:PHE:HB3	1:D:224:ILE:HD11	1.47	0.96
1:F:269:LEU:HB3	1:F:346:VAL:CG2	1.95	0.96
1:F:273:GLN:N	1:F:273:GLN:NE2	2.13	0.96
1:A:280:ILE:HD11	1:A:322:PHE:HE2	1.31	0.96
1:D:153:PRO:HB3	1:D:222:TRP:CZ3	2.01	0.96
1:F:118:LYS:HE2	1:F:148:PHE:O	1.65	0.96
1:H:114:LYS:HZ1	1:H:115:VAL:H	1.06	0.96
1:C:120:TYR:HB2	1:D:149:ASP:OD1	1.66	0.95
1:H:279:LYS:HE3	1:H:282:VAL:HG22	1.47	0.95
1:A:154:VAL:HG12	1:A:221:LEU:HB2	1.44	0.95
1:C:190:THR:HG22	1:C:191:SER:H	1.30	0.95
1:E:280:ILE:CD1	1:E:322:PHE:CE2	2.50	0.95
1:G:134:VAL:HG11	1:G:268:ALA:HA	1.44	0.95
1:H:211:ASP:CG	2:H:401:CMP:H5'1	1.85	0.95
1:A:251:VAL:HG13	1:A:254:LEU:HD21	1.45	0.95
1:C:120:TYR:CE1	1:D:148:PHE:CD1	2.53	0.95
1:C:274:PHE:CD2	1:C:343:LEU:HD23	1.99	0.95
1:G:255:GLU:OE1	1:G:255:GLU:HA	1.65	0.95
1:H:158:ALA:HB2	1:H:217:THR:C	1.86	0.95
1:B:230:ARG:O	1:B:234:MET:HB3	1.63	0.95
1:C:182:VAL:HG23	1:C:182:VAL:O	1.66	0.95
1:D:200:GLU:HG2	1:D:201:LEU:N	1.78	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:148:PHE:CB	1:H:120:TYR:HD1	1.79	0.95
1:G:165:GLN:H	1:G:212:THR:HG23	0.80	0.95
1:A:112:VAL:HG22	1:D:115:VAL:HG21	1.46	0.95
1:E:251:VAL:O	1:E:254:LEU:HD11	1.65	0.95
1:F:329:MET:HB2	1:F:331:ARG:HG3	1.48	0.95
1:A:291:PHE:N	1:A:291:PHE:HD1	1.60	0.95
1:B:175:ILE:HD13	1:B:194:GLU:HA	1.45	0.95
1:C:365:LYS:O	1:C:368:ILE:HG13	1.64	0.95
1:A:269:LEU:HD22	1:A:346:VAL:CG2	1.97	0.95
1:B:200:GLU:HG2	1:B:201:LEU:N	1.78	0.95
1:F:259:LYS:O	1:F:262:ARG:HG3	1.63	0.95
1:G:226:ARG:HG3	1:G:226:ARG:NH1	1.72	0.95
1:H:172:PHE:HB3	1:H:224:ILE:HD11	1.49	0.95
1:A:112:VAL:C	1:A:112:VAL:HA	1.86	0.95
1:C:272:VAL:CA	1:C:273:GLN:NE2	2.30	0.95
1:G:259:LYS:O	1:G:262:ARG:HG3	1.66	0.95
1:A:196:GLY:HA2	1:A:355:ARG:NH2	1.81	0.94
1:C:120:TYR:HD1	1:D:148:PHE:CB	1.80	0.94
1:A:158:ALA:HB2	1:A:217:THR:C	1.87	0.94
1:B:200:GLU:CG	1:B:201:LEU:H	1.79	0.94
1:B:251:VAL:HG23	1:B:319:SER:O	1.66	0.94
1:E:243:MET:HE3	1:G:157:ILE:CD1	1.97	0.94
1:E:255:GLU:OE1	1:E:255:GLU:HA	1.65	0.94
1:C:172:PHE:HB3	1:C:224:ILE:HD11	1.46	0.94
1:F:300:VAL:HG22	1:F:337:VAL:HG22	1.48	0.94
1:G:148:PHE:CD1	1:H:120:TYR:HE1	1.85	0.94
1:G:173:TYR:HB2	1:G:198:PHE:CE1	2.02	0.94
1:H:229:TYR:CE1	1:H:233:LEU:HD13	2.01	0.94
1:H:233:LEU:H	1:H:233:LEU:HD12	1.32	0.94
1:C:265:VAL:CG1	1:C:269:LEU:HD21	1.98	0.94
1:B:157:ILE:HD12	1:B:157:ILE:O	1.68	0.94
1:B:253:ILE:HG13	1:B:254:LEU:H	1.30	0.94
1:F:175:ILE:HA	1:F:221:LEU:CD2	1.97	0.94
1:G:260:TRP:HE1	2:G:401:CMP:H2'	1.27	0.94
1:H:365:LYS:O	1:H:368:ILE:HG13	1.66	0.94
1:E:273:GLN:HE21	1:E:273:GLN:H	1.07	0.94
1:A:115:VAL:HG21	1:D:112:VAL:N	1.83	0.94
1:B:291:PHE:N	1:B:291:PHE:HD1	1.66	0.94
1:C:356:VAL:HG23	1:C:357:LEU:CD1	1.96	0.94
1:F:114:LYS:NZ	1:F:115:VAL:CG2	2.30	0.94
1:F:279:LYS:HB2	1:F:279:LYS:NZ	1.81	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:300:VAL:CG1	1:F:335:ALA:HB1	1.96	0.94
1:B:350:ARG:HB3	1:B:351:PRO:HD3	1.47	0.94
1:C:120:TYR:HE1	1:D:148:PHE:CD1	1.86	0.94
1:E:211:ASP:OD2	2:E:401:CMP:H3'	1.67	0.94
1:D:279:LYS:HB2	1:D:279:LYS:HZ3	0.85	0.94
1:A:294:LEU:HD13	1:A:344:LYS:O	1.67	0.93
1:F:229:TYR:HD1	1:F:233:LEU:CD1	1.81	0.93
1:F:294:LEU:HD12	1:F:294:LEU:H	1.31	0.93
1:G:204:ILE:HG12	1:G:234:MET:SD	2.08	0.93
1:H:114:LYS:HZ1	1:H:115:VAL:N	1.65	0.93
1:C:251:VAL:HG13	1:C:254:LEU:HD21	1.50	0.93
1:D:165:GLN:H	1:D:212:THR:HG23	0.78	0.93
1:E:171:ASN:HB3	1:E:224:ILE:O	1.68	0.93
1:E:173:TYR:HB2	1:E:198:PHE:CE1	2.04	0.93
1:F:294:LEU:CD1	1:F:345:CYS:HA	1.98	0.93
1:H:300:VAL:HG11	2:H:402:CMP:C8	1.98	0.93
1:A:156:PHE:CE2	1:A:162:VAL:HG12	2.03	0.93
1:C:182:VAL:HG12	1:C:213:VAL:HG13	1.51	0.93
1:B:259:LYS:HG3	1:B:260:TRP:H	1.34	0.93
1:F:171:ASN:HB3	1:F:224:ILE:O	1.69	0.93
1:A:175:ILE:CD1	1:A:194:GLU:HA	1.98	0.93
1:A:182:VAL:HG12	1:A:213:VAL:HG22	1.48	0.93
1:C:115:VAL:CG2	1:F:110:SER:HB2	1.98	0.93
1:D:161:THR:HA	1:D:214:LYS:HD2	1.49	0.93
1:D:324:GLU:HG2	1:D:325:ILE:H	1.21	0.93
1:F:162:VAL:CG2	1:F:163:ILE:HG13	1.99	0.93
1:F:179:GLU:HG2	1:F:216:LYS:HD3	1.50	0.93
1:A:162:VAL:HG23	1:A:163:ILE:HG13	1.49	0.93
1:B:182:VAL:O	1:B:182:VAL:HG23	1.69	0.93
1:G:251:VAL:O	1:G:254:LEU:HD11	1.68	0.93
1:H:182:VAL:HG12	1:H:213:VAL:HG22	1.48	0.93
1:H:280:ILE:HG13	1:H:281:VAL:N	1.82	0.93
1:A:211:ASP:OD2	2:A:401:CMP:H3'	1.69	0.93
1:B:255:GLU:OE1	1:B:255:GLU:HA	1.66	0.93
1:D:175:ILE:HA	1:D:221:LEU:CD2	1.99	0.93
1:D:371:TYR:HE1	2:D:402:CMP:N7	1.66	0.93
1:G:371:TYR:CE1	2:G:402:CMP:C5	2.56	0.93
1:H:269:LEU:HB3	1:H:346:VAL:CG2	1.99	0.93
1:B:247:PHE:CE1	1:B:294:LEU:HA	2.03	0.93
1:D:273:GLN:HE21	1:D:273:GLN:H	0.99	0.93
1:H:262:ARG:O	1:H:265:VAL:HB	1.69	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:325:ILE:HD11	2:D:402:CMP:O1P	1.69	0.92
1:E:233:LEU:H	1:E:233:LEU:HD12	1.32	0.92
1:F:157:ILE:CD1	1:H:243:MET:HE3	1.98	0.92
1:F:226:ARG:HG3	1:F:226:ARG:NH1	1.74	0.92
1:H:156:PHE:CD2	1:H:162:VAL:CG1	2.52	0.92
1:H:279:LYS:HZ1	1:H:336:THR:HG23	1.31	0.92
1:B:279:LYS:HE3	1:B:282:VAL:HG22	1.51	0.92
1:C:161:THR:HA	1:C:214:LYS:HD2	1.51	0.92
1:C:179:GLU:HG2	1:C:216:LYS:HD2	1.52	0.92
1:D:293:ILE:CD1	1:D:343:LEU:HD11	1.99	0.92
1:F:161:THR:HA	1:F:214:LYS:HD2	1.49	0.92
1:B:325:ILE:HG13	1:B:326:ALA:H	1.34	0.92
1:D:157:ILE:HB	1:D:218:ASN:OD1	1.70	0.92
1:H:294:LEU:CD1	1:H:295:GLU:N	2.32	0.92
1:A:357:LEU:HD12	1:A:357:LEU:H	1.31	0.92
1:C:270:GLU:O	1:C:346:VAL:HA	1.68	0.92
1:C:126:LEU:HD12	1:C:126:LEU:O	1.68	0.92
1:E:172:PHE:HB3	1:E:224:ILE:HD11	1.47	0.92
1:H:356:VAL:HG23	1:H:357:LEU:CD1	1.98	0.92
1:A:280:ILE:CD1	1:A:322:PHE:HE2	1.80	0.92
1:E:265:VAL:HG12	1:E:269:LEU:HD21	1.50	0.92
1:F:280:ILE:HD11	1:F:322:PHE:HE2	1.33	0.92
1:H:139:LEU:H	1:H:139:LEU:HD12	1.35	0.92
1:B:266:ALA:HA	1:B:269:LEU:HD12	1.51	0.92
1:D:204:ILE:HG12	1:D:234:MET:SD	2.08	0.92
1:G:247:PHE:CE1	1:G:294:LEU:HA	2.05	0.92
1:A:249:SER:N	1:A:262:ARG:HH22	1.67	0.92
1:A:259:LYS:HG3	1:A:260:TRP:H	1.31	0.92
1:D:279:LYS:HB2	1:D:279:LYS:HZ2	1.34	0.92
1:H:302:GLN:NE2	1:H:374:PHE:CB	2.32	0.92
1:B:280:ILE:HD13	1:B:322:PHE:CZ	2.04	0.92
1:C:175:ILE:HA	1:C:221:LEU:HD22	1.51	0.92
1:G:302:GLN:HG3	1:G:313:VAL:HG11	0.96	0.92
1:D:118:LYS:HE2	1:D:148:PHE:O	1.70	0.92
1:F:294:LEU:HD11	1:F:345:CYS:HA	1.50	0.92
1:G:153:PRO:HB3	1:G:222:TRP:CZ3	2.05	0.92
1:B:118:LYS:HE2	1:B:148:PHE:O	1.70	0.91
1:C:243:MET:HE1	1:E:157:ILE:HD12	1.52	0.91
1:E:113:ARG:O	1:H:112:VAL:HB	1.69	0.91
1:G:265:VAL:HG12	1:G:269:LEU:CD1	1.99	0.91
1:G:279:LYS:NZ	1:G:279:LYS:CB	2.16	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:350:ARG:HB3	1:G:351:PRO:HD3	1.52	0.91
1:H:234:MET:HG3	1:H:238:LEU:HD12	1.52	0.91
1:H:285:GLU:OE1	1:H:285:GLU:HA	1.69	0.91
1:D:196:GLY:HA2	1:D:355:ARG:NH2	1.84	0.91
1:E:289:GLU:HG3	1:E:347:LYS:NZ	1.83	0.91
1:G:301:LEU:HD13	1:G:310:PHE:HB3	1.50	0.91
1:H:274:PHE:CD2	1:H:343:LEU:HD23	2.05	0.91
1:A:247:PHE:CE1	1:A:294:LEU:HA	2.05	0.91
1:B:200:GLU:HG2	1:B:201:LEU:CD1	1.98	0.91
1:C:226:ARG:HG3	1:C:226:ARG:NH1	1.74	0.91
1:H:294:LEU:HD12	1:H:294:LEU:C	1.87	0.91
1:B:175:ILE:CD1	1:B:194:GLU:HA	2.00	0.91
1:A:115:VAL:HG21	1:D:112:VAL:CG2	2.00	0.91
1:B:259:LYS:O	1:B:262:ARG:HG3	1.70	0.91
1:B:313:VAL:HG23	1:B:313:VAL:O	1.67	0.91
1:E:228:SER:O	1:E:232:ILE:HG22	1.70	0.91
1:F:152:PHE:HE2	1:F:223:GLY:HA3	1.33	0.91
1:B:247:PHE:HE1	1:B:294:LEU:HA	1.33	0.91
1:C:156:PHE:CD2	1:C:162:VAL:CG1	2.53	0.91
1:E:280:ILE:HD11	1:E:322:PHE:HE2	1.34	0.91
1:F:179:GLU:HG2	1:F:216:LYS:CD	1.99	0.91
1:G:251:VAL:HG23	1:G:319:SER:O	1.70	0.91
1:F:293:ILE:HG13	1:F:345:CYS:SG	2.09	0.91
1:A:273:GLN:HE21	1:A:273:GLN:H	0.99	0.91
1:C:253:ILE:HG13	1:C:254:LEU:H	1.36	0.91
1:E:111:TYR:HE2	1:H:111:TYR:HE2	1.06	0.91
1:A:180:MET:HB2	1:A:192:VAL:HB	1.51	0.91
1:C:224:ILE:HD12	1:C:224:ILE:N	1.86	0.91
1:H:293:ILE:HD11	1:H:343:LEU:HD11	1.51	0.91
1:A:230:ARG:O	1:A:234:MET:HB3	1.71	0.91
1:B:278:GLN:CG	1:B:279:LYS:H	1.84	0.91
1:C:111:TYR:CE1	1:F:111:TYR:HE2	1.87	0.91
1:D:301:LEU:CD2	1:D:310:PHE:HB3	2.00	0.91
1:E:279:LYS:HB2	1:E:279:LYS:HZ2	1.00	0.91
1:F:113:ARG:HD3	1:F:146:ASP:CG	1.91	0.91
1:F:251:VAL:O	1:F:254:LEU:HD11	1.70	0.91
1:B:111:TYR:CD2	1:B:112:VAL:N	2.39	0.90
1:B:365:LYS:O	1:B:368:ILE:HG13	1.70	0.90
1:D:324:GLU:OE2	1:D:371:TYR:CE2	2.24	0.90
1:E:161:THR:HA	1:E:214:LYS:HD2	1.52	0.90
1:H:114:LYS:HZ2	1:H:114:LYS:HA	1.33	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:280:ILE:HG13	1:C:281:VAL:N	1.84	0.90
1:A:134:VAL:HG11	1:A:268:ALA:HA	1.53	0.90
1:E:123:MET:HE3	1:F:123:MET:CE	2.02	0.90
1:E:274:PHE:CE2	1:E:280:ILE:HG22	2.05	0.90
1:F:278:GLN:HG3	1:F:279:LYS:H	1.34	0.90
1:H:259:LYS:HG3	1:H:260:TRP:N	1.84	0.90
1:C:228:SER:O	1:C:232:ILE:HG22	1.72	0.90
1:C:233:LEU:HD12	1:C:233:LEU:H	1.36	0.90
1:D:131:GLU:OE1	1:D:131:GLU:N	2.03	0.90
1:D:347:LYS:O	1:D:348:LEU:HD12	1.71	0.90
1:H:281:VAL:HG11	1:H:333:ARG:HD2	1.54	0.90
1:H:298:ALA:O	1:H:315:ARG:HA	1.70	0.90
1:B:371:TYR:CE1	2:B:402:CMP:C8	2.54	0.90
1:H:173:TYR:HD2	1:H:198:PHE:CE1	1.90	0.90
1:H:175:ILE:O	1:H:175:ILE:CD1	2.18	0.90
1:A:371:TYR:CE1	2:A:402:CMP:N7	2.39	0.90
1:E:111:TYR:CG	1:E:112:VAL:N	2.37	0.90
1:F:291:PHE:CE1	1:F:347:LYS:NZ	2.40	0.90
1:F:294:LEU:O	1:F:318:PRO:HB3	1.72	0.90
1:G:175:ILE:HA	1:G:221:LEU:CD2	2.02	0.90
1:A:293:ILE:HG13	1:A:345:CYS:SG	2.12	0.90
1:C:243:MET:HE3	1:E:157:ILE:CD1	2.01	0.90
1:D:200:GLU:CG	1:D:201:LEU:H	1.84	0.90
1:F:175:ILE:HA	1:F:221:LEU:HD22	1.54	0.90
1:C:291:PHE:N	1:C:291:PHE:HD1	1.69	0.90
1:F:365:LYS:O	1:F:368:ILE:HG13	1.72	0.90
1:B:158:ALA:HB2	1:B:217:THR:O	1.70	0.89
1:B:301:LEU:HD13	1:B:310:PHE:HB2	1.52	0.89
1:E:294:LEU:CD1	1:E:294:LEU:H	1.85	0.89
1:E:262:ARG:O	1:E:265:VAL:HB	1.70	0.89
1:F:130:ILE:HG13	1:F:136:PHE:CD2	2.06	0.89
1:G:249:SER:N	1:G:262:ARG:HH22	1.68	0.89
1:H:175:ILE:HA	1:H:221:LEU:CD2	2.01	0.89
1:A:325:ILE:CD1	2:A:402:CMP:O2P	2.20	0.89
1:C:259:LYS:HG3	1:C:260:TRP:N	1.88	0.89
1:D:234:MET:HG3	1:D:238:LEU:HD12	1.53	0.89
1:C:269:LEU:CB	1:C:346:VAL:CG2	2.49	0.89
1:A:139:LEU:HD12	1:A:139:LEU:N	1.87	0.89
1:D:233:LEU:H	1:D:233:LEU:CD1	1.78	0.89
1:D:371:TYR:CE1	2:D:402:CMP:C8	2.55	0.89
1:E:164:GLN:HA	1:E:212:THR:HG22	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:303:ARG:HA	1:E:309:GLU:O	1.72	0.89
1:H:272:VAL:C	1:H:273:GLN:HE21	1.75	0.89
1:H:323:GLY:HA2	2:H:402:CMP:O2P	1.72	0.89
1:B:175:ILE:HA	1:B:221:LEU:HD22	1.52	0.89
1:B:229:TYR:HD1	1:B:233:LEU:CD1	1.85	0.89
1:C:272:VAL:HA	1:C:273:GLN:HE22	1.33	0.89
1:F:247:PHE:HE1	1:F:294:LEU:HA	1.34	0.89
1:H:198:PHE:CD1	1:H:198:PHE:C	2.43	0.89
1:B:249:SER:N	1:B:262:ARG:HH22	1.69	0.89
1:E:118:LYS:HE2	1:E:148:PHE:O	1.71	0.89
1:E:182:VAL:O	1:E:182:VAL:HG23	1.71	0.89
1:A:280:ILE:HG13	1:A:281:VAL:N	1.87	0.89
1:F:229:TYR:CD1	1:F:233:LEU:CD1	2.56	0.89
1:C:260:TRP:HE1	2:C:401:CMP:H2'	1.36	0.89
1:E:280:ILE:HG13	1:E:281:VAL:H	1.36	0.89
1:F:263:LEU:O	1:F:266:ALA:HB3	1.73	0.89
1:A:113:ARG:HH21	1:D:115:VAL:HG13	1.35	0.88
1:B:120:TYR:HD2	1:B:120:TYR:C	1.75	0.88
1:B:211:ASP:OD2	2:B:401:CMP:H3'	1.73	0.88
1:B:226:ARG:HG3	1:B:226:ARG:NH1	1.83	0.88
1:E:266:ALA:HA	1:E:269:LEU:CD1	2.02	0.88
1:F:251:VAL:HG12	1:F:254:LEU:HD21	0.92	0.88
1:G:280:ILE:HG13	1:G:281:VAL:N	1.88	0.88
1:H:115:VAL:HA	1:H:149:ASP:HB3	1.55	0.88
1:H:255:GLU:HA	1:H:255:GLU:OE1	1.73	0.88
1:H:280:ILE:HD11	1:H:337:VAL:HB	1.54	0.88
1:A:114:LYS:CG	1:A:115:VAL:N	2.30	0.88
1:A:269:LEU:HB3	1:A:346:VAL:HG23	1.54	0.88
1:A:313:VAL:HG13	1:A:313:VAL:O	1.73	0.88
1:B:154:VAL:HG12	1:B:221:LEU:HB2	1.54	0.88
1:D:324:GLU:CG	1:D:325:ILE:H	1.85	0.88
1:D:371:TYR:CE1	2:D:402:CMP:C5	2.61	0.88
1:E:226:ARG:HG3	1:E:226:ARG:NH1	1.80	0.88
1:E:279:LYS:HE3	1:E:282:VAL:HG22	1.54	0.88
1:A:111:TYR:O	1:A:112:VAL:HG22	1.73	0.88
1:D:269:LEU:HD22	1:D:346:VAL:CG2	2.04	0.88
1:F:260:TRP:HE1	2:F:401:CMP:C2'	1.86	0.88
1:F:279:LYS:HZ3	1:F:279:LYS:CB	1.87	0.88
1:E:356:VAL:HG23	1:E:357:LEU:CD1	2.02	0.88
1:F:356:VAL:HG23	1:F:357:LEU:HD13	1.55	0.88
1:E:259:LYS:O	1:E:262:ARG:HG3	1.72	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:356:VAL:HG23	1:E:357:LEU:HD13	1.56	0.88
1:F:152:PHE:O	1:F:152:PHE:HD2	1.56	0.88
1:H:180:MET:HB2	1:H:192:VAL:HB	1.55	0.88
1:H:260:TRP:NE1	2:H:401:CMP:H2'	1.87	0.88
1:H:302:GLN:O	1:H:310:PHE:CD1	2.26	0.88
1:A:272:VAL:HG22	1:A:273:GLN:H	1.39	0.88
1:B:260:TRP:CD1	2:B:401:CMP:C5	2.62	0.88
1:C:300:VAL:O	1:C:301:LEU:HD12	1.74	0.88
1:E:111:TYR:CE2	1:H:112:VAL:CG1	2.54	0.88
1:G:229:TYR:HD1	1:G:233:LEU:CD1	1.86	0.88
1:H:122:THR:O	1:H:125:ALA:HB3	1.72	0.88
1:C:247:PHE:HE1	1:C:294:LEU:HA	1.36	0.88
1:D:226:ARG:HG3	1:D:226:ARG:NH1	1.81	0.88
1:F:182:VAL:HG23	1:F:182:VAL:O	1.71	0.88
1:F:229:TYR:CE1	1:F:233:LEU:HD13	2.09	0.88
1:A:280:ILE:CD1	1:A:322:PHE:CE2	2.57	0.88
1:B:371:TYR:CE1	2:B:402:CMP:N7	2.42	0.88
1:C:234:MET:HG3	1:C:238:LEU:HD12	1.56	0.88
1:E:165:GLN:H	1:E:212:THR:HG23	0.75	0.88
1:F:229:TYR:HD1	1:F:233:LEU:HD13	1.32	0.88
1:A:120:TYR:C	1:A:120:TYR:CD2	2.46	0.87
1:B:280:ILE:HD13	1:B:322:PHE:CE2	2.08	0.87
1:F:178:GLY:HA3	1:F:219:VAL:HG12	1.54	0.87
1:G:148:PHE:HB3	1:H:120:TYR:HD1	1.39	0.87
1:A:131:GLU:OE1	1:A:131:GLU:N	2.07	0.87
1:C:229:TYR:CE1	1:C:233:LEU:HD13	2.09	0.87
1:E:139:LEU:H	1:E:139:LEU:HD12	1.39	0.87
1:B:134:VAL:HG11	1:B:268:ALA:HA	1.55	0.87
1:E:249:SER:N	1:E:262:ARG:NH2	2.22	0.87
1:F:280:ILE:HD13	1:F:322:PHE:CE2	2.09	0.87
1:E:211:ASP:CG	2:E:401:CMP:H5'1	1.95	0.87
1:E:269:LEU:HB3	1:E:346:VAL:CG2	2.05	0.87
1:F:139:LEU:H	1:F:139:LEU:HD12	1.39	0.87
1:G:120:TYR:C	1:G:120:TYR:CD2	2.48	0.87
1:C:255:GLU:HA	1:C:255:GLU:OE1	1.75	0.87
1:E:203:LEU:HD22	1:E:226:ARG:HB3	1.57	0.87
1:F:350:ARG:O	1:F:353:PHE:HB3	1.73	0.87
1:H:291:PHE:CE1	1:H:347:LYS:NZ	2.43	0.87
1:H:300:VAL:HG23	1:H:314:GLY:H	1.39	0.87
1:B:356:VAL:HG23	1:B:357:LEU:CD1	2.04	0.87
1:C:173:TYR:HD2	1:C:198:PHE:CZ	1.92	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:162:VAL:HG23	1:H:163:ILE:HG13	1.55	0.87
1:H:273:GLN:NE2	1:H:273:GLN:N	2.22	0.87
1:A:118:LYS:HE2	1:A:148:PHE:O	1.73	0.87
1:C:266:ALA:CA	1:C:269:LEU:HD12	2.02	0.87
1:D:175:ILE:HD11	1:D:196:GLY:H	1.38	0.87
1:E:251:VAL:CG1	1:E:254:LEU:HD21	2.03	0.87
1:H:126:LEU:HD12	1:H:126:LEU:O	1.74	0.87
1:A:115:VAL:CG2	1:D:112:VAL:H	1.88	0.87
1:A:120:TYR:HD1	1:B:148:PHE:HB2	1.37	0.87
1:A:230:ARG:O	1:A:234:MET:CB	2.22	0.87
1:A:324:GLU:HG2	1:A:325:ILE:N	1.89	0.87
1:B:111:TYR:C	1:B:112:VAL:HG22	1.92	0.87
1:C:158:ALA:HB1	1:C:216:LYS:O	1.75	0.87
1:C:198:PHE:C	1:C:198:PHE:CD1	2.38	0.87
1:H:272:VAL:C	1:H:273:GLN:NE2	2.28	0.87
1:C:329:MET:HA	1:C:329:MET:CE	2.05	0.86
1:D:204:ILE:HG22	1:D:205:TYR:CD2	2.09	0.86
1:B:262:ARG:O	1:B:265:VAL:HB	1.75	0.86
1:B:325:ILE:HD11	2:B:402:CMP:O1P	1.75	0.86
1:C:300:VAL:HG21	1:C:313:VAL:HG12	1.56	0.86
1:E:229:TYR:HD1	1:E:233:LEU:HD13	1.40	0.86
1:G:204:ILE:HG22	1:G:205:TYR:CD2	2.09	0.86
1:G:229:TYR:CD1	1:G:233:LEU:CD1	2.58	0.86
1:H:230:ARG:O	1:H:234:MET:HB3	1.74	0.86
1:A:152:PHE:HE2	1:A:223:GLY:HA3	1.40	0.86
1:B:158:ALA:HB1	1:B:216:LYS:O	1.75	0.86
1:C:139:LEU:HD12	1:C:139:LEU:N	1.89	0.86
1:C:269:LEU:CB	1:C:346:VAL:HG21	2.06	0.86
1:F:278:GLN:CG	1:F:279:LYS:H	1.88	0.86
1:H:275:GLU:O	1:H:278:GLN:HB2	1.73	0.86
1:F:273:GLN:HE21	1:F:273:GLN:H	1.15	0.86
1:A:226:ARG:HG3	1:A:226:ARG:NH1	1.84	0.86
1:F:190:THR:HG22	1:F:191:SER:H	1.39	0.86
1:B:139:LEU:HD12	1:B:139:LEU:N	1.86	0.86
1:G:139:LEU:HD12	1:G:139:LEU:N	1.91	0.86
1:C:198:PHE:CD1	1:C:198:PHE:O	2.27	0.86
1:E:353:PHE:CE1	1:E:357:LEU:HD22	2.10	0.86
1:D:211:ASP:CG	2:D:401:CMP:H5'1	1.95	0.86
1:F:274:PHE:CE2	1:F:280:ILE:HG22	2.11	0.86
1:A:188:TRP:CZ3	1:A:190:THR:C	2.48	0.86
1:B:279:LYS:HZ3	1:B:279:LYS:HB2	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:329:MET:HA	1:C:329:MET:HE3	1.58	0.86
1:G:178:GLY:HA3	1:G:219:VAL:HG12	1.57	0.86
1:B:371:TYR:HE1	2:B:402:CMP:N7	1.74	0.85
1:E:328:LEU:CD2	1:E:365:LYS:HE3	2.06	0.85
1:B:120:TYR:C	1:B:120:TYR:CD2	2.45	0.85
1:D:300:VAL:CG2	1:D:335:ALA:HB1	2.05	0.85
1:E:291:PHE:N	1:E:291:PHE:HD1	1.74	0.85
1:G:294:LEU:CD1	1:G:294:LEU:H	1.88	0.85
1:E:293:ILE:CD1	1:E:317:GLY:O	2.24	0.85
1:F:152:PHE:O	1:F:152:PHE:CD2	2.28	0.85
1:F:165:GLN:HA	1:F:211:ASP:O	1.76	0.85
1:D:301:LEU:HD21	1:D:310:PHE:CB	2.04	0.85
1:E:131:GLU:N	1:E:131:GLU:OE1	2.09	0.85
1:G:131:GLU:OE1	1:G:131:GLU:N	2.08	0.85
1:F:291:PHE:N	1:F:291:PHE:HD1	1.68	0.85
1:H:175:ILE:HA	1:H:221:LEU:HD22	1.59	0.85
1:H:204:ILE:HG22	1:H:205:TYR:CD2	2.12	0.85
1:B:112:VAL:HG12	1:B:231:ARG:NE	1.91	0.85
1:G:229:TYR:HD1	1:G:233:LEU:HD13	1.41	0.85
1:H:114:LYS:NZ	1:H:115:VAL:N	2.21	0.85
1:A:293:ILE:HD11	1:A:343:LEU:CD1	2.05	0.85
1:B:249:SER:CA	1:B:262:ARG:HH22	1.90	0.85
1:G:198:PHE:CD1	1:G:198:PHE:C	2.45	0.85
1:G:249:SER:CA	1:G:262:ARG:HH22	1.89	0.85
1:A:111:TYR:HA	1:D:115:VAL:HG23	1.59	0.85
1:A:175:ILE:HD11	1:A:193:GLY:O	1.76	0.85
1:C:278:GLN:HG3	1:C:279:LYS:H	1.42	0.85
1:D:273:GLN:NE2	1:D:273:GLN:H	1.70	0.85
1:F:182:VAL:CG2	1:F:190:THR:O	2.24	0.85
1:H:156:PHE:HE2	1:H:162:VAL:HG12	1.40	0.85
1:A:361:SER:C	1:A:365:LYS:HZ2	1.80	0.85
1:C:198:PHE:O	1:C:198:PHE:HD1	1.60	0.85
1:C:363:ILE:O	1:C:366:ARG:HG2	1.75	0.85
1:D:126:LEU:HB2	1:D:222:TRP:CZ2	2.11	0.85
1:E:259:LYS:HG3	1:E:260:TRP:N	1.92	0.85
1:F:348:LEU:HD21	1:F:356:VAL:HG21	1.57	0.85
1:D:230:ARG:O	1:D:234:MET:HB3	1.76	0.85
1:E:156:PHE:CD2	1:E:162:VAL:CG1	2.59	0.85
1:G:118:LYS:HE2	1:G:148:PHE:O	1.75	0.85
1:G:291:PHE:N	1:G:291:PHE:HD1	1.74	0.85
1:C:163:ILE:HB	1:C:213:VAL:HG23	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:170:ASP:H	1:C:209:ARG:NH2	1.75	0.84
1:D:269:LEU:HB3	1:D:346:VAL:CG2	2.07	0.84
1:E:173:TYR:HB2	1:E:198:PHE:HE1	1.42	0.84
1:F:325:ILE:HD11	2:F:402:CMP:O1P	1.76	0.84
1:C:112:VAL:O	1:F:112:VAL:CG1	2.25	0.84
1:E:279:LYS:HB2	1:E:279:LYS:HZ3	1.40	0.84
1:F:164:GLN:HA	1:F:212:THR:HG22	1.59	0.84
1:F:259:LYS:HG3	1:F:260:TRP:N	1.91	0.84
1:F:293:ILE:HD11	1:F:343:LEU:CD1	2.06	0.84
1:H:172:PHE:HB3	1:H:224:ILE:CD1	2.07	0.84
1:E:175:ILE:HA	1:E:221:LEU:HD22	1.57	0.84
1:H:251:VAL:CG1	1:H:254:LEU:HD21	2.07	0.84
1:B:165:GLN:HA	1:B:211:ASP:O	1.78	0.84
1:B:200:GLU:HG2	1:B:201:LEU:HD12	1.57	0.84
1:B:278:GLN:HG2	1:B:279:LYS:H	1.41	0.84
1:E:156:PHE:HD2	1:E:162:VAL:HG12	1.42	0.84
1:E:175:ILE:HD11	1:E:196:GLY:N	1.90	0.84
1:F:280:ILE:HD13	1:F:322:PHE:CZ	2.12	0.84
1:B:118:LYS:HB3	1:B:123:MET:HE2	1.58	0.84
1:D:188:TRP:HH2	1:D:191:SER:HG	1.21	0.84
1:H:296:GLY:O	1:H:318:PRO:HD3	1.78	0.84
1:C:293:ILE:HD11	1:C:343:LEU:CD1	2.07	0.84
1:D:301:LEU:HD23	1:D:310:PHE:CD1	2.12	0.84
1:F:114:LYS:HZ2	1:F:115:VAL:CG2	1.88	0.84
1:F:153:PRO:HB3	1:F:222:TRP:CZ3	2.12	0.84
1:A:182:VAL:HG23	1:A:182:VAL:O	1.76	0.84
1:E:190:THR:HG22	1:E:191:SER:H	1.41	0.84
1:E:300:VAL:HG21	2:E:402:CMP:C8	2.05	0.84
1:G:259:LYS:HG3	1:G:260:TRP:N	1.90	0.84
1:A:115:VAL:HG11	1:D:112:VAL:CG2	2.08	0.84
1:C:120:TYR:CB	1:D:149:ASP:OD1	2.25	0.84
1:E:278:GLN:HG3	1:E:279:LYS:H	1.43	0.84
1:F:173:TYR:HB2	1:F:198:PHE:CE1	2.13	0.84
1:F:247:PHE:CE1	1:F:294:LEU:HA	2.11	0.84
1:G:175:ILE:HD11	1:G:196:GLY:H	1.40	0.84
1:H:113:ARG:CD	1:H:114:LYS:H	1.91	0.84
1:D:139:LEU:HD12	1:D:139:LEU:N	1.91	0.84
1:D:280:ILE:HG13	1:D:281:VAL:N	1.93	0.84
1:A:350:ARG:O	1:A:353:PHE:HB3	1.78	0.84
1:H:247:PHE:HE1	1:H:294:LEU:HA	1.41	0.84
1:H:260:TRP:CE2	2:H:401:CMP:C8	2.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:THR:CG2	1:A:191:SER:H	1.91	0.83
1:D:139:LEU:HD12	1:D:139:LEU:H	1.42	0.83
1:C:179:GLU:HG2	1:C:216:LYS:CD	2.07	0.83
1:C:269:LEU:HD23	1:C:348:LEU:HD13	1.60	0.83
1:C:323:GLY:HA2	2:C:402:CMP:O1P	1.78	0.83
1:F:139:LEU:HD12	1:F:139:LEU:N	1.93	0.83
1:A:229:TYR:CE1	1:A:233:LEU:HD13	2.14	0.83
1:C:110:SER:HB3	1:F:114:LYS:CE	2.08	0.83
1:C:122:THR:O	1:C:125:ALA:HB3	1.78	0.83
1:C:173:TYR:HD2	1:C:198:PHE:CE1	1.95	0.83
1:F:230:ARG:HG2	1:F:234:MET:HE1	1.60	0.83
1:A:313:VAL:O	1:A:313:VAL:CG1	2.26	0.83
1:B:182:VAL:HG12	1:B:213:VAL:HG22	1.60	0.83
1:B:291:PHE:N	1:B:291:PHE:CD1	2.37	0.83
1:B:350:ARG:O	1:B:353:PHE:HB3	1.78	0.83
1:H:249:SER:N	1:H:262:ARG:HH22	1.75	0.83
1:A:273:GLN:HB2	1:A:343:LEU:O	1.78	0.83
1:B:230:ARG:HG2	1:B:234:MET:HE1	1.57	0.83
1:C:211:ASP:OD2	2:C:401:CMP:H3'	1.77	0.83
1:D:259:LYS:HG3	1:D:260:TRP:H	1.37	0.83
1:A:147:ILE:HG23	1:A:232:ILE:HD13	1.61	0.83
1:E:242:LYS:N	1:E:242:LYS:HD3	1.92	0.83
1:E:247:PHE:HE1	1:E:294:LEU:HA	1.42	0.83
1:F:157:ILE:CD1	1:H:243:MET:CE	2.53	0.83
1:H:179:GLU:HG2	1:H:216:LYS:CD	2.08	0.83
1:C:120:TYR:HD1	1:D:148:PHE:HB2	1.42	0.83
1:D:163:ILE:HD12	1:D:213:VAL:HB	1.59	0.83
1:D:175:ILE:HA	1:D:221:LEU:HD22	1.60	0.83
1:D:230:ARG:HG2	1:D:234:MET:HE1	1.61	0.83
1:G:148:PHE:CB	1:H:120:TYR:CD1	2.61	0.83
1:H:175:ILE:HD13	1:H:194:GLU:HA	1.60	0.83
1:H:279:LYS:HB2	1:H:279:LYS:HZ2	1.41	0.83
1:B:280:ILE:HG13	1:B:281:VAL:N	1.91	0.83
1:C:224:ILE:HD12	1:C:224:ILE:H	1.41	0.83
1:C:284:GLY:O	1:C:332:PRO:CB	2.26	0.83
1:D:249:SER:CA	1:D:262:ARG:HH22	1.91	0.83
1:C:204:ILE:HG22	1:C:205:TYR:HD2	1.40	0.83
1:F:175:ILE:HD11	1:F:196:GLY:N	1.93	0.83
1:H:156:PHE:HD2	1:H:162:VAL:CG1	1.92	0.83
1:B:324:GLU:OE2	1:B:371:TYR:HE2	1.61	0.83
1:C:312:GLU:OE1	1:C:312:GLU:HA	1.79	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:198:PHE:O	1:G:198:PHE:HD1	1.62	0.82
1:A:203:LEU:HD22	1:A:226:ARG:HB3	1.60	0.82
1:C:279:LYS:CE	1:C:336:THR:HG23	2.06	0.82
1:F:347:LYS:O	1:F:348:LEU:HD12	1.78	0.82
1:G:139:LEU:HD12	1:G:139:LEU:H	1.45	0.82
1:G:234:MET:HG3	1:G:238:LEU:HD12	1.61	0.82
1:G:266:ALA:CA	1:G:269:LEU:HD12	2.05	0.82
1:C:259:LYS:HG3	1:C:260:TRP:H	1.44	0.82
1:H:259:LYS:HG3	1:H:260:TRP:H	1.40	0.82
1:H:294:LEU:O	1:H:318:PRO:HB3	1.77	0.82
1:A:114:LYS:C	1:A:115:VAL:HG22	2.00	0.82
1:A:147:ILE:CG2	1:A:232:ILE:HD13	2.09	0.82
1:A:224:ILE:O	1:A:224:ILE:HD13	1.79	0.82
1:B:130:ILE:CG2	1:B:131:GLU:N	2.41	0.82
1:D:135:LEU:HD12	1:D:136:PHE:N	1.94	0.82
1:D:156:PHE:HD2	1:D:162:VAL:HG12	1.43	0.82
1:A:229:TYR:HD1	1:A:233:LEU:CD1	1.92	0.82
1:A:259:LYS:O	1:A:262:ARG:HG3	1.78	0.82
1:B:135:LEU:HD12	1:B:136:PHE:H	1.45	0.82
1:D:294:LEU:HD13	1:D:344:LYS:O	1.79	0.82
1:D:300:VAL:HG12	1:D:314:GLY:O	1.78	0.82
1:H:111:TYR:CG	1:H:112:VAL:N	2.46	0.82
1:C:241:ARG:NH1	1:C:263:LEU:HG	1.94	0.82
1:D:260:TRP:NE1	2:D:401:CMP:H2'	1.93	0.82
1:D:325:ILE:HG12	2:D:402:CMP:O3'	1.80	0.82
1:E:260:TRP:CE2	2:E:401:CMP:C8	2.62	0.82
1:G:279:LYS:HE3	1:G:282:VAL:HG22	1.59	0.82
1:B:165:GLN:H	1:B:212:THR:HG23	0.71	0.82
1:E:263:LEU:O	1:E:266:ALA:HB3	1.78	0.82
1:G:229:TYR:CE1	1:G:233:LEU:HD13	2.14	0.82
1:A:249:SER:N	1:A:262:ARG:NH2	2.27	0.82
1:B:263:LEU:O	1:B:266:ALA:HB3	1.77	0.82
1:C:230:ARG:O	1:C:234:MET:HB3	1.80	0.82
1:D:291:PHE:N	1:D:291:PHE:HD1	1.72	0.82
1:E:139:LEU:HD12	1:E:139:LEU:N	1.91	0.82
1:C:259:LYS:O	1:C:262:ARG:HG3	1.79	0.82
1:D:255:GLU:OE1	1:D:255:GLU:HA	1.78	0.82
1:F:269:LEU:HB3	1:F:346:VAL:HG21	1.62	0.82
1:G:347:LYS:O	1:G:348:LEU:HD12	1.80	0.82
1:G:350:ARG:O	1:G:353:PHE:HB3	1.79	0.82
1:A:228:SER:O	1:A:232:ILE:HG22	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:VAL:O	1:B:254:LEU:HD11	1.80	0.82
1:C:247:PHE:CE1	1:C:294:LEU:HA	2.15	0.82
1:C:350:ARG:O	1:C:353:PHE:HB3	1.79	0.82
1:D:156:PHE:CD2	1:D:162:VAL:CG1	2.60	0.82
1:F:356:VAL:HG23	1:F:357:LEU:CD1	2.09	0.82
1:H:280:ILE:HD13	1:H:322:PHE:CZ	2.15	0.82
1:A:158:ALA:HB1	1:A:216:LYS:O	1.80	0.81
1:H:266:ALA:HA	1:H:269:LEU:HD12	1.60	0.81
1:B:156:PHE:HD2	1:B:162:VAL:HG12	1.43	0.81
1:B:281:VAL:HG11	1:B:333:ARG:HD2	1.59	0.81
1:E:229:TYR:CD1	1:E:233:LEU:CD1	2.63	0.81
1:E:229:TYR:CE1	1:E:233:LEU:HD13	2.15	0.81
1:F:157:ILE:O	1:F:160:GLU:HB2	1.78	0.81
1:H:280:ILE:HD11	1:H:322:PHE:HE2	1.44	0.81
1:A:350:ARG:HB3	1:A:351:PRO:HD3	1.61	0.81
1:A:365:LYS:HA	1:A:368:ILE:HG13	1.62	0.81
1:B:211:ASP:N	1:B:211:ASP:OD1	2.13	0.81
1:B:269:LEU:HD22	1:B:346:VAL:HG21	1.62	0.81
1:B:325:ILE:HG13	1:B:326:ALA:N	1.93	0.81
1:C:120:TYR:CD1	1:D:148:PHE:CB	2.62	0.81
1:C:316:LEU:HA	1:C:320:ASP:OD2	1.81	0.81
1:D:229:TYR:CD1	1:D:233:LEU:CD1	2.63	0.81
1:D:291:PHE:CD1	1:D:347:LYS:NZ	2.48	0.81
1:E:247:PHE:CE1	1:E:294:LEU:HA	2.14	0.81
1:G:261:GLU:O	1:G:265:VAL:HG23	1.79	0.81
1:H:285:GLU:O	1:H:332:PRO:HA	1.79	0.81
1:B:179:GLU:HG2	1:B:216:LYS:CD	2.11	0.81
1:B:348:LEU:HD21	1:B:356:VAL:HG21	1.62	0.81
1:B:156:PHE:CE2	1:B:162:VAL:HG12	2.15	0.81
1:C:120:TYR:CD1	1:D:148:PHE:HB2	2.15	0.81
1:D:178:GLY:HA3	1:D:219:VAL:HG12	1.61	0.81
1:D:229:TYR:CE1	1:D:233:LEU:HD13	2.14	0.81
1:G:246:GLU:O	1:G:247:PHE:C	2.18	0.81
1:G:324:GLU:HG2	1:G:325:ILE:N	1.95	0.81
1:H:294:LEU:HD12	1:H:295:GLU:H	1.44	0.81
1:B:230:ARG:O	1:B:234:MET:CB	2.28	0.81
1:C:233:LEU:CD1	1:C:233:LEU:H	1.90	0.81
1:D:251:VAL:O	1:D:252:SER:O	1.98	0.81
1:F:230:ARG:O	1:F:234:MET:HB3	1.81	0.81
1:A:142:ASN:HB2	1:C:121:LYS:HE3	1.61	0.81
1:A:249:SER:CA	1:A:262:ARG:HH22	1.92	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:180:MET:HB2	1:C:192:VAL:HB	1.62	0.81
1:G:196:GLY:HA2	1:G:355:ARG:HH21	1.43	0.81
1:H:350:ARG:O	1:H:353:PHE:HB3	1.80	0.81
1:A:148:PHE:HB2	1:B:120:TYR:HD1	1.45	0.81
1:A:371:TYR:HE1	2:A:402:CMP:N7	1.77	0.81
1:C:111:TYR:HE1	1:F:111:TYR:CD2	1.99	0.81
1:E:292:ILE:HB	1:E:346:VAL:HG13	1.62	0.81
1:A:173:TYR:HD2	1:A:198:PHE:CE1	1.98	0.81
1:B:153:PRO:CB	1:B:222:TRP:CZ3	2.64	0.81
1:B:251:VAL:CG1	1:B:254:LEU:HD21	2.10	0.81
1:A:188:TRP:HZ3	1:A:190:THR:C	1.83	0.80
1:F:156:PHE:HD2	1:F:162:VAL:HG12	1.46	0.80
1:C:154:VAL:HG12	1:C:221:LEU:HB2	1.63	0.80
1:C:251:VAL:O	1:C:254:LEU:HD11	1.81	0.80
1:C:272:VAL:HG22	1:C:273:GLN:H	1.47	0.80
1:E:204:ILE:HG22	1:E:205:TYR:CD2	2.15	0.80
1:E:280:ILE:HG13	1:E:281:VAL:N	1.94	0.80
1:E:294:LEU:HD13	1:E:344:LYS:O	1.81	0.80
1:G:211:ASP:OD2	2:G:401:CMP:H5'1	1.82	0.80
1:A:280:ILE:HD13	1:A:322:PHE:CZ	2.16	0.80
1:A:325:ILE:HG13	1:A:326:ALA:H	1.47	0.80
1:B:371:TYR:HE1	2:B:402:CMP:C8	1.93	0.80
1:C:172:PHE:HB3	1:C:224:ILE:CD1	2.12	0.80
1:C:280:ILE:HD13	1:C:322:PHE:CZ	2.16	0.80
1:D:144:ARG:HG2	1:D:145:SER:N	1.94	0.80
1:D:353:PHE:CE1	1:D:357:LEU:CD2	2.63	0.80
1:F:279:LYS:NZ	1:F:279:LYS:CB	2.36	0.80
1:F:280:ILE:HG13	1:F:281:VAL:N	1.95	0.80
1:G:116:ILE:HG22	1:G:118:LYS:HG3	1.63	0.80
1:B:162:VAL:HG23	1:B:163:ILE:HG13	1.64	0.80
1:C:300:VAL:O	1:C:301:LEU:CD1	2.30	0.80
1:E:243:MET:CE	1:G:157:ILE:CD1	2.59	0.80
1:F:329:MET:CB	1:F:331:ARG:HG3	2.10	0.80
1:A:120:TYR:C	1:A:120:TYR:HD2	1.84	0.80
1:B:175:ILE:HD11	1:B:193:GLY:O	1.81	0.80
1:B:273:GLN:H	1:B:273:GLN:HE21	0.82	0.80
1:C:365:LYS:HA	1:C:368:ILE:HD11	1.64	0.80
1:D:198:PHE:CD1	1:D:198:PHE:C	2.53	0.80
1:D:361:SER:C	1:D:365:LYS:HZ2	1.85	0.80
1:E:123:MET:HE3	1:F:123:MET:HE2	1.63	0.80
1:G:249:SER:N	1:G:262:ARG:NH2	2.29	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:291:PHE:CE1	1:G:347:LYS:NZ	2.50	0.80
1:E:293:ILE:HG21	1:E:317:GLY:O	1.82	0.80
1:F:228:SER:O	1:F:232:ILE:HG22	1.81	0.80
1:A:251:VAL:O	1:A:254:LEU:HD11	1.80	0.80
1:A:291:PHE:N	1:A:291:PHE:CD1	2.38	0.80
1:B:229:TYR:CD1	1:B:233:LEU:CD1	2.63	0.80
1:B:249:SER:N	1:B:262:ARG:NH2	2.29	0.80
1:E:229:TYR:HD1	1:E:233:LEU:CD1	1.93	0.80
1:E:265:VAL:HG12	1:E:269:LEU:CD1	2.12	0.80
1:C:165:GLN:HA	1:C:211:ASP:O	1.81	0.80
1:C:299:ALA:HB1	1:C:312:GLU:CD	2.02	0.80
1:G:228:SER:O	1:G:232:ILE:HG22	1.82	0.80
1:G:253:ILE:HD13	1:G:321:TYR:CD2	2.17	0.80
1:A:375:VAL:HG13	1:A:376:SER:N	1.97	0.80
1:C:249:SER:N	1:C:262:ARG:HH22	1.79	0.80
1:D:224:ILE:O	1:D:224:ILE:HD13	1.82	0.80
1:B:323:GLY:HA2	2:B:402:CMP:O2P	1.82	0.80
1:B:375:VAL:CG2	1:B:376:SER:H	1.95	0.80
1:C:175:ILE:O	1:C:175:ILE:CD1	2.29	0.80
1:D:269:LEU:HD22	1:D:346:VAL:HG21	1.64	0.80
1:E:156:PHE:HE2	1:E:162:VAL:HG12	1.46	0.80
1:F:112:VAL:HG13	1:F:113:ARG:N	1.96	0.80
1:F:278:GLN:CG	1:F:279:LYS:N	2.45	0.80
1:B:229:TYR:CE1	1:B:233:LEU:HD13	2.17	0.79
1:C:278:GLN:O	1:C:338:VAL:HA	1.82	0.79
1:C:291:PHE:N	1:C:291:PHE:CD1	2.46	0.79
1:G:182:VAL:HG23	1:G:182:VAL:O	1.79	0.79
1:G:325:ILE:HG23	1:G:329:MET:HG3	1.65	0.79
1:H:279:LYS:HB2	1:H:279:LYS:HZ3	1.47	0.79
1:A:260:TRP:CD1	2:A:401:CMP:C5	2.70	0.79
1:C:287:GLY:HA3	1:C:326:ALA:HB1	1.64	0.79
1:C:371:TYR:HE1	2:C:402:CMP:C8	1.94	0.79
1:D:251:VAL:HG13	1:D:254:LEU:CD1	2.06	0.79
1:E:111:TYR:HE2	1:H:111:TYR:CE2	1.94	0.79
1:E:280:ILE:HD11	1:E:322:PHE:CE2	2.14	0.79
1:G:120:TYR:HD2	1:G:121:LYS:HA	1.46	0.79
1:H:249:SER:N	1:H:262:ARG:NH2	2.29	0.79
1:H:281:VAL:CG1	1:H:333:ARG:HD2	2.11	0.79
1:C:281:VAL:CG1	1:C:333:ARG:CD	2.59	0.79
1:E:350:ARG:O	1:E:353:PHE:HB3	1.81	0.79
1:F:324:GLU:HB2	1:F:364:LEU:HD13	1.62	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:PHE:CD1	1:B:198:PHE:C	2.49	0.79
1:F:175:ILE:CD1	1:F:195:GLY:H	1.95	0.79
1:A:135:LEU:CD1	1:A:136:PHE:N	2.45	0.79
1:A:253:ILE:HG13	1:A:254:LEU:H	1.47	0.79
1:C:280:ILE:CG1	1:C:337:VAL:HB	2.13	0.79
1:D:291:PHE:N	1:D:291:PHE:CD1	2.47	0.79
1:E:239:ARG:HH11	1:G:157:ILE:HG23	1.46	0.79
1:F:204:ILE:HG22	1:F:205:TYR:CD2	2.18	0.79
1:F:291:PHE:N	1:F:291:PHE:CD1	2.44	0.79
1:B:190:THR:CG2	1:B:191:SER:H	1.96	0.79
1:B:211:ASP:OD2	2:B:401:CMP:C3'	2.31	0.79
1:C:196:GLY:CA	1:C:355:ARG:NH2	2.42	0.79
1:C:294:LEU:CD1	1:C:294:LEU:H	1.95	0.79
1:C:188:TRP:CZ3	1:C:190:THR:C	2.56	0.79
1:D:112:VAL:HG12	1:D:231:ARG:CZ	2.11	0.79
1:A:165:GLN:H	1:A:212:THR:HG23	0.67	0.79
1:A:190:THR:HG22	1:A:191:SER:N	1.95	0.79
1:B:321:TYR:CD1	1:B:321:TYR:C	2.56	0.79
1:E:175:ILE:HG22	1:E:221:LEU:HD21	1.65	0.79
1:E:196:GLY:HA2	1:E:355:ARG:HH21	1.48	0.79
1:F:262:ARG:O	1:F:265:VAL:HB	1.83	0.79
1:G:348:LEU:HD21	1:G:356:VAL:HG21	1.65	0.79
1:E:291:PHE:CE1	1:E:347:LYS:NZ	2.50	0.79
1:F:134:VAL:HG11	1:F:268:ALA:HA	1.62	0.79
1:F:203:LEU:HD13	1:F:226:ARG:HB3	1.63	0.79
1:A:113:ARG:HH21	1:D:115:VAL:CG1	1.94	0.79
1:D:157:ILE:CD1	1:F:243:MET:HE3	2.12	0.79
1:E:179:GLU:HG2	1:E:216:LYS:CD	2.13	0.79
1:F:156:PHE:CD2	1:F:162:VAL:CG1	2.65	0.79
1:H:112:VAL:HG13	1:H:113:ARG:N	1.98	0.79
1:H:139:LEU:HD12	1:H:139:LEU:N	1.97	0.79
1:A:114:LYS:HG2	1:A:115:VAL:N	1.96	0.78
1:B:175:ILE:CD1	1:B:193:GLY:O	2.31	0.78
1:C:281:VAL:HG13	1:C:333:ARG:CD	2.13	0.78
1:D:120:TYR:C	1:D:120:TYR:CD2	2.54	0.78
1:D:233:LEU:HD12	1:D:233:LEU:N	1.92	0.78
1:A:156:PHE:HD2	1:A:162:VAL:HG12	1.40	0.78
1:C:269:LEU:HD23	1:C:348:LEU:CD1	2.13	0.78
1:F:172:PHE:HB3	1:F:224:ILE:CD1	2.12	0.78
1:F:269:LEU:HB3	1:F:346:VAL:HG23	1.63	0.78
1:G:116:ILE:CG2	1:G:118:LYS:HZ2	1.94	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:262:ARG:O	1:G:265:VAL:HB	1.83	0.78
1:H:249:SER:HA	1:H:262:ARG:HH22	1.48	0.78
1:H:279:LYS:NZ	1:H:279:LYS:CB	2.44	0.78
1:H:287:GLY:HA3	1:H:326:ALA:HB1	1.65	0.78
1:A:229:TYR:CD1	1:A:233:LEU:CD1	2.65	0.78
1:B:312:GLU:CD	1:B:314:GLY:H	1.85	0.78
1:C:234:MET:O	1:C:238:LEU:HD12	1.83	0.78
1:D:165:GLN:HA	1:D:211:ASP:O	1.83	0.78
1:E:204:ILE:HG22	1:E:205:TYR:HD2	1.47	0.78
1:A:172:PHE:HB3	1:A:224:ILE:CD1	2.14	0.78
1:A:201:LEU:HD12	1:A:201:LEU:H	1.49	0.78
1:A:269:LEU:HB3	1:A:346:VAL:HG21	1.64	0.78
1:B:203:LEU:HD13	1:B:226:ARG:HB3	1.63	0.78
1:B:312:GLU:OE1	1:B:312:GLU:HA	1.81	0.78
1:B:313:VAL:CG2	2:B:402:CMP:N6	2.42	0.78
1:D:269:LEU:HB3	1:D:346:VAL:HG23	1.65	0.78
1:E:260:TRP:HE1	2:E:401:CMP:H2'	1.47	0.78
1:F:196:GLY:HA2	1:F:355:ARG:HH21	1.44	0.78
1:H:280:ILE:HG13	1:H:281:VAL:H	1.48	0.78
1:E:203:LEU:HD12	1:E:229:TYR:CD2	2.19	0.78
1:F:325:ILE:HG13	1:F:326:ALA:H	1.46	0.78
1:G:120:TYR:C	1:G:120:TYR:HD2	1.87	0.78
1:G:368:ILE:O	1:G:371:TYR:HB2	1.82	0.78
1:H:328:LEU:CD2	1:H:365:LYS:HE3	2.12	0.78
1:A:266:ALA:HA	1:A:269:LEU:CD1	2.11	0.78
1:C:112:VAL:O	1:F:112:VAL:HG12	1.83	0.78
1:C:294:LEU:N	1:C:294:LEU:CD1	2.42	0.78
1:F:175:ILE:CD1	1:F:195:GLY:N	2.46	0.78
1:G:120:TYR:CD1	1:H:148:PHE:CD1	2.71	0.78
1:G:224:ILE:HD13	1:G:224:ILE:O	1.83	0.78
1:H:300:VAL:C	1:H:301:LEU:HD23	2.02	0.78
1:E:112:VAL:CG1	1:E:231:ARG:CZ	2.60	0.78
1:F:294:LEU:HD13	1:F:344:LYS:O	1.83	0.78
1:G:269:LEU:HD23	1:G:348:LEU:CD1	2.14	0.78
1:G:356:VAL:HG23	1:G:357:LEU:HD13	1.64	0.78
1:H:224:ILE:H	1:H:224:ILE:HD12	1.47	0.78
1:H:324:GLU:O	1:H:328:LEU:HD12	1.83	0.78
1:A:144:ARG:HD2	1:B:120:TYR:OH	1.84	0.78
1:C:171:ASN:HB3	1:C:224:ILE:O	1.83	0.78
1:E:203:LEU:HD13	1:E:226:ARG:HB3	1.66	0.78
1:F:242:LYS:HD3	1:F:242:LYS:N	1.90	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:158:ALA:HB1	1:H:216:LYS:O	1.84	0.78
1:H:198:PHE:O	1:H:198:PHE:HD1	1.67	0.78
1:H:224:ILE:HD12	1:H:224:ILE:N	1.99	0.78
1:H:234:MET:O	1:H:238:LEU:HD12	1.83	0.78
1:A:165:GLN:HA	1:A:211:ASP:O	1.82	0.78
1:C:324:GLU:HB2	1:C:364:LEU:HD13	1.66	0.78
1:D:203:LEU:HD22	1:D:226:ARG:HB3	1.64	0.78
1:E:249:SER:CA	1:E:262:ARG:HH22	1.97	0.78
1:F:203:LEU:HD12	1:F:229:TYR:CD2	2.19	0.78
1:G:294:LEU:HD11	1:G:345:CYS:CA	2.13	0.78
1:H:260:TRP:CD2	2:H:401:CMP:C8	2.67	0.78
1:H:293:ILE:HD11	1:H:343:LEU:CD1	2.14	0.78
1:D:112:VAL:HG12	1:D:231:ARG:NE	1.99	0.78
1:D:302:GLN:HG3	1:D:313:VAL:HG11	1.64	0.78
1:G:280:ILE:CD1	1:G:322:PHE:HE2	1.96	0.78
1:H:153:PRO:HB3	1:H:222:TRP:CZ3	2.19	0.78
1:C:293:ILE:HG21	1:C:317:GLY:O	1.84	0.77
1:E:260:TRP:CD1	2:E:401:CMP:C5	2.72	0.77
1:F:173:TYR:HB2	1:F:198:PHE:HE1	1.49	0.77
1:F:255:GLU:OE1	1:F:255:GLU:CA	2.28	0.77
1:B:325:ILE:CG1	2:B:402:CMP:O1P	2.32	0.77
1:E:175:ILE:CD1	1:E:195:GLY:N	2.47	0.77
1:G:253:ILE:HD13	1:G:321:TYR:CE2	2.18	0.77
1:H:201:LEU:H	1:H:201:LEU:HD12	1.49	0.77
1:C:204:ILE:HG12	1:C:234:MET:SD	2.24	0.77
1:E:289:GLU:HG3	1:E:347:LYS:HZ3	1.46	0.77
1:G:164:GLN:HA	1:G:212:THR:HG22	1.65	0.77
1:B:246:GLU:O	1:B:247:PHE:C	2.18	0.77
1:B:278:GLN:CG	1:B:279:LYS:N	2.39	0.77
1:E:135:LEU:HD12	1:E:136:PHE:H	1.48	0.77
1:F:300:VAL:HG21	2:F:402:CMP:H8	1.66	0.77
1:G:116:ILE:HG21	1:G:118:LYS:HZ2	1.46	0.77
1:A:301:LEU:HD13	1:A:310:PHE:CE2	2.19	0.77
1:A:316:LEU:C	1:A:316:LEU:HD12	2.05	0.77
1:B:260:TRP:HE1	2:B:401:CMP:C2'	1.97	0.77
1:E:272:VAL:HA	1:E:273:GLN:NE2	1.99	0.77
1:F:175:ILE:HD13	1:F:194:GLU:HA	1.66	0.77
1:F:246:GLU:O	1:F:247:PHE:C	2.22	0.77
1:G:203:LEU:HD22	1:G:226:ARG:HB3	1.66	0.77
1:A:224:ILE:CD1	1:A:224:ILE:N	2.48	0.77
1:A:247:PHE:HZ	1:A:293:ILE:O	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:313:VAL:HG11	2:C:402:CMP:HN61	1.50	0.77
1:H:295:GLU:HA	1:H:318:PRO:HG3	1.67	0.77
1:A:269:LEU:CD2	1:A:346:VAL:HG21	2.13	0.77
1:C:144:ARG:CG	1:C:145:SER:N	2.48	0.77
1:E:246:GLU:O	1:E:247:PHE:C	2.20	0.77
1:E:325:ILE:HG13	1:E:326:ALA:H	1.47	0.77
1:F:318:PRO:O	1:F:319:SER:HB3	1.85	0.77
1:G:179:GLU:HG2	1:G:216:LYS:CD	2.15	0.77
1:G:233:LEU:HD12	1:G:233:LEU:N	1.96	0.77
1:G:237:THR:O	1:G:241:ARG:HG3	1.84	0.77
1:C:294:LEU:CD1	1:C:344:LYS:O	2.30	0.77
1:C:325:ILE:CG1	2:C:402:CMP:O2P	2.32	0.77
1:D:198:PHE:HD1	1:D:198:PHE:O	1.67	0.77
1:E:172:PHE:HB3	1:E:224:ILE:CD1	2.15	0.77
1:E:175:ILE:CD1	1:E:195:GLY:H	1.98	0.77
1:F:180:MET:HB2	1:F:192:VAL:HB	1.67	0.77
1:H:247:PHE:CE1	1:H:294:LEU:HA	2.20	0.77
1:A:281:VAL:CG1	1:A:333:ARG:HG3	2.15	0.77
1:C:265:VAL:CG1	1:C:269:LEU:HD11	2.07	0.77
1:E:280:ILE:HD13	1:E:322:PHE:CZ	2.19	0.77
1:D:296:GLY:HA3	1:D:342:PRO:O	1.85	0.77
1:E:126:LEU:HB2	1:E:222:TRP:CZ2	2.20	0.77
1:F:325:ILE:HG13	1:F:326:ALA:N	2.00	0.77
1:G:173:TYR:HD2	1:G:198:PHE:CE1	2.03	0.77
1:A:170:ASP:H	1:A:209:ARG:NH2	1.83	0.76
1:A:324:GLU:HB2	1:A:364:LEU:CD1	2.15	0.76
1:D:229:TYR:HD1	1:D:233:LEU:HD13	1.49	0.76
1:H:285:GLU:OE1	1:H:285:GLU:CA	2.33	0.76
1:A:280:ILE:HD13	1:A:322:PHE:CE2	2.20	0.76
1:B:294:LEU:CD1	1:B:344:LYS:O	2.31	0.76
1:C:111:TYR:CD1	1:F:111:TYR:CE2	2.73	0.76
1:C:281:VAL:HG13	1:C:333:ARG:CG	2.16	0.76
1:H:188:TRP:CZ3	1:H:190:THR:C	2.58	0.76
1:H:200:GLU:OE1	1:H:201:LEU:HD12	1.84	0.76
1:B:175:ILE:HG22	1:B:221:LEU:HD21	1.66	0.76
1:E:154:VAL:HG12	1:E:221:LEU:HB2	1.66	0.76
1:E:165:GLN:HA	1:E:211:ASP:O	1.84	0.76
1:E:299:ALA:CB	1:E:312:GLU:OE2	2.33	0.76
1:F:293:ILE:HG23	1:F:318:PRO:HA	1.66	0.76
1:H:211:ASP:OD1	2:H:401:CMP:H5'1	1.85	0.76
1:A:179:GLU:HG2	1:A:216:LYS:HD2	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:110:SER:O	1:F:114:LYS:HD3	1.85	0.76
1:E:328:LEU:HD22	1:E:365:LYS:HE3	1.66	0.76
1:A:274:PHE:HD2	1:A:343:LEU:HD23	1.50	0.76
1:B:224:ILE:O	1:B:224:ILE:HD13	1.84	0.76
1:B:375:VAL:CG2	1:B:376:SER:N	2.48	0.76
1:B:376:SER:N	1:C:306:GLU:HA	1.99	0.76
1:C:252:SER:OG	1:C:253:ILE:HG23	1.84	0.76
1:C:278:GLN:O	1:C:338:VAL:HG22	1.85	0.76
1:D:157:ILE:CD1	1:F:243:MET:CE	2.63	0.76
1:D:190:THR:HG22	1:D:191:SER:N	1.99	0.76
1:E:152:PHE:HE2	1:E:223:GLY:HA3	1.51	0.76
1:E:175:ILE:HD13	1:E:194:GLU:HA	1.65	0.76
1:E:300:VAL:CG1	1:E:335:ALA:HB1	2.16	0.76
1:H:115:VAL:HG23	1:H:115:VAL:O	1.85	0.76
1:H:311:VAL:HG23	1:H:312:GLU:N	1.99	0.76
1:C:224:ILE:N	1:C:224:ILE:CD1	2.47	0.76
1:C:249:SER:CA	1:C:262:ARG:NH2	2.38	0.76
1:G:294:LEU:HD13	1:G:344:LYS:O	1.85	0.76
1:H:173:TYR:HD2	1:H:198:PHE:CZ	2.03	0.76
1:A:115:VAL:HG11	1:D:112:VAL:HG21	1.66	0.76
1:A:153:PRO:CB	1:A:222:TRP:CZ3	2.69	0.76
1:B:190:THR:HG22	1:B:191:SER:N	1.99	0.76
1:C:279:LYS:CE	1:C:336:THR:CG2	2.63	0.76
1:C:298:ALA:O	1:C:315:ARG:HA	1.85	0.76
1:E:179:GLU:HB3	1:E:217:THR:HG23	1.68	0.76
1:F:184:VAL:O	1:F:184:VAL:HG13	1.85	0.76
1:G:131:GLU:OE1	1:G:131:GLU:CA	2.24	0.76
1:G:365:LYS:HA	1:G:368:ILE:HG13	1.67	0.76
1:H:131:GLU:N	1:H:131:GLU:OE1	2.19	0.76
1:H:247:PHE:C	1:H:247:PHE:CD2	2.59	0.76
1:A:113:ARG:O	1:A:113:ARG:HG2	1.84	0.76
1:A:253:ILE:HG13	1:A:254:LEU:CD2	2.16	0.76
1:C:135:LEU:HD12	1:C:136:PHE:H	1.49	0.76
1:C:226:ARG:HH11	1:C:226:ARG:CG	1.98	0.76
1:C:280:ILE:HD11	1:C:322:PHE:HE2	1.49	0.76
1:E:243:MET:CE	1:G:157:ILE:HD12	2.15	0.76
1:F:156:PHE:HE2	1:F:162:VAL:HG12	1.50	0.76
1:F:251:VAL:HG22	1:F:319:SER:O	1.86	0.76
1:A:157:ILE:HG13	1:A:160:GLU:OE1	1.86	0.76
1:B:282:VAL:O	1:B:285:GLU:HG2	1.84	0.76
1:D:279:LYS:CB	1:D:279:LYS:HZ2	1.93	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:111:TYR:O	1:E:112:VAL:HG13	1.86	0.76
1:F:157:ILE:HG13	1:F:160:GLU:OE1	1.85	0.76
1:G:291:PHE:N	1:G:291:PHE:CD1	2.54	0.76
1:H:144:ARG:CG	1:H:145:SER:N	2.49	0.76
1:H:293:ILE:HG21	1:H:317:GLY:O	1.85	0.76
1:B:173:TYR:HD2	1:B:198:PHE:CZ	2.04	0.76
1:B:197:SER:O	1:B:198:PHE:HB3	1.85	0.76
1:C:113:ARG:HD2	1:F:112:VAL:CB	2.12	0.76
1:D:316:LEU:HA	1:D:320:ASP:OD2	1.85	0.76
1:D:325:ILE:HG13	1:D:326:ALA:H	1.50	0.76
1:E:291:PHE:N	1:E:291:PHE:CD1	2.51	0.76
1:H:260:TRP:CG	2:H:401:CMP:N7	2.54	0.76
1:B:234:MET:HG3	1:B:238:LEU:HD12	1.68	0.75
1:C:224:ILE:O	1:C:224:ILE:HD13	1.86	0.75
1:C:375:VAL:HG23	1:C:376:SER:H	1.51	0.75
1:E:134:VAL:HG11	1:E:268:ALA:HA	1.68	0.75
1:F:293:ILE:CG2	1:F:318:PRO:HA	2.15	0.75
1:H:305:SER:O	1:H:306:GLU:O	2.04	0.75
1:D:292:ILE:HB	1:D:346:VAL:HG13	1.68	0.75
1:E:112:VAL:HG12	1:E:231:ARG:NH2	2.01	0.75
1:E:329:MET:HA	1:E:329:MET:CE	2.17	0.75
1:F:260:TRP:CD1	2:F:401:CMP:C5	2.75	0.75
1:H:284:GLY:O	1:H:332:PRO:CB	2.29	0.75
1:A:324:GLU:HG2	1:A:325:ILE:H	1.51	0.75
1:D:126:LEU:HD12	1:D:126:LEU:C	2.07	0.75
1:D:196:GLY:HA2	1:D:355:ARG:HH21	1.49	0.75
1:F:224:ILE:O	1:F:224:ILE:HD13	1.85	0.75
1:G:173:TYR:HB2	1:G:198:PHE:HE1	1.47	0.75
1:C:175:ILE:HD13	1:C:194:GLU:HA	1.67	0.75
1:C:273:GLN:HE21	1:C:273:GLN:H	1.33	0.75
1:A:111:TYR:C	1:D:115:VAL:CG2	2.55	0.75
1:B:291:PHE:HD1	1:B:291:PHE:H	1.34	0.75
1:C:269:LEU:HB2	1:C:346:VAL:HG21	1.68	0.75
1:E:204:ILE:HG12	1:E:234:MET:SD	2.26	0.75
1:G:226:ARG:HH11	1:G:226:ARG:CG	1.97	0.75
1:H:113:ARG:HD3	1:H:114:LYS:H	1.49	0.75
1:A:115:VAL:CB	1:D:112:VAL:CG2	2.65	0.75
1:C:251:VAL:CG1	1:C:254:LEU:HD21	2.16	0.75
1:E:348:LEU:HD21	1:E:356:VAL:CG2	2.17	0.75
1:H:179:GLU:HG2	1:H:216:LYS:HD2	1.69	0.75
1:C:120:TYR:C	1:C:120:TYR:CD2	2.59	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:211:ASP:CG	2:C:401:CMP:H5'1	2.06	0.75
1:D:179:GLU:HG2	1:D:216:LYS:HD3	1.69	0.75
1:E:301:LEU:HD21	1:E:338:VAL:HB	1.69	0.75
1:F:126:LEU:HB2	1:F:222:TRP:CZ2	2.22	0.75
1:G:211:ASP:N	1:G:211:ASP:OD1	2.19	0.75
1:G:230:ARG:O	1:G:234:MET:HB3	1.87	0.75
1:A:118:LYS:HB3	1:A:123:MET:HE2	1.66	0.75
1:B:251:VAL:CG2	1:B:319:SER:O	2.34	0.75
1:B:298:ALA:O	1:B:316:LEU:HB2	1.87	0.75
1:D:253:ILE:CG1	1:D:254:LEU:HD13	2.16	0.75
1:D:294:LEU:CD1	1:D:344:LYS:O	2.34	0.75
1:D:371:TYR:HE1	2:D:402:CMP:C8	1.98	0.75
1:F:154:VAL:HG12	1:F:221:LEU:HB2	1.67	0.75
1:F:274:PHE:HD2	1:F:343:LEU:HD23	1.51	0.75
1:G:324:GLU:HG2	1:G:325:ILE:H	1.50	0.75
1:A:113:ARG:NH2	1:D:114:LYS:C	2.39	0.75
1:B:179:GLU:HG2	1:B:216:LYS:HD3	1.68	0.75
1:C:156:PHE:HD2	1:C:162:VAL:CG1	1.99	0.75
1:C:272:VAL:C	1:C:273:GLN:NE2	2.29	0.75
1:C:365:LYS:HA	1:C:368:ILE:CD1	2.16	0.75
1:E:200:GLU:OE2	1:E:241:ARG:NH2	2.20	0.75
1:A:325:ILE:CG1	2:A:402:CMP:O2P	2.35	0.74
1:B:375:VAL:HG22	1:B:376:SER:N	2.02	0.74
1:C:203:LEU:HD22	1:C:226:ARG:HB3	1.68	0.74
1:C:230:ARG:NH1	1:C:234:MET:HE1	2.01	0.74
1:E:184:VAL:HG13	1:E:184:VAL:O	1.85	0.74
1:E:269:LEU:CB	1:E:346:VAL:CG2	2.65	0.74
1:F:328:LEU:HD13	1:F:364:LEU:HD11	1.69	0.74
1:G:190:THR:CG2	1:G:191:SER:H	1.99	0.74
1:B:293:ILE:HD11	1:B:343:LEU:HD11	1.69	0.74
1:C:201:LEU:H	1:C:201:LEU:HD12	1.52	0.74
1:C:321:TYR:CD1	1:C:321:TYR:C	2.59	0.74
1:D:249:SER:HA	1:D:262:ARG:HH22	1.53	0.74
1:F:204:ILE:HG12	1:F:234:MET:SD	2.27	0.74
1:G:280:ILE:CD1	1:G:322:PHE:CE2	2.70	0.74
1:C:273:GLN:NE2	1:C:273:GLN:H	1.83	0.74
1:E:182:VAL:CG2	1:E:190:THR:O	2.29	0.74
1:F:294:LEU:N	1:F:294:LEU:CD1	2.49	0.74
1:G:198:PHE:CD1	1:G:198:PHE:O	2.39	0.74
1:G:295:GLU:HB2	1:G:344:LYS:HB3	1.69	0.74
1:B:278:GLN:HG2	1:B:279:LYS:N	2.01	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:293:ILE:HG13	1:H:345:CYS:SG	2.26	0.74
1:A:234:MET:HG3	1:A:238:LEU:HD12	1.69	0.74
1:A:291:PHE:CE1	1:A:347:LYS:NZ	2.56	0.74
1:C:120:TYR:HD1	1:D:148:PHE:HB3	1.53	0.74
1:C:325:ILE:HD11	2:C:402:CMP:O2P	1.85	0.74
1:D:204:ILE:HD13	1:D:238:LEU:HD11	1.68	0.74
1:D:251:VAL:CG2	1:D:319:SER:O	2.35	0.74
1:G:171:ASN:HB3	1:G:224:ILE:O	1.86	0.74
1:G:210:ALA:N	1:G:211:ASP:OD1	2.21	0.74
1:H:175:ILE:HD11	1:H:196:GLY:H	1.53	0.74
1:H:230:ARG:HG2	1:H:234:MET:HE1	1.70	0.74
1:H:269:LEU:HD22	1:H:346:VAL:HG21	1.69	0.74
1:H:293:ILE:CG2	1:H:317:GLY:O	2.36	0.74
1:A:211:ASP:OD1	1:A:211:ASP:N	2.21	0.74
1:A:253:ILE:HD13	1:A:321:TYR:CE2	2.23	0.74
1:B:300:VAL:CG1	1:B:335:ALA:HB1	2.18	0.74
1:B:313:VAL:O	1:B:313:VAL:CG2	2.35	0.74
1:B:365:LYS:HA	1:B:368:ILE:HG13	1.68	0.74
1:C:293:ILE:CG2	1:C:317:GLY:O	2.35	0.74
1:C:324:GLU:HB2	1:C:364:LEU:CD1	2.18	0.74
1:D:260:TRP:HA	1:D:263:LEU:HD12	1.70	0.74
1:D:328:LEU:HD22	1:D:365:LYS:HE3	1.69	0.74
1:E:135:LEU:HD12	1:E:136:PHE:N	2.01	0.74
1:E:353:PHE:CE1	1:E:357:LEU:CD2	2.70	0.74
1:G:261:GLU:OE2	1:G:359:PRO:HG2	1.86	0.74
1:A:114:LYS:HA	1:D:111:TYR:HE2	1.51	0.74
1:B:130:ILE:CG2	1:B:131:GLU:H	2.01	0.74
1:C:198:PHE:C	1:C:198:PHE:HD1	1.91	0.74
1:C:200:GLU:OE1	1:C:201:LEU:HD12	1.87	0.74
1:C:366:ARG:HG3	1:C:367:ASN:N	2.00	0.74
1:D:152:PHE:H	1:D:152:PHE:HD1	1.35	0.74
1:G:204:ILE:HG22	1:G:205:TYR:HD2	1.49	0.74
1:H:175:ILE:CD1	1:H:194:GLU:HA	2.17	0.74
1:A:211:ASP:OD2	2:A:401:CMP:C3'	2.36	0.74
1:C:280:ILE:HG12	1:C:337:VAL:HB	1.70	0.74
1:C:284:GLY:CA	1:C:332:PRO:HB3	2.17	0.74
1:E:347:LYS:O	1:E:348:LEU:HD12	1.87	0.74
1:F:211:ASP:OD2	2:F:401:CMP:N3	2.21	0.74
1:G:188:TRP:CZ3	1:G:190:THR:C	2.61	0.74
1:B:313:VAL:HG21	2:B:402:CMP:HN61	1.49	0.74
1:D:153:PRO:HB3	1:D:222:TRP:HZ3	1.48	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:157:ILE:O	1:E:160:GLU:HB2	1.88	0.74
1:F:306:GLU:CB	1:G:307:ASN:CB	2.65	0.74
1:A:156:PHE:CD2	1:A:162:VAL:CG1	2.70	0.74
1:A:246:GLU:O	1:A:247:PHE:C	2.20	0.74
1:B:211:ASP:CG	2:B:401:CMP:H5'1	2.07	0.74
1:B:269:LEU:HB3	1:B:346:VAL:HG23	1.66	0.74
1:C:111:TYR:CD1	1:F:111:TYR:HE2	2.06	0.74
1:C:230:ARG:NH1	1:C:234:MET:CE	2.50	0.74
1:D:192:VAL:O	1:D:192:VAL:HG12	1.88	0.74
1:D:280:ILE:HG13	1:D:281:VAL:H	1.51	0.74
1:E:123:MET:HE3	1:F:123:MET:HE3	1.68	0.74
1:E:198:PHE:CD1	1:E:198:PHE:C	2.58	0.74
1:E:243:MET:HE3	1:G:157:ILE:HD11	1.70	0.74
1:H:173:TYR:CD2	1:H:198:PHE:CE1	2.75	0.74
1:D:198:PHE:CD1	1:D:198:PHE:O	2.41	0.73
1:D:204:ILE:HG22	1:D:205:TYR:HD2	1.52	0.73
1:D:294:LEU:H	1:D:294:LEU:CD1	1.98	0.73
1:D:301:LEU:CD2	1:D:310:PHE:CD1	2.70	0.73
1:E:126:LEU:HD12	1:E:126:LEU:C	2.08	0.73
1:F:254:LEU:HD12	1:F:255:GLU:N	2.02	0.73
1:F:260:TRP:NE1	2:F:401:CMP:H2'	2.02	0.73
1:F:290:PHE:C	1:F:291:PHE:HD1	1.89	0.73
1:G:112:VAL:HG12	1:G:231:ARG:NH2	2.03	0.73
1:G:172:PHE:HB3	1:G:224:ILE:CD1	2.18	0.73
1:H:316:LEU:HA	1:H:320:ASP:OD2	1.88	0.73
1:A:144:ARG:NH1	1:A:144:ARG:HB2	2.03	0.73
1:C:113:ARG:HG3	1:F:112:VAL:HG12	1.69	0.73
1:C:175:ILE:HD11	1:C:196:GLY:H	1.53	0.73
1:C:246:GLU:O	1:C:247:PHE:C	2.23	0.73
1:F:234:MET:HG3	1:F:238:LEU:HD12	1.71	0.73
1:G:371:TYR:HE1	2:G:402:CMP:N7	1.86	0.73
1:A:112:VAL:O	1:A:231:ARG:NH1	2.21	0.73
1:A:115:VAL:CG1	1:D:112:VAL:HG23	2.19	0.73
1:A:135:LEU:HD13	1:A:136:PHE:CD1	2.23	0.73
1:A:365:LYS:CA	1:A:368:ILE:HG13	2.18	0.73
1:C:234:MET:HG3	1:C:238:LEU:CD1	2.17	0.73
1:F:114:LYS:HD2	1:F:115:VAL:H	1.52	0.73
1:F:301:LEU:HD22	1:F:311:VAL:O	1.86	0.73
1:G:183:TYR:CE1	1:G:188:TRP:HB2	2.23	0.73
1:H:233:LEU:CD1	1:H:233:LEU:H	1.95	0.73
1:A:204:ILE:HG22	1:A:205:TYR:CD2	2.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:162:VAL:HG22	1:D:213:VAL:O	1.88	0.73
1:E:173:TYR:CB	1:E:198:PHE:HE1	2.01	0.73
1:A:328:LEU:HD22	1:A:365:LYS:HE3	1.68	0.73
1:B:252:SER:O	1:B:254:LEU:HG	1.88	0.73
1:C:153:PRO:HB3	1:C:222:TRP:CZ3	2.24	0.73
1:C:280:ILE:HD11	1:C:337:VAL:HB	1.68	0.73
1:G:211:ASP:OD2	2:G:401:CMP:H3'	1.88	0.73
1:H:204:ILE:HG22	1:H:205:TYR:HD2	1.49	0.73
1:H:280:ILE:HB	1:H:291:PHE:HE2	1.53	0.73
1:H:291:PHE:CD2	1:H:322:PHE:CZ	2.76	0.73
1:A:111:TYR:HA	1:D:115:VAL:CG2	2.19	0.73
1:C:280:ILE:HG13	1:C:281:VAL:H	1.53	0.73
1:E:152:PHE:CD2	1:E:152:PHE:O	2.41	0.73
1:E:230:ARG:HG2	1:E:234:MET:HE1	1.69	0.73
1:F:204:ILE:HD13	1:F:238:LEU:HD11	1.69	0.73
1:H:273:GLN:HB2	1:H:343:LEU:O	1.89	0.73
1:H:280:ILE:CD1	1:H:337:VAL:HB	2.19	0.73
1:A:325:ILE:HG13	1:A:326:ALA:N	2.03	0.73
1:B:294:LEU:H	1:B:294:LEU:CD1	1.97	0.73
1:C:194:GLU:O	1:C:355:ARG:HD2	1.88	0.73
1:F:175:ILE:HD11	1:F:195:GLY:N	2.02	0.73
1:H:249:SER:CA	1:H:262:ARG:NH2	2.52	0.73
1:A:279:LYS:HB3	1:A:338:VAL:HG23	1.69	0.73
1:B:147:ILE:HG23	1:B:232:ILE:HD13	1.69	0.73
1:B:325:ILE:CD1	2:B:402:CMP:O1P	2.35	0.73
1:C:120:TYR:HD2	1:C:121:LYS:HA	1.52	0.73
1:C:130:ILE:HG23	1:C:131:GLU:N	2.04	0.73
1:C:269:LEU:HB3	1:C:346:VAL:HG22	1.70	0.73
1:C:287:GLY:HA3	1:C:326:ALA:CB	2.18	0.73
1:E:243:MET:HE1	1:G:158:ALA:O	1.88	0.73
1:E:325:ILE:HG13	1:E:326:ALA:N	2.03	0.73
1:A:260:TRP:CG	2:A:401:CMP:N7	2.57	0.73
1:B:269:LEU:HD22	1:B:346:VAL:CG2	2.19	0.73
1:B:273:GLN:HB2	1:B:343:LEU:O	1.87	0.73
1:B:312:GLU:OE1	1:B:313:VAL:N	2.21	0.73
1:C:111:TYR:O	1:C:112:VAL:CG1	2.36	0.73
1:C:275:GLU:O	1:C:339:ALA:HB3	1.89	0.73
1:E:294:LEU:O	1:E:318:PRO:HB3	1.89	0.73
1:G:148:PHE:HB3	1:H:120:TYR:CD1	2.24	0.73
1:G:161:THR:CA	1:G:214:LYS:HD2	2.18	0.73
1:A:175:ILE:HA	1:A:221:LEU:HD22	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:ILE:HD12	1:A:281:VAL:HG23	1.71	0.73
1:B:130:ILE:HG23	1:B:131:GLU:N	2.03	0.73
1:C:293:ILE:HG13	1:C:345:CYS:SG	2.29	0.73
1:C:371:TYR:CE1	2:C:402:CMP:C8	2.71	0.73
1:D:172:PHE:HB3	1:D:224:ILE:CD1	2.19	0.73
1:E:239:ARG:NH1	1:G:157:ILE:HG23	2.02	0.73
1:F:279:LYS:HE3	1:F:282:VAL:HG22	1.70	0.73
1:F:280:ILE:HD11	1:F:322:PHE:CE2	2.20	0.73
1:A:203:LEU:HD12	1:A:229:TYR:CD2	2.24	0.72
1:B:111:TYR:C	1:B:112:VAL:CG2	2.57	0.72
1:C:204:ILE:CG2	1:C:205:TYR:CD2	2.71	0.72
1:F:301:LEU:HD12	1:F:310:PHE:HB3	1.71	0.72
1:H:135:LEU:HD12	1:H:136:PHE:H	1.52	0.72
1:A:272:VAL:HA	1:A:273:GLN:NE2	2.03	0.72
1:B:302:GLN:O	1:B:310:PHE:HA	1.90	0.72
1:D:157:ILE:CB	1:D:218:ASN:OD1	2.36	0.72
1:G:165:GLN:HA	1:G:211:ASP:O	1.89	0.72
1:A:112:VAL:O	1:A:231:ARG:CZ	2.37	0.72
1:A:365:LYS:HA	1:A:368:ILE:CG1	2.19	0.72
1:B:135:LEU:HD13	1:B:136:PHE:CD1	2.23	0.72
1:C:283:GLN:HG3	1:C:335:ALA:N	2.04	0.72
1:D:153:PRO:CB	1:D:222:TRP:CZ3	2.73	0.72
1:E:158:ALA:N	1:E:218:ASN:OD1	2.22	0.72
1:E:179:GLU:HG2	1:E:216:LYS:HD3	1.69	0.72
1:E:265:VAL:HG12	1:E:269:LEU:CD2	2.18	0.72
1:F:328:LEU:CD2	1:F:365:LYS:HE3	2.20	0.72
1:F:328:LEU:CD1	1:F:364:LEU:HD11	2.19	0.72
1:G:152:PHE:CD2	1:G:152:PHE:O	2.42	0.72
1:H:111:TYR:CE2	1:H:112:VAL:HG12	2.24	0.72
1:H:237:THR:O	1:H:241:ARG:HG3	1.89	0.72
1:A:142:ASN:HB2	1:C:121:LYS:CE	2.20	0.72
1:B:130:ILE:HG22	1:B:131:GLU:H	1.54	0.72
1:B:172:PHE:HB3	1:B:224:ILE:CD1	2.17	0.72
1:B:280:ILE:HD11	1:B:322:PHE:CE2	2.08	0.72
1:B:327:LEU:HD23	1:B:353:PHE:CE2	2.25	0.72
1:C:152:PHE:CD2	1:C:152:PHE:O	2.42	0.72
1:C:156:PHE:CE2	1:C:162:VAL:CG1	2.60	0.72
1:C:313:VAL:HG13	1:C:313:VAL:O	1.87	0.72
1:D:156:PHE:HD2	1:D:162:VAL:CG1	2.01	0.72
1:G:233:LEU:H	1:G:233:LEU:CD1	1.87	0.72
1:B:228:SER:O	1:B:232:ILE:HG22	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:171:ASN:HB3	1:D:224:ILE:O	1.88	0.72
1:A:165:GLN:N	1:A:212:THR:CG2	2.30	0.72
1:C:280:ILE:CD1	1:C:337:VAL:HB	2.20	0.72
1:C:291:PHE:CE1	1:C:347:LYS:NZ	2.58	0.72
1:E:112:VAL:CG1	1:E:231:ARG:NH2	2.53	0.72
1:E:278:GLN:CG	1:E:279:LYS:H	2.02	0.72
1:E:324:GLU:HB2	1:E:364:LEU:HD13	1.72	0.72
1:H:120:TYR:C	1:H:120:TYR:CD2	2.63	0.72
1:H:304:ARG:H	1:H:308:GLU:CB	2.00	0.72
1:A:153:PRO:CA	1:A:222:TRP:CZ3	2.73	0.72
1:A:182:VAL:CG2	1:A:190:THR:O	2.32	0.72
1:C:281:VAL:HG13	1:C:333:ARG:HG3	1.69	0.72
1:D:131:GLU:OE1	1:D:131:GLU:CA	2.34	0.72
1:D:157:ILE:O	1:D:160:GLU:HB2	1.89	0.72
1:D:280:ILE:CD1	1:D:322:PHE:CE2	2.73	0.72
1:E:279:LYS:CB	1:E:279:LYS:HZ2	1.83	0.72
1:F:162:VAL:HG23	1:F:163:ILE:N	2.04	0.72
1:F:211:ASP:OD2	2:F:401:CMP:H3'	1.89	0.72
1:A:260:TRP:CD2	2:A:401:CMP:N7	2.57	0.72
1:A:347:LYS:O	1:A:348:LEU:HD12	1.89	0.72
1:B:203:LEU:HD12	1:B:229:TYR:CD2	2.24	0.72
1:D:120:TYR:C	1:D:120:TYR:HD2	1.92	0.72
1:D:190:THR:CG2	1:D:191:SER:H	1.97	0.72
1:E:293:ILE:CG2	1:E:317:GLY:O	2.37	0.72
1:F:280:ILE:HD11	1:F:337:VAL:HB	1.71	0.72
1:F:301:LEU:HA	1:F:311:VAL:O	1.89	0.72
1:G:328:LEU:CD2	1:G:365:LYS:HE3	2.20	0.72
1:A:175:ILE:HG22	1:A:221:LEU:HD21	1.70	0.72
1:B:152:PHE:CD2	1:B:152:PHE:O	2.43	0.72
1:B:170:ASP:H	1:B:209:ARG:NH2	1.88	0.72
1:D:290:PHE:C	1:D:291:PHE:HD1	1.92	0.72
1:E:272:VAL:HG22	1:E:273:GLN:H	1.55	0.72
1:G:148:PHE:HB2	1:H:120:TYR:CD1	2.25	0.72
1:H:265:VAL:O	1:H:269:LEU:HG	1.90	0.72
1:C:144:ARG:HG2	1:C:145:SER:N	2.03	0.72
1:C:348:LEU:HD21	1:C:356:VAL:HG21	1.72	0.72
1:E:230:ARG:O	1:E:234:MET:HB3	1.89	0.72
1:E:329:MET:HA	1:E:329:MET:HE3	1.71	0.72
1:H:198:PHE:C	1:H:198:PHE:HD1	1.88	0.72
1:A:147:ILE:HG23	1:A:232:ILE:CD1	2.19	0.71
1:A:183:TYR:CD1	1:A:188:TRP:HB2	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:TRP:CE3	1:A:222:TRP:HA	2.25	0.71
1:H:365:LYS:HA	1:H:368:ILE:HG13	1.71	0.71
1:A:179:GLU:HG2	1:A:216:LYS:CD	2.19	0.71
1:A:183:TYR:CE1	1:A:188:TRP:HB2	2.25	0.71
1:A:365:LYS:C	1:A:368:ILE:HG13	2.09	0.71
1:B:175:ILE:O	1:B:175:ILE:CD1	2.28	0.71
1:B:275:GLU:O	1:B:278:GLN:HB3	1.90	0.71
1:C:130:ILE:CG2	1:C:131:GLU:H	2.02	0.71
1:C:249:SER:N	1:C:262:ARG:NH2	2.39	0.71
1:G:328:LEU:HD22	1:G:365:LYS:HE3	1.72	0.71
1:H:251:VAL:HG23	1:H:319:SER:O	1.89	0.71
1:B:272:VAL:HG22	1:B:273:GLN:H	1.55	0.71
1:E:203:LEU:HD22	1:E:226:ARG:CB	2.20	0.71
1:H:184:VAL:O	1:H:184:VAL:HG13	1.88	0.71
1:C:188:TRP:CH2	1:C:190:THR:HA	2.25	0.71
1:D:368:ILE:O	1:D:371:TYR:HB2	1.90	0.71
1:E:280:ILE:CD1	1:E:281:VAL:HG23	2.20	0.71
1:F:272:VAL:HG22	1:F:273:GLN:H	1.55	0.71
1:G:253:ILE:HG21	1:G:321:TYR:CE2	2.25	0.71
1:H:270:GLU:O	1:H:346:VAL:HA	1.89	0.71
1:H:284:GLY:N	1:H:333:ARG:O	2.23	0.71
1:B:120:TYR:HD2	1:B:120:TYR:O	1.72	0.71
1:C:113:ARG:CG	1:F:112:VAL:CG1	2.59	0.71
1:F:259:LYS:HG3	1:F:260:TRP:H	1.55	0.71
1:G:280:ILE:HD11	1:G:337:VAL:HB	1.71	0.71
1:H:135:LEU:HD12	1:H:136:PHE:N	2.05	0.71
1:A:113:ARG:HH22	1:D:115:VAL:HA	1.55	0.71
1:B:247:PHE:HZ	1:B:293:ILE:O	1.73	0.71
1:D:325:ILE:HG12	2:D:402:CMP:P	2.31	0.71
1:E:183:TYR:CE1	1:E:188:TRP:HB2	2.26	0.71
1:E:251:VAL:CG2	1:E:319:SER:O	2.37	0.71
1:H:171:ASN:HB3	1:H:224:ILE:O	1.91	0.71
1:A:224:ILE:N	1:A:224:ILE:HD12	2.06	0.71
1:A:281:VAL:HG13	1:A:333:ARG:HG3	1.72	0.71
1:C:356:VAL:CG2	1:C:357:LEU:HD13	2.16	0.71
1:D:157:ILE:HD11	1:F:243:MET:HE3	1.72	0.71
1:E:156:PHE:HD2	1:E:162:VAL:CG1	1.98	0.71
1:G:278:GLN:HG2	1:G:279:LYS:H	1.56	0.71
1:G:280:ILE:HG13	1:G:281:VAL:H	1.53	0.71
1:H:313:VAL:HG11	2:H:402:CMP:HN61	1.56	0.71
1:A:156:PHE:HD2	1:A:162:VAL:CG1	2.03	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:TYR:C	1:A:321:TYR:CD1	2.64	0.71
1:B:157:ILE:HG22	1:B:218:ASN:OD1	1.89	0.71
1:B:158:ALA:CB	1:B:217:THR:O	2.36	0.71
1:G:148:PHE:HD1	1:H:120:TYR:CE1	2.08	0.71
1:G:278:GLN:HG2	1:G:279:LYS:N	2.06	0.71
1:G:278:GLN:CG	1:G:279:LYS:H	2.03	0.71
1:A:111:TYR:O	1:D:115:VAL:HG21	1.90	0.71
1:A:113:ARG:NH1	1:D:114:LYS:N	2.39	0.71
1:B:198:PHE:CD1	1:B:198:PHE:O	2.43	0.71
1:B:210:ALA:N	1:B:211:ASP:OD1	2.23	0.71
1:C:300:VAL:O	1:C:301:LEU:CG	2.38	0.71
1:D:175:ILE:HD13	1:D:194:GLU:HA	1.70	0.71
1:G:265:VAL:O	1:G:269:LEU:CG	2.32	0.71
1:H:179:GLU:HG2	1:H:216:LYS:HD3	1.71	0.71
1:H:253:ILE:HG13	1:H:254:LEU:N	2.03	0.71
1:H:259:LYS:O	1:H:262:ARG:HG3	1.89	0.71
1:H:260:TRP:HE1	2:H:401:CMP:C2'	1.99	0.71
1:A:175:ILE:CD1	1:A:193:GLY:O	2.38	0.71
1:C:298:ALA:HB1	1:C:338:VAL:O	1.91	0.71
1:F:278:GLN:HG3	1:F:279:LYS:N	2.03	0.71
1:G:126:LEU:HB2	1:G:222:TRP:CZ2	2.26	0.71
1:G:282:VAL:O	1:G:285:GLU:HG2	1.91	0.71
1:A:239:ARG:NH2	1:C:156:PHE:CE1	2.58	0.70
1:A:251:VAL:CG1	1:A:254:LEU:HD21	2.20	0.70
1:A:294:LEU:CD1	1:A:344:LYS:O	2.38	0.70
1:C:130:ILE:HG23	1:C:131:GLU:H	1.54	0.70
1:C:182:VAL:CG2	1:C:190:THR:H	2.02	0.70
1:C:283:GLN:HG3	1:C:334:ALA:C	2.11	0.70
1:H:198:PHE:CD1	1:H:198:PHE:O	2.43	0.70
1:A:293:ILE:CD1	1:A:343:LEU:HD11	2.21	0.70
1:B:175:ILE:HD11	1:B:195:GLY:N	2.05	0.70
1:B:211:ASP:OD2	2:B:401:CMP:C4'	2.40	0.70
1:B:293:ILE:HG13	1:B:345:CYS:SG	2.30	0.70
1:C:182:VAL:HG12	1:C:213:VAL:CG1	2.19	0.70
1:C:230:ARG:HG2	1:C:230:ARG:HH11	1.56	0.70
1:D:224:ILE:CD1	1:D:224:ILE:N	2.52	0.70
1:F:260:TRP:CD1	2:F:401:CMP:C4	2.79	0.70
1:H:220:LYS:O	1:H:221:LEU:HD23	1.91	0.70
1:H:328:LEU:HD23	1:H:365:LYS:HE3	1.71	0.70
1:A:140:ASP:C	1:A:140:ASP:OD1	2.29	0.70
1:A:197:SER:O	1:A:198:PHE:HB3	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:114:LYS:CD	1:F:115:VAL:H	2.05	0.70
1:F:293:ILE:CD1	1:F:343:LEU:HD11	2.21	0.70
1:G:116:ILE:CG2	1:G:118:LYS:NZ	2.53	0.70
1:A:182:VAL:HG12	1:A:213:VAL:CG2	2.21	0.70
1:A:251:VAL:CG2	1:A:319:SER:O	2.38	0.70
1:B:175:ILE:CD1	1:B:195:GLY:H	2.04	0.70
1:D:246:GLU:O	1:D:249:SER:N	2.24	0.70
1:E:162:VAL:CG2	1:E:163:ILE:HG13	2.16	0.70
1:F:200:GLU:OE2	1:F:241:ARG:NH2	2.24	0.70
1:G:117:PRO:O	1:G:118:LYS:HB2	1.90	0.70
1:G:365:LYS:C	1:G:368:ILE:HG13	2.11	0.70
1:H:230:ARG:NH1	1:H:234:MET:HE1	2.05	0.70
1:D:282:VAL:O	1:D:285:GLU:HG2	1.91	0.70
1:D:327:LEU:HD23	1:D:353:PHE:CD2	2.26	0.70
1:F:179:GLU:HG2	1:F:216:LYS:HD2	1.73	0.70
1:G:324:GLU:HB2	1:G:364:LEU:CD1	2.20	0.70
1:H:301:LEU:O	1:H:302:GLN:HG3	1.91	0.70
1:D:211:ASP:OD1	2:D:401:CMP:H5'1	1.91	0.70
1:E:175:ILE:HD11	1:E:195:GLY:N	2.05	0.70
1:G:175:ILE:HD13	1:G:194:GLU:HA	1.71	0.70
1:C:300:VAL:HG11	2:C:402:CMP:C8	2.21	0.70
1:D:280:ILE:HD11	1:D:337:VAL:HB	1.72	0.70
1:G:135:LEU:HD12	1:G:136:PHE:N	2.06	0.70
1:G:361:SER:C	1:G:365:LYS:HZ2	1.94	0.70
1:H:247:PHE:CD2	1:H:247:PHE:O	2.44	0.70
1:H:291:PHE:N	1:H:291:PHE:CD1	2.59	0.70
1:H:329:MET:HA	1:H:329:MET:HE3	1.73	0.70
1:A:130:ILE:CD1	1:A:151:MET:CE	2.70	0.70
1:A:348:LEU:HD21	1:A:356:VAL:HG21	1.71	0.70
1:B:295:GLU:O	1:B:344:LYS:N	2.23	0.70
1:E:153:PRO:HB3	1:E:222:TRP:CZ3	2.27	0.70
1:E:278:GLN:CG	1:E:279:LYS:N	2.55	0.70
1:F:230:ARG:CG	1:F:234:MET:HE1	2.21	0.70
1:G:135:LEU:HD12	1:G:136:PHE:H	1.56	0.70
1:B:246:GLU:O	1:B:249:SER:N	2.24	0.70
1:C:265:VAL:O	1:C:269:LEU:CG	2.31	0.70
1:E:211:ASP:OD1	2:E:401:CMP:H5'1	1.91	0.70
1:B:280:ILE:HG13	1:B:281:VAL:H	1.56	0.70
1:D:269:LEU:HD22	1:D:346:VAL:HG22	1.73	0.70
1:G:182:VAL:HG12	1:G:213:VAL:HG22	1.73	0.70
1:A:203:LEU:HD13	1:A:226:ARG:HB3	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:ARG:HG2	1:A:234:MET:HE1	1.71	0.69
1:C:183:TYR:HD1	1:C:188:TRP:HA	1.57	0.69
1:C:285:GLU:O	1:C:332:PRO:CA	2.36	0.69
1:C:311:VAL:HG23	1:C:312:GLU:N	2.07	0.69
1:D:252:SER:O	1:D:254:LEU:HD22	1.91	0.69
1:D:325:ILE:CD1	2:D:402:CMP:O1P	2.39	0.69
1:G:156:PHE:HD2	1:G:162:VAL:HG12	1.56	0.69
1:G:175:ILE:CD1	1:G:195:GLY:H	2.05	0.69
1:H:234:MET:HG3	1:H:238:LEU:CD1	2.20	0.69
1:H:253:ILE:HG13	1:H:254:LEU:CD2	2.21	0.69
1:A:175:ILE:O	1:A:175:ILE:CD1	2.29	0.69
1:A:224:ILE:CD1	1:A:224:ILE:H	2.04	0.69
1:B:198:PHE:O	1:B:198:PHE:HD1	1.75	0.69
1:C:224:ILE:H	1:C:224:ILE:CD1	2.04	0.69
1:D:162:VAL:CG2	1:D:163:ILE:HG13	2.18	0.69
1:D:280:ILE:CD1	1:D:322:PHE:HE2	2.05	0.69
1:D:285:GLU:OE1	1:D:285:GLU:HA	1.93	0.69
1:E:245:GLU:OE1	1:E:246:GLU:OE1	2.08	0.69
1:G:279:LYS:CB	1:G:279:LYS:HZ2	1.98	0.69
1:H:203:LEU:HD12	1:H:229:TYR:CD2	2.27	0.69
1:A:263:LEU:O	1:A:267:ASP:N	2.24	0.69
1:B:140:ASP:C	1:B:140:ASP:OD1	2.31	0.69
1:C:174:VAL:O	1:C:174:VAL:HG13	1.90	0.69
1:C:365:LYS:O	1:C:368:ILE:CG1	2.39	0.69
1:D:194:GLU:O	1:D:355:ARG:HD2	1.92	0.69
1:H:182:VAL:HG12	1:H:213:VAL:CG2	2.22	0.69
1:D:222:TRP:CE3	1:D:222:TRP:HA	2.26	0.69
1:F:130:ILE:HG13	1:F:136:PHE:CG	2.27	0.69
1:F:158:ALA:HB2	1:F:217:THR:C	2.12	0.69
1:G:179:GLU:HG2	1:G:216:LYS:HD3	1.74	0.69
1:G:266:ALA:CA	1:G:269:LEU:CD1	2.68	0.69
1:G:275:GLU:O	1:G:278:GLN:HB3	1.92	0.69
1:H:347:LYS:O	1:H:348:LEU:HD12	1.93	0.69
1:A:282:VAL:O	1:A:285:GLU:HG2	1.93	0.69
1:D:259:LYS:O	1:D:262:ARG:CG	2.33	0.69
1:D:329:MET:CE	1:D:329:MET:HA	2.21	0.69
1:E:116:ILE:HG22	1:E:118:LYS:HG3	1.74	0.69
1:F:222:TRP:CE3	1:F:222:TRP:HA	2.27	0.69
1:F:328:LEU:HD22	1:F:365:LYS:HE3	1.74	0.69
1:H:288:ASP:OD1	1:H:288:ASP:O	2.10	0.69
1:H:329:MET:HA	1:H:329:MET:CE	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:266:ALA:HA	1:B:269:LEU:CD1	2.23	0.69
1:C:247:PHE:C	1:C:247:PHE:CD2	2.63	0.69
1:C:266:ALA:CA	1:C:269:LEU:CD1	2.66	0.69
1:F:266:ALA:HA	1:F:269:LEU:HD12	1.74	0.69
1:A:204:ILE:HG22	1:A:205:TYR:HD2	1.57	0.69
1:A:253:ILE:HG21	1:A:321:TYR:CE2	2.27	0.69
1:B:153:PRO:CA	1:B:222:TRP:CZ3	2.75	0.69
1:C:190:THR:CG2	1:C:191:SER:H	2.03	0.69
1:D:164:GLN:HA	1:D:212:THR:HG22	1.75	0.69
1:G:152:PHE:O	1:G:152:PHE:HD2	1.74	0.69
1:G:175:ILE:O	1:G:175:ILE:CD1	2.32	0.69
1:G:280:ILE:HD11	1:G:322:PHE:HE2	1.56	0.69
1:G:280:ILE:HD13	1:G:322:PHE:CZ	2.27	0.69
1:G:298:ALA:HB1	1:G:338:VAL:O	1.93	0.69
1:A:188:TRP:CH2	1:A:190:THR:HA	2.27	0.69
1:A:323:GLY:HA2	2:A:402:CMP:O1P	1.93	0.69
1:B:135:LEU:HD12	1:B:136:PHE:N	2.07	0.69
1:B:161:THR:CA	1:B:214:LYS:HD2	2.17	0.69
1:B:211:ASP:OD2	2:B:401:CMP:H5'1	1.91	0.69
1:B:280:ILE:HD11	1:B:337:VAL:HB	1.73	0.69
1:C:327:LEU:HD23	1:C:353:PHE:CE2	2.27	0.69
1:D:153:PRO:CB	1:D:222:TRP:HZ3	2.05	0.69
1:D:161:THR:CA	1:D:214:LYS:HD2	2.20	0.69
1:D:173:TYR:HB2	1:D:198:PHE:CE1	2.27	0.69
1:D:296:GLY:CA	1:D:342:PRO:O	2.40	0.69
1:D:298:ALA:CB	1:D:338:VAL:O	2.38	0.69
1:E:152:PHE:H	1:E:152:PHE:HD2	1.39	0.69
1:E:253:ILE:HG21	1:E:321:TYR:CE2	2.27	0.69
1:F:253:ILE:HG13	1:F:254:LEU:H	1.57	0.69
1:H:144:ARG:O	1:H:147:ILE:HG12	1.93	0.69
1:H:156:PHE:HD2	1:H:162:VAL:HG12	1.45	0.69
1:H:289:GLU:HB3	1:H:347:LYS:HZ1	1.56	0.69
1:H:365:LYS:HA	1:H:368:ILE:CG1	2.23	0.69
1:D:183:TYR:CE1	1:D:188:TRP:HB2	2.28	0.69
1:F:158:ALA:N	1:F:218:ASN:OD1	2.25	0.69
1:F:260:TRP:CE2	2:F:401:CMP:C8	2.76	0.69
1:G:148:PHE:HB2	1:H:120:TYR:HD1	1.55	0.69
1:H:222:TRP:HA	1:H:222:TRP:CE3	2.26	0.69
1:B:361:SER:C	1:B:365:LYS:HZ2	1.96	0.69
1:C:173:TYR:CD2	1:C:198:PHE:CZ	2.80	0.69
1:E:224:ILE:O	1:E:224:ILE:HD13	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:TYR:O	1:A:112:VAL:CG2	2.40	0.68
1:B:171:ASN:H	1:B:209:ARG:HH22	1.41	0.68
1:E:148:PHE:CD1	1:F:120:TYR:CD1	2.80	0.68
1:E:365:LYS:HA	1:E:368:ILE:HG13	1.75	0.68
1:G:371:TYR:CE1	2:G:402:CMP:C4	2.81	0.68
1:H:224:ILE:CD1	1:H:224:ILE:H	2.06	0.68
1:H:226:ARG:HH11	1:H:226:ARG:CG	2.02	0.68
1:H:300:VAL:O	1:H:312:GLU:HB2	1.93	0.68
1:B:321:TYR:CD1	1:B:321:TYR:O	2.46	0.68
1:C:300:VAL:N	1:C:312:GLU:OE2	2.25	0.68
1:D:173:TYR:HD2	1:D:198:PHE:CE1	2.11	0.68
1:E:116:ILE:N	1:E:149:ASP:O	2.25	0.68
1:E:123:MET:CE	1:F:123:MET:CE	2.72	0.68
1:G:182:VAL:CG2	1:G:190:THR:H	2.06	0.68
1:G:253:ILE:HG13	1:G:254:LEU:H	1.57	0.68
1:H:249:SER:HA	1:H:262:ARG:NH2	2.08	0.68
1:A:183:TYR:CD1	1:A:188:TRP:CB	2.77	0.68
1:B:254:LEU:C	1:B:254:LEU:HD12	2.13	0.68
1:C:233:LEU:HD12	1:C:233:LEU:N	2.06	0.68
1:D:123:MET:O	1:D:127:ALA:N	2.20	0.68
1:E:360:CYS:O	1:E:364:LEU:HD23	1.92	0.68
1:G:157:ILE:O	1:G:160:GLU:HB2	1.92	0.68
1:G:251:VAL:CG2	1:G:319:SER:O	2.39	0.68
1:G:371:TYR:HE1	2:G:402:CMP:C5	2.09	0.68
1:H:182:VAL:O	1:H:182:VAL:CG2	2.37	0.68
1:H:283:GLN:HG3	1:H:335:ALA:N	2.09	0.68
1:H:290:PHE:C	1:H:291:PHE:HD1	1.97	0.68
1:B:183:TYR:CE1	1:B:188:TRP:HB2	2.29	0.68
1:F:174:VAL:HG23	1:F:196:GLY:O	1.94	0.68
1:H:301:LEU:HA	1:H:311:VAL:O	1.94	0.68
1:A:126:LEU:HB2	1:A:222:TRP:CZ2	2.28	0.68
1:A:209:ARG:HD2	2:A:401:CMP:O5'	1.93	0.68
1:B:135:LEU:CD1	1:B:136:PHE:N	2.57	0.68
1:B:254:LEU:HD12	1:B:255:GLU:N	2.09	0.68
1:B:269:LEU:CB	1:B:346:VAL:HG21	2.20	0.68
1:C:173:TYR:CD2	1:C:198:PHE:CE1	2.80	0.68
1:E:300:VAL:HA	1:E:336:THR:O	1.93	0.68
1:F:265:VAL:O	1:F:269:LEU:HG	1.93	0.68
1:G:269:LEU:HB3	1:G:346:VAL:CG2	2.23	0.68
1:H:118:LYS:HB2	1:H:123:MET:HE1	1.75	0.68
1:H:190:THR:CG2	1:H:191:SER:H	2.00	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:324:GLU:HB2	1:B:364:LEU:CD1	2.24	0.68
1:F:260:TRP:NE1	2:F:401:CMP:C2'	2.57	0.68
1:H:365:LYS:HA	1:H:368:ILE:CD1	2.24	0.68
1:B:279:LYS:O	1:B:279:LYS:HG3	1.91	0.68
1:C:297:SER:HA	1:C:316:LEU:O	1.94	0.68
1:E:148:PHE:CD1	1:F:120:TYR:CE1	2.82	0.68
1:F:156:PHE:HD2	1:F:162:VAL:CG1	2.02	0.68
1:F:280:ILE:HD12	1:F:281:VAL:HG23	1.74	0.68
1:G:272:VAL:C	1:G:273:GLN:NE2	2.46	0.68
1:H:282:VAL:O	1:H:285:GLU:HG2	1.94	0.68
1:H:294:LEU:CD1	1:H:295:GLU:H	2.01	0.68
1:H:294:LEU:O	1:H:295:GLU:HG3	1.93	0.68
1:A:164:GLN:HA	1:A:212:THR:HG22	1.76	0.68
1:B:111:TYR:CG	1:B:112:VAL:N	2.47	0.68
1:C:144:ARG:O	1:C:147:ILE:HG12	1.94	0.68
1:C:230:ARG:CG	1:C:234:MET:HE1	2.23	0.68
1:D:278:GLN:HG3	1:D:279:LYS:H	1.58	0.68
1:E:253:ILE:HD13	1:E:321:TYR:CD2	2.29	0.68
1:E:294:LEU:HD13	1:E:345:CYS:HA	1.74	0.68
1:F:114:LYS:HD2	1:F:115:VAL:N	2.09	0.68
1:G:203:LEU:HD12	1:G:229:TYR:CD2	2.29	0.68
1:H:112:VAL:HG22	1:H:113:ARG:N	2.08	0.68
1:H:183:TYR:CE1	1:H:188:TRP:HB2	2.28	0.68
1:A:327:LEU:HD23	1:A:353:PHE:CE1	2.29	0.68
1:D:229:TYR:HD1	1:D:233:LEU:CD1	2.03	0.68
1:D:254:LEU:HD22	1:D:255:GLU:N	2.09	0.68
1:D:263:LEU:O	1:D:266:ALA:HB3	1.94	0.68
1:D:266:ALA:HA	1:D:269:LEU:HD12	1.76	0.68
1:F:135:LEU:HD12	1:F:135:LEU:N	2.08	0.68
1:F:226:ARG:HH11	1:F:226:ARG:CG	1.98	0.68
1:F:249:SER:CA	1:F:262:ARG:HH22	2.06	0.68
1:F:353:PHE:CE1	1:F:357:LEU:HD22	2.29	0.68
1:G:230:ARG:HG2	1:G:234:MET:HE1	1.74	0.68
1:A:152:PHE:O	1:A:152:PHE:CD2	2.47	0.68
1:C:183:TYR:CE1	1:C:188:TRP:HB2	2.28	0.68
1:C:290:PHE:C	1:C:291:PHE:HD1	1.96	0.68
1:C:362:ASP:N	1:C:365:LYS:NZ	2.42	0.68
1:D:126:LEU:O	1:D:126:LEU:CD1	2.32	0.68
1:D:254:LEU:HD13	1:D:254:LEU:H	1.59	0.68
1:D:275:GLU:O	1:D:278:GLN:HB3	1.94	0.68
1:E:300:VAL:HG12	1:E:335:ALA:HB1	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:200:GLU:OE2	1:G:241:ARG:NH2	2.26	0.68
1:H:120:TYR:HD2	1:H:121:LYS:HA	1.58	0.68
1:A:260:TRP:HA	1:A:263:LEU:HD12	1.76	0.67
1:A:275:GLU:O	1:A:278:GLN:HB3	1.94	0.67
1:B:157:ILE:HG13	1:B:160:GLU:OE1	1.94	0.67
1:C:118:LYS:HB2	1:C:123:MET:HE1	1.76	0.67
1:C:196:GLY:HA2	1:C:355:ARG:HH21	1.57	0.67
1:C:294:LEU:O	1:C:295:GLU:HG3	1.93	0.67
1:C:361:SER:C	1:C:365:LYS:HZ2	1.97	0.67
1:D:135:LEU:CD1	1:D:136:PHE:H	2.03	0.67
1:D:203:LEU:HD13	1:D:226:ARG:HB3	1.77	0.67
1:D:278:GLN:CG	1:D:279:LYS:H	2.07	0.67
1:E:328:LEU:HD23	1:E:365:LYS:HE3	1.74	0.67
1:F:112:VAL:HG22	1:F:113:ARG:N	2.09	0.67
1:F:131:GLU:OE1	1:F:132:LYS:N	2.28	0.67
1:G:116:ILE:HB	1:G:118:LYS:NZ	2.09	0.67
1:G:157:ILE:HB	1:G:218:ASN:OD1	1.94	0.67
1:H:170:ASP:H	1:H:209:ARG:NH2	1.92	0.67
1:H:224:ILE:CD1	1:H:224:ILE:N	2.55	0.67
1:H:288:ASP:OD1	1:H:288:ASP:C	2.23	0.67
1:A:112:VAL:CG2	1:D:115:VAL:HG21	2.21	0.67
1:A:226:ARG:HH11	1:A:226:ARG:CG	2.05	0.67
1:D:348:LEU:HD21	1:D:356:VAL:HG21	1.76	0.67
1:F:173:TYR:CB	1:F:198:PHE:HE1	2.07	0.67
1:F:177:GLN:HA	1:F:194:GLU:CG	2.24	0.67
1:F:249:SER:N	1:F:262:ARG:HH22	1.91	0.67
1:H:246:GLU:O	1:H:247:PHE:C	2.30	0.67
1:A:183:TYR:HD1	1:A:188:TRP:HA	1.58	0.67
1:A:230:ARG:O	1:A:234:MET:HB2	1.93	0.67
1:B:281:VAL:HG11	1:B:333:ARG:CD	2.23	0.67
1:C:115:VAL:CA	1:C:149:ASP:HB3	2.21	0.67
1:D:294:LEU:HD11	1:D:345:CYS:CA	2.17	0.67
1:F:130:ILE:HG21	1:F:148:PHE:HE2	1.59	0.67
1:F:275:GLU:O	1:F:278:GLN:HB3	1.94	0.67
1:G:260:TRP:CD1	2:G:401:CMP:C5	2.83	0.67
1:H:200:GLU:OE1	1:H:201:LEU:CD1	2.42	0.67
1:B:175:ILE:HD11	1:B:196:GLY:H	1.60	0.67
1:B:188:TRP:CZ3	1:B:190:THR:C	2.67	0.67
1:D:262:ARG:O	1:D:265:VAL:HB	1.94	0.67
1:E:131:GLU:OE1	1:E:131:GLU:CA	2.42	0.67
1:E:175:ILE:HD12	1:E:195:GLY:H	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:266:ALA:O	1:F:267:ASP:C	2.31	0.67
1:G:274:PHE:CE2	1:G:280:ILE:HG22	2.30	0.67
1:H:371:TYR:CE1	2:H:402:CMP:C5	2.82	0.67
1:B:224:ILE:CD1	1:B:224:ILE:N	2.57	0.67
1:E:163:ILE:HD12	1:E:213:VAL:HB	1.76	0.67
1:F:300:VAL:HG21	2:F:402:CMP:C8	2.24	0.67
1:G:263:LEU:O	1:G:266:ALA:HB3	1.94	0.67
1:G:278:GLN:CG	1:G:279:LYS:N	2.56	0.67
1:H:299:ALA:HA	1:H:314:GLY:O	1.95	0.67
1:A:120:TYR:CE1	1:B:148:PHE:CD1	2.81	0.67
1:B:130:ILE:CD1	1:B:151:MET:CE	2.73	0.67
1:C:158:ALA:HB2	1:C:217:THR:O	1.94	0.67
1:C:283:GLN:CA	1:C:333:ARG:O	2.40	0.67
1:E:173:TYR:HD2	1:E:198:PHE:CE1	2.12	0.67
1:F:365:LYS:HA	1:F:368:ILE:HG13	1.76	0.67
1:G:120:TYR:HD1	1:H:148:PHE:CD1	2.12	0.67
1:G:246:GLU:O	1:G:249:SER:N	2.26	0.67
1:B:278:GLN:O	1:B:338:VAL:HG22	1.94	0.67
1:B:300:VAL:HG12	1:B:335:ALA:HB1	1.77	0.67
1:D:224:ILE:CD1	1:D:224:ILE:H	2.06	0.67
1:F:114:LYS:CD	1:F:115:VAL:N	2.58	0.67
1:F:175:ILE:HD12	1:F:195:GLY:H	1.57	0.67
1:G:230:ARG:NH1	1:G:234:MET:HE1	2.10	0.67
1:A:175:ILE:HD11	1:A:196:GLY:H	1.58	0.67
1:A:211:ASP:CG	2:A:401:CMP:H5'1	2.15	0.67
1:B:126:LEU:HD12	1:B:126:LEU:C	2.15	0.67
1:D:247:PHE:C	1:D:247:PHE:CD2	2.68	0.67
1:E:243:MET:HE1	1:G:157:ILE:HD12	1.75	0.67
1:G:149:ASP:OD1	1:H:120:TYR:CB	2.43	0.67
1:G:294:LEU:CD1	1:G:344:LYS:O	2.41	0.67
1:B:135:LEU:HD12	1:B:135:LEU:N	2.10	0.67
1:B:175:ILE:CD1	1:B:194:GLU:CA	2.73	0.67
1:B:226:ARG:HH11	1:B:226:ARG:CG	2.06	0.67
1:C:237:THR:O	1:C:241:ARG:HG3	1.95	0.67
1:F:198:PHE:C	1:F:198:PHE:CD1	2.66	0.67
1:F:203:LEU:HD22	1:F:226:ARG:HB3	1.76	0.67
1:G:175:ILE:HD11	1:G:195:GLY:N	2.10	0.67
1:G:260:TRP:NE1	2:G:401:CMP:H2'	2.07	0.67
1:H:287:GLY:HA3	1:H:326:ALA:CB	2.24	0.67
1:H:293:ILE:HG23	1:H:318:PRO:HA	1.77	0.67
1:A:158:ALA:HB2	1:A:217:THR:O	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:153:PRO:HB3	1:B:222:TRP:HZ3	1.55	0.67
1:B:253:ILE:HG13	1:B:254:LEU:N	2.08	0.67
1:C:293:ILE:CD1	1:C:343:LEU:HD11	2.22	0.67
1:D:247:PHE:HE1	1:D:294:LEU:CA	2.04	0.67
1:D:249:SER:N	1:D:262:ARG:NH2	2.43	0.67
1:E:158:ALA:HB2	1:E:217:THR:C	2.15	0.67
1:G:365:LYS:HA	1:G:368:ILE:CG1	2.25	0.67
1:A:239:ARG:HH22	1:C:156:PHE:HD1	1.42	0.66
1:A:350:ARG:O	1:A:353:PHE:N	2.28	0.66
1:C:274:PHE:CE2	1:C:280:ILE:HG22	2.30	0.66
1:C:353:PHE:O	1:C:357:LEU:HB2	1.93	0.66
1:D:192:VAL:O	1:D:192:VAL:CG1	2.42	0.66
1:D:298:ALA:O	1:D:316:LEU:HD22	1.94	0.66
1:E:182:VAL:HG12	1:E:213:VAL:HG22	1.76	0.66
1:E:325:ILE:CD1	2:E:402:CMP:O2P	2.38	0.66
1:G:126:LEU:HD12	1:G:126:LEU:C	2.15	0.66
1:G:153:PRO:CB	1:G:222:TRP:CZ3	2.78	0.66
1:H:188:TRP:CH2	1:H:190:THR:HA	2.30	0.66
1:H:279:LYS:HZ3	1:H:279:LYS:CB	2.06	0.66
1:H:365:LYS:C	1:H:368:ILE:HG13	2.16	0.66
1:B:252:SER:O	1:B:253:ILE:CG1	2.43	0.66
1:D:136:PHE:O	1:D:139:LEU:HD11	1.95	0.66
1:D:228:SER:O	1:D:232:ILE:HG22	1.96	0.66
1:D:245:GLU:OE1	1:D:246:GLU:OE1	2.12	0.66
1:H:273:GLN:N	1:H:273:GLN:CD	2.49	0.66
1:A:254:LEU:HD12	1:A:254:LEU:C	2.15	0.66
1:A:269:LEU:CD2	1:A:346:VAL:CG2	2.72	0.66
1:B:179:GLU:HG2	1:B:216:LYS:HD2	1.76	0.66
1:C:269:LEU:HB3	1:C:346:VAL:HG21	1.68	0.66
1:D:179:GLU:HG2	1:D:216:LYS:CD	2.26	0.66
1:D:300:VAL:HG22	1:D:335:ALA:HB1	1.76	0.66
1:D:316:LEU:HD22	1:D:316:LEU:O	1.95	0.66
1:E:280:ILE:HD13	1:E:322:PHE:CE2	2.29	0.66
1:F:252:SER:O	1:F:255:GLU:HB2	1.95	0.66
1:G:175:ILE:HA	1:G:221:LEU:HD22	1.76	0.66
1:G:269:LEU:HD23	1:G:348:LEU:HD13	1.76	0.66
1:B:296:GLY:O	1:B:318:PRO:HD3	1.96	0.66
1:D:183:TYR:HD1	1:D:188:TRP:HA	1.59	0.66
1:E:173:TYR:HD2	1:E:198:PHE:CZ	2.13	0.66
1:F:203:LEU:HD12	1:F:229:TYR:HD2	1.58	0.66
1:A:198:PHE:O	1:A:198:PHE:CD1	2.39	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:ALA:N	1:A:211:ASP:OD1	2.28	0.66
1:A:290:PHE:C	1:A:291:PHE:HD1	1.98	0.66
1:B:324:GLU:O	1:B:328:LEU:CD1	2.37	0.66
1:D:165:GLN:N	1:D:212:THR:CG2	2.38	0.66
1:F:131:GLU:OE1	1:F:131:GLU:N	2.28	0.66
1:F:144:ARG:CG	1:F:145:SER:N	2.58	0.66
1:F:158:ALA:O	1:H:243:MET:SD	2.54	0.66
1:F:175:ILE:O	1:F:175:ILE:CD1	2.34	0.66
1:G:283:GLN:HB2	1:G:336:THR:OG1	1.96	0.66
1:H:260:TRP:HZ2	2:H:401:CMP:HO2'	1.44	0.66
1:A:175:ILE:CD1	1:A:194:GLU:CA	2.72	0.66
1:B:173:TYR:HD2	1:B:198:PHE:CE1	2.12	0.66
1:B:331:ARG:NH2	1:B:376:SER:HB3	2.11	0.66
1:D:365:LYS:C	1:D:368:ILE:HG13	2.15	0.66
1:E:152:PHE:HE2	1:E:223:GLY:CA	2.08	0.66
1:G:162:VAL:CG2	1:G:163:ILE:HG13	2.22	0.66
1:H:230:ARG:NH1	1:H:234:MET:CE	2.58	0.66
1:H:327:LEU:HD23	1:H:353:PHE:CE2	2.30	0.66
1:A:375:VAL:HG13	1:A:376:SER:H	1.61	0.66
1:C:200:GLU:OE1	1:C:201:LEU:CD1	2.43	0.66
1:C:243:MET:CE	1:E:157:ILE:CD1	2.58	0.66
1:C:243:MET:SD	1:E:158:ALA:O	2.54	0.66
1:C:258:ASP:O	1:C:262:ARG:CG	2.43	0.66
1:C:353:PHE:CE1	1:C:357:LEU:CD2	2.78	0.66
1:F:254:LEU:HD12	1:F:254:LEU:C	2.15	0.66
1:A:253:ILE:HD13	1:A:321:TYR:CD2	2.29	0.66
1:A:261:GLU:OE2	1:A:359:PRO:HG2	1.96	0.66
1:A:285:GLU:OE1	1:A:285:GLU:HA	1.96	0.66
1:B:184:VAL:HG13	1:B:184:VAL:O	1.95	0.66
1:D:278:GLN:CG	1:D:279:LYS:N	2.58	0.66
1:D:371:TYR:CD1	2:D:402:CMP:C5	2.84	0.66
1:E:260:TRP:CD1	2:E:401:CMP:C4	2.83	0.66
1:F:247:PHE:C	1:F:247:PHE:CD2	2.69	0.66
1:G:365:LYS:CA	1:G:368:ILE:HG13	2.26	0.66
1:H:302:GLN:C	1:H:310:PHE:CE1	2.69	0.66
1:A:253:ILE:HG13	1:A:254:LEU:HD23	1.78	0.66
1:A:280:ILE:HB	1:A:291:PHE:HE2	1.61	0.66
1:B:242:LYS:N	1:B:242:LYS:HD3	2.09	0.66
1:B:263:LEU:O	1:B:267:ASP:N	2.27	0.66
1:F:144:ARG:HG2	1:F:145:SER:N	2.11	0.66
1:F:179:GLU:HB3	1:F:217:THR:HG23	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:321:TYR:CD1	1:F:321:TYR:C	2.69	0.66
1:C:152:PHE:HE2	1:C:223:GLY:HA3	1.59	0.66
1:C:175:ILE:CD1	1:C:193:GLY:O	2.44	0.66
1:C:347:LYS:O	1:C:348:LEU:HD12	1.96	0.66
1:D:251:VAL:O	1:D:254:LEU:HD21	1.96	0.66
1:E:243:MET:HE2	1:G:159:GLY:O	1.96	0.66
1:E:247:PHE:C	1:E:247:PHE:CD2	2.69	0.66
1:E:295:GLU:O	1:E:344:LYS:N	2.29	0.66
1:F:114:LYS:NZ	1:F:115:VAL:HG23	2.11	0.66
1:F:230:ARG:O	1:F:234:MET:CB	2.44	0.66
1:G:175:ILE:CD1	1:G:195:GLY:N	2.59	0.66
1:G:260:TRP:HA	1:G:263:LEU:HD12	1.78	0.66
1:H:365:LYS:HA	1:H:368:ILE:HD11	1.78	0.66
1:A:148:PHE:HB2	1:B:120:TYR:CD1	2.31	0.65
1:B:153:PRO:HB3	1:B:222:TRP:CH2	2.31	0.65
1:B:200:GLU:CG	1:B:201:LEU:CD1	2.74	0.65
1:C:148:PHE:CD1	1:D:120:TYR:CD1	2.84	0.65
1:C:371:TYR:HE1	2:C:402:CMP:N7	1.94	0.65
1:E:321:TYR:CD1	1:E:321:TYR:C	2.69	0.65
1:G:224:ILE:CD1	1:G:224:ILE:N	2.59	0.65
1:H:266:ALA:O	1:H:269:LEU:N	2.24	0.65
1:A:222:TRP:HA	1:A:222:TRP:HE3	1.62	0.65
1:B:312:GLU:OE2	1:B:314:GLY:N	2.29	0.65
1:C:263:LEU:O	1:C:266:ALA:HB3	1.96	0.65
1:C:292:ILE:HB	1:C:346:VAL:HG13	1.78	0.65
1:D:274:PHE:CE2	1:D:280:ILE:HG22	2.31	0.65
1:F:178:GLY:H	1:F:194:GLU:HG3	1.61	0.65
1:F:224:ILE:N	1:F:224:ILE:HD12	2.10	0.65
1:G:293:ILE:CG1	1:G:345:CYS:SG	2.75	0.65
1:H:298:ALA:HB1	1:H:338:VAL:O	1.95	0.65
1:A:280:ILE:HG13	1:A:281:VAL:H	1.60	0.65
1:A:324:GLU:O	1:A:328:LEU:HD12	1.97	0.65
1:B:203:LEU:HD12	1:B:229:TYR:HD2	1.61	0.65
1:B:265:VAL:O	1:B:269:LEU:HG	1.96	0.65
1:B:278:GLN:HG3	1:B:279:LYS:H	1.60	0.65
1:C:111:TYR:O	1:C:112:VAL:HG13	1.97	0.65
1:F:245:GLU:OE1	1:F:246:GLU:OE1	2.12	0.65
1:H:126:LEU:HB2	1:H:222:TRP:CZ2	2.31	0.65
1:H:222:TRP:HA	1:H:222:TRP:HE3	1.60	0.65
1:H:273:GLN:CB	1:H:343:LEU:O	2.44	0.65
1:A:115:VAL:CG1	1:D:112:VAL:CG2	2.73	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:VAL:HG22	1:A:273:GLN:N	2.09	0.65
1:A:362:ASP:N	1:A:365:LYS:HZ2	1.94	0.65
1:B:183:TYR:HD1	1:B:188:TRP:HA	1.62	0.65
1:B:301:LEU:HB2	1:B:336:THR:HB	1.77	0.65
1:F:173:TYR:HD2	1:F:198:PHE:CE1	2.14	0.65
1:C:251:VAL:HG23	1:C:319:SER:O	1.95	0.65
1:E:198:PHE:CD1	1:E:198:PHE:O	2.49	0.65
1:E:296:GLY:HA2	1:E:342:PRO:HG2	1.79	0.65
1:F:170:ASP:H	1:F:209:ARG:NH2	1.94	0.65
1:G:179:GLU:HG2	1:G:216:LYS:HD2	1.77	0.65
1:G:269:LEU:HD23	1:G:348:LEU:HD11	1.78	0.65
1:G:329:MET:HA	1:G:329:MET:CE	2.26	0.65
1:G:375:VAL:HG12	1:G:376:SER:H	1.59	0.65
1:H:175:ILE:CD1	1:H:193:GLY:O	2.45	0.65
1:H:247:PHE:HE1	1:H:294:LEU:CA	2.10	0.65
1:A:229:TYR:HD1	1:A:233:LEU:HD13	1.42	0.65
1:A:272:VAL:CA	1:A:273:GLN:NE2	2.60	0.65
1:A:350:ARG:O	1:A:353:PHE:CB	2.44	0.65
1:B:153:PRO:HA	1:B:222:TRP:CE3	2.31	0.65
1:B:161:THR:HA	1:B:214:LYS:CD	2.19	0.65
1:B:222:TRP:CE3	1:B:222:TRP:HA	2.31	0.65
1:B:294:LEU:HD11	1:B:345:CYS:CA	2.19	0.65
1:D:135:LEU:CD1	1:D:136:PHE:N	2.60	0.65
1:D:151:MET:HA	1:D:224:ILE:HG22	1.77	0.65
1:D:246:GLU:O	1:D:247:PHE:C	2.35	0.65
1:E:120:TYR:C	1:E:120:TYR:CD2	2.68	0.65
1:E:246:GLU:O	1:E:249:SER:N	2.30	0.65
1:E:353:PHE:HE1	1:E:357:LEU:HD22	1.61	0.65
1:F:173:TYR:HD2	1:F:198:PHE:CZ	2.14	0.65
1:H:252:SER:O	1:H:255:GLU:HB2	1.96	0.65
1:H:269:LEU:CB	1:H:346:VAL:HG21	2.25	0.65
1:A:115:VAL:HG11	1:D:112:VAL:HG23	1.78	0.65
1:A:184:VAL:O	1:A:184:VAL:HG13	1.95	0.65
1:A:280:ILE:HD11	1:A:337:VAL:HB	1.78	0.65
1:B:294:LEU:O	1:B:318:PRO:HB3	1.96	0.65
1:B:327:LEU:HD23	1:B:353:PHE:CD2	2.32	0.65
1:B:366:ARG:HG2	1:B:367:ASN:N	2.12	0.65
1:C:300:VAL:O	1:C:301:LEU:HG	1.96	0.65
1:F:183:TYR:CE1	1:F:188:TRP:HB2	2.31	0.65
1:F:289:GLU:CG	1:F:347:LYS:NZ	2.55	0.65
1:A:356:VAL:HG23	1:A:357:LEU:N	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:GLN:N	1:B:212:THR:CG2	2.38	0.65
1:B:325:ILE:HG13	2:B:402:CMP:O1P	1.96	0.65
1:C:209:ARG:HD2	2:C:401:CMP:O5'	1.97	0.65
1:C:253:ILE:HG13	1:C:254:LEU:N	2.08	0.65
1:D:293:ILE:CG1	1:D:345:CYS:SG	2.80	0.65
1:D:327:LEU:HD23	1:D:353:PHE:CE2	2.32	0.65
1:F:114:LYS:HZ1	1:F:115:VAL:HG23	1.61	0.65
1:G:198:PHE:C	1:G:198:PHE:HD1	1.91	0.65
1:B:118:LYS:CB	1:B:123:MET:HE2	2.27	0.65
1:D:111:TYR:OH	1:D:113:ARG:C	2.35	0.65
1:D:222:TRP:HA	1:D:222:TRP:HE3	1.62	0.65
1:G:184:VAL:HG13	1:G:184:VAL:O	1.96	0.65
1:G:301:LEU:HD13	1:G:310:PHE:CB	2.26	0.65
1:H:365:LYS:CA	1:H:368:ILE:HG13	2.27	0.65
1:A:113:ARG:HG2	1:D:113:ARG:O	1.97	0.65
1:A:158:ALA:N	1:A:218:ASN:OD1	2.28	0.65
1:C:152:PHE:O	1:C:152:PHE:HD2	1.79	0.65
1:C:252:SER:O	1:C:255:GLU:HB2	1.97	0.65
1:D:234:MET:O	1:D:238:LEU:HD12	1.97	0.65
1:D:328:LEU:CD2	1:D:365:LYS:HE3	2.26	0.65
1:A:113:ARG:NE	1:D:113:ARG:C	2.51	0.64
1:A:280:ILE:HD11	1:A:322:PHE:CE2	2.22	0.64
1:B:188:TRP:CH2	1:B:190:THR:HA	2.31	0.64
1:B:233:LEU:HD12	1:B:233:LEU:N	2.02	0.64
1:B:260:TRP:CD1	2:B:401:CMP:C4	2.84	0.64
1:F:224:ILE:CD1	1:F:224:ILE:N	2.59	0.64
1:G:203:LEU:HD13	1:G:226:ARG:HB3	1.78	0.64
1:A:131:GLU:OE1	1:A:131:GLU:CA	2.42	0.64
1:B:224:ILE:CD1	1:B:224:ILE:H	2.10	0.64
1:F:272:VAL:O	1:F:345:CYS:N	2.27	0.64
1:H:356:VAL:CG2	1:H:357:LEU:HD13	2.19	0.64
1:B:287:GLY:HA3	1:B:326:ALA:HB1	1.79	0.64
1:C:182:VAL:O	1:C:182:VAL:CG2	2.42	0.64
1:E:164:GLN:HA	1:E:212:THR:CG2	2.25	0.64
1:E:325:ILE:O	1:E:328:LEU:N	2.31	0.64
1:F:262:ARG:HA	1:F:265:VAL:CG2	2.27	0.64
1:F:274:PHE:CD2	1:F:343:LEU:HD23	2.32	0.64
1:A:260:TRP:HE1	2:A:401:CMP:H2'	1.60	0.64
1:B:224:ILE:HD13	1:B:224:ILE:H	1.61	0.64
1:B:272:VAL:HA	1:B:273:GLN:NE2	2.12	0.64
1:C:260:TRP:CE2	2:C:401:CMP:C8	2.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:312:GLU:OE1	1:C:312:GLU:CA	2.46	0.64
1:D:188:TRP:CH2	1:D:190:THR:HA	2.33	0.64
1:E:253:ILE:HG13	1:E:254:LEU:H	1.61	0.64
1:E:254:LEU:HD12	1:E:255:GLU:N	2.12	0.64
1:F:211:ASP:CG	2:F:401:CMP:H5'1	2.18	0.64
1:B:252:SER:O	1:B:253:ILE:HG13	1.97	0.64
1:B:293:ILE:HG21	1:B:317:GLY:O	1.97	0.64
1:B:375:VAL:HG23	1:B:376:SER:H	1.63	0.64
1:D:273:GLN:HB2	1:D:343:LEU:O	1.98	0.64
1:D:321:TYR:C	1:D:321:TYR:CD1	2.71	0.64
1:D:325:ILE:HG13	1:D:326:ALA:N	2.13	0.64
1:E:224:ILE:HD12	1:E:224:ILE:N	2.12	0.64
1:F:205:TYR:HD2	1:F:205:TYR:N	1.96	0.64
1:G:272:VAL:HA	1:G:273:GLN:NE2	2.11	0.64
1:H:246:GLU:O	1:H:249:SER:N	2.30	0.64
1:A:114:LYS:HA	1:D:111:TYR:CE2	2.32	0.64
1:A:200:GLU:OE2	1:A:241:ARG:NH2	2.31	0.64
1:B:356:VAL:CG2	1:B:357:LEU:HD13	2.20	0.64
1:C:184:VAL:O	1:C:184:VAL:HG13	1.97	0.64
1:C:325:ILE:CD1	2:C:402:CMP:O2P	2.45	0.64
1:E:260:TRP:HE1	2:E:401:CMP:C2'	2.10	0.64
1:E:272:VAL:CA	1:E:273:GLN:NE2	2.60	0.64
1:F:152:PHE:HE2	1:F:223:GLY:CA	2.07	0.64
1:F:233:LEU:HD12	1:F:233:LEU:N	2.05	0.64
1:F:233:LEU:H	1:F:233:LEU:CD1	2.02	0.64
1:G:290:PHE:C	1:G:291:PHE:HD1	2.01	0.64
1:B:147:ILE:CG2	1:B:232:ILE:HD13	2.26	0.64
1:B:152:PHE:O	1:B:152:PHE:HD2	1.81	0.64
1:C:120:TYR:CE1	1:D:148:PHE:HD1	2.11	0.64
1:C:130:ILE:CG2	1:C:131:GLU:N	2.60	0.64
1:C:147:ILE:HG13	1:C:148:PHE:HD2	1.63	0.64
1:C:365:LYS:C	1:C:368:ILE:HG13	2.17	0.64
1:E:230:ARG:O	1:E:234:MET:CB	2.45	0.64
1:H:263:LEU:O	1:H:266:ALA:HB3	1.98	0.64
1:B:135:LEU:CD1	1:B:136:PHE:H	2.11	0.64
1:C:279:LYS:HB3	1:C:338:VAL:HG23	1.78	0.64
1:E:260:TRP:CG	2:E:401:CMP:C5	2.85	0.64
1:E:289:GLU:HG3	1:E:347:LYS:HZ1	1.60	0.64
1:F:153:PRO:CB	1:F:222:TRP:CZ3	2.81	0.64
1:G:156:PHE:CD2	1:G:162:VAL:HG12	2.32	0.64
1:H:260:TRP:NE1	2:H:401:CMP:C2'	2.60	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:291:PHE:N	1:H:291:PHE:HD1	1.93	0.64
1:H:335:ALA:HB3	2:H:402:CMP:H5'1	1.80	0.64
1:D:325:ILE:CG1	2:D:402:CMP:O1P	2.46	0.64
1:E:183:TYR:CD1	1:E:188:TRP:HB2	2.33	0.64
1:E:280:ILE:HD11	1:E:337:VAL:HB	1.79	0.64
1:E:280:ILE:HB	1:E:291:PHE:HE2	1.63	0.64
1:F:113:ARG:CD	1:F:146:ASP:CG	2.63	0.64
1:F:165:GLN:CA	1:F:211:ASP:O	2.45	0.64
1:F:198:PHE:CD1	1:F:198:PHE:N	2.64	0.64
1:F:329:MET:HA	1:F:329:MET:CE	2.27	0.64
1:G:272:VAL:CA	1:G:273:GLN:NE2	2.61	0.64
1:A:173:TYR:CD2	1:A:198:PHE:HE1	2.16	0.64
1:E:274:PHE:HD2	1:E:343:LEU:HD23	1.62	0.64
1:E:313:VAL:HG22	1:E:313:VAL:O	1.98	0.64
1:B:260:TRP:CG	2:B:401:CMP:N7	2.66	0.63
1:C:260:TRP:HE1	2:C:401:CMP:C2'	2.09	0.63
1:E:162:VAL:HG23	1:E:163:ILE:N	2.12	0.63
1:E:177:GLN:HA	1:E:194:GLU:CG	2.28	0.63
1:E:328:LEU:CD1	1:E:364:LEU:HD11	2.28	0.63
1:H:272:VAL:CA	1:H:273:GLN:HE21	2.00	0.63
1:H:363:ILE:O	1:H:366:ARG:HG2	1.98	0.63
1:A:183:TYR:CE1	1:A:188:TRP:CB	2.81	0.63
1:A:316:LEU:HA	1:A:320:ASP:OD2	1.98	0.63
1:A:375:VAL:CG1	1:A:376:SER:N	2.61	0.63
1:B:183:TYR:CD1	1:B:188:TRP:HB2	2.33	0.63
1:B:200:GLU:HG2	1:B:201:LEU:CG	2.28	0.63
1:B:312:GLU:OE1	1:B:312:GLU:CA	2.46	0.63
1:C:211:ASP:OD2	2:C:401:CMP:N3	2.32	0.63
1:C:222:TRP:HA	1:C:222:TRP:CE3	2.33	0.63
1:E:239:ARG:NH2	1:G:156:PHE:HD1	1.96	0.63
1:E:272:VAL:HA	1:E:273:GLN:HE22	1.60	0.63
1:E:361:SER:C	1:E:365:LYS:HZ2	2.02	0.63
1:F:163:ILE:HD12	1:F:213:VAL:HB	1.81	0.63
1:H:260:TRP:HA	1:H:263:LEU:HD12	1.80	0.63
1:B:111:TYR:O	1:B:112:VAL:CG2	2.42	0.63
1:B:126:LEU:HB2	1:B:222:TRP:CZ2	2.34	0.63
1:D:350:ARG:O	1:D:353:PHE:HB3	1.97	0.63
1:E:179:GLU:HG2	1:E:216:LYS:HD2	1.78	0.63
1:E:280:ILE:HG13	1:E:281:VAL:HG23	1.80	0.63
1:E:284:GLY:O	1:E:332:PRO:HB3	1.98	0.63
1:B:156:PHE:HD2	1:B:162:VAL:CG1	2.10	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:GLN:HA	1:B:212:THR:HG22	1.80	0.63
1:D:153:PRO:CA	1:D:222:TRP:CZ3	2.81	0.63
1:E:178:GLY:H	1:E:194:GLU:HG3	1.63	0.63
1:E:328:LEU:HD13	1:E:364:LEU:HD11	1.81	0.63
1:G:154:VAL:HG12	1:G:221:LEU:HB2	1.80	0.63
1:G:175:ILE:HD12	1:G:195:GLY:H	1.63	0.63
1:G:183:TYR:HD1	1:G:188:TRP:HA	1.64	0.63
1:H:183:TYR:HD1	1:H:188:TRP:HA	1.63	0.63
1:A:274:PHE:CD2	1:A:343:LEU:HD23	2.33	0.63
1:B:200:GLU:HG2	1:B:201:LEU:HG	1.80	0.63
1:E:246:GLU:O	1:E:248:LEU:N	2.31	0.63
1:G:165:GLN:N	1:G:212:THR:CG2	2.42	0.63
1:G:183:TYR:CD1	1:G:188:TRP:HB2	2.34	0.63
1:H:204:ILE:CG2	1:H:205:TYR:CD2	2.81	0.63
1:B:280:ILE:HD13	1:B:322:PHE:HZ	1.63	0.63
1:C:110:SER:HB3	1:F:114:LYS:NZ	2.13	0.63
1:C:247:PHE:CD2	1:C:247:PHE:O	2.51	0.63
1:C:253:ILE:HG13	1:C:254:LEU:CD2	2.27	0.63
1:C:285:GLU:OE1	1:C:285:GLU:HA	1.98	0.63
1:E:224:ILE:CD1	1:E:224:ILE:N	2.61	0.63
1:F:135:LEU:HD12	1:F:136:PHE:H	1.62	0.63
1:F:183:TYR:HD1	1:F:188:TRP:HA	1.63	0.63
1:G:162:VAL:HG22	1:G:213:VAL:O	1.99	0.63
1:G:262:ARG:HA	1:G:265:VAL:CG2	2.29	0.63
1:H:203:LEU:HD13	1:H:226:ARG:HB3	1.80	0.63
1:A:114:LYS:HG3	1:A:115:VAL:N	2.01	0.63
1:C:164:GLN:HA	1:C:212:THR:HG22	1.81	0.63
1:D:188:TRP:CZ3	1:D:190:THR:C	2.71	0.63
1:E:269:LEU:HD23	1:E:348:LEU:CD1	2.28	0.63
1:E:308:GLU:C	1:E:309:GLU:HG2	2.17	0.63
1:E:350:ARG:HB3	1:E:351:PRO:HD3	1.81	0.63
1:F:290:PHE:HB2	1:F:327:LEU:CD2	2.29	0.63
1:F:301:LEU:CD1	1:F:310:PHE:HB3	2.28	0.63
1:B:175:ILE:CD1	1:B:195:GLY:N	2.62	0.63
1:F:247:PHE:HZ	1:F:293:ILE:O	1.81	0.63
1:G:224:ILE:N	1:G:224:ILE:HD12	2.13	0.63
1:G:324:GLU:O	1:G:328:LEU:HD12	1.97	0.63
1:H:281:VAL:CG1	1:H:333:ARG:CD	2.76	0.63
1:A:237:THR:O	1:A:241:ARG:HG3	1.98	0.63
1:A:295:GLU:O	1:A:343:LEU:HD12	1.98	0.63
1:B:157:ILE:CB	1:B:218:ASN:OD1	2.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:PHE:HD2	1:B:343:LEU:HD23	1.64	0.63
1:B:365:LYS:CA	1:B:368:ILE:HG13	2.29	0.63
1:C:135:LEU:HD13	1:C:136:PHE:CD1	2.34	0.63
1:C:258:ASP:O	1:C:262:ARG:HG2	1.98	0.63
1:D:269:LEU:HB3	1:D:346:VAL:HG21	1.79	0.63
1:E:188:TRP:CZ3	1:E:190:THR:C	2.71	0.63
1:H:294:LEU:HG	1:H:344:LYS:O	1.98	0.63
1:A:272:VAL:HA	1:A:273:GLN:HE22	1.62	0.62
1:B:324:GLU:OE2	1:B:371:TYR:CE2	2.47	0.62
1:B:350:ARG:HB3	1:B:351:PRO:CD	2.25	0.62
1:C:276:ASP:HA	1:C:339:ALA:O	1.99	0.62
1:D:211:ASP:OD2	2:D:401:CMP:N3	2.32	0.62
1:D:253:ILE:HD13	1:D:321:TYR:CD2	2.34	0.62
1:D:362:ASP:OD1	1:D:362:ASP:N	2.30	0.62
1:F:272:VAL:HA	1:F:273:GLN:NE2	2.14	0.62
1:F:280:ILE:HG13	1:F:281:VAL:H	1.61	0.62
1:H:229:TYR:HE1	1:H:233:LEU:HD13	1.62	0.62
1:A:260:TRP:CD2	2:A:401:CMP:C8	2.82	0.62
1:B:175:ILE:HD12	1:B:195:GLY:H	1.64	0.62
1:B:253:ILE:HG13	1:B:254:LEU:CD2	2.29	0.62
1:D:116:ILE:HG22	1:D:118:LYS:HG3	1.81	0.62
1:D:198:PHE:C	1:D:198:PHE:HD1	1.98	0.62
1:D:247:PHE:HZ	1:D:293:ILE:O	1.82	0.62
1:E:296:GLY:HA3	1:E:342:PRO:O	1.99	0.62
1:F:204:ILE:HG22	1:F:205:TYR:HD2	1.61	0.62
1:G:265:VAL:HA	1:G:356:VAL:HG11	1.79	0.62
1:G:273:GLN:HE21	1:G:273:GLN:CA	2.07	0.62
1:H:173:TYR:HB2	1:H:198:PHE:CE1	2.34	0.62
1:A:176:ASP:O	1:A:194:GLU:HG2	1.99	0.62
1:C:279:LYS:CE	1:C:282:VAL:HG22	2.30	0.62
1:C:365:LYS:O	1:C:368:ILE:N	2.27	0.62
1:D:365:LYS:HA	1:D:368:ILE:HG13	1.80	0.62
1:F:126:LEU:HD12	1:F:126:LEU:C	2.19	0.62
1:F:153:PRO:CA	1:F:222:TRP:CZ3	2.82	0.62
1:F:284:GLY:O	1:F:332:PRO:HB3	2.00	0.62
1:H:130:ILE:CD1	1:H:136:PHE:CD2	2.82	0.62
1:H:165:GLN:HA	1:H:211:ASP:O	1.99	0.62
1:A:153:PRO:HA	1:A:222:TRP:CE3	2.34	0.62
1:B:248:LEU:CB	1:B:262:ARG:HH21	2.13	0.62
1:C:116:ILE:HB	1:C:149:ASP:O	2.00	0.62
1:C:157:ILE:HD12	1:C:157:ILE:C	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:120:TYR:HE2	1:D:124:ALA:HB2	1.64	0.62
1:D:298:ALA:HB3	1:D:316:LEU:HD21	1.80	0.62
1:E:211:ASP:OD2	2:E:401:CMP:N3	2.32	0.62
1:F:222:TRP:HA	1:F:222:TRP:HE3	1.61	0.62
1:G:111:TYR:CD1	1:G:112:VAL:N	2.66	0.62
1:A:255:GLU:OE1	1:A:255:GLU:CA	2.37	0.62
1:B:156:PHE:CD2	1:B:162:VAL:CG1	2.78	0.62
1:B:279:LYS:NZ	1:B:279:LYS:CB	2.62	0.62
1:E:174:VAL:HG23	1:E:196:GLY:O	1.98	0.62
1:E:279:LYS:CB	1:E:279:LYS:HZ3	2.03	0.62
1:F:230:ARG:CB	1:F:234:MET:HE1	2.29	0.62
1:G:175:ILE:HD11	1:G:196:GLY:N	2.13	0.62
1:H:202:ALA:HB1	1:H:207:THR:O	2.00	0.62
1:A:154:VAL:O	1:A:221:LEU:N	2.28	0.62
1:A:366:ARG:HG2	1:A:367:ASN:N	2.15	0.62
1:C:118:LYS:CB	1:C:123:MET:HE1	2.30	0.62
1:C:302:GLN:O	1:C:310:PHE:CD1	2.52	0.62
1:C:325:ILE:CD1	1:C:334:ALA:HB3	2.28	0.62
1:D:253:ILE:HG21	1:D:321:TYR:CE2	2.35	0.62
1:E:211:ASP:OD2	2:E:401:CMP:C3'	2.44	0.62
1:E:266:ALA:CA	1:E:269:LEU:HD12	2.19	0.62
1:G:116:ILE:HB	1:G:118:LYS:HZ3	1.63	0.62
1:G:253:ILE:CG2	1:G:321:TYR:HE2	2.12	0.62
1:H:325:ILE:CG1	2:H:402:CMP:O1P	2.47	0.62
1:C:174:VAL:HG13	1:C:222:TRP:HB2	1.80	0.62
1:C:260:TRP:CD1	2:C:401:CMP:C5	2.87	0.62
1:D:347:LYS:O	1:D:348:LEU:CD1	2.46	0.62
1:D:356:VAL:CG2	1:D:357:LEU:CD1	2.73	0.62
1:E:116:ILE:CG2	1:E:118:LYS:HZ2	2.11	0.62
1:G:247:PHE:HZ	1:G:293:ILE:O	1.81	0.62
1:G:265:VAL:HG12	1:G:269:LEU:HD21	1.80	0.62
1:H:162:VAL:CG2	1:H:163:ILE:HG13	2.29	0.62
1:H:283:GLN:HA	1:H:333:ARG:O	2.00	0.62
1:H:353:PHE:CE1	1:H:357:LEU:CD2	2.82	0.62
1:A:242:LYS:HD3	1:A:242:LYS:N	2.09	0.62
1:A:247:PHE:HE1	1:A:294:LEU:CA	2.06	0.62
1:A:311:VAL:HG22	1:A:312:GLU:N	2.15	0.62
1:C:158:ALA:N	1:C:218:ASN:OD1	2.33	0.62
1:C:230:ARG:HG2	1:C:230:ARG:NH1	2.15	0.62
1:D:162:VAL:HG23	1:D:163:ILE:N	2.15	0.62
1:E:198:PHE:O	1:E:198:PHE:HD1	1.83	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:259:LYS:HG3	1:E:260:TRP:H	1.63	0.62
1:G:152:PHE:HE2	1:G:223:GLY:HA3	1.65	0.62
1:H:260:TRP:CD1	2:H:401:CMP:C5	2.88	0.62
1:A:115:VAL:HB	1:D:112:VAL:CG2	2.29	0.62
1:B:248:LEU:HB2	1:B:262:ARG:HH21	1.65	0.62
1:C:243:MET:HE1	1:E:158:ALA:O	2.00	0.62
1:D:234:MET:HG3	1:D:238:LEU:CD1	2.28	0.62
1:E:366:ARG:HG3	1:E:367:ASN:N	2.15	0.62
1:F:182:VAL:HG12	1:F:213:VAL:HG22	1.81	0.62
1:G:292:ILE:HB	1:G:346:VAL:HG13	1.81	0.62
1:H:246:GLU:HA	1:H:249:SER:OG	1.99	0.62
1:A:173:TYR:HD2	1:A:198:PHE:CZ	2.18	0.62
1:A:175:ILE:HD11	1:A:195:GLY:N	2.15	0.62
1:B:375:VAL:O	1:B:376:SER:OXT	2.18	0.62
1:C:247:PHE:HE1	1:C:294:LEU:CA	2.08	0.62
1:C:265:VAL:HG12	1:C:269:LEU:HD21	1.82	0.62
1:C:296:GLY:O	1:C:318:PRO:HD3	1.99	0.62
1:D:205:TYR:HD2	1:D:205:TYR:N	1.98	0.62
1:D:259:LYS:CG	1:D:260:TRP:N	2.56	0.62
1:D:350:ARG:HB3	1:D:351:PRO:HD3	1.80	0.62
1:H:175:ILE:HD11	1:H:193:GLY:O	2.00	0.62
1:H:298:ALA:O	1:H:315:ARG:CA	2.46	0.62
1:A:152:PHE:O	1:A:152:PHE:HD2	1.82	0.61
1:A:153:PRO:HB3	1:A:222:TRP:CH2	2.34	0.61
1:A:260:TRP:CE2	2:A:401:CMP:H8	2.35	0.61
1:A:263:LEU:O	1:A:266:ALA:HB3	2.00	0.61
1:B:161:THR:HG23	1:B:214:LYS:HD3	1.82	0.61
1:B:204:ILE:HG22	1:B:205:TYR:CD2	2.34	0.61
1:C:174:VAL:HA	1:C:196:GLY:O	1.99	0.61
1:E:115:VAL:CG2	1:H:110:SER:HB3	2.31	0.61
1:E:190:THR:CG2	1:E:191:SER:H	2.13	0.61
1:F:327:LEU:HD23	1:F:353:PHE:CZ	2.35	0.61
1:G:260:TRP:HE1	2:G:401:CMP:C2'	2.07	0.61
1:H:173:TYR:CD2	1:H:198:PHE:CZ	2.86	0.61
1:H:269:LEU:HD22	1:H:346:VAL:CG2	2.30	0.61
1:A:120:TYR:CD2	1:A:120:TYR:O	2.53	0.61
1:B:265:VAL:HA	1:B:356:VAL:HG11	1.82	0.61
1:B:279:LYS:HB2	1:B:279:LYS:NZ	2.12	0.61
1:C:174:VAL:O	1:C:174:VAL:CG1	2.47	0.61
1:E:135:LEU:CD1	1:E:136:PHE:N	2.62	0.61
1:H:112:VAL:CG1	1:H:113:ARG:H	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:118:LYS:CB	1:H:123:MET:HE1	2.29	0.61
1:H:280:ILE:CG1	1:H:337:VAL:HB	2.30	0.61
1:A:115:VAL:CG2	1:D:112:VAL:CG2	2.67	0.61
1:A:280:ILE:HD13	1:A:322:PHE:HZ	1.66	0.61
1:B:289:GLU:HG3	1:B:347:LYS:NZ	2.14	0.61
1:C:321:TYR:CD1	1:C:321:TYR:O	2.53	0.61
1:E:152:PHE:O	1:E:152:PHE:HD2	1.80	0.61
1:F:114:LYS:HZ1	1:F:115:VAL:CG2	2.10	0.61
1:F:165:GLN:N	1:F:212:THR:CG2	2.46	0.61
1:G:316:LEU:HD12	1:G:316:LEU:N	2.16	0.61
1:G:375:VAL:HG12	1:G:376:SER:N	2.14	0.61
1:H:260:TRP:O	1:H:263:LEU:HB2	2.00	0.61
1:H:279:LYS:CE	1:H:336:THR:HG23	2.30	0.61
1:A:181:ASP:OD1	1:A:191:SER:HB3	2.00	0.61
1:B:196:GLY:HA2	1:B:355:ARG:HH21	1.61	0.61
1:B:324:GLU:HB2	1:B:364:LEU:HD13	1.82	0.61
1:D:329:MET:HA	1:D:329:MET:HE3	1.81	0.61
1:F:260:TRP:HA	1:F:263:LEU:HD12	1.83	0.61
1:F:294:LEU:H	1:F:294:LEU:CD1	2.08	0.61
1:G:158:ALA:N	1:G:218:ASN:OD1	2.30	0.61
1:H:144:ARG:HG2	1:H:145:SER:N	2.14	0.61
1:H:147:ILE:HG13	1:H:148:PHE:HD2	1.65	0.61
1:A:327:LEU:HD23	1:A:353:PHE:CZ	2.35	0.61
1:C:130:ILE:CD1	1:C:136:PHE:CD2	2.83	0.61
1:C:234:MET:HG3	1:C:234:MET:O	2.00	0.61
1:C:324:GLU:N	1:C:324:GLU:OE1	2.33	0.61
1:D:120:TYR:O	1:D:121:LYS:C	2.36	0.61
1:D:182:VAL:HG23	1:D:182:VAL:O	2.00	0.61
1:E:157:ILE:HG13	1:E:160:GLU:OE1	2.01	0.61
1:E:254:LEU:HD12	1:E:254:LEU:C	2.21	0.61
1:C:112:VAL:HB	1:C:231:ARG:CZ	2.31	0.61
1:C:177:GLN:HA	1:C:194:GLU:HG3	1.82	0.61
1:C:247:PHE:HZ	1:C:293:ILE:O	1.82	0.61
1:C:315:ARG:NH2	1:C:340:ARG:HH22	1.97	0.61
1:D:183:TYR:CD1	1:D:188:TRP:HB2	2.36	0.61
1:D:198:PHE:CD1	1:D:198:PHE:N	2.66	0.61
1:D:224:ILE:N	1:D:224:ILE:HD12	2.15	0.61
1:F:140:ASP:C	1:F:140:ASP:OD1	2.38	0.61
1:H:350:ARG:HB3	1:H:351:PRO:HD3	1.83	0.61
1:A:362:ASP:O	1:A:365:LYS:HG3	2.01	0.61
1:B:371:TYR:CE1	2:B:402:CMP:C5	2.88	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:243:MET:CE	1:E:158:ALA:O	2.49	0.61
1:E:165:GLN:N	1:E:212:THR:CG2	2.42	0.61
1:G:173:TYR:CB	1:G:198:PHE:HE1	2.12	0.61
1:G:211:ASP:OD2	2:G:401:CMP:C3'	2.49	0.61
1:G:222:TRP:HA	1:G:222:TRP:CE3	2.34	0.61
1:H:305:SER:O	1:H:306:GLU:C	2.37	0.61
1:H:321:TYR:CD1	1:H:321:TYR:C	2.73	0.61
1:A:113:ARG:CG	1:D:113:ARG:HB2	2.31	0.61
1:A:260:TRP:CG	2:A:401:CMP:C5	2.89	0.61
1:A:272:VAL:C	1:A:273:GLN:NE2	2.54	0.61
1:B:205:TYR:N	1:B:205:TYR:HD2	1.96	0.61
1:C:353:PHE:CE1	1:C:357:LEU:HD22	2.36	0.61
1:H:194:GLU:O	1:H:355:ARG:HD2	2.01	0.61
1:A:120:TYR:HB2	1:B:149:ASP:OD1	2.00	0.61
1:A:229:TYR:O	1:A:233:LEU:HD12	2.00	0.61
1:B:165:GLN:CA	1:B:211:ASP:O	2.49	0.61
1:C:220:LYS:O	1:C:221:LEU:HD23	2.01	0.61
1:D:247:PHE:CE1	1:D:294:LEU:HB3	2.36	0.61
1:E:222:TRP:HA	1:E:222:TRP:CE3	2.36	0.61
1:E:260:TRP:HA	1:E:263:LEU:HD12	1.82	0.61
1:G:316:LEU:HA	1:G:320:ASP:OD2	2.01	0.61
1:A:171:ASN:HB3	1:A:224:ILE:O	2.01	0.61
1:B:201:LEU:O	1:B:204:ILE:N	2.34	0.61
1:B:222:TRP:HA	1:B:222:TRP:HE3	1.66	0.61
1:C:298:ALA:N	1:C:316:LEU:O	2.32	0.61
1:C:353:PHE:CE1	1:C:357:LEU:HD23	2.36	0.61
1:D:279:LYS:HG3	1:D:279:LYS:O	1.99	0.61
1:E:280:ILE:HD13	1:E:322:PHE:HZ	1.66	0.61
1:E:293:ILE:HA	1:E:345:CYS:SG	2.40	0.61
1:G:209:ARG:HD2	2:G:401:CMP:O5'	2.00	0.61
1:G:247:PHE:C	1:G:247:PHE:CD2	2.74	0.61
1:G:266:ALA:O	1:G:267:ASP:C	2.38	0.61
1:H:115:VAL:CA	1:H:149:ASP:HB3	2.29	0.61
1:A:120:TYR:CD1	1:B:148:PHE:HB2	2.27	0.60
1:A:233:LEU:HD12	1:A:233:LEU:N	2.03	0.60
1:B:158:ALA:CA	1:B:217:THR:O	2.49	0.60
1:B:182:VAL:HG12	1:B:213:VAL:CG2	2.31	0.60
1:B:375:VAL:HG22	1:B:376:SER:OG	2.00	0.60
1:C:205:TYR:HD2	1:C:205:TYR:N	1.99	0.60
1:H:152:PHE:CD2	1:H:152:PHE:O	2.54	0.60
1:H:242:LYS:HD3	1:H:242:LYS:N	2.07	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:263:LEU:O	1:H:267:ASP:N	2.30	0.60
1:H:275:GLU:O	1:H:339:ALA:HB3	2.01	0.60
1:H:311:VAL:CG2	1:H:312:GLU:N	2.64	0.60
1:A:203:LEU:HD22	1:A:226:ARG:CB	2.30	0.60
1:A:230:ARG:HH12	1:A:234:MET:CE	2.12	0.60
1:A:248:LEU:CB	1:A:262:ARG:HH21	2.14	0.60
1:C:241:ARG:CZ	1:C:263:LEU:HG	2.31	0.60
1:D:325:ILE:CG1	2:D:402:CMP:P	2.89	0.60
1:G:157:ILE:HD12	1:G:157:ILE:O	2.01	0.60
1:G:253:ILE:CG2	1:G:321:TYR:CE2	2.84	0.60
1:G:329:MET:HA	1:G:329:MET:HE3	1.83	0.60
1:G:356:VAL:HG23	1:G:357:LEU:HD12	1.80	0.60
1:H:211:ASP:OD2	2:H:401:CMP:H3'	2.00	0.60
1:H:247:PHE:HZ	1:H:293:ILE:O	1.82	0.60
1:H:328:LEU:HD22	1:H:365:LYS:HE3	1.82	0.60
1:A:139:LEU:CD2	1:A:147:ILE:HD13	2.32	0.60
1:B:120:TYR:HE2	1:B:124:ALA:HB2	1.66	0.60
1:C:282:VAL:O	1:C:285:GLU:CG	2.46	0.60
1:C:294:LEU:HD11	1:C:345:CYS:CA	2.14	0.60
1:G:230:ARG:O	1:G:234:MET:CB	2.49	0.60
1:G:257:LEU:HD21	1:G:360:CYS:SG	2.41	0.60
1:G:299:ALA:HB3	1:G:338:VAL:HG12	1.82	0.60
1:A:120:TYR:O	1:A:121:LYS:C	2.39	0.60
1:A:230:ARG:NH1	1:A:234:MET:HE3	2.16	0.60
1:A:260:TRP:CZ2	2:A:401:CMP:H8	2.37	0.60
1:C:151:MET:HA	1:C:224:ILE:HG22	1.83	0.60
1:C:178:GLY:CA	1:C:219:VAL:HG12	2.15	0.60
1:D:112:VAL:HG12	1:D:231:ARG:NH2	2.15	0.60
1:D:175:ILE:HD11	1:D:196:GLY:N	2.12	0.60
1:D:232:ILE:HG23	1:D:233:LEU:HG	1.83	0.60
1:E:123:MET:CE	1:F:123:MET:HE2	2.30	0.60
1:E:294:LEU:N	1:E:294:LEU:CD1	2.38	0.60
1:H:361:SER:C	1:H:365:LYS:HZ2	2.05	0.60
1:A:188:TRP:HH2	1:A:191:SER:HG	1.48	0.60
1:A:294:LEU:CD1	1:A:294:LEU:H	2.01	0.60
1:B:260:TRP:CD2	2:B:401:CMP:C8	2.85	0.60
1:B:327:LEU:HD23	1:B:353:PHE:CZ	2.37	0.60
1:E:300:VAL:HG22	1:E:337:VAL:HG22	1.84	0.60
1:F:177:GLN:HA	1:F:194:GLU:HG3	1.82	0.60
1:F:325:ILE:CD1	2:F:402:CMP:O1P	2.49	0.60
1:G:262:ARG:HA	1:G:265:VAL:HG23	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:272:VAL:O	1:H:345:CYS:N	2.32	0.60
1:A:152:PHE:HE2	1:A:223:GLY:CA	2.11	0.60
1:B:209:ARG:HD2	2:B:401:CMP:O5'	2.01	0.60
1:B:365:LYS:C	1:B:368:ILE:HG13	2.21	0.60
1:C:126:LEU:HB2	1:C:222:TRP:CZ2	2.37	0.60
1:C:229:TYR:CD1	1:C:233:LEU:HD12	2.36	0.60
1:D:283:GLN:OE1	1:D:302:GLN:HA	2.02	0.60
1:G:190:THR:HG22	1:G:191:SER:N	2.07	0.60
1:G:272:VAL:HA	1:G:273:GLN:HE22	1.65	0.60
1:G:325:ILE:HG23	1:G:329:MET:CG	2.31	0.60
1:H:281:VAL:HG13	1:H:333:ARG:CD	2.31	0.60
1:A:139:LEU:HD21	1:A:147:ILE:HD13	1.83	0.60
1:A:188:TRP:CZ3	1:A:190:THR:CA	2.84	0.60
1:A:362:ASP:N	1:A:362:ASP:OD1	2.32	0.60
1:B:152:PHE:HE2	1:B:223:GLY:HA3	1.65	0.60
1:B:273:GLN:N	1:B:273:GLN:CD	2.50	0.60
1:D:184:VAL:HG13	1:D:184:VAL:O	2.01	0.60
1:E:113:ARG:O	1:H:112:VAL:CB	2.47	0.60
1:E:115:VAL:HG23	1:H:110:SER:HB3	1.84	0.60
1:F:114:LYS:CE	1:F:115:VAL:H	2.15	0.60
1:G:173:TYR:HD2	1:G:198:PHE:CZ	2.18	0.60
1:G:175:ILE:HD11	1:G:193:GLY:O	2.01	0.60
1:G:327:LEU:HD23	1:G:353:PHE:CE2	2.36	0.60
1:H:230:ARG:HG2	1:H:230:ARG:HH11	1.66	0.60
1:H:322:PHE:CD1	1:H:322:PHE:N	2.68	0.60
1:A:254:LEU:HD12	1:A:255:GLU:N	2.17	0.60
1:A:366:ARG:O	1:A:369:GLN:HB2	2.02	0.60
1:B:273:GLN:HB3	1:B:344:LYS:HA	1.84	0.60
1:B:310:PHE:O	1:B:311:VAL:HG23	2.02	0.60
1:C:182:VAL:CG2	1:C:190:THR:O	2.38	0.60
1:C:301:LEU:HA	1:C:311:VAL:O	2.02	0.60
1:C:371:TYR:CE1	2:C:402:CMP:N7	2.69	0.60
1:D:205:TYR:CD2	1:D:205:TYR:N	2.70	0.60
1:D:353:PHE:CD1	1:D:357:LEU:HD22	2.33	0.60
1:F:130:ILE:CG1	1:F:136:PHE:CD2	2.81	0.60
1:F:158:ALA:O	1:H:243:MET:CE	2.49	0.60
1:F:190:THR:CG2	1:F:191:SER:H	2.12	0.60
1:H:147:ILE:O	1:H:148:PHE:C	2.37	0.60
1:H:200:GLU:OE2	1:H:241:ARG:NH2	2.35	0.60
1:A:211:ASP:OD2	2:A:401:CMP:N3	2.34	0.60
1:A:298:ALA:HB1	1:A:338:VAL:O	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:GLN:HE22	1:B:185:ASN:ND2	2.00	0.60
1:B:229:TYR:O	1:B:233:LEU:HD12	2.02	0.60
1:C:130:ILE:HG13	1:C:136:PHE:CD2	2.36	0.60
1:D:179:GLU:HB3	1:D:217:THR:HG23	1.84	0.60
1:D:298:ALA:O	1:D:316:LEU:CD2	2.49	0.60
1:E:266:ALA:CA	1:E:269:LEU:CD1	2.76	0.60
1:F:249:SER:N	1:F:262:ARG:NH2	2.49	0.60
1:G:279:LYS:HB2	1:G:279:LYS:HZ2	1.56	0.60
1:B:182:VAL:O	1:B:182:VAL:CG2	2.44	0.60
1:C:284:GLY:N	1:C:333:ARG:O	2.32	0.60
1:D:175:ILE:HD11	1:D:195:GLY:N	2.17	0.60
1:D:249:SER:N	1:D:262:ARG:HH22	2.00	0.60
1:D:280:ILE:HD13	1:D:322:PHE:CZ	2.37	0.60
1:F:175:ILE:HG22	1:F:221:LEU:HD21	1.83	0.60
1:A:126:LEU:HD12	1:A:126:LEU:C	2.18	0.59
1:A:311:VAL:CG2	1:A:312:GLU:N	2.65	0.59
1:A:316:LEU:CA	1:A:320:ASP:OD2	2.50	0.59
1:B:273:GLN:CB	1:B:344:LYS:HA	2.31	0.59
1:B:333:ARG:NH1	2:B:402:CMP:O2P	2.34	0.59
1:F:131:GLU:O	1:F:133:ASN:N	2.35	0.59
1:F:301:LEU:HD13	1:F:311:VAL:O	2.02	0.59
1:G:111:TYR:CG	1:G:112:VAL:N	2.70	0.59
1:H:230:ARG:CZ	1:H:234:MET:CE	2.80	0.59
1:H:325:ILE:HD11	2:H:402:CMP:O1P	2.02	0.59
1:A:117:PRO:HG2	1:D:110:SER:CB	2.32	0.59
1:A:230:ARG:HH11	1:A:234:MET:HE1	1.61	0.59
1:A:329:MET:CE	1:A:329:MET:HA	2.32	0.59
1:B:135:LEU:HD13	1:B:136:PHE:CG	2.37	0.59
1:B:203:LEU:HD22	1:B:226:ARG:HB3	1.84	0.59
1:B:211:ASP:OD2	2:B:401:CMP:C5'	2.49	0.59
1:C:293:ILE:HA	1:C:345:CYS:SG	2.42	0.59
1:D:294:LEU:CD1	1:D:294:LEU:N	2.49	0.59
1:E:230:ARG:NH1	1:E:234:MET:HE1	2.17	0.59
1:G:260:TRP:CD1	2:G:401:CMP:C4	2.90	0.59
1:H:295:GLU:HG2	1:H:318:PRO:HG3	1.83	0.59
1:B:153:PRO:CB	1:B:222:TRP:HZ3	2.13	0.59
1:C:278:GLN:O	1:C:338:VAL:CG2	2.49	0.59
1:D:111:TYR:CG	1:D:112:VAL:N	2.70	0.59
1:E:177:GLN:HA	1:E:194:GLU:HG3	1.83	0.59
1:E:272:VAL:C	1:E:273:GLN:NE2	2.55	0.59
1:F:158:ALA:O	1:H:243:MET:HE1	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:313:VAL:O	1:F:313:VAL:HG22	2.01	0.59
1:H:182:VAL:CG2	1:H:190:THR:H	2.13	0.59
1:H:203:LEU:HD22	1:H:226:ARG:HB3	1.84	0.59
1:A:162:VAL:CG2	1:A:163:ILE:HG13	2.29	0.59
1:A:173:TYR:HD2	1:A:198:PHE:HE1	1.43	0.59
1:B:272:VAL:CG2	1:B:273:GLN:NE2	2.66	0.59
1:C:118:LYS:HE2	1:C:148:PHE:O	2.01	0.59
1:C:298:ALA:CB	1:C:338:VAL:O	2.50	0.59
1:F:174:VAL:HG13	1:F:222:TRP:HB2	1.84	0.59
1:H:279:LYS:HB3	1:H:338:VAL:HG23	1.84	0.59
1:H:376:SER:O	1:H:376:SER:OG	2.14	0.59
1:A:157:ILE:CA	1:A:218:ASN:OD1	2.51	0.59
1:A:158:ALA:CA	1:A:217:THR:O	2.50	0.59
1:B:144:ARG:O	1:B:147:ILE:HG12	2.02	0.59
1:B:293:ILE:HD11	1:B:343:LEU:CD1	2.32	0.59
1:C:204:ILE:CG2	1:C:205:TYR:HD2	2.10	0.59
1:F:152:PHE:CE2	1:F:223:GLY:HA3	2.25	0.59
1:H:157:ILE:O	1:H:160:GLU:HB2	2.02	0.59
1:H:247:PHE:HE1	1:H:294:LEU:CB	2.14	0.59
1:H:348:LEU:HD21	1:H:356:VAL:HG21	1.83	0.59
1:A:116:ILE:HB	1:A:118:LYS:NZ	2.17	0.59
1:A:145:SER:HA	1:B:120:TYR:CD1	2.36	0.59
1:B:247:PHE:CE1	1:B:294:LEU:HB3	2.38	0.59
1:B:272:VAL:CA	1:B:273:GLN:NE2	2.66	0.59
1:B:313:VAL:HG21	2:B:402:CMP:C6	2.32	0.59
1:C:120:TYR:C	1:C:120:TYR:HD2	2.04	0.59
1:C:165:GLN:CA	1:C:211:ASP:O	2.49	0.59
1:C:266:ALA:O	1:C:267:ASP:C	2.39	0.59
1:D:235:GLY:O	1:D:239:ARG:HG3	2.02	0.59
1:E:183:TYR:HD1	1:E:188:TRP:HA	1.68	0.59
1:E:290:PHE:C	1:E:291:PHE:HD1	2.05	0.59
1:E:365:LYS:C	1:E:368:ILE:HG13	2.21	0.59
1:F:205:TYR:CD2	1:F:205:TYR:N	2.69	0.59
1:F:296:GLY:HA3	1:F:342:PRO:O	2.02	0.59
1:G:151:MET:HA	1:G:224:ILE:HG22	1.84	0.59
1:H:113:ARG:HB3	1:H:231:ARG:HH12	1.66	0.59
1:H:183:TYR:CD1	1:H:188:TRP:HB2	2.37	0.59
1:H:294:LEU:O	1:H:318:PRO:CB	2.47	0.59
1:H:353:PHE:CE1	1:H:357:LEU:HD23	2.38	0.59
1:B:205:TYR:CD2	1:B:205:TYR:N	2.68	0.59
1:B:260:TRP:CG	2:B:401:CMP:C5	2.90	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:129:ALA:HA	1:C:132:LYS:HE3	1.85	0.59
1:C:243:MET:HE2	1:E:159:GLY:O	2.03	0.59
1:C:271:PRO:HA	1:C:345:CYS:O	2.02	0.59
1:D:291:PHE:CZ	1:D:347:LYS:NZ	2.71	0.59
1:G:152:PHE:CD2	1:G:152:PHE:C	2.73	0.59
1:G:173:TYR:CD2	1:G:198:PHE:CE1	2.87	0.59
1:G:365:LYS:O	1:G:368:ILE:CG1	2.42	0.59
1:H:252:SER:OG	1:H:253:ILE:N	2.34	0.59
1:H:278:GLN:O	1:H:338:VAL:HG22	2.00	0.59
1:A:112:VAL:CB	1:A:112:VAL:N	2.62	0.59
1:A:375:VAL:CG1	1:A:376:SER:H	2.15	0.59
1:B:253:ILE:HG13	1:B:254:LEU:HG	1.84	0.59
1:D:293:ILE:CG1	1:D:343:LEU:HD11	2.32	0.59
1:E:353:PHE:HE1	1:E:357:LEU:CD2	2.12	0.59
1:F:176:ASP:O	1:F:194:GLU:HG2	2.03	0.59
1:G:120:TYR:CD2	1:G:121:LYS:HA	2.35	0.59
1:H:230:ARG:CG	1:H:234:MET:HE1	2.33	0.59
1:H:284:GLY:CA	1:H:332:PRO:HB3	2.32	0.59
1:A:111:TYR:O	1:D:115:VAL:CG2	2.51	0.59
1:A:152:PHE:CE2	1:A:223:GLY:HA3	2.31	0.59
1:A:188:TRP:HZ3	1:A:190:THR:O	1.85	0.59
1:A:260:TRP:NE1	2:A:401:CMP:C8	2.65	0.59
1:A:262:ARG:HA	1:A:265:VAL:CG2	2.32	0.59
1:A:278:GLN:O	1:A:338:VAL:HG22	2.03	0.59
1:D:175:ILE:CD1	1:D:195:GLY:N	2.66	0.59
1:E:259:LYS:CG	1:E:260:TRP:N	2.66	0.59
1:H:204:ILE:HG12	1:H:234:MET:SD	2.43	0.59
1:H:205:TYR:HD2	1:H:205:TYR:N	2.00	0.59
1:B:173:TYR:HD1	1:B:223:GLY:HA3	1.68	0.59
1:D:200:GLU:HG2	1:D:201:LEU:HG	1.84	0.59
1:D:211:ASP:OD2	2:D:401:CMP:H3'	2.03	0.59
1:D:247:PHE:CE1	1:D:294:LEU:CA	2.79	0.59
1:D:293:ILE:HA	1:D:345:CYS:SG	2.43	0.59
1:H:173:TYR:CD2	1:H:198:PHE:HE1	2.18	0.59
1:H:177:GLN:HA	1:H:194:GLU:HG3	1.84	0.59
1:H:294:LEU:HD11	1:H:344:LYS:HG2	1.85	0.59
1:H:365:LYS:O	1:H:368:ILE:CG1	2.48	0.59
1:A:113:ARG:NH2	1:D:115:VAL:HA	2.16	0.58
1:A:273:GLN:NE2	1:A:273:GLN:H	1.79	0.58
1:B:131:GLU:C	1:B:133:ASN:H	2.06	0.58
1:D:366:ARG:HG2	1:D:367:ASN:N	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:362:ASP:OD1	1:E:362:ASP:N	2.36	0.58
1:F:131:GLU:OE1	1:F:131:GLU:CA	2.50	0.58
1:F:194:GLU:O	1:F:355:ARG:HD2	2.03	0.58
1:G:180:MET:HB2	1:G:192:VAL:HB	1.84	0.58
1:H:161:THR:CA	1:H:214:LYS:HD2	2.25	0.58
1:H:253:ILE:HG13	1:H:254:LEU:HG	1.85	0.58
1:A:144:ARG:HD2	1:B:120:TYR:HH	1.68	0.58
1:A:175:ILE:CD1	1:A:195:GLY:N	2.66	0.58
1:A:262:ARG:O	1:A:265:VAL:CB	2.43	0.58
1:A:294:LEU:HD11	1:A:345:CYS:CA	2.22	0.58
1:B:292:ILE:HB	1:B:346:VAL:HG13	1.84	0.58
1:C:143:GLU:HB3	1:C:232:ILE:HD11	1.85	0.58
1:C:281:VAL:CG1	1:C:333:ARG:CG	2.81	0.58
1:D:296:GLY:HA3	1:D:343:LEU:HA	1.85	0.58
1:E:111:TYR:C	1:E:112:VAL:HG22	2.24	0.58
1:E:198:PHE:CD1	1:E:198:PHE:N	2.70	0.58
1:F:220:LYS:O	1:F:221:LEU:HD23	2.03	0.58
1:G:117:PRO:HA	1:H:119:ASP:HA	1.84	0.58
1:H:293:ILE:HG21	1:H:317:GLY:C	2.23	0.58
1:A:135:LEU:HD13	1:A:136:PHE:CG	2.37	0.58
1:B:310:PHE:O	1:B:310:PHE:HD2	1.86	0.58
1:B:322:PHE:CD2	1:B:337:VAL:HG21	2.38	0.58
1:C:293:ILE:HG21	1:C:317:GLY:C	2.23	0.58
1:C:361:SER:HB2	1:C:365:LYS:HZ1	1.67	0.58
1:E:165:GLN:CA	1:E:211:ASP:O	2.50	0.58
1:F:180:MET:O	1:F:191:SER:HA	2.02	0.58
1:F:198:PHE:N	1:F:198:PHE:HD1	2.01	0.58
1:G:321:TYR:C	1:G:321:TYR:CD1	2.77	0.58
1:B:133:ASN:O	1:B:135:LEU:HD12	2.02	0.58
1:B:262:ARG:HA	1:B:265:VAL:CG2	2.34	0.58
1:B:281:VAL:CG1	1:B:333:ARG:CD	2.81	0.58
1:C:173:TYR:HB2	1:C:198:PHE:CE1	2.38	0.58
1:C:350:ARG:O	1:C:353:PHE:CB	2.51	0.58
1:D:144:ARG:O	1:D:145:SER:C	2.40	0.58
1:E:120:TYR:CD1	1:F:148:PHE:CD1	2.92	0.58
1:E:203:LEU:HD12	1:E:229:TYR:HD2	1.67	0.58
1:G:112:VAL:HG12	1:G:231:ARG:CZ	2.33	0.58
1:G:144:ARG:O	1:G:147:ILE:HG12	2.02	0.58
1:G:164:GLN:HA	1:G:212:THR:CG2	2.32	0.58
1:H:280:ILE:HD11	1:H:337:VAL:CB	2.29	0.58
1:H:300:VAL:O	1:H:301:LEU:CD2	2.44	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:325:ILE:HG13	2:H:402:CMP:O1P	2.04	0.58
1:A:120:TYR:OH	1:B:144:ARG:HD2	2.03	0.58
1:A:259:LYS:CG	1:A:260:TRP:N	2.57	0.58
1:B:325:ILE:CD1	1:B:334:ALA:HB3	2.34	0.58
1:C:112:VAL:O	1:C:113:ARG:HG3	2.04	0.58
1:C:247:PHE:CE1	1:C:294:LEU:HB3	2.38	0.58
1:C:263:LEU:O	1:C:267:ASP:N	2.33	0.58
1:C:292:ILE:HB	1:C:346:VAL:CG1	2.33	0.58
1:D:122:THR:O	1:D:125:ALA:HB3	2.03	0.58
1:D:200:GLU:HG2	1:D:201:LEU:HD12	1.84	0.58
1:E:144:ARG:CG	1:E:145:SER:N	2.67	0.58
1:E:161:THR:CA	1:E:214:LYS:HD2	2.32	0.58
1:E:173:TYR:CD2	1:E:198:PHE:CE1	2.91	0.58
1:E:182:VAL:CG2	1:E:190:THR:H	2.16	0.58
1:E:248:LEU:CB	1:E:262:ARG:HH21	2.17	0.58
1:G:269:LEU:CB	1:G:346:VAL:CG2	2.81	0.58
1:H:308:GLU:O	1:H:309:GLU:OE2	2.21	0.58
1:C:205:TYR:CD2	1:C:205:TYR:N	2.71	0.58
1:C:272:VAL:HG22	1:C:273:GLN:N	2.14	0.58
1:D:318:PRO:O	1:D:319:SER:HB3	2.03	0.58
1:E:201:LEU:HD13	2:E:401:CMP:H2'	1.83	0.58
1:F:152:PHE:CD2	1:F:152:PHE:C	2.76	0.58
1:A:188:TRP:CZ3	1:A:190:THR:HA	2.38	0.58
1:B:163:ILE:O	1:B:212:THR:HG22	2.04	0.58
1:C:302:GLN:NE2	1:C:374:PHE:CB	2.67	0.58
1:D:162:VAL:CG2	1:D:213:VAL:O	2.50	0.58
1:D:175:ILE:CD1	1:D:194:GLU:HA	2.33	0.58
1:E:262:ARG:HA	1:E:265:VAL:CG2	2.33	0.58
1:F:113:ARG:HD3	1:F:146:ASP:CB	2.34	0.58
1:G:158:ALA:HB2	1:G:217:THR:C	2.24	0.58
1:G:254:LEU:HD12	1:G:255:GLU:N	2.18	0.58
1:A:142:ASN:CB	1:C:121:LYS:HE3	2.33	0.58
1:B:200:GLU:CG	1:B:201:LEU:N	2.42	0.58
1:B:260:TRP:HA	1:B:263:LEU:HD12	1.84	0.58
1:C:139:LEU:N	1:C:139:LEU:CD1	2.63	0.58
1:D:161:THR:HG23	1:D:214:LYS:CD	2.34	0.58
1:D:199:GLY:HA2	2:D:401:CMP:P	2.44	0.58
1:D:204:ILE:CG2	1:D:205:TYR:CD2	2.83	0.58
1:E:180:MET:HB2	1:E:192:VAL:HB	1.86	0.58
1:E:274:PHE:CD2	1:E:280:ILE:HG22	2.39	0.58
1:E:296:GLY:CA	1:E:342:PRO:O	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:157:ILE:CB	1:G:218:ASN:OD1	2.51	0.58
1:H:325:ILE:O	1:H:328:LEU:N	2.36	0.58
1:A:113:ARG:HG2	1:D:113:ARG:HB2	1.84	0.58
1:A:113:ARG:CZ	1:D:114:LYS:N	2.67	0.58
1:B:120:TYR:CD2	1:B:120:TYR:O	2.52	0.58
1:B:177:GLN:HA	1:B:194:GLU:HG3	1.84	0.58
1:B:260:TRP:NE1	2:B:401:CMP:H2'	2.12	0.58
1:B:348:LEU:HD21	1:B:356:VAL:CG2	2.32	0.58
1:C:161:THR:OG1	1:C:214:LYS:NZ	2.32	0.58
1:C:371:TYR:CE1	2:C:402:CMP:C5	2.92	0.58
1:D:152:PHE:HD1	1:D:152:PHE:N	1.97	0.58
1:D:226:ARG:HH11	1:D:226:ARG:CG	2.04	0.58
1:E:293:ILE:CG1	1:E:317:GLY:O	2.51	0.58
1:E:300:VAL:HG11	2:E:402:CMP:C8	2.33	0.58
1:F:270:GLU:O	1:F:346:VAL:HA	2.04	0.58
1:B:269:LEU:CD2	1:B:346:VAL:HG21	2.34	0.58
1:B:294:LEU:O	1:B:295:GLU:HG3	2.03	0.58
1:C:175:ILE:HD11	1:C:193:GLY:O	2.04	0.58
1:C:229:TYR:HD1	1:C:233:LEU:HD11	1.66	0.58
1:D:129:ALA:CB	1:D:222:TRP:HE1	2.17	0.58
1:D:292:ILE:HB	1:D:346:VAL:CG1	2.33	0.58
1:D:324:GLU:O	1:D:325:ILE:C	2.42	0.58
1:E:151:MET:HA	1:E:224:ILE:HG22	1.85	0.58
1:E:152:PHE:CD2	1:E:152:PHE:N	2.68	0.58
1:F:300:VAL:HG11	1:F:335:ALA:HB1	1.85	0.58
1:F:361:SER:O	1:F:365:LYS:HD2	2.03	0.58
1:H:158:ALA:HA	1:H:215:ALA:CB	2.34	0.58
1:H:302:GLN:C	1:H:310:PHE:CD1	2.77	0.58
1:A:175:ILE:HA	1:A:221:LEU:HD23	1.81	0.57
1:D:135:LEU:HD12	1:D:135:LEU:N	2.19	0.57
1:D:242:LYS:N	1:D:242:LYS:HD3	2.11	0.57
1:E:269:LEU:CB	1:E:346:VAL:HG21	2.32	0.57
1:E:290:PHE:HB2	1:E:327:LEU:CD2	2.34	0.57
1:F:118:LYS:NZ	1:F:151:MET:O	2.32	0.57
1:F:183:TYR:CD1	1:F:188:TRP:HB2	2.38	0.57
1:F:230:ARG:HG2	1:F:230:ARG:HH11	1.69	0.57
1:G:247:PHE:HE1	1:G:294:LEU:CA	2.10	0.57
1:H:152:PHE:O	1:H:152:PHE:HD2	1.87	0.57
1:H:205:TYR:CD2	1:H:205:TYR:N	2.71	0.57
1:H:247:PHE:C	1:H:247:PHE:HD2	2.05	0.57
1:A:111:TYR:O	1:A:112:VAL:CB	2.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:HIS:CD2	1:C:157:ILE:CG2	2.86	0.57
1:B:188:TRP:HH2	1:B:191:SER:HG	1.51	0.57
1:D:113:ARG:CZ	1:D:146:ASP:OD1	2.51	0.57
1:D:120:TYR:CE2	1:D:124:ALA:HB2	2.39	0.57
1:D:299:ALA:HB3	1:D:338:VAL:HG12	1.85	0.57
1:A:151:MET:HG2	1:A:224:ILE:CG2	2.34	0.57
1:B:347:LYS:O	1:B:348:LEU:HD12	2.04	0.57
1:C:158:ALA:HA	1:C:215:ALA:CB	2.34	0.57
1:D:158:ALA:O	1:F:243:MET:HE1	2.04	0.57
1:D:230:ARG:CG	1:D:234:MET:HE1	2.31	0.57
1:F:188:TRP:CH2	1:F:190:THR:HA	2.39	0.57
1:G:126:LEU:O	1:G:126:LEU:CD1	2.39	0.57
1:G:130:ILE:CG2	1:G:131:GLU:N	2.67	0.57
1:A:313:VAL:HG11	2:A:402:CMP:N6	2.19	0.57
1:B:157:ILE:CG2	1:B:218:ASN:OD1	2.52	0.57
1:B:246:GLU:O	1:B:248:LEU:N	2.37	0.57
1:C:222:TRP:HA	1:C:222:TRP:HE3	1.67	0.57
1:C:260:TRP:O	1:C:263:LEU:HB2	2.04	0.57
1:C:344:LYS:HE2	1:E:216:LYS:HA	1.86	0.57
1:D:365:LYS:CA	1:D:368:ILE:HG13	2.34	0.57
1:G:161:THR:OG1	1:G:214:LYS:NZ	2.22	0.57
1:G:254:LEU:HD12	1:G:254:LEU:C	2.25	0.57
1:H:129:ALA:CB	1:H:222:TRP:HE1	2.18	0.57
1:H:297:SER:O	1:H:340:ARG:HB2	2.04	0.57
1:A:175:ILE:HD12	1:A:195:GLY:H	1.69	0.57
1:B:152:PHE:HE2	1:B:223:GLY:CA	2.17	0.57
1:B:312:GLU:CD	1:B:313:VAL:N	2.57	0.57
1:B:365:LYS:HA	1:B:368:ILE:CG1	2.35	0.57
1:D:201:LEU:O	1:D:204:ILE:N	2.38	0.57
1:E:233:LEU:HD12	1:E:233:LEU:N	2.08	0.57
1:F:164:GLN:HA	1:F:212:THR:CG2	2.31	0.57
1:F:363:ILE:O	1:F:366:ARG:HG2	2.04	0.57
1:G:234:MET:HG3	1:G:238:LEU:CD1	2.33	0.57
1:G:246:GLU:O	1:G:248:LEU:N	2.38	0.57
1:G:265:VAL:CG1	1:G:269:LEU:CD2	2.70	0.57
1:G:348:LEU:HD21	1:G:356:VAL:CG2	2.34	0.57
1:A:138:HIS:CD2	1:C:157:ILE:HG21	2.39	0.57
1:B:251:VAL:O	1:B:252:SER:O	2.21	0.57
1:C:120:TYR:HD2	1:C:121:LYS:CA	2.17	0.57
1:C:157:ILE:O	1:C:157:ILE:CD1	2.37	0.57
1:C:172:PHE:O	1:C:224:ILE:HD12	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:204:ILE:CG2	1:C:205:TYR:CE2	2.88	0.57
1:C:325:ILE:HG13	2:C:402:CMP:O2P	2.02	0.57
1:D:139:LEU:HD21	1:D:147:ILE:HD11	1.87	0.57
1:D:174:VAL:CG1	1:D:222:TRP:HB2	2.35	0.57
1:E:127:ALA:O	1:E:130:ILE:N	2.38	0.57
1:E:356:VAL:HG23	1:E:357:LEU:HD12	1.86	0.57
1:F:114:LYS:HE3	1:F:115:VAL:N	2.19	0.57
1:F:122:THR:O	1:F:125:ALA:HB3	2.04	0.57
1:F:198:PHE:CD1	1:F:198:PHE:O	2.57	0.57
1:F:294:LEU:CD1	1:F:344:LYS:O	2.52	0.57
1:F:312:GLU:OE1	1:F:340:ARG:NH1	2.37	0.57
1:G:112:VAL:HG12	1:G:231:ARG:HH21	1.69	0.57
1:G:153:PRO:HB3	1:G:222:TRP:HZ3	1.61	0.57
1:G:249:SER:CA	1:G:262:ARG:NH2	2.66	0.57
1:G:375:VAL:CG1	1:G:376:SER:N	2.68	0.57
1:H:111:TYR:CE2	1:H:112:VAL:CG1	2.86	0.57
1:A:248:LEU:HB2	1:A:262:ARG:HH21	1.69	0.57
1:B:293:ILE:HG23	1:B:318:PRO:HA	1.87	0.57
1:C:248:LEU:HD21	1:C:265:VAL:HG11	1.87	0.57
1:G:182:VAL:O	1:G:182:VAL:CG2	2.52	0.57
1:G:285:GLU:OE1	1:G:285:GLU:HA	2.04	0.57
1:H:153:PRO:CA	1:H:222:TRP:CZ3	2.88	0.57
1:H:269:LEU:HB3	1:H:346:VAL:HG23	1.84	0.57
1:H:278:GLN:O	1:H:338:VAL:HA	2.04	0.57
1:H:368:ILE:O	1:H:371:TYR:HB2	2.04	0.57
1:A:153:PRO:CB	1:A:222:TRP:HZ3	2.16	0.57
1:A:309:GLU:HG3	1:A:310:PHE:N	2.19	0.57
1:C:135:LEU:HD12	1:C:136:PHE:N	2.19	0.57
1:C:172:PHE:O	1:C:224:ILE:CD1	2.52	0.57
1:D:113:ARG:NH2	1:D:146:ASP:OD1	2.38	0.57
1:D:247:PHE:CE1	1:D:294:LEU:CB	2.87	0.57
1:E:365:LYS:CA	1:E:368:ILE:HG13	2.34	0.57
1:F:293:ILE:HA	1:F:345:CYS:SG	2.45	0.57
1:G:252:SER:O	1:G:255:GLU:HB2	2.04	0.57
1:G:253:ILE:HG23	1:G:321:TYR:HE2	1.70	0.57
1:A:171:ASN:H	1:A:209:ARG:HH22	1.53	0.57
1:A:292:ILE:HB	1:A:346:VAL:HG13	1.86	0.57
1:A:324:GLU:CG	1:A:325:ILE:N	2.67	0.57
1:B:121:LYS:O	1:B:124:ALA:N	2.38	0.57
1:B:284:GLY:O	1:B:332:PRO:HB3	2.05	0.57
1:C:281:VAL:O	1:C:336:THR:HA	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:PHE:O	1:D:139:LEU:CD1	2.52	0.57
1:E:170:ASP:H	1:E:209:ARG:NH2	2.02	0.57
1:E:269:LEU:HB3	1:E:346:VAL:HG22	1.85	0.57
1:E:291:PHE:CD1	1:E:347:LYS:NZ	2.73	0.57
1:F:153:PRO:HB3	1:F:222:TRP:HZ3	1.67	0.57
1:F:366:ARG:CG	1:F:367:ASN:N	2.67	0.57
1:G:118:LYS:NZ	1:G:151:MET:O	2.34	0.57
1:G:140:ASP:OD1	1:G:140:ASP:C	2.43	0.57
1:G:175:ILE:CD1	1:G:194:GLU:HA	2.34	0.57
1:H:162:VAL:HG22	1:H:213:VAL:O	2.05	0.57
1:H:327:LEU:HD23	1:H:353:PHE:CD2	2.40	0.57
1:B:272:VAL:HG22	1:B:273:GLN:N	2.20	0.57
1:B:329:MET:HA	1:B:329:MET:CE	2.35	0.57
1:C:247:PHE:HE1	1:C:294:LEU:HB3	1.70	0.57
1:C:325:ILE:HG13	1:C:326:ALA:H	1.70	0.57
1:D:152:PHE:N	1:D:152:PHE:CD1	2.68	0.57
1:E:140:ASP:C	1:E:140:ASP:OD1	2.43	0.57
1:E:178:GLY:HA3	1:E:219:VAL:CG1	2.26	0.57
1:E:226:ARG:HA	1:E:229:TYR:HB3	1.86	0.57
1:E:294:LEU:CD1	1:E:344:LYS:O	2.51	0.57
1:E:365:LYS:HA	1:E:368:ILE:CG1	2.35	0.57
1:F:151:MET:HA	1:F:224:ILE:HG22	1.85	0.57
1:F:278:GLN:O	1:F:338:VAL:HG22	2.05	0.57
1:H:120:TYR:C	1:H:120:TYR:HD2	2.04	0.57
1:H:211:ASP:OD2	2:H:401:CMP:N3	2.38	0.57
1:A:224:ILE:HD12	1:A:224:ILE:H	1.68	0.56
1:B:239:ARG:C	1:B:241:ARG:N	2.53	0.56
1:B:274:PHE:CD2	1:B:343:LEU:HD23	2.40	0.56
1:F:129:ALA:CB	1:F:222:TRP:HE1	2.18	0.56
1:F:269:LEU:HD23	1:F:348:LEU:CD1	2.35	0.56
1:G:177:GLN:HA	1:G:194:GLU:HG3	1.86	0.56
1:G:296:GLY:HA3	1:G:342:PRO:O	2.05	0.56
1:G:324:GLU:HB2	1:G:364:LEU:HD13	1.86	0.56
1:H:293:ILE:CD1	1:H:343:LEU:HD11	2.32	0.56
1:A:180:MET:O	1:A:191:SER:HA	2.05	0.56
1:A:247:PHE:C	1:A:247:PHE:CD2	2.77	0.56
1:B:162:VAL:CG2	1:B:163:ILE:HG13	2.34	0.56
1:E:281:VAL:HG12	1:E:333:ARG:HG3	1.86	0.56
1:G:222:TRP:HA	1:G:222:TRP:HE3	1.69	0.56
1:H:152:PHE:HD2	1:H:152:PHE:H	1.54	0.56
1:H:154:VAL:O	1:H:221:LEU:N	2.29	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:LYS:CB	1:A:123:MET:HE2	2.33	0.56
1:A:194:GLU:O	1:A:355:ARG:HD2	2.05	0.56
1:A:201:LEU:HD13	2:A:401:CMP:H2'	1.87	0.56
1:A:366:ARG:O	1:A:369:GLN:CB	2.54	0.56
1:C:138:HIS:HE2	1:C:236:SER:HB3	1.69	0.56
1:C:252:SER:OG	1:C:253:ILE:N	2.37	0.56
1:C:266:ALA:N	1:C:269:LEU:HD11	2.20	0.56
1:C:294:LEU:O	1:C:318:PRO:HB3	2.04	0.56
1:D:263:LEU:O	1:D:266:ALA:N	2.39	0.56
1:D:365:LYS:HA	1:D:368:ILE:CG1	2.36	0.56
1:E:246:GLU:C	1:E:248:LEU:N	2.55	0.56
1:E:253:ILE:HD13	1:E:321:TYR:CE2	2.40	0.56
1:F:210:ALA:N	1:F:211:ASP:OD1	2.38	0.56
1:G:139:LEU:HD22	1:G:144:ARG:HA	1.88	0.56
1:G:204:ILE:CG2	1:G:205:TYR:CD2	2.84	0.56
1:G:259:LYS:HG3	1:G:260:TRP:H	1.68	0.56
1:G:293:ILE:HG23	1:G:318:PRO:HA	1.87	0.56
1:G:366:ARG:O	1:G:369:GLN:HB2	2.05	0.56
1:H:114:LYS:HZ2	1:H:114:LYS:CA	2.11	0.56
1:H:130:ILE:HD13	1:H:151:MET:CE	2.35	0.56
1:H:172:PHE:HD2	1:H:224:ILE:HD11	1.70	0.56
1:H:253:ILE:HG13	1:H:254:LEU:HD23	1.87	0.56
1:H:301:LEU:HB3	1:H:311:VAL:O	2.04	0.56
1:H:371:TYR:CE1	2:H:402:CMP:C4	2.94	0.56
1:A:175:ILE:CD1	1:A:195:GLY:H	2.18	0.56
1:B:120:TYR:O	1:B:121:LYS:C	2.41	0.56
1:B:266:ALA:O	1:B:267:ASP:C	2.43	0.56
1:F:130:ILE:CD1	1:F:136:PHE:CD2	2.89	0.56
1:F:133:ASN:ND2	1:F:174:VAL:HG21	2.19	0.56
1:A:175:ILE:HD12	1:A:175:ILE:C	2.22	0.56
1:A:298:ALA:HB3	1:A:316:LEU:HD11	1.86	0.56
1:A:325:ILE:CD1	1:A:334:ALA:CB	2.84	0.56
1:B:246:GLU:C	1:B:248:LEU:N	2.59	0.56
1:C:365:LYS:HA	1:C:368:ILE:CG1	2.36	0.56
1:D:153:PRO:HA	1:D:222:TRP:CE3	2.40	0.56
1:H:190:THR:HG22	1:H:191:SER:N	2.07	0.56
1:H:291:PHE:HB2	1:H:322:PHE:CE1	2.40	0.56
1:A:183:TYR:HD1	1:A:188:TRP:CB	2.19	0.56
1:A:246:GLU:O	1:A:249:SER:N	2.38	0.56
1:B:139:LEU:HD21	1:B:147:ILE:HD13	1.86	0.56
1:B:362:ASP:OD1	1:B:362:ASP:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:118:LYS:NZ	1:C:151:MET:O	2.32	0.56
1:C:350:ARG:HB3	1:C:351:PRO:HD3	1.87	0.56
1:D:118:LYS:NZ	1:D:151:MET:O	2.32	0.56
1:D:324:GLU:HB2	1:D:364:LEU:CD1	2.36	0.56
1:E:203:LEU:CD2	1:E:226:ARG:HB3	2.31	0.56
1:F:161:THR:HG23	1:F:214:LYS:HD3	1.87	0.56
1:H:158:ALA:HB2	1:H:217:THR:O	2.05	0.56
1:H:266:ALA:O	1:H:268:ALA:N	2.39	0.56
1:H:362:ASP:N	1:H:365:LYS:HZ2	2.03	0.56
1:A:120:TYR:HD1	1:B:148:PHE:CB	2.14	0.56
1:A:163:ILE:O	1:A:212:THR:HG22	2.06	0.56
1:A:278:GLN:HG3	1:A:279:LYS:H	1.69	0.56
1:A:279:LYS:HB2	1:A:337:VAL:O	2.05	0.56
1:A:290:PHE:HB2	1:A:327:LEU:CD2	2.36	0.56
1:B:278:GLN:HG3	1:B:279:LYS:N	2.17	0.56
1:B:281:VAL:CG1	1:B:333:ARG:HG3	2.35	0.56
1:C:300:VAL:C	1:C:301:LEU:HD12	2.24	0.56
1:C:325:ILE:O	1:C:328:LEU:N	2.39	0.56
1:D:171:ASN:OD1	1:D:225:ASP:HA	2.06	0.56
1:D:230:ARG:O	1:D:234:MET:CB	2.52	0.56
1:E:188:TRP:CH2	1:E:190:THR:HA	2.40	0.56
1:E:247:PHE:CD2	1:E:247:PHE:O	2.58	0.56
1:E:260:TRP:CG	2:E:401:CMP:N7	2.74	0.56
1:E:327:LEU:HD23	1:E:353:PHE:CE2	2.40	0.56
1:F:365:LYS:CA	1:F:368:ILE:HG13	2.35	0.56
1:G:280:ILE:HD13	1:G:322:PHE:CE2	2.41	0.56
1:G:280:ILE:HD13	1:G:322:PHE:HZ	1.69	0.56
1:H:172:PHE:O	1:H:224:ILE:CD1	2.53	0.56
1:H:289:GLU:HB3	1:H:347:LYS:NZ	2.21	0.56
1:A:113:ARG:O	1:D:113:ARG:O	2.24	0.56
1:A:246:GLU:C	1:A:248:LEU:N	2.53	0.56
1:B:281:VAL:HG13	1:B:333:ARG:HG3	1.86	0.56
1:B:353:PHE:O	1:B:357:LEU:HB2	2.06	0.56
1:E:130:ILE:CD1	1:E:151:MET:CE	2.84	0.56
1:E:148:PHE:CD1	1:F:120:TYR:HD1	2.24	0.56
1:E:203:LEU:CD1	1:E:226:ARG:HB3	2.36	0.56
1:E:204:ILE:CG2	1:E:205:TYR:CD2	2.88	0.56
1:G:245:GLU:OE1	1:G:246:GLU:OE1	2.23	0.56
1:A:158:ALA:CB	1:A:217:THR:O	2.54	0.56
1:A:316:LEU:C	1:A:316:LEU:CD1	2.69	0.56
1:B:272:VAL:CG2	1:B:273:GLN:HE22	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:350:ARG:O	1:B:353:PHE:CB	2.51	0.56
1:C:139:LEU:HD22	1:C:144:ARG:HA	1.86	0.56
1:C:175:ILE:HD11	1:C:196:GLY:N	2.20	0.56
1:C:282:VAL:O	1:C:333:ARG:HB2	2.06	0.56
1:C:295:GLU:O	1:C:344:LYS:N	2.39	0.56
1:D:293:ILE:HG23	1:D:318:PRO:HA	1.88	0.56
1:E:269:LEU:HD23	1:E:348:LEU:HD11	1.87	0.56
1:F:269:LEU:HD23	1:F:348:LEU:HD11	1.87	0.56
1:G:170:ASP:H	1:G:209:ARG:NH2	2.03	0.56
1:G:366:ARG:CG	1:G:367:ASN:N	2.68	0.56
1:H:350:ARG:O	1:H:353:PHE:CB	2.54	0.56
1:A:157:ILE:HA	1:A:218:ASN:OD1	2.06	0.56
1:B:247:PHE:CE1	1:B:294:LEU:CA	2.86	0.56
1:B:311:VAL:CG1	1:B:312:GLU:N	2.69	0.56
1:B:366:ARG:O	1:B:369:GLN:CB	2.54	0.56
1:C:162:VAL:HG23	1:C:163:ILE:HG13	1.86	0.56
1:E:120:TYR:CE1	1:F:148:PHE:CD1	2.94	0.56
1:E:203:LEU:HD22	1:E:226:ARG:CG	2.36	0.56
1:H:174:VAL:HA	1:H:196:GLY:O	2.06	0.56
1:H:182:VAL:HA	1:H:212:THR:O	2.06	0.56
1:B:282:VAL:O	1:B:285:GLU:CG	2.51	0.55
1:C:179:GLU:HG2	1:C:216:LYS:HD3	1.86	0.55
1:C:196:GLY:HA2	1:C:355:ARG:HH22	1.62	0.55
1:D:200:GLU:HG2	1:D:201:LEU:CD1	2.36	0.55
1:D:295:GLU:O	1:D:343:LEU:HD12	2.06	0.55
1:D:366:ARG:O	1:D:369:GLN:CB	2.54	0.55
1:E:130:ILE:HD13	1:E:151:MET:HE2	1.86	0.55
1:E:278:GLN:HG3	1:E:279:LYS:N	2.10	0.55
1:F:113:ARG:HD3	1:F:146:ASP:OD2	2.05	0.55
1:G:162:VAL:HG23	1:G:163:ILE:N	2.21	0.55
1:G:174:VAL:CG1	1:G:222:TRP:HB2	2.37	0.55
1:A:144:ARG:CG	1:A:145:SER:N	2.69	0.55
1:A:158:ALA:HA	1:A:217:THR:O	2.07	0.55
1:A:183:TYR:HD1	1:A:188:TRP:CA	2.19	0.55
1:B:122:THR:O	1:B:125:ALA:HB3	2.07	0.55
1:B:260:TRP:CD2	2:B:401:CMP:N7	2.75	0.55
1:B:260:TRP:NE1	2:B:401:CMP:C8	2.68	0.55
1:C:131:GLU:C	1:C:133:ASN:N	2.58	0.55
1:C:158:ALA:CB	1:C:217:THR:O	2.54	0.55
1:F:300:VAL:HA	1:F:336:THR:O	2.06	0.55
1:G:226:ARG:NH1	1:G:226:ARG:CG	2.56	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:182:VAL:CG2	1:H:190:THR:O	2.41	0.55
1:A:134:VAL:O	1:A:137:SER:HB3	2.07	0.55
1:A:205:TYR:HD2	1:A:205:TYR:N	2.04	0.55
1:A:273:GLN:CB	1:A:344:LYS:HA	2.36	0.55
1:A:278:GLN:CG	1:A:279:LYS:N	2.69	0.55
1:B:249:SER:CA	1:B:262:ARG:NH2	2.65	0.55
1:C:140:ASP:C	1:C:140:ASP:OD1	2.45	0.55
1:C:285:GLU:OE1	1:C:285:GLU:CA	2.54	0.55
1:C:293:ILE:HG23	1:C:318:PRO:HA	1.87	0.55
1:D:173:TYR:HB2	1:D:198:PHE:HE1	1.70	0.55
1:E:230:ARG:CZ	1:E:234:MET:HE1	2.37	0.55
1:G:350:ARG:HB3	1:G:351:PRO:CD	2.32	0.55
1:H:224:ILE:O	1:H:224:ILE:HD13	2.07	0.55
1:H:353:PHE:O	1:H:357:LEU:HB2	2.05	0.55
1:A:266:ALA:O	1:A:267:ASP:C	2.44	0.55
1:B:200:GLU:O	1:B:201:LEU:C	2.45	0.55
1:C:158:ALA:CA	1:C:217:THR:O	2.54	0.55
1:C:171:ASN:H	1:C:209:ARG:HH22	1.53	0.55
1:C:327:LEU:HD23	1:C:353:PHE:CZ	2.41	0.55
1:C:329:MET:HA	1:C:329:MET:HE2	1.87	0.55
1:E:131:GLU:H	1:E:131:GLU:CD	2.09	0.55
1:E:260:TRP:NE1	2:E:401:CMP:H2'	2.20	0.55
1:G:242:LYS:HD3	1:G:242:LYS:N	2.15	0.55
1:G:246:GLU:C	1:G:248:LEU:N	2.53	0.55
1:G:371:TYR:OH	2:G:402:CMP:C2'	2.55	0.55
1:H:127:ALA:O	1:H:130:ILE:HG22	2.07	0.55
1:H:153:PRO:CB	1:H:222:TRP:CZ3	2.88	0.55
1:H:303:ARG:CB	1:H:310:PHE:CZ	2.90	0.55
1:H:353:PHE:CE1	1:H:357:LEU:HD22	2.41	0.55
1:A:112:VAL:CA	1:A:112:VAL:HB	2.17	0.55
1:A:144:ARG:O	1:A:147:ILE:HG12	2.06	0.55
1:A:173:TYR:CD2	1:A:198:PHE:CE1	2.85	0.55
1:A:254:LEU:HA	1:A:360:CYS:SG	2.46	0.55
1:B:182:VAL:CG2	1:B:190:THR:H	2.20	0.55
1:B:291:PHE:CD2	1:B:347:LYS:NZ	2.66	0.55
1:B:366:ARG:O	1:B:369:GLN:HB2	2.07	0.55
1:C:188:TRP:CZ3	1:C:190:THR:O	2.59	0.55
1:C:278:GLN:O	1:C:338:VAL:CA	2.53	0.55
1:E:120:TYR:C	1:E:120:TYR:HD2	2.09	0.55
1:E:154:VAL:O	1:E:221:LEU:N	2.29	0.55
1:E:260:TRP:CD2	2:E:401:CMP:C8	2.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:342:PRO:O	1:F:342:PRO:HG2	2.06	0.55
1:G:353:PHE:CE1	1:G:357:LEU:CD2	2.89	0.55
1:H:172:PHE:CE1	1:H:200:GLU:HB3	2.41	0.55
1:H:283:GLN:CG	1:H:333:ARG:O	2.55	0.55
1:A:126:LEU:O	1:A:126:LEU:CD1	2.41	0.55
1:B:210:ALA:C	1:B:211:ASP:OD1	2.45	0.55
1:B:253:ILE:C	1:B:255:GLU:H	2.10	0.55
1:C:247:PHE:HE1	1:C:294:LEU:CB	2.18	0.55
1:D:175:ILE:HG21	1:D:180:MET:HG3	1.87	0.55
1:E:280:ILE:HB	1:E:291:PHE:CE2	2.41	0.55
1:F:133:ASN:O	1:F:135:LEU:HD12	2.07	0.55
1:F:173:TYR:CD2	1:F:198:PHE:CE1	2.94	0.55
1:F:310:PHE:O	1:F:311:VAL:HG13	2.07	0.55
1:G:153:PRO:CA	1:G:222:TRP:CZ3	2.89	0.55
1:G:247:PHE:CE1	1:G:294:LEU:HB3	2.41	0.55
1:G:256:SER:OG	1:G:363:ILE:CD1	2.55	0.55
1:A:111:TYR:CA	1:D:115:VAL:HG23	2.33	0.55
1:A:270:GLU:O	1:A:346:VAL:HA	2.06	0.55
1:B:260:TRP:NE1	2:B:401:CMP:N9	2.54	0.55
1:D:220:LYS:O	1:D:221:LEU:HD23	2.06	0.55
1:D:224:ILE:HD13	1:D:224:ILE:H	1.71	0.55
1:D:260:TRP:NE1	2:D:401:CMP:C2'	2.69	0.55
1:E:148:PHE:HD1	1:F:120:TYR:CD1	2.24	0.55
1:F:134:VAL:O	1:F:137:SER:HB3	2.06	0.55
1:F:246:GLU:O	1:F:248:LEU:N	2.39	0.55
1:H:247:PHE:CE1	1:H:294:LEU:CB	2.89	0.55
1:H:266:ALA:O	1:H:267:ASP:C	2.45	0.55
1:H:274:PHE:CE2	1:H:280:ILE:HG22	2.42	0.55
1:H:365:LYS:O	1:H:368:ILE:N	2.30	0.55
1:A:113:ARG:NH2	1:D:115:VAL:CA	2.70	0.55
1:A:203:LEU:HD12	1:A:229:TYR:HD2	1.70	0.55
1:B:272:VAL:HG23	1:B:273:GLN:HE22	1.71	0.55
1:C:174:VAL:CG1	1:C:222:TRP:HB2	2.37	0.55
1:C:183:TYR:CD1	1:C:188:TRP:HB2	2.41	0.55
1:C:198:PHE:CD1	1:C:198:PHE:N	2.73	0.55
1:D:127:ALA:O	1:D:130:ILE:N	2.38	0.55
1:D:152:PHE:CD1	1:D:152:PHE:O	2.60	0.55
1:D:324:GLU:CG	1:D:325:ILE:N	2.44	0.55
1:E:162:VAL:HG22	1:E:213:VAL:O	2.07	0.55
1:E:302:GLN:O	1:E:309:GLU:O	2.24	0.55
1:F:179:GLU:CG	1:F:216:LYS:HD2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:353:PHE:CE1	1:F:357:LEU:CD2	2.90	0.55
1:G:291:PHE:CD1	1:G:347:LYS:NZ	2.74	0.55
1:A:113:ARG:NH2	1:D:115:VAL:N	2.55	0.55
1:A:144:ARG:HG2	1:A:145:SER:N	2.22	0.55
1:A:278:GLN:HG3	1:A:279:LYS:N	2.22	0.55
1:B:352:ARG:O	1:B:355:ARG:HB2	2.07	0.55
1:C:160:GLU:O	1:C:214:LYS:HA	2.06	0.55
1:C:259:LYS:O	1:C:260:TRP:C	2.45	0.55
1:C:260:TRP:NE1	2:C:401:CMP:H2'	2.16	0.55
1:D:317:GLY:O	1:D:320:ASP:HB2	2.06	0.55
1:E:175:ILE:HG22	1:E:221:LEU:CD2	2.37	0.55
1:E:230:ARG:CG	1:E:234:MET:HE1	2.35	0.55
1:E:282:VAL:O	1:E:285:GLU:CG	2.47	0.55
1:F:251:VAL:CG1	1:F:254:LEU:CD2	2.66	0.55
1:G:149:ASP:OD1	1:H:120:TYR:N	2.39	0.55
1:G:149:ASP:OD1	1:H:120:TYR:HB2	2.06	0.55
1:G:300:VAL:CG1	1:G:335:ALA:HB1	2.36	0.55
1:H:175:ILE:CD1	1:H:194:GLU:CA	2.85	0.55
1:H:196:GLY:HA2	1:H:355:ARG:HH21	1.70	0.55
1:A:111:TYR:CE2	1:A:113:ARG:N	2.75	0.55
1:A:151:MET:HA	1:A:224:ILE:HG22	1.88	0.55
1:A:175:ILE:HA	1:A:221:LEU:HD21	1.83	0.55
1:B:139:LEU:CD2	1:B:147:ILE:HD13	2.36	0.55
1:C:280:ILE:HD12	1:C:281:VAL:HG23	1.88	0.55
1:D:353:PHE:HE1	1:D:357:LEU:HD22	1.61	0.55
1:E:265:VAL:HG12	1:E:269:LEU:CG	2.36	0.55
1:H:300:VAL:CG2	1:H:314:GLY:O	2.55	0.55
1:A:301:LEU:CB	1:A:310:PHE:HE2	1.95	0.54
1:A:328:LEU:CD2	1:A:365:LYS:HE3	2.34	0.54
1:B:253:ILE:O	1:B:255:GLU:N	2.40	0.54
1:C:179:GLU:CG	1:C:216:LYS:HD2	2.32	0.54
1:G:188:TRP:CH2	1:G:190:THR:HA	2.42	0.54
1:A:115:VAL:CG2	1:D:111:TYR:CD2	2.90	0.54
1:A:253:ILE:CG2	1:A:321:TYR:HE2	2.21	0.54
1:A:325:ILE:CD1	1:A:334:ALA:HB3	2.37	0.54
1:B:134:VAL:HG11	1:B:268:ALA:CA	2.33	0.54
1:B:368:ILE:O	1:B:371:TYR:HB2	2.08	0.54
1:C:246:GLU:O	1:C:248:LEU:N	2.40	0.54
1:C:329:MET:CE	1:C:329:MET:CA	2.81	0.54
1:D:175:ILE:HD11	1:D:193:GLY:O	2.07	0.54
1:E:270:GLU:HB2	1:E:271:PRO:CD	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:289:GLU:CG	1:E:347:LYS:NZ	2.66	0.54
1:E:318:PRO:O	1:E:319:SER:HB3	2.07	0.54
1:F:211:ASP:OD1	1:F:211:ASP:N	2.39	0.54
1:F:300:VAL:O	1:F:312:GLU:HA	2.07	0.54
1:G:198:PHE:CD1	1:G:198:PHE:N	2.73	0.54
1:H:172:PHE:CD2	1:H:224:ILE:HD11	2.43	0.54
1:A:120:TYR:HD2	1:A:120:TYR:O	1.86	0.54
1:A:177:GLN:HA	1:A:194:GLU:HG3	1.88	0.54
1:D:153:PRO:CA	1:D:222:TRP:HZ3	2.20	0.54
1:B:131:GLU:C	1:B:133:ASN:N	2.59	0.54
1:B:204:ILE:HG23	1:B:234:MET:SD	2.47	0.54
1:C:120:TYR:CD1	1:D:148:PHE:HB3	2.37	0.54
1:C:135:LEU:CD1	1:C:136:PHE:N	2.71	0.54
1:C:363:ILE:O	1:C:366:ARG:CG	2.54	0.54
1:D:247:PHE:CZ	1:D:294:LEU:HA	2.41	0.54
1:D:357:LEU:O	1:D:360:CYS:HB2	2.08	0.54
1:D:361:SER:C	1:D:365:LYS:NZ	2.57	0.54
1:E:280:ILE:HD12	1:E:281:VAL:CG2	2.37	0.54
1:F:153:PRO:CB	1:F:222:TRP:HZ3	2.19	0.54
1:F:253:ILE:HG21	1:F:321:TYR:CE2	2.42	0.54
1:F:260:TRP:CG	2:F:401:CMP:N7	2.75	0.54
1:F:325:ILE:O	1:F:328:LEU:N	2.41	0.54
1:G:116:ILE:CB	1:G:118:LYS:NZ	2.71	0.54
1:A:164:GLN:HA	1:A:212:THR:CG2	2.38	0.54
1:A:294:LEU:O	1:A:295:GLU:HG3	2.07	0.54
1:B:173:TYR:CD2	1:B:198:PHE:CE1	2.94	0.54
1:C:110:SER:CB	1:F:114:LYS:NZ	2.71	0.54
1:C:171:ASN:OD1	1:C:225:ASP:HA	2.07	0.54
1:E:220:LYS:O	1:E:221:LEU:HD23	2.08	0.54
1:E:226:ARG:NH1	1:E:226:ARG:CG	2.61	0.54
1:E:348:LEU:CD2	1:E:356:VAL:CG2	2.86	0.54
1:E:368:ILE:O	1:E:371:TYR:HB2	2.07	0.54
1:F:130:ILE:CD1	1:F:151:MET:CE	2.85	0.54
1:F:182:VAL:O	1:F:182:VAL:CG2	2.45	0.54
1:G:260:TRP:CE2	2:G:401:CMP:C8	2.90	0.54
1:G:363:ILE:O	1:G:366:ARG:HG2	2.08	0.54
1:H:164:GLN:HA	1:H:212:THR:HG22	1.89	0.54
1:H:291:PHE:HD2	1:H:322:PHE:CZ	2.20	0.54
1:H:295:GLU:HG2	1:H:318:PRO:CG	2.37	0.54
1:A:175:ILE:HD11	1:A:194:GLU:CA	2.37	0.54
1:A:316:LEU:CB	1:A:320:ASP:OD2	2.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:GLU:HG3	1:B:347:LYS:HZ1	1.71	0.54
1:C:131:GLU:O	1:C:133:ASN:N	2.40	0.54
1:C:246:GLU:O	1:C:249:SER:N	2.40	0.54
1:C:247:PHE:C	1:C:247:PHE:HD2	2.08	0.54
1:C:327:LEU:HD23	1:C:353:PHE:CD2	2.42	0.54
1:E:175:ILE:HD11	1:E:193:GLY:O	2.07	0.54
1:F:280:ILE:HD13	1:F:322:PHE:HZ	1.68	0.54
1:F:365:LYS:C	1:F:368:ILE:HG13	2.26	0.54
1:H:188:TRP:CZ3	1:H:190:THR:O	2.60	0.54
1:B:120:TYR:CE2	1:B:124:ALA:HB2	2.41	0.54
1:B:147:ILE:HG23	1:B:232:ILE:CD1	2.38	0.54
1:B:350:ARG:O	1:B:353:PHE:N	2.40	0.54
1:C:211:ASP:OD1	1:C:211:ASP:N	2.41	0.54
1:D:262:ARG:HA	1:D:265:VAL:CG2	2.38	0.54
1:D:300:VAL:HG13	1:D:314:GLY:H	1.72	0.54
1:E:265:VAL:O	1:E:269:LEU:CG	2.42	0.54
1:E:280:ILE:CD1	1:E:281:VAL:CG2	2.86	0.54
1:F:365:LYS:HA	1:F:368:ILE:CG1	2.38	0.54
1:G:183:TYR:HE1	1:G:188:TRP:HB2	1.70	0.54
1:G:230:ARG:NH1	1:G:234:MET:CE	2.70	0.54
1:G:255:GLU:OE1	1:G:255:GLU:CA	2.44	0.54
1:A:113:ARG:NH2	1:D:115:VAL:CG1	2.68	0.54
1:A:139:LEU:HB3	1:A:143:GLU:HB2	1.90	0.54
1:A:265:VAL:O	1:A:269:LEU:HG	2.08	0.54
1:A:273:GLN:HB3	1:A:344:LYS:HA	1.89	0.54
1:A:365:LYS:O	1:A:368:ILE:CG1	2.45	0.54
1:C:115:VAL:HA	1:C:149:ASP:CB	2.27	0.54
1:D:151:MET:HA	1:D:224:ILE:CG2	2.37	0.54
1:E:165:GLN:HG2	1:E:166:GLY:N	2.22	0.54
1:E:182:VAL:O	1:E:182:VAL:CG2	2.45	0.54
1:E:299:ALA:HB3	1:E:338:VAL:HG12	1.89	0.54
1:G:130:ILE:HG23	1:G:131:GLU:N	2.23	0.54
1:G:201:LEU:H	1:G:201:LEU:HD12	1.72	0.54
1:G:201:LEU:HD13	2:G:401:CMP:H2'	1.89	0.54
1:G:251:VAL:CG1	1:G:254:LEU:CD2	2.78	0.54
1:G:282:VAL:O	1:G:285:GLU:CG	2.56	0.54
1:H:300:VAL:O	1:H:312:GLU:CB	2.55	0.54
1:B:152:PHE:CD2	1:B:152:PHE:C	2.77	0.54
1:B:360:CYS:O	1:B:364:LEU:HD23	2.08	0.54
1:C:175:ILE:CD1	1:C:194:GLU:HA	2.35	0.54
1:C:246:GLU:C	1:C:248:LEU:N	2.60	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:147:ILE:HG23	1:D:232:ILE:HD13	1.89	0.54
1:E:226:ARG:HH11	1:E:226:ARG:CG	2.02	0.54
1:E:263:LEU:O	1:E:267:ASP:N	2.34	0.54
1:E:280:ILE:CG1	1:E:281:VAL:HG23	2.37	0.54
1:E:366:ARG:CG	1:E:367:ASN:N	2.70	0.54
1:F:120:TYR:C	1:F:120:TYR:CD2	2.81	0.54
1:F:188:TRP:CZ3	1:F:190:THR:C	2.81	0.54
1:F:246:GLU:C	1:F:248:LEU:N	2.57	0.54
1:H:152:PHE:CD2	1:H:152:PHE:N	2.76	0.54
1:H:172:PHE:O	1:H:224:ILE:HD12	2.08	0.54
1:H:230:ARG:CZ	1:H:234:MET:HE3	2.38	0.54
1:H:252:SER:OG	1:H:253:ILE:HG23	2.08	0.54
1:H:270:GLU:OE1	1:H:347:LYS:HB2	2.08	0.54
1:H:324:GLU:HB2	1:H:364:LEU:HD13	1.90	0.54
1:B:247:PHE:CZ	1:B:294:LEU:HA	2.43	0.54
1:C:112:VAL:HB	1:C:231:ARG:NH2	2.23	0.54
1:C:202:ALA:HB1	1:C:207:THR:O	2.08	0.54
1:C:279:LYS:CE	1:C:336:THR:HG21	2.37	0.54
1:D:198:PHE:HD1	1:D:198:PHE:N	2.05	0.54
1:D:260:TRP:CD1	2:D:401:CMP:C5	2.96	0.54
1:E:285:GLU:OE1	1:E:285:GLU:HA	2.07	0.54
1:E:361:SER:O	1:E:364:LEU:HG	2.08	0.54
1:F:201:LEU:HD13	2:F:401:CMP:H2'	1.89	0.54
1:F:230:ARG:HG2	1:F:230:ARG:NH1	2.23	0.54
1:G:289:GLU:HG2	1:G:347:LYS:HZ3	1.73	0.54
1:H:165:GLN:HG2	1:H:166:GLY:N	2.21	0.54
1:H:245:GLU:OE1	1:H:246:GLU:N	2.40	0.54
1:H:273:GLN:HG3	1:H:344:LYS:HD2	1.90	0.54
1:H:325:ILE:HG13	1:H:326:ALA:H	1.72	0.54
1:A:153:PRO:HB3	1:A:222:TRP:HZ3	1.64	0.53
1:A:224:ILE:HD13	1:A:224:ILE:H	1.72	0.53
1:A:269:LEU:HD22	1:A:346:VAL:HG22	1.88	0.53
1:B:247:PHE:C	1:B:247:PHE:CD2	2.81	0.53
1:B:375:VAL:C	1:C:306:GLU:HA	2.28	0.53
1:C:118:LYS:O	1:D:117:PRO:O	2.26	0.53
1:C:328:LEU:CD2	1:C:365:LYS:HE3	2.37	0.53
1:C:365:LYS:CA	1:C:368:ILE:HG13	2.37	0.53
1:D:175:ILE:HG22	1:D:221:LEU:HD21	1.89	0.53
1:E:116:ILE:CG2	1:E:118:LYS:NZ	2.70	0.53
1:E:135:LEU:HD12	1:E:135:LEU:N	2.23	0.53
1:E:173:TYR:CD2	1:E:198:PHE:CZ	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:274:PHE:CD2	1:F:280:ILE:HG22	2.43	0.53
1:F:316:LEU:HA	1:F:320:ASP:OD2	2.08	0.53
1:H:300:VAL:HA	1:H:336:THR:O	2.08	0.53
1:A:113:ARG:HE	1:D:113:ARG:C	2.10	0.53
1:A:324:GLU:HB2	1:A:364:LEU:HD13	1.90	0.53
1:B:311:VAL:HG12	1:B:312:GLU:N	2.23	0.53
1:E:224:ILE:CD1	1:E:224:ILE:H	2.22	0.53
1:F:175:ILE:HD11	1:F:193:GLY:O	2.08	0.53
1:F:224:ILE:CD1	1:F:224:ILE:H	2.20	0.53
1:F:263:LEU:O	1:F:267:ASP:N	2.35	0.53
1:G:153:PRO:CB	1:G:222:TRP:HZ3	2.19	0.53
1:G:253:ILE:HG13	1:G:254:LEU:CD2	2.38	0.53
1:H:162:VAL:CG2	1:H:213:VAL:O	2.56	0.53
1:H:230:ARG:HG2	1:H:230:ARG:NH1	2.23	0.53
1:A:153:PRO:HA	1:A:222:TRP:CZ3	2.42	0.53
1:A:269:LEU:CB	1:A:346:VAL:HG21	2.36	0.53
1:B:116:ILE:N	1:B:149:ASP:O	2.40	0.53
1:B:272:VAL:HG22	1:B:273:GLN:NE2	2.23	0.53
1:B:315:ARG:O	1:B:316:LEU:HD13	2.09	0.53
1:C:203:LEU:HD13	1:C:226:ARG:HB3	1.89	0.53
1:C:270:GLU:OE1	1:C:347:LYS:HB2	2.08	0.53
1:E:266:ALA:O	1:E:267:ASP:C	2.46	0.53
1:F:289:GLU:HG3	1:F:347:LYS:HZ1	1.64	0.53
1:F:290:PHE:HB2	1:F:327:LEU:HD21	1.90	0.53
1:F:357:LEU:O	1:F:360:CYS:HB2	2.08	0.53
1:G:186:ASN:OD1	1:G:186:ASN:N	2.41	0.53
1:G:263:LEU:O	1:G:267:ASP:N	2.33	0.53
1:G:276:ASP:C	1:G:278:GLN:H	2.09	0.53
1:G:362:ASP:OD1	1:G:362:ASP:N	2.38	0.53
1:G:366:ARG:HG2	1:G:367:ASN:H	1.73	0.53
1:H:118:LYS:NZ	1:H:151:MET:O	2.35	0.53
1:H:253:ILE:O	1:H:255:GLU:N	2.41	0.53
1:H:325:ILE:CD1	1:H:334:ALA:HB3	2.37	0.53
1:A:165:GLN:CA	1:A:211:ASP:O	2.54	0.53
1:B:302:GLN:O	1:B:310:PHE:HB3	2.09	0.53
1:D:200:GLU:OE2	1:D:201:LEU:HD11	2.08	0.53
1:D:229:TYR:O	1:D:233:LEU:HD12	2.08	0.53
1:D:254:LEU:C	1:D:254:LEU:CD2	2.76	0.53
1:E:116:ILE:HG13	1:E:152:PHE:HB3	1.89	0.53
1:E:123:MET:CE	1:F:123:MET:HE3	2.35	0.53
1:F:158:ALA:HB1	1:F:216:LYS:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:159:GLY:O	1:H:243:MET:HE2	2.09	0.53
1:F:362:ASP:N	1:F:362:ASP:OD1	2.41	0.53
1:G:203:LEU:HD12	1:G:229:TYR:HD2	1.73	0.53
1:G:371:TYR:HE1	2:G:402:CMP:C8	2.22	0.53
1:H:114:LYS:HZ2	1:H:115:VAL:N	2.05	0.53
1:H:265:VAL:HG12	1:H:269:LEU:HD11	1.91	0.53
1:A:309:GLU:CG	1:A:310:PHE:N	2.72	0.53
1:B:158:ALA:CB	1:B:216:LYS:O	2.53	0.53
1:C:126:LEU:HD12	1:C:126:LEU:C	2.29	0.53
1:C:210:ALA:N	1:C:211:ASP:OD1	2.42	0.53
1:D:175:ILE:O	1:D:175:ILE:CD1	2.34	0.53
1:E:152:PHE:CE2	1:E:223:GLY:C	2.82	0.53
1:E:198:PHE:HD1	1:E:198:PHE:N	2.06	0.53
1:E:222:TRP:HA	1:E:222:TRP:HE3	1.73	0.53
1:E:247:PHE:HZ	1:E:293:ILE:O	1.92	0.53
1:G:175:ILE:CD1	1:G:193:GLY:O	2.57	0.53
1:H:229:TYR:CE1	1:H:233:LEU:CD1	2.79	0.53
1:A:111:TYR:O	1:A:112:VAL:HG13	2.08	0.53
1:A:293:ILE:HG21	1:A:317:GLY:O	2.08	0.53
1:B:152:PHE:HD2	1:B:152:PHE:H	1.57	0.53
1:B:249:SER:HA	1:B:262:ARG:HH22	1.72	0.53
1:B:285:GLU:HA	1:B:285:GLU:OE1	2.08	0.53
1:B:325:ILE:CD1	1:B:334:ALA:CB	2.86	0.53
1:C:325:ILE:HG13	1:C:326:ALA:N	2.23	0.53
1:D:142:ASN:O	1:D:143:GLU:C	2.43	0.53
1:E:128:LYS:O	1:E:131:GLU:OE1	2.27	0.53
1:E:270:GLU:CB	1:E:271:PRO:CD	2.83	0.53
1:F:247:PHE:CD2	1:F:247:PHE:O	2.61	0.53
1:G:129:ALA:HA	1:G:132:LYS:HE3	1.89	0.53
1:G:280:ILE:HB	1:G:291:PHE:HE2	1.73	0.53
1:H:120:TYR:HD2	1:H:121:LYS:CA	2.20	0.53
1:H:204:ILE:CG2	1:H:205:TYR:HD2	2.18	0.53
1:H:230:ARG:CZ	1:H:234:MET:HE1	2.38	0.53
1:H:279:LYS:HZ3	1:H:336:THR:HG23	1.70	0.53
1:A:260:TRP:CZ2	2:A:401:CMP:C8	2.91	0.53
1:C:300:VAL:HG23	1:C:313:VAL:H	1.73	0.53
1:D:201:LEU:HD13	2:D:401:CMP:H2'	1.90	0.53
1:D:211:ASP:OD1	1:D:211:ASP:N	2.40	0.53
1:E:274:PHE:CD2	1:E:343:LEU:HD23	2.43	0.53
1:F:203:LEU:HD22	1:F:226:ARG:CG	2.38	0.53
1:G:135:LEU:CD1	1:G:136:PHE:N	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:129:ALA:HA	1:H:132:LYS:HE3	1.90	0.53
1:H:134:VAL:O	1:H:137:SER:HB3	2.08	0.53
1:A:118:LYS:NZ	1:A:151:MET:O	2.36	0.53
1:A:130:ILE:HD13	1:A:151:MET:CE	2.38	0.53
1:B:157:ILE:HB	1:B:218:ASN:OD1	2.08	0.53
1:B:233:LEU:O	1:B:234:MET:C	2.47	0.53
1:C:134:VAL:HG11	1:C:268:ALA:CA	2.24	0.53
1:C:229:TYR:CE1	1:C:233:LEU:CD1	2.81	0.53
1:C:253:ILE:C	1:C:255:GLU:H	2.11	0.53
1:D:203:LEU:HD22	1:D:226:ARG:CB	2.38	0.53
1:D:260:TRP:CD1	2:D:401:CMP:C4	2.96	0.53
1:D:294:LEU:O	1:D:295:GLU:HG3	2.09	0.53
1:E:205:TYR:HD2	1:E:205:TYR:N	2.07	0.53
1:E:273:GLN:HB2	1:E:343:LEU:O	2.09	0.53
1:E:289:GLU:CG	1:E:347:LYS:HZ1	2.22	0.53
1:E:325:ILE:HG12	2:E:402:CMP:P	2.49	0.53
1:F:297:SER:O	1:F:340:ARG:HB2	2.08	0.53
1:F:328:LEU:HD23	1:F:365:LYS:HE3	1.90	0.53
1:G:205:TYR:HD2	1:G:205:TYR:N	2.06	0.53
1:H:139:LEU:N	1:H:139:LEU:CD1	2.69	0.53
1:H:140:ASP:C	1:H:140:ASP:OD1	2.47	0.53
1:A:291:PHE:HB2	1:A:322:PHE:CE1	2.44	0.53
1:B:261:GLU:O	1:B:262:ARG:C	2.47	0.53
1:B:261:GLU:O	1:B:265:VAL:HG23	2.08	0.53
1:B:321:TYR:C	1:B:321:TYR:HD1	2.09	0.53
1:C:204:ILE:HG21	1:C:205:TYR:CE2	2.44	0.53
1:D:180:MET:HB2	1:D:192:VAL:HG12	1.91	0.53
1:D:233:LEU:CD1	1:D:233:LEU:N	2.46	0.53
1:D:371:TYR:CZ	2:D:402:CMP:C8	2.91	0.53
1:E:203:LEU:HD13	1:E:226:ARG:CB	2.37	0.53
1:F:203:LEU:CD1	1:F:229:TYR:HD2	2.22	0.53
1:G:116:ILE:HG21	1:G:118:LYS:NZ	2.22	0.53
1:H:147:ILE:CG1	1:H:148:PHE:N	2.72	0.53
1:H:220:LYS:C	1:H:221:LEU:HD23	2.28	0.53
1:A:147:ILE:HG22	1:A:232:ILE:HD13	1.90	0.53
1:B:291:PHE:CE2	1:B:347:LYS:NZ	2.77	0.53
1:C:135:LEU:CD1	1:C:136:PHE:H	2.20	0.53
1:C:203:LEU:HD12	1:C:229:TYR:CD2	2.44	0.53
1:C:248:LEU:HD21	1:C:265:VAL:CG1	2.39	0.53
1:C:253:ILE:HG13	1:C:254:LEU:HD23	1.90	0.53
1:C:350:ARG:O	1:C:353:PHE:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:138:HIS:H	1:D:138:HIS:HD1	1.57	0.53
1:D:175:ILE:CD1	1:D:195:GLY:H	2.22	0.53
1:F:131:GLU:O	1:F:132:LYS:C	2.44	0.53
1:F:153:PRO:CA	1:F:222:TRP:HZ3	2.21	0.53
1:F:235:GLY:O	1:F:236:SER:C	2.46	0.53
1:G:353:PHE:CE1	1:G:357:LEU:HD22	2.44	0.53
1:H:300:VAL:O	1:H:312:GLU:HA	2.09	0.53
1:H:313:VAL:CG1	1:H:314:GLY:N	2.71	0.53
1:A:178:GLY:HA3	1:A:219:VAL:CG1	2.17	0.52
1:A:182:VAL:O	1:A:182:VAL:CG2	2.51	0.52
1:A:356:VAL:CG2	1:A:357:LEU:N	2.71	0.52
1:B:133:ASN:C	1:B:133:ASN:OD1	2.47	0.52
1:B:161:THR:OG1	1:B:214:LYS:NZ	2.31	0.52
1:B:177:GLN:O	1:B:219:VAL:HB	2.08	0.52
1:D:159:GLY:O	1:F:243:MET:HE2	2.09	0.52
1:D:272:VAL:HG22	1:D:273:GLN:H	1.74	0.52
1:F:203:LEU:HD22	1:F:226:ARG:CB	2.39	0.52
1:F:254:LEU:HB2	1:F:257:LEU:HD12	1.91	0.52
1:F:329:MET:HA	1:F:329:MET:HE2	1.91	0.52
1:G:196:GLY:HA2	1:G:355:ARG:CZ	2.37	0.52
1:G:280:ILE:HD12	1:G:281:VAL:HG23	1.90	0.52
1:H:111:TYR:HE2	1:H:112:VAL:HG12	1.69	0.52
1:C:120:TYR:CD2	1:C:121:LYS:HA	2.41	0.52
1:D:139:LEU:N	1:D:139:LEU:CD1	2.65	0.52
1:G:122:THR:O	1:G:125:ALA:HB3	2.09	0.52
1:G:171:ASN:H	1:G:209:ARG:HH22	1.58	0.52
1:A:120:TYR:HD2	1:A:121:LYS:N	2.07	0.52
1:A:130:ILE:CD1	1:A:151:MET:HE3	2.39	0.52
1:A:233:LEU:H	1:A:233:LEU:CD1	2.00	0.52
1:A:253:ILE:CG2	1:A:321:TYR:CE2	2.93	0.52
1:C:152:PHE:CD2	1:C:152:PHE:C	2.81	0.52
1:C:175:ILE:CD1	1:C:195:GLY:N	2.73	0.52
1:C:230:ARG:CZ	1:C:234:MET:HE3	2.39	0.52
1:C:284:GLY:HA2	1:C:332:PRO:HB3	1.88	0.52
1:C:352:ARG:HA	1:C:355:ARG:HB2	1.91	0.52
1:D:280:ILE:HD11	1:D:322:PHE:CE2	2.43	0.52
1:E:164:GLN:O	1:E:167:ASP:HB2	2.10	0.52
1:F:224:ILE:HD13	1:F:224:ILE:C	2.28	0.52
1:F:280:ILE:HB	1:F:291:PHE:HE2	1.74	0.52
1:F:282:VAL:O	1:F:285:GLU:HG3	2.09	0.52
1:G:130:ILE:CD1	1:G:151:MET:CE	2.87	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:LEU:O	1:A:234:MET:C	2.48	0.52
1:A:365:LYS:O	1:A:368:ILE:N	2.32	0.52
1:B:225:ASP:OD1	1:B:225:ASP:N	2.32	0.52
1:B:247:PHE:HE1	1:B:294:LEU:CA	2.12	0.52
1:B:253:ILE:HG13	1:B:254:LEU:CG	2.40	0.52
1:B:328:LEU:HD22	1:B:365:LYS:HE3	1.90	0.52
1:C:301:LEU:HD12	1:C:336:THR:O	2.10	0.52
1:E:253:ILE:CG2	1:E:321:TYR:HE2	2.21	0.52
1:F:262:ARG:HA	1:F:265:VAL:HG21	1.91	0.52
1:G:182:VAL:CG2	1:G:190:THR:O	2.41	0.52
1:G:280:ILE:HD11	1:G:322:PHE:CE2	2.39	0.52
1:H:300:VAL:HG23	1:H:314:GLY:O	2.09	0.52
1:A:154:VAL:CG1	1:A:221:LEU:HB2	2.28	0.52
1:B:316:LEU:HD12	1:B:320:ASP:OD2	2.10	0.52
1:C:229:TYR:HE1	1:C:233:LEU:HD13	1.70	0.52
1:D:246:GLU:O	1:D:248:LEU:N	2.42	0.52
1:D:280:ILE:HD11	1:D:322:PHE:HE2	1.74	0.52
1:E:162:VAL:HG23	1:E:163:ILE:H	1.75	0.52
1:E:239:ARG:HD3	1:G:157:ILE:HG12	1.91	0.52
1:F:348:LEU:HD21	1:F:356:VAL:CG2	2.33	0.52
1:G:211:ASP:OD2	2:G:401:CMP:C5'	2.53	0.52
1:G:318:PRO:O	1:G:319:SER:HB3	2.10	0.52
1:G:357:LEU:HD12	1:G:357:LEU:N	2.16	0.52
1:H:125:ALA:O	1:H:128:LYS:HB3	2.09	0.52
1:H:253:ILE:C	1:H:255:GLU:H	2.13	0.52
1:B:129:ALA:HA	1:B:132:LYS:HE3	1.92	0.52
1:B:183:TYR:CD1	1:B:188:TRP:CB	2.92	0.52
1:B:198:PHE:CD1	1:B:198:PHE:N	2.71	0.52
1:C:183:TYR:HE1	1:C:188:TRP:HB2	1.72	0.52
1:C:230:ARG:NH1	1:C:234:MET:HE3	2.25	0.52
1:C:279:LYS:HE3	1:C:282:VAL:HG22	1.91	0.52
1:D:156:PHE:HE2	1:D:162:VAL:HG12	1.61	0.52
1:D:182:VAL:CG2	1:D:190:THR:H	2.22	0.52
1:D:186:ASN:OD1	1:D:186:ASN:N	2.41	0.52
1:F:161:THR:CA	1:F:214:LYS:HD2	2.30	0.52
1:G:327:LEU:HD23	1:G:353:PHE:CZ	2.45	0.52
1:H:272:VAL:N	1:H:345:CYS:O	2.42	0.52
1:H:298:ALA:N	1:H:316:LEU:O	2.42	0.52
1:A:204:ILE:HD13	1:A:238:LEU:HD11	1.91	0.52
1:A:247:PHE:CE1	1:A:294:LEU:HB3	2.45	0.52
1:A:291:PHE:CD1	1:A:347:LYS:NZ	2.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:131:GLU:H	1:D:131:GLU:CD	2.13	0.52
1:E:241:ARG:O	1:E:242:LYS:C	2.47	0.52
1:E:270:GLU:OE1	1:E:270:GLU:N	2.42	0.52
1:F:112:VAL:CG1	1:F:113:ARG:H	2.00	0.52
1:F:164:GLN:O	1:F:167:ASP:HB2	2.10	0.52
1:G:285:GLU:OE1	1:G:285:GLU:CA	2.53	0.52
1:H:175:ILE:CD1	1:H:195:GLY:N	2.73	0.52
1:A:205:TYR:CD2	1:A:205:TYR:N	2.76	0.52
1:B:180:MET:O	1:B:191:SER:HA	2.10	0.52
1:B:204:ILE:HG22	1:B:205:TYR:HD2	1.74	0.52
1:B:280:ILE:CD1	1:B:337:VAL:HB	2.39	0.52
1:B:322:PHE:N	1:B:322:PHE:CD1	2.76	0.52
1:C:111:TYR:C	1:C:112:VAL:HG13	2.30	0.52
1:C:119:ASP:HA	1:D:117:PRO:HA	1.92	0.52
1:C:269:LEU:HB2	1:C:346:VAL:CG2	2.28	0.52
1:C:300:VAL:HG22	1:C:312:GLU:OE2	2.10	0.52
1:D:182:VAL:HG12	1:D:213:VAL:CG2	2.27	0.52
1:D:324:GLU:HB2	1:D:364:LEU:HD13	1.92	0.52
1:E:176:ASP:O	1:E:194:GLU:HG2	2.09	0.52
1:E:252:SER:O	1:E:255:GLU:HB2	2.10	0.52
1:E:260:TRP:CD2	2:E:401:CMP:N7	2.77	0.52
1:F:248:LEU:HD11	1:F:265:VAL:HG11	1.92	0.52
1:G:205:TYR:CD2	1:G:205:TYR:N	2.78	0.52
1:H:266:ALA:HA	1:H:269:LEU:CD1	2.37	0.52
1:A:113:ARG:CZ	1:D:114:LYS:C	2.78	0.52
1:A:182:VAL:CG2	1:A:190:THR:H	2.23	0.52
1:A:327:LEU:HD23	1:A:353:PHE:CD1	2.45	0.52
1:B:173:TYR:HD1	1:B:223:GLY:CA	2.23	0.52
1:C:158:ALA:HA	1:C:217:THR:O	2.09	0.52
1:C:161:THR:CA	1:C:214:LYS:HD2	2.32	0.52
1:C:198:PHE:HD1	1:C:198:PHE:N	2.07	0.52
1:C:204:ILE:HG21	1:C:205:TYR:HE2	1.75	0.52
1:D:126:LEU:C	1:D:126:LEU:CD1	2.68	0.52
1:D:366:ARG:O	1:D:369:GLN:HB2	2.09	0.52
1:E:121:LYS:O	1:E:125:ALA:N	2.36	0.52
1:E:153:PRO:CA	1:E:222:TRP:CZ3	2.93	0.52
1:F:130:ILE:HG21	1:F:148:PHE:CE2	2.43	0.52
1:F:131:GLU:C	1:F:133:ASN:N	2.60	0.52
1:F:253:ILE:HD13	1:F:321:TYR:CD2	2.45	0.52
1:F:272:VAL:CA	1:F:273:GLN:NE2	2.73	0.52
1:F:273:GLN:CB	1:F:344:LYS:HA	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:283:GLN:HG3	1:F:335:ALA:N	2.25	0.52
1:G:274:PHE:HD2	1:G:343:LEU:HD23	1.75	0.52
1:H:130:ILE:CD1	1:H:151:MET:CE	2.88	0.52
1:H:130:ILE:HD12	1:H:136:PHE:CE2	2.45	0.52
1:H:135:LEU:HD13	1:H:136:PHE:CD1	2.45	0.52
1:A:130:ILE:HD13	1:A:151:MET:HE3	1.92	0.52
1:A:175:ILE:HG21	1:A:180:MET:HG3	1.92	0.52
1:B:176:ASP:O	1:B:194:GLU:HG2	2.10	0.52
1:B:200:GLU:CG	1:B:201:LEU:HD12	2.36	0.52
1:C:113:ARG:HG2	1:F:112:VAL:HG11	1.88	0.52
1:C:262:ARG:O	1:C:265:VAL:HB	2.11	0.52
1:D:325:ILE:CD1	1:D:334:ALA:HB3	2.39	0.52
1:E:293:ILE:HG22	1:E:320:ASP:O	2.10	0.52
1:F:325:ILE:HD11	1:F:334:ALA:H	1.75	0.52
1:F:325:ILE:CD1	1:F:334:ALA:CB	2.88	0.52
1:H:157:ILE:HD12	1:H:157:ILE:C	2.26	0.52
1:H:175:ILE:HD11	1:H:195:GLY:N	2.25	0.52
1:H:272:VAL:HG22	1:H:273:GLN:H	1.75	0.52
1:H:285:GLU:HB3	1:H:286:PRO:CD	2.39	0.52
1:A:121:LYS:O	1:A:124:ALA:N	2.44	0.51
1:B:139:LEU:HD21	1:B:147:ILE:CD1	2.40	0.51
1:B:151:MET:HA	1:B:224:ILE:HG22	1.91	0.51
1:B:211:ASP:OD2	2:B:401:CMP:O4'	2.27	0.51
1:B:366:ARG:CG	1:B:367:ASN:N	2.72	0.51
1:C:110:SER:CA	1:F:114:LYS:HZ3	2.24	0.51
1:C:116:ILE:HB	1:C:118:LYS:NZ	2.26	0.51
1:D:112:VAL:HB	1:D:113:ARG:HG3	1.92	0.51
1:D:135:LEU:HD13	1:D:136:PHE:CD1	2.45	0.51
1:D:325:ILE:O	1:D:328:LEU:N	2.43	0.51
1:E:129:ALA:CB	1:E:222:TRP:HE1	2.23	0.51
1:G:253:ILE:HG13	1:G:254:LEU:N	2.25	0.51
1:H:261:GLU:O	1:H:265:VAL:HG23	2.09	0.51
1:H:324:GLU:HB2	1:H:364:LEU:CD1	2.40	0.51
1:A:174:VAL:HA	1:A:196:GLY:O	2.11	0.51
1:B:136:PHE:HE1	1:B:233:LEU:CD2	2.23	0.51
1:B:362:ASP:N	1:B:365:LYS:HZ2	2.07	0.51
1:C:152:PHE:HD2	1:C:152:PHE:H	1.59	0.51
1:C:157:ILE:O	1:C:158:ALA:O	2.28	0.51
1:C:165:GLN:HG2	1:C:166:GLY:N	2.24	0.51
1:C:265:VAL:CG1	1:C:269:LEU:CD2	2.83	0.51
1:C:311:VAL:HG23	1:C:312:GLU:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:113:ARG:HH22	1:D:142:ASN:HD21	1.58	0.51
1:D:266:ALA:O	1:D:267:ASP:C	2.48	0.51
1:D:293:ILE:CG2	1:D:318:PRO:HA	2.40	0.51
1:E:120:TYR:HD2	1:E:121:LYS:HA	1.75	0.51
1:E:161:THR:HA	1:E:214:LYS:CD	2.35	0.51
1:F:173:TYR:CD2	1:F:198:PHE:CZ	2.98	0.51
1:F:327:LEU:HD23	1:F:353:PHE:CE2	2.44	0.51
1:G:154:VAL:O	1:G:221:LEU:N	2.30	0.51
1:G:203:LEU:HD22	1:G:226:ARG:CB	2.39	0.51
1:G:247:PHE:CE1	1:G:294:LEU:CA	2.88	0.51
1:G:371:TYR:CE1	2:G:402:CMP:C8	2.93	0.51
1:A:152:PHE:CD2	1:A:152:PHE:C	2.78	0.51
1:A:200:GLU:HG2	1:A:201:LEU:N	2.24	0.51
1:A:366:ARG:CG	1:A:367:ASN:N	2.72	0.51
1:B:164:GLN:HA	1:B:212:THR:CG2	2.40	0.51
1:C:162:VAL:CG2	1:C:213:VAL:O	2.58	0.51
1:D:247:PHE:HE1	1:D:294:LEU:CB	2.23	0.51
1:E:262:ARG:HA	1:E:265:VAL:HG21	1.93	0.51
1:F:174:VAL:CG1	1:F:222:TRP:HB2	2.41	0.51
1:F:241:ARG:O	1:F:242:LYS:C	2.45	0.51
1:F:310:PHE:O	1:F:311:VAL:CG1	2.58	0.51
1:G:201:LEU:O	1:G:204:ILE:N	2.44	0.51
1:A:135:LEU:CD1	1:A:136:PHE:CG	2.94	0.51
1:A:269:LEU:CB	1:A:346:VAL:CG2	2.80	0.51
1:B:239:ARG:O	1:B:240:LYS:C	2.46	0.51
1:C:114:LYS:HD2	1:C:225:ASP:OD1	2.11	0.51
1:C:135:LEU:HD13	1:C:136:PHE:CG	2.45	0.51
1:C:243:MET:HE2	1:E:159:GLY:C	2.31	0.51
1:C:348:LEU:HD21	1:C:356:VAL:CG2	2.39	0.51
1:E:111:TYR:CD2	1:E:112:VAL:N	2.65	0.51
1:E:275:GLU:O	1:E:278:GLN:HB3	2.10	0.51
1:F:198:PHE:HD1	1:F:198:PHE:O	1.93	0.51
1:G:174:VAL:HG13	1:G:222:TRP:HB2	1.92	0.51
1:G:253:ILE:CD1	1:G:321:TYR:CD2	2.92	0.51
1:H:294:LEU:O	1:H:295:GLU:CG	2.59	0.51
1:A:135:LEU:HD12	1:A:135:LEU:N	2.24	0.51
1:A:290:PHE:HB2	1:A:327:LEU:HD21	1.92	0.51
1:A:296:GLY:O	1:A:318:PRO:HD3	2.09	0.51
1:A:371:TYR:CD1	2:A:402:CMP:C5	2.98	0.51
1:C:110:SER:C	1:F:114:LYS:HD3	2.30	0.51
1:C:120:TYR:CE1	1:D:148:PHE:CG	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:130:ILE:HG13	1:C:136:PHE:CG	2.45	0.51
1:C:224:ILE:HD13	1:C:224:ILE:C	2.31	0.51
1:C:279:LYS:CB	1:C:337:VAL:O	2.59	0.51
1:E:109:ALA:HB1	1:H:114:LYS:HE2	1.92	0.51
1:E:140:ASP:N	1:E:143:GLU:OE1	2.42	0.51
1:E:196:GLY:HA2	1:E:355:ARG:CZ	2.35	0.51
1:F:226:ARG:HA	1:F:229:TYR:HB3	1.92	0.51
1:F:266:ALA:O	1:F:268:ALA:N	2.44	0.51
1:G:293:ILE:CG2	1:G:318:PRO:HA	2.41	0.51
1:H:283:GLN:HG3	1:H:334:ALA:C	2.31	0.51
1:A:309:GLU:CG	1:A:310:PHE:H	2.23	0.51
1:A:329:MET:HA	1:A:329:MET:HE3	1.93	0.51
1:A:371:TYR:CE1	2:A:402:CMP:C5	2.98	0.51
1:C:120:TYR:CD2	1:C:120:TYR:O	2.64	0.51
1:C:247:PHE:CE1	1:C:294:LEU:CB	2.93	0.51
1:C:335:ALA:HB3	2:C:402:CMP:H5'1	1.93	0.51
1:D:158:ALA:HB2	1:D:217:THR:C	2.31	0.51
1:E:130:ILE:HD13	1:E:151:MET:CE	2.41	0.51
1:E:211:ASP:OD1	1:E:211:ASP:N	2.43	0.51
1:G:230:ARG:CG	1:G:234:MET:HE1	2.40	0.51
1:G:342:PRO:O	1:G:342:PRO:HG2	2.10	0.51
1:H:311:VAL:HG23	1:H:312:GLU:H	1.76	0.51
1:A:285:GLU:OE1	1:A:285:GLU:CA	2.59	0.51
1:B:325:ILE:HG12	2:B:402:CMP:O3'	2.11	0.51
1:D:134:VAL:O	1:D:137:SER:HB3	2.11	0.51
1:D:173:TYR:CB	1:D:198:PHE:HE1	2.24	0.51
1:D:324:GLU:HG2	1:D:325:ILE:HG23	1.93	0.51
1:E:152:PHE:HD2	1:E:152:PHE:N	2.02	0.51
1:F:144:ARG:O	1:F:147:ILE:HG12	2.11	0.51
1:F:253:ILE:HD13	1:F:321:TYR:CE2	2.46	0.51
1:F:350:ARG:O	1:F:353:PHE:CB	2.53	0.51
1:G:177:GLN:HA	1:G:194:GLU:CG	2.40	0.51
1:G:249:SER:HA	1:G:262:ARG:HH22	1.73	0.51
1:G:265:VAL:C	1:G:269:LEU:HG	2.26	0.51
1:A:246:GLU:O	1:A:248:LEU:N	2.43	0.51
1:A:261:GLU:O	1:A:262:ARG:C	2.49	0.51
1:B:226:ARG:O	1:B:227:ASP:C	2.50	0.51
1:B:260:TRP:NE1	2:B:401:CMP:C4	2.78	0.51
1:C:158:ALA:HA	1:C:215:ALA:HB1	1.92	0.51
1:C:235:GLY:O	1:C:238:LEU:N	2.43	0.51
1:C:365:LYS:HA	1:C:368:ILE:HG13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:165:GLN:CA	1:D:211:ASP:O	2.56	0.51
1:D:261:GLU:O	1:D:264:THR:N	2.44	0.51
1:D:302:GLN:HG3	1:D:313:VAL:CG1	2.40	0.51
1:E:113:ARG:NH1	1:H:112:VAL:HG23	2.25	0.51
1:E:316:LEU:HA	1:E:320:ASP:OD2	2.10	0.51
1:F:182:VAL:CG2	1:F:190:THR:H	2.23	0.51
1:F:274:PHE:HB2	1:F:343:LEU:HB3	1.93	0.51
1:G:224:ILE:CD1	1:G:224:ILE:H	2.23	0.51
1:G:293:ILE:HA	1:G:345:CYS:SG	2.51	0.51
1:H:173:TYR:HB3	1:H:222:TRP:O	2.11	0.51
1:H:255:GLU:OE1	1:H:255:GLU:CA	2.51	0.51
1:A:177:GLN:HA	1:A:194:GLU:CG	2.40	0.51
1:A:183:TYR:HD1	1:A:188:TRP:HB2	1.76	0.51
1:B:253:ILE:C	1:B:255:GLU:N	2.64	0.51
1:C:152:PHE:CD2	1:C:152:PHE:N	2.79	0.51
1:C:190:THR:HG22	1:C:191:SER:N	2.11	0.51
1:D:209:ARG:HD2	2:D:401:CMP:O5'	2.10	0.51
1:E:269:LEU:HB2	1:E:346:VAL:CG2	2.39	0.51
1:E:269:LEU:HB2	1:E:346:VAL:HG21	1.92	0.51
1:E:293:ILE:HG23	1:E:318:PRO:HA	1.91	0.51
1:F:113:ARG:HB3	1:F:146:ASP:OD2	2.11	0.51
1:F:162:VAL:HG23	1:F:163:ILE:H	1.73	0.51
1:G:300:VAL:HG23	1:G:316:LEU:HD11	1.91	0.51
1:H:118:LYS:HE2	1:H:148:PHE:O	2.10	0.51
1:H:186:ASN:N	1:H:186:ASN:OD1	2.43	0.51
1:H:285:GLU:HB2	1:H:333:ARG:HG3	1.92	0.51
1:A:204:ILE:CG2	1:A:205:TYR:CD2	2.92	0.51
1:B:110:SER:O	1:B:111:TYR:HB2	2.10	0.51
1:B:174:VAL:HA	1:B:196:GLY:O	2.10	0.51
1:C:158:ALA:CB	1:C:216:LYS:O	2.55	0.51
1:C:272:VAL:N	1:C:345:CYS:O	2.44	0.51
1:D:157:ILE:HG23	1:F:239:ARG:NH1	2.26	0.51
1:E:269:LEU:HD23	1:E:348:LEU:HD13	1.92	0.51
1:F:296:GLY:CA	1:F:342:PRO:O	2.58	0.51
1:F:331:ARG:HB3	1:F:332:PRO:HD2	1.91	0.51
1:G:116:ILE:HG13	1:G:152:PHE:HB3	1.93	0.51
1:G:135:LEU:HD12	1:G:135:LEU:N	2.26	0.51
1:G:248:LEU:CB	1:G:262:ARG:HH21	2.24	0.51
1:H:251:VAL:CG2	1:H:319:SER:O	2.58	0.51
1:H:280:ILE:HB	1:H:291:PHE:CE2	2.40	0.51
1:H:300:VAL:HG23	1:H:314:GLY:N	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:TYR:C	1:D:115:VAL:HG21	2.27	0.50
1:A:296:GLY:HA3	1:A:343:LEU:HA	1.93	0.50
1:A:366:ARG:HG2	1:A:367:ASN:H	1.75	0.50
1:B:126:LEU:C	1:B:126:LEU:CD1	2.79	0.50
1:B:249:SER:HA	1:B:262:ARG:NH2	2.26	0.50
1:C:265:VAL:HG12	1:C:269:LEU:CD2	2.41	0.50
1:F:116:ILE:N	1:F:149:ASP:O	2.36	0.50
1:H:143:GLU:HB3	1:H:232:ILE:HD11	1.92	0.50
1:H:203:LEU:HD12	1:H:229:TYR:HD2	1.71	0.50
1:H:362:ASP:N	1:H:362:ASP:OD1	2.44	0.50
1:A:161:THR:HG23	1:A:214:LYS:HD3	1.93	0.50
1:A:247:PHE:CE1	1:A:294:LEU:CA	2.85	0.50
1:B:115:VAL:O	1:B:115:VAL:HG23	2.11	0.50
1:B:162:VAL:HG23	1:B:163:ILE:N	2.25	0.50
1:C:157:ILE:O	1:C:160:GLU:HB2	2.11	0.50
1:C:180:MET:O	1:C:191:SER:HA	2.11	0.50
1:C:260:TRP:CD1	2:C:401:CMP:C4	2.99	0.50
1:D:139:LEU:HD21	1:D:147:ILE:CD1	2.41	0.50
1:D:230:ARG:HG2	1:D:230:ARG:HH11	1.75	0.50
1:F:153:PRO:HA	1:F:222:TRP:CE3	2.46	0.50
1:F:300:VAL:HG13	1:F:335:ALA:HB1	1.84	0.50
1:G:268:ALA:O	1:G:352:ARG:NH1	2.44	0.50
1:H:357:LEU:N	1:H:357:LEU:HD12	2.19	0.50
1:H:366:ARG:O	1:H:369:GLN:HB2	2.11	0.50
1:A:130:ILE:CG2	1:A:131:GLU:N	2.74	0.50
1:B:171:ASN:HB3	1:B:224:ILE:O	2.10	0.50
1:C:147:ILE:O	1:C:148:PHE:C	2.48	0.50
1:C:165:GLN:N	1:C:212:THR:CG2	2.50	0.50
1:C:254:LEU:C	1:C:254:LEU:HD12	2.31	0.50
1:D:300:VAL:HG12	1:D:314:GLY:C	2.30	0.50
1:E:131:GLU:N	1:E:131:GLU:CD	2.65	0.50
1:E:158:ALA:HA	1:E:215:ALA:HB1	1.94	0.50
1:E:179:GLU:CG	1:E:216:LYS:HD2	2.42	0.50
1:E:230:ARG:HG2	1:E:230:ARG:HH11	1.76	0.50
1:F:111:TYR:CD2	1:F:111:TYR:C	2.81	0.50
1:F:152:PHE:CE2	1:F:223:GLY:CA	2.91	0.50
1:F:293:ILE:HG21	1:F:317:GLY:O	2.11	0.50
1:G:175:ILE:HG22	1:G:221:LEU:HD21	1.94	0.50
1:G:371:TYR:CD1	2:G:402:CMP:C6	2.99	0.50
1:H:158:ALA:HB2	1:H:218:ASN:N	2.24	0.50
1:H:185:ASN:N	1:H:185:ASN:OD1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:294:LEU:CD1	1:H:294:LEU:C	2.69	0.50
1:A:293:ILE:HG23	1:A:318:PRO:HA	1.93	0.50
1:B:152:PHE:CE2	1:B:223:GLY:C	2.84	0.50
1:B:297:SER:O	1:B:340:ARG:HB2	2.11	0.50
1:B:362:ASP:HA	1:B:365:LYS:NZ	2.26	0.50
1:D:157:ILE:HD13	1:F:243:MET:CE	2.41	0.50
1:D:239:ARG:O	1:D:240:LYS:C	2.49	0.50
1:D:253:ILE:HG13	1:D:254:LEU:CD1	2.24	0.50
1:E:144:ARG:HG2	1:E:145:SER:N	2.26	0.50
1:E:204:ILE:CG2	1:E:205:TYR:HD2	2.21	0.50
1:E:324:GLU:HB2	1:E:364:LEU:CD1	2.40	0.50
1:F:157:ILE:HD11	1:H:243:MET:HE3	1.90	0.50
1:F:269:LEU:HD22	1:F:346:VAL:CG2	2.41	0.50
1:H:253:ILE:HD13	1:H:321:TYR:CE2	2.46	0.50
1:H:259:LYS:CG	1:H:260:TRP:N	2.62	0.50
1:H:260:TRP:CD1	2:H:401:CMP:C4	2.99	0.50
1:A:164:GLN:O	1:A:167:ASP:HB2	2.12	0.50
1:A:239:ARG:NH2	1:C:156:PHE:HE1	2.09	0.50
1:B:182:VAL:CG2	1:B:190:THR:O	2.45	0.50
1:B:281:VAL:CG1	1:B:333:ARG:CG	2.90	0.50
1:C:291:PHE:HB2	1:C:322:PHE:CE1	2.47	0.50
1:C:297:SER:O	1:C:340:ARG:HB2	2.11	0.50
1:D:165:GLN:HG2	1:D:166:GLY:N	2.26	0.50
1:D:173:TYR:CD2	1:D:198:PHE:CE1	2.95	0.50
1:F:230:ARG:HB3	1:F:234:MET:CE	2.41	0.50
1:F:248:LEU:HD11	1:F:265:VAL:CG1	2.41	0.50
1:F:260:TRP:CG	2:F:401:CMP:C5	3.00	0.50
1:F:327:LEU:HD23	1:F:353:PHE:CE1	2.46	0.50
1:G:173:TYR:CD2	1:G:198:PHE:HE1	2.28	0.50
1:H:271:PRO:O	1:H:272:VAL:HB	2.12	0.50
1:B:255:GLU:OE1	1:B:255:GLU:CA	2.45	0.50
1:B:350:ARG:CB	1:B:351:PRO:HD3	2.25	0.50
1:C:153:PRO:CB	1:C:222:TRP:CZ3	2.94	0.50
1:C:173:TYR:CD2	1:C:198:PHE:HE1	2.27	0.50
1:D:157:ILE:HG23	1:F:239:ARG:HH11	1.76	0.50
1:D:269:LEU:CD2	1:D:346:VAL:HG21	2.37	0.50
1:D:280:ILE:CD1	1:D:322:PHE:CZ	2.94	0.50
1:D:285:GLU:OE1	1:D:285:GLU:CA	2.56	0.50
1:D:298:ALA:O	1:D:316:LEU:HD13	2.12	0.50
1:D:300:VAL:HA	1:D:336:THR:O	2.11	0.50
1:E:152:PHE:CD2	1:E:152:PHE:C	2.81	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:269:LEU:HD22	1:F:346:VAL:HG21	1.94	0.50
1:G:356:VAL:CG2	1:G:357:LEU:HD13	2.38	0.50
1:H:324:GLU:O	1:H:328:LEU:CD1	2.58	0.50
1:A:224:ILE:HD13	1:A:224:ILE:C	2.30	0.50
1:A:279:LYS:O	1:A:279:LYS:HG2	2.11	0.50
1:B:112:VAL:HG12	1:B:231:ARG:HE	1.72	0.50
1:D:182:VAL:CG2	1:D:190:THR:O	2.41	0.50
1:D:259:LYS:C	1:D:262:ARG:HG2	2.25	0.50
1:D:309:GLU:O	1:D:311:VAL:HG12	2.12	0.50
1:D:362:ASP:N	1:D:365:LYS:HZ2	2.08	0.50
1:E:205:TYR:CD2	1:E:205:TYR:N	2.79	0.50
1:G:165:GLN:CA	1:G:211:ASP:O	2.57	0.50
1:G:247:PHE:CD2	1:G:247:PHE:O	2.64	0.50
1:G:283:GLN:OE1	1:G:302:GLN:HA	2.12	0.50
1:H:130:ILE:HD12	1:H:136:PHE:CD2	2.46	0.50
1:H:174:VAL:HG13	1:H:222:TRP:HB2	1.93	0.50
1:A:161:THR:CA	1:A:214:LYS:HD2	2.30	0.50
1:B:201:LEU:HD13	2:B:401:CMP:H2'	1.92	0.50
1:B:300:VAL:HG13	1:B:335:ALA:HB1	1.92	0.50
1:B:366:ARG:HG2	1:B:367:ASN:H	1.75	0.50
1:C:121:LYS:HG3	1:C:122:THR:N	2.26	0.50
1:C:211:ASP:OD1	2:C:401:CMP:H5'1	2.12	0.50
1:D:174:VAL:HA	1:D:196:GLY:O	2.12	0.50
1:D:357:LEU:HD12	1:D:357:LEU:N	2.26	0.50
1:D:365:LYS:O	1:D:368:ILE:CG1	2.43	0.50
1:E:147:ILE:O	1:E:148:PHE:C	2.50	0.50
1:E:290:PHE:HB2	1:E:327:LEU:HD21	1.94	0.50
1:E:356:VAL:CG2	1:E:357:LEU:HD13	2.37	0.50
1:F:204:ILE:CG2	1:F:205:TYR:CD2	2.93	0.50
1:F:247:PHE:HE1	1:F:294:LEU:CA	2.16	0.50
1:G:163:ILE:HD12	1:G:213:VAL:HB	1.94	0.50
1:G:272:VAL:HG22	1:G:273:GLN:H	1.77	0.50
1:G:273:GLN:HE21	1:G:273:GLN:H	0.53	0.50
1:G:362:ASP:N	1:G:365:LYS:HZ2	2.09	0.50
1:G:366:ARG:HG2	1:G:367:ASN:N	2.26	0.50
1:A:262:ARG:HA	1:A:265:VAL:HG21	1.93	0.50
1:B:152:PHE:CD2	1:B:152:PHE:N	2.77	0.50
1:B:290:PHE:HB2	1:B:327:LEU:CD2	2.42	0.50
1:B:331:ARG:NH2	1:B:376:SER:CB	2.73	0.50
1:C:114:LYS:HD2	1:C:225:ASP:CG	2.32	0.50
1:C:161:THR:HG23	1:C:214:LYS:HD3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:253:ILE:O	1:C:255:GLU:N	2.45	0.50
1:D:266:ALA:HA	1:D:269:LEU:CD1	2.41	0.50
1:E:110:SER:OG	1:H:115:VAL:HG23	2.12	0.50
1:F:230:ARG:HB3	1:F:234:MET:HE1	1.92	0.50
1:F:273:GLN:HB3	1:F:344:LYS:HA	1.94	0.50
1:G:224:ILE:HD13	1:G:224:ILE:C	2.30	0.50
1:A:163:ILE:HD11	1:A:198:PHE:CZ	2.47	0.49
1:A:247:PHE:CE1	1:A:294:LEU:CB	2.95	0.49
1:A:335:ALA:HB3	2:A:402:CMP:O4'	2.12	0.49
1:B:144:ARG:CG	1:B:145:SER:N	2.75	0.49
1:B:230:ARG:CG	1:B:234:MET:HE1	2.37	0.49
1:B:253:ILE:HD13	1:B:321:TYR:CE2	2.46	0.49
1:D:264:THR:O	1:D:265:VAL:C	2.49	0.49
1:D:278:GLN:HG3	1:D:279:LYS:N	2.23	0.49
1:E:127:ALA:O	1:E:130:ILE:HG22	2.11	0.49
1:E:139:LEU:HD22	1:E:144:ARG:HA	1.93	0.49
1:E:175:ILE:CD1	1:E:193:GLY:O	2.60	0.49
1:G:371:TYR:CD1	2:G:402:CMP:C5	3.00	0.49
1:H:115:VAL:HA	1:H:149:ASP:CB	2.36	0.49
1:A:154:VAL:O	1:A:154:VAL:CG1	2.57	0.49
1:A:239:ARG:O	1:A:240:LYS:C	2.48	0.49
1:A:348:LEU:HD21	1:A:356:VAL:CG2	2.42	0.49
1:B:157:ILE:O	1:B:160:GLU:HB2	2.11	0.49
1:C:186:ASN:N	1:C:186:ASN:OD1	2.43	0.49
1:C:261:GLU:O	1:C:265:VAL:HG23	2.12	0.49
1:D:161:THR:HG23	1:D:214:LYS:HD3	1.94	0.49
1:D:175:ILE:HD12	1:D:195:GLY:H	1.78	0.49
1:D:226:ARG:O	1:D:227:ASP:C	2.51	0.49
1:D:279:LYS:O	1:D:279:LYS:CG	2.60	0.49
1:D:300:VAL:O	1:D:313:VAL:HG13	2.11	0.49
1:E:163:ILE:CD1	1:E:213:VAL:HB	2.42	0.49
1:E:260:TRP:O	1:E:263:LEU:HB2	2.12	0.49
1:G:294:LEU:N	1:G:294:LEU:CD1	2.45	0.49
1:G:327:LEU:HD23	1:G:353:PHE:CD2	2.46	0.49
1:H:253:ILE:HG13	1:H:254:LEU:CG	2.41	0.49
1:H:324:GLU:OE1	1:H:324:GLU:N	2.45	0.49
1:A:274:PHE:CE2	1:A:280:ILE:HG22	2.48	0.49
1:A:318:PRO:O	1:A:319:SER:HB3	2.11	0.49
1:B:139:LEU:HB3	1:B:143:GLU:HB2	1.95	0.49
1:B:140:ASP:OD1	1:B:140:ASP:O	2.31	0.49
1:B:144:ARG:HG2	1:B:145:SER:N	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:129:ALA:HB2	1:C:222:TRP:HE1	1.76	0.49
1:C:144:ARG:O	1:C:145:SER:C	2.49	0.49
1:C:269:LEU:HD23	1:C:348:LEU:HD11	1.92	0.49
1:C:289:GLU:N	1:C:327:LEU:HD11	2.26	0.49
1:C:294:LEU:HD13	1:C:344:LYS:C	2.28	0.49
1:C:333:ARG:NH1	2:C:402:CMP:O1P	2.43	0.49
1:D:144:ARG:O	1:D:147:ILE:N	2.44	0.49
1:D:177:GLN:HA	1:D:194:GLU:CG	2.43	0.49
1:D:251:VAL:O	1:D:254:LEU:CD2	2.58	0.49
1:E:229:TYR:O	1:E:233:LEU:HD12	2.12	0.49
1:F:162:VAL:CG2	1:F:163:ILE:N	2.75	0.49
1:F:165:GLN:HG2	1:F:166:GLY:N	2.26	0.49
1:G:120:TYR:CE1	1:H:148:PHE:CD1	3.00	0.49
1:G:179:GLU:CG	1:G:216:LYS:HD2	2.42	0.49
1:H:116:ILE:N	1:H:149:ASP:O	2.26	0.49
1:H:129:ALA:HB2	1:H:222:TRP:HE1	1.77	0.49
1:H:131:GLU:H	1:H:131:GLU:CD	2.15	0.49
1:H:144:ARG:O	1:H:147:ILE:N	2.45	0.49
1:H:160:GLU:O	1:H:214:LYS:HA	2.12	0.49
1:H:246:GLU:C	1:H:248:LEU:N	2.59	0.49
1:A:135:LEU:CD1	1:A:135:LEU:C	2.78	0.49
1:A:226:ARG:O	1:A:227:ASP:C	2.50	0.49
1:B:135:LEU:HD13	1:B:136:PHE:N	2.28	0.49
1:C:129:ALA:CB	1:C:222:TRP:HE1	2.25	0.49
1:D:356:VAL:HG23	1:D:357:LEU:HD13	1.88	0.49
1:G:175:ILE:HG21	1:G:180:MET:HG3	1.95	0.49
1:G:248:LEU:HB2	1:G:262:ARG:HH21	1.78	0.49
1:H:153:PRO:HA	1:H:222:TRP:CE3	2.46	0.49
1:H:260:TRP:CG	2:H:401:CMP:C8	2.96	0.49
1:A:175:ILE:HD11	1:A:194:GLU:C	2.32	0.49
1:B:120:TYR:HE2	1:B:124:ALA:CB	2.26	0.49
1:B:198:PHE:HD1	1:B:198:PHE:N	2.09	0.49
1:B:200:GLU:OE2	1:B:241:ARG:NH2	2.45	0.49
1:D:210:ALA:N	1:D:211:ASP:OD1	2.46	0.49
1:E:112:VAL:HG12	1:E:231:ARG:HE	1.71	0.49
1:E:113:ARG:H	1:H:112:VAL:HG11	1.77	0.49
1:E:263:LEU:O	1:E:266:ALA:CB	2.57	0.49
1:E:283:GLN:HG3	1:E:335:ALA:N	2.28	0.49
1:F:252:SER:OG	1:F:253:ILE:N	2.42	0.49
1:F:300:VAL:CG1	1:F:335:ALA:CB	2.83	0.49
1:F:366:ARG:O	1:F:369:GLN:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:135:LEU:HD13	1:G:136:PHE:CG	2.47	0.49
1:H:260:TRP:CG	2:H:401:CMP:C5	3.01	0.49
1:A:363:ILE:O	1:A:366:ARG:HG2	2.13	0.49
1:B:224:ILE:HD13	1:B:224:ILE:N	2.25	0.49
1:C:131:GLU:C	1:C:133:ASN:H	2.14	0.49
1:C:177:GLN:HA	1:C:194:GLU:CG	2.42	0.49
1:C:284:GLY:HA2	1:C:332:PRO:CB	2.43	0.49
1:D:116:ILE:CG2	1:D:118:LYS:NZ	2.75	0.49
1:D:280:ILE:HD13	1:D:322:PHE:HZ	1.76	0.49
1:D:297:SER:O	1:D:340:ARG:N	2.39	0.49
1:E:152:PHE:HE2	1:E:223:GLY:C	2.16	0.49
1:E:153:PRO:CB	1:E:222:TRP:CZ3	2.95	0.49
1:E:253:ILE:HG13	1:E:254:LEU:HG	1.93	0.49
1:F:272:VAL:N	1:F:345:CYS:O	2.41	0.49
1:G:120:TYR:O	1:G:121:LYS:C	2.49	0.49
1:G:158:ALA:HB1	1:G:216:LYS:O	2.13	0.49
1:H:278:GLN:O	1:H:339:ALA:N	2.32	0.49
1:H:292:ILE:HB	1:H:346:VAL:HG13	1.93	0.49
1:H:325:ILE:HG13	1:H:326:ALA:N	2.27	0.49
1:A:247:PHE:HE1	1:A:294:LEU:CB	2.25	0.49
1:B:173:TYR:HB2	1:B:198:PHE:CE1	2.47	0.49
1:C:173:TYR:CD2	1:C:198:PHE:HZ	2.29	0.49
1:C:242:LYS:HD3	1:C:242:LYS:N	1.95	0.49
1:D:183:TYR:CD1	1:D:188:TRP:HA	2.45	0.49
1:D:203:LEU:HD12	1:D:229:TYR:CD2	2.47	0.49
1:D:273:GLN:HE21	1:D:273:GLN:CA	2.25	0.49
1:E:281:VAL:HG11	1:E:333:ARG:NE	2.28	0.49
1:F:261:GLU:O	1:F:265:VAL:HG23	2.12	0.49
1:G:116:ILE:HB	1:G:149:ASP:O	2.12	0.49
1:G:121:LYS:O	1:G:122:THR:C	2.50	0.49
1:G:360:CYS:O	1:G:364:LEU:HD23	2.13	0.49
1:H:113:ARG:CD	1:H:114:LYS:N	2.71	0.49
1:H:230:ARG:CB	1:H:234:MET:HE1	2.43	0.49
1:H:261:GLU:O	1:H:262:ARG:C	2.48	0.49
1:A:139:LEU:HD21	1:A:147:ILE:CD1	2.42	0.49
1:A:249:SER:HA	1:A:262:ARG:HH22	1.75	0.49
1:B:147:ILE:O	1:B:148:PHE:C	2.47	0.49
1:B:290:PHE:HB2	1:B:327:LEU:HD21	1.95	0.49
1:C:254:LEU:HD12	1:C:255:GLU:N	2.28	0.49
1:C:265:VAL:HG12	1:C:269:LEU:CG	2.41	0.49
1:C:325:ILE:CD1	1:C:334:ALA:CB	2.90	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:269:LEU:O	1:D:270:GLU:CB	2.59	0.49
1:E:287:GLY:HA3	1:E:326:ALA:HB1	1.95	0.49
1:F:224:ILE:HD12	1:F:224:ILE:H	1.73	0.49
1:F:289:GLU:HG2	1:F:291:PHE:HE1	1.77	0.49
1:G:139:LEU:HD21	1:G:147:ILE:CD1	2.42	0.49
1:A:116:ILE:N	1:A:149:ASP:O	2.43	0.49
1:A:122:THR:O	1:A:125:ALA:HB3	2.12	0.49
1:A:352:ARG:HA	1:A:355:ARG:HB2	1.95	0.49
1:B:253:ILE:HG21	1:B:321:TYR:CE2	2.48	0.49
1:C:120:TYR:HE1	1:D:148:PHE:CG	2.29	0.49
1:C:280:ILE:HB	1:C:291:PHE:HE2	1.77	0.49
1:C:366:ARG:O	1:C:369:GLN:HB2	2.13	0.49
1:D:120:TYR:HD2	1:D:121:LYS:N	2.11	0.49
1:D:121:LYS:O	1:D:124:ALA:N	2.46	0.49
1:F:118:LYS:CE	1:F:148:PHE:O	2.51	0.49
1:F:135:LEU:HD12	1:F:136:PHE:N	2.27	0.49
1:H:129:ALA:CB	1:H:222:TRP:NE1	2.76	0.49
1:H:131:GLU:C	1:H:133:ASN:N	2.65	0.49
1:H:139:LEU:HD22	1:H:144:ARG:HA	1.94	0.49
1:H:158:ALA:N	1:H:218:ASN:OD1	2.40	0.49
1:A:174:VAL:CG1	1:A:222:TRP:HB2	2.42	0.49
1:A:297:SER:O	1:A:340:ARG:HB2	2.13	0.49
1:A:371:TYR:CD1	2:A:402:CMP:N7	2.80	0.49
1:B:111:TYR:CE2	1:B:112:VAL:O	2.66	0.49
1:B:272:VAL:HA	1:B:273:GLN:HE22	1.75	0.49
1:C:144:ARG:HG2	1:C:145:SER:H	1.74	0.49
1:C:144:ARG:O	1:C:147:ILE:N	2.46	0.49
1:C:153:PRO:CA	1:C:222:TRP:CZ3	2.96	0.49
1:C:211:ASP:OD1	2:C:401:CMP:O2P	2.30	0.49
1:C:315:ARG:HH21	1:C:340:ARG:HH22	1.61	0.49
1:D:183:TYR:HE1	1:D:188:TRP:HB2	1.76	0.49
1:D:188:TRP:HH2	1:D:191:SER:OG	1.90	0.49
1:E:201:LEU:HD13	2:E:401:CMP:C2'	2.43	0.49
1:G:211:ASP:OD2	2:G:401:CMP:N3	2.46	0.49
1:H:196:GLY:CA	1:H:355:ARG:NH2	2.65	0.49
1:H:229:TYR:HD1	1:H:233:LEU:HD11	1.73	0.49
1:A:284:GLY:O	1:A:332:PRO:HB3	2.13	0.48
1:A:296:GLY:CA	1:A:342:PRO:O	2.61	0.48
1:B:154:VAL:O	1:B:221:LEU:N	2.32	0.48
1:B:293:ILE:CG2	1:B:317:GLY:O	2.59	0.48
1:D:293:ILE:HG21	1:D:317:GLY:C	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:249:SER:CA	1:E:262:ARG:NH2	2.70	0.48
1:E:324:GLU:O	1:E:328:LEU:CD1	2.42	0.48
1:E:325:ILE:CD1	1:E:334:ALA:CB	2.92	0.48
1:F:157:ILE:O	1:H:243:MET:HE1	2.13	0.48
1:F:260:TRP:CD2	2:F:401:CMP:C8	2.96	0.48
1:F:291:PHE:CZ	1:F:347:LYS:NZ	2.79	0.48
1:G:153:PRO:HB3	1:G:222:TRP:CH2	2.46	0.48
1:G:256:SER:OG	1:G:363:ILE:HD12	2.13	0.48
1:H:177:GLN:HA	1:H:194:GLU:CG	2.43	0.48
1:H:235:GLY:O	1:H:238:LEU:N	2.46	0.48
1:H:261:GLU:O	1:H:264:THR:N	2.46	0.48
1:H:262:ARG:HA	1:H:265:VAL:CG2	2.42	0.48
1:H:269:LEU:CD2	1:H:346:VAL:HG21	2.38	0.48
1:H:304:ARG:CB	1:H:308:GLU:CB	2.90	0.48
1:A:162:VAL:HG22	1:A:213:VAL:O	2.13	0.48
1:A:324:GLU:CG	1:A:325:ILE:H	2.24	0.48
1:B:175:ILE:HD11	1:B:194:GLU:CA	2.43	0.48
1:B:200:GLU:CD	1:B:201:LEU:HD11	2.33	0.48
1:C:163:ILE:HD12	1:C:213:VAL:HG21	1.95	0.48
1:C:211:ASP:OD2	2:C:401:CMP:C3'	2.56	0.48
1:C:284:GLY:O	1:C:332:PRO:CG	2.61	0.48
1:D:247:PHE:HE1	1:D:294:LEU:HB3	1.77	0.48
1:E:126:LEU:O	1:E:130:ILE:N	2.44	0.48
1:E:139:LEU:N	1:E:139:LEU:CD1	2.66	0.48
1:F:234:MET:HG3	1:F:238:LEU:CD1	2.41	0.48
1:F:235:GLY:O	1:F:238:LEU:N	2.47	0.48
1:F:273:GLN:HE21	1:F:273:GLN:CA	2.22	0.48
1:F:352:ARG:HA	1:F:355:ARG:HB2	1.95	0.48
1:G:258:ASP:O	1:G:262:ARG:HG2	2.13	0.48
1:H:241:ARG:O	1:H:242:LYS:C	2.50	0.48
1:A:179:GLU:HG2	1:A:216:LYS:HD3	1.93	0.48
1:C:290:PHE:HB2	1:C:327:LEU:CD2	2.43	0.48
1:D:161:THR:HG23	1:D:214:LYS:HD2	1.95	0.48
1:E:234:MET:HG3	1:E:238:LEU:HD12	1.95	0.48
1:E:281:VAL:HG11	1:E:333:ARG:CD	2.43	0.48
1:F:171:ASN:OD1	1:F:225:ASP:HA	2.14	0.48
1:F:249:SER:CB	1:F:262:ARG:HH22	2.26	0.48
1:F:293:ILE:HG21	1:F:317:GLY:C	2.34	0.48
1:F:349:ASP:O	1:F:353:PHE:HB2	2.13	0.48
1:G:116:ILE:N	1:G:149:ASP:O	2.41	0.48
1:G:135:LEU:HD13	1:G:136:PHE:CD1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:353:PHE:CE1	1:G:357:LEU:HD23	2.48	0.48
1:H:324:GLU:OE2	1:H:371:TYR:HE2	1.96	0.48
1:A:153:PRO:CA	1:A:222:TRP:HZ3	2.23	0.48
1:B:113:ARG:HG3	1:B:113:ARG:O	2.13	0.48
1:B:260:TRP:CE2	2:B:401:CMP:H8	2.47	0.48
1:C:260:TRP:CG	2:C:401:CMP:N7	2.81	0.48
1:D:164:GLN:O	1:D:167:ASP:HB2	2.14	0.48
1:D:224:ILE:H	1:D:224:ILE:HD12	1.75	0.48
1:D:296:GLY:HA2	1:D:342:PRO:HG2	1.95	0.48
1:E:134:VAL:O	1:E:137:SER:HB3	2.12	0.48
1:E:289:GLU:HG2	1:E:291:PHE:CE1	2.48	0.48
1:F:163:ILE:O	1:F:213:VAL:N	2.43	0.48
1:F:183:TYR:HE1	1:F:188:TRP:HB2	1.78	0.48
1:F:246:GLU:O	1:F:249:SER:N	2.46	0.48
1:G:116:ILE:HG22	1:G:118:LYS:CG	2.39	0.48
1:G:120:TYR:HD2	1:G:121:LYS:N	2.11	0.48
1:G:247:PHE:CE1	1:G:294:LEU:CB	2.96	0.48
1:H:153:PRO:HB3	1:H:222:TRP:HZ3	1.76	0.48
1:H:163:ILE:O	1:H:212:THR:HG22	2.14	0.48
1:H:165:GLN:N	1:H:212:THR:CG2	2.50	0.48
1:H:183:TYR:HE1	1:H:188:TRP:HB2	1.75	0.48
1:H:260:TRP:CE2	2:H:401:CMP:H8	2.44	0.48
1:H:333:ARG:NH1	2:H:402:CMP:O2P	2.37	0.48
1:A:186:ASN:OD1	1:A:186:ASN:N	2.47	0.48
1:A:309:GLU:HG3	1:A:310:PHE:H	1.79	0.48
1:C:113:ARG:NE	1:C:146:ASP:OD1	2.41	0.48
1:C:188:TRP:CH2	1:C:190:THR:CA	2.94	0.48
1:C:254:LEU:HB2	1:C:257:LEU:HD12	1.94	0.48
1:C:294:LEU:HD13	1:C:345:CYS:HA	1.87	0.48
1:C:318:PRO:O	1:C:319:SER:HB3	2.12	0.48
1:C:325:ILE:HG12	2:C:402:CMP:O3'	2.12	0.48
1:C:361:SER:C	1:C:365:LYS:NZ	2.67	0.48
1:D:343:LEU:HA	1:D:343:LEU:HD12	1.55	0.48
1:E:324:GLU:OE1	1:E:324:GLU:N	2.46	0.48
1:E:325:ILE:HG22	1:E:368:ILE:HG21	1.94	0.48
1:E:353:PHE:CE1	1:E:357:LEU:HD23	2.48	0.48
1:F:280:ILE:HD12	1:F:281:VAL:CG2	2.43	0.48
1:H:115:VAL:O	1:H:115:VAL:CG2	2.54	0.48
1:H:147:ILE:HG13	1:H:148:PHE:N	2.28	0.48
1:H:157:ILE:O	1:H:158:ALA:O	2.31	0.48
1:H:157:ILE:HG13	1:H:160:GLU:OE1	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:171:ASN:H	1:H:209:ARG:HH22	1.60	0.48
1:H:180:MET:O	1:H:191:SER:HA	2.12	0.48
1:H:204:ILE:CG2	1:H:205:TYR:CE2	2.97	0.48
1:H:245:GLU:OE1	1:H:245:GLU:C	2.52	0.48
1:A:113:ARG:CD	1:D:113:ARG:HB3	2.43	0.48
1:B:298:ALA:HB1	1:B:338:VAL:O	2.14	0.48
1:C:129:ALA:CB	1:C:222:TRP:NE1	2.77	0.48
1:C:203:LEU:HD22	1:C:226:ARG:CB	2.38	0.48
1:C:278:GLN:O	1:C:339:ALA:N	2.42	0.48
1:C:291:PHE:CD1	1:C:347:LYS:NZ	2.81	0.48
1:D:172:PHE:O	1:D:224:ILE:CD1	2.61	0.48
1:D:200:GLU:HG2	1:D:201:LEU:CG	2.43	0.48
1:D:253:ILE:HD13	1:D:321:TYR:CE2	2.49	0.48
1:F:262:ARG:HA	1:F:265:VAL:HG23	1.94	0.48
1:F:329:MET:HB3	1:F:331:ARG:HG3	1.95	0.48
1:G:123:MET:O	1:G:127:ALA:N	2.37	0.48
1:G:211:ASP:OD2	2:G:401:CMP:C4'	2.62	0.48
1:G:233:LEU:CD1	1:G:233:LEU:N	2.53	0.48
1:H:144:ARG:O	1:H:145:SER:C	2.51	0.48
1:H:215:ALA:HB1	1:H:217:THR:O	2.13	0.48
1:H:298:ALA:CB	1:H:338:VAL:O	2.62	0.48
1:H:366:ARG:HG2	1:H:367:ASN:N	2.29	0.48
1:B:260:TRP:CZ2	2:B:401:CMP:C8	2.95	0.48
1:B:325:ILE:O	1:B:328:LEU:N	2.46	0.48
1:C:324:GLU:OE2	1:C:371:TYR:HE2	1.97	0.48
1:D:221:LEU:HD23	1:D:221:LEU:HA	1.46	0.48
1:F:130:ILE:CG1	1:F:136:PHE:CG	2.95	0.48
1:F:186:ASN:OD1	1:F:186:ASN:N	2.47	0.48
1:F:318:PRO:O	1:F:319:SER:CB	2.58	0.48
1:F:325:ILE:CD1	1:F:334:ALA:HB3	2.44	0.48
1:G:232:ILE:HG23	1:G:233:LEU:HG	1.95	0.48
1:G:294:LEU:HD11	1:G:345:CYS:C	2.34	0.48
1:H:158:ALA:HA	1:H:215:ALA:HB3	1.95	0.48
1:H:162:VAL:HG23	1:H:163:ILE:N	2.28	0.48
1:H:198:PHE:CD1	1:H:198:PHE:N	2.78	0.48
1:H:247:PHE:CE1	1:H:294:LEU:HB3	2.49	0.48
1:A:135:LEU:CD1	1:A:136:PHE:H	2.07	0.48
1:A:152:PHE:CD2	1:A:152:PHE:N	2.82	0.48
1:A:174:VAL:HG13	1:A:222:TRP:HB2	1.96	0.48
1:A:211:ASP:OD2	2:A:401:CMP:C4'	2.62	0.48
1:A:324:GLU:HB2	1:A:364:LEU:HD11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:SER:C	1:A:365:LYS:NZ	2.61	0.48
1:B:183:TYR:CE1	1:B:188:TRP:CB	2.95	0.48
1:B:315:ARG:C	1:B:316:LEU:HD13	2.34	0.48
1:B:318:PRO:O	1:B:319:SER:HB3	2.14	0.48
1:C:130:ILE:HD12	1:C:136:PHE:CE2	2.48	0.48
1:E:243:MET:CE	1:G:158:ALA:O	2.61	0.48
1:E:261:GLU:O	1:E:265:VAL:HG23	2.14	0.48
1:F:113:ARG:NE	1:F:146:ASP:CG	2.67	0.48
1:G:139:LEU:N	1:G:139:LEU:CD1	2.67	0.48
1:G:229:TYR:O	1:G:233:LEU:HD12	2.14	0.48
1:H:157:ILE:O	1:H:158:ALA:C	2.51	0.48
1:H:246:GLU:O	1:H:248:LEU:N	2.47	0.48
1:A:112:VAL:CA	1:A:112:VAL:CG1	2.84	0.48
1:A:133:ASN:C	1:A:133:ASN:OD1	2.51	0.48
1:A:296:GLY:HA3	1:A:342:PRO:O	2.13	0.48
1:B:210:ALA:CA	1:B:211:ASP:OD1	2.61	0.48
1:B:252:SER:C	1:B:253:ILE:HG12	2.33	0.48
1:C:266:ALA:N	1:C:269:LEU:CD1	2.77	0.48
1:D:204:ILE:CG2	1:D:205:TYR:CE2	2.96	0.48
1:D:253:ILE:HG13	1:D:254:LEU:H	1.78	0.48
1:D:254:LEU:HB2	1:D:257:LEU:CD1	2.43	0.48
1:E:184:VAL:O	1:E:185:ASN:HB2	2.14	0.48
1:F:118:LYS:HB2	1:F:123:MET:HE1	1.95	0.48
1:F:259:LYS:HA	1:F:262:ARG:HD3	1.95	0.48
1:F:312:GLU:CD	1:F:340:ARG:HH12	2.16	0.48
1:G:144:ARG:CG	1:G:145:SER:N	2.76	0.48
1:H:300:VAL:HG11	2:H:402:CMP:H8	1.90	0.48
1:A:115:VAL:HA	1:A:149:ASP:HB3	1.94	0.48
1:A:120:TYR:CE2	1:A:124:ALA:HB2	2.49	0.48
1:A:129:ALA:HA	1:A:132:LYS:HE3	1.95	0.48
1:A:203:LEU:HD22	1:A:226:ARG:CG	2.44	0.48
1:A:261:GLU:O	1:A:265:VAL:HG23	2.14	0.48
1:B:200:GLU:HG3	1:B:201:LEU:H	1.74	0.48
1:C:152:PHE:HE2	1:C:223:GLY:CA	2.26	0.48
1:C:266:ALA:O	1:C:268:ALA:N	2.47	0.48
1:D:285:GLU:HB3	1:D:286:PRO:HD2	1.96	0.48
1:E:148:PHE:CD1	1:F:120:TYR:HE1	2.29	0.48
1:E:289:GLU:HG2	1:E:291:PHE:HE1	1.78	0.48
1:F:114:LYS:CE	1:F:115:VAL:N	2.77	0.48
1:F:273:GLN:HB2	1:F:343:LEU:O	2.14	0.48
1:H:120:TYR:HD2	1:H:121:LYS:N	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:VAL:HG23	1:A:163:ILE:N	2.28	0.47
1:A:260:TRP:HB2	2:A:401:CMP:N6	2.28	0.47
1:B:328:LEU:CD2	1:B:365:LYS:HE3	2.44	0.47
1:B:357:LEU:HA	1:B:357:LEU:HD12	1.58	0.47
1:B:376:SER:CA	1:C:306:GLU:HA	2.44	0.47
1:C:120:TYR:HD2	1:C:121:LYS:N	2.12	0.47
1:C:230:ARG:CZ	1:C:234:MET:CE	2.91	0.47
1:E:128:LYS:O	1:E:129:ALA:C	2.52	0.47
1:F:120:TYR:HD2	1:F:121:LYS:HA	1.78	0.47
1:G:226:ARG:NH1	1:G:227:ASP:OD1	2.37	0.47
1:G:269:LEU:CB	1:G:346:VAL:HG21	2.44	0.47
1:G:328:LEU:HD23	1:G:365:LYS:HE3	1.93	0.47
1:H:260:TRP:CD2	2:H:401:CMP:N7	2.82	0.47
1:A:153:PRO:N	1:A:222:TRP:HZ3	2.12	0.47
1:A:204:ILE:HG12	1:A:234:MET:SD	2.54	0.47
1:A:265:VAL:HA	1:A:356:VAL:HG11	1.96	0.47
1:B:207:THR:OG1	1:B:208:PRO:O	2.32	0.47
1:B:224:ILE:N	1:B:224:ILE:HD12	2.29	0.47
1:B:247:PHE:CE1	1:B:294:LEU:CB	2.97	0.47
1:B:309:GLU:OE1	1:B:310:PHE:CE2	2.67	0.47
1:C:121:LYS:O	1:C:122:THR:C	2.52	0.47
1:C:279:LYS:HB2	1:C:337:VAL:O	2.14	0.47
1:C:347:LYS:HE3	1:C:347:LYS:HB3	1.22	0.47
1:D:128:LYS:O	1:D:129:ALA:C	2.49	0.47
1:D:130:ILE:CD1	1:D:136:PHE:CD2	2.97	0.47
1:D:270:GLU:O	1:D:346:VAL:HA	2.14	0.47
1:D:300:VAL:CG1	1:D:314:GLY:H	2.27	0.47
1:D:352:ARG:HA	1:D:355:ARG:HB2	1.96	0.47
1:E:111:TYR:CD1	1:E:112:VAL:N	2.82	0.47
1:E:158:ALA:HB1	1:E:216:LYS:O	2.14	0.47
1:F:295:GLU:O	1:F:344:LYS:N	2.40	0.47
1:G:293:ILE:CG1	1:G:343:LEU:HD11	2.43	0.47
1:H:174:VAL:HG13	1:H:174:VAL:O	2.13	0.47
1:H:190:THR:CG2	1:H:191:SER:N	2.74	0.47
1:H:233:LEU:HD12	1:H:233:LEU:N	2.05	0.47
1:A:365:LYS:HA	1:A:368:ILE:CD1	2.44	0.47
1:B:152:PHE:CD2	1:B:223:GLY:O	2.68	0.47
1:B:260:TRP:NE1	2:B:401:CMP:C2'	2.72	0.47
1:B:356:VAL:HG23	1:B:357:LEU:N	2.29	0.47
1:C:176:ASP:HB2	1:C:222:TRP:CD1	2.49	0.47
1:C:229:TYR:O	1:C:233:LEU:HD12	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:160:GLU:O	1:D:214:LYS:HE3	2.15	0.47
1:E:158:ALA:HA	1:E:215:ALA:CB	2.45	0.47
1:E:230:ARG:NH1	1:E:234:MET:CE	2.78	0.47
1:E:233:LEU:O	1:E:234:MET:C	2.51	0.47
1:F:165:GLN:CB	1:F:211:ASP:O	2.62	0.47
1:F:229:TYR:O	1:F:233:LEU:HD12	2.14	0.47
1:F:300:VAL:HG12	1:F:335:ALA:HB1	1.93	0.47
1:G:361:SER:C	1:G:365:LYS:NZ	2.66	0.47
1:H:173:TYR:HB2	1:H:198:PHE:HE1	1.80	0.47
1:H:280:ILE:HG12	1:H:337:VAL:HB	1.96	0.47
1:H:301:LEU:O	1:H:302:GLN:CG	2.61	0.47
1:B:252:SER:C	1:B:253:ILE:CG1	2.83	0.47
1:B:311:VAL:CG1	1:B:312:GLU:H	2.28	0.47
1:C:120:TYR:HB3	1:D:149:ASP:OD1	2.12	0.47
1:C:124:ALA:O	1:C:127:ALA:HB3	2.14	0.47
1:C:280:ILE:HD11	1:C:322:PHE:CE2	2.33	0.47
1:D:230:ARG:NH1	1:D:234:MET:HE1	2.29	0.47
1:F:126:LEU:O	1:F:127:ALA:C	2.51	0.47
1:F:171:ASN:H	1:F:209:ARG:HH22	1.61	0.47
1:F:272:VAL:HA	1:F:273:GLN:HE22	1.79	0.47
1:F:366:ARG:HG2	1:F:367:ASN:H	1.79	0.47
1:G:173:TYR:CD2	1:G:198:PHE:CZ	3.02	0.47
1:H:176:ASP:O	1:H:194:GLU:HG2	2.15	0.47
1:H:289:GLU:N	1:H:327:LEU:HD11	2.30	0.47
1:H:327:LEU:HD23	1:H:353:PHE:CZ	2.48	0.47
1:H:356:VAL:HG23	1:H:357:LEU:N	2.29	0.47
1:H:366:ARG:O	1:H:369:GLN:CB	2.63	0.47
1:A:148:PHE:CD1	1:B:120:TYR:CE1	3.02	0.47
1:A:188:TRP:CZ3	1:A:190:THR:O	2.63	0.47
1:A:196:GLY:HA2	1:A:355:ARG:CZ	2.43	0.47
1:A:325:ILE:HD11	1:A:334:ALA:H	1.79	0.47
1:B:332:PRO:HD3	1:C:332:PRO:HG2	1.97	0.47
1:C:134:VAL:O	1:C:137:SER:HB3	2.14	0.47
1:C:138:HIS:O	1:C:139:LEU:C	2.50	0.47
1:E:266:ALA:O	1:E:268:ALA:N	2.47	0.47
1:E:272:VAL:HG22	1:E:273:GLN:N	2.27	0.47
1:F:126:LEU:O	1:F:126:LEU:CD1	2.46	0.47
1:F:199:GLY:H	2:F:401:CMP:H4'	1.79	0.47
1:F:247:PHE:C	1:F:247:PHE:HD2	2.17	0.47
1:H:178:GLY:CA	1:H:219:VAL:HG12	2.23	0.47
1:H:234:MET:HG3	1:H:234:MET:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:298:ALA:O	1:H:316:LEU:N	2.45	0.47
1:C:162:VAL:HG23	1:C:163:ILE:N	2.29	0.47
1:C:253:ILE:HG13	1:C:254:LEU:HG	1.96	0.47
1:C:298:ALA:O	1:C:316:LEU:N	2.46	0.47
1:C:302:GLN:CD	1:C:374:PHE:CB	2.83	0.47
1:D:164:GLN:HA	1:D:212:THR:CG2	2.43	0.47
1:D:353:PHE:O	1:D:357:LEU:HB2	2.14	0.47
1:F:248:LEU:CD1	1:F:265:VAL:HG11	2.44	0.47
1:H:293:ILE:HA	1:H:345:CYS:SG	2.55	0.47
1:A:110:SER:HB3	1:A:111:TYR:H	1.53	0.47
1:A:139:LEU:HB3	1:A:143:GLU:CB	2.43	0.47
1:A:253:ILE:C	1:A:255:GLU:H	2.16	0.47
1:B:158:ALA:HA	1:B:217:THR:O	2.13	0.47
1:B:183:TYR:HD1	1:B:188:TRP:CA	2.27	0.47
1:B:279:LYS:CE	1:B:282:VAL:HG22	2.34	0.47
1:C:265:VAL:C	1:C:269:LEU:HD11	2.35	0.47
1:C:366:ARG:CG	1:C:367:ASN:N	2.75	0.47
1:D:124:ALA:O	1:D:127:ALA:HB3	2.14	0.47
1:D:173:TYR:HD2	1:D:198:PHE:CZ	2.32	0.47
1:D:234:MET:HG3	1:D:234:MET:O	2.14	0.47
1:D:371:TYR:CE1	2:D:402:CMP:C4	3.03	0.47
1:E:175:ILE:O	1:E:175:ILE:CD1	2.39	0.47
1:E:230:ARG:CZ	1:E:234:MET:CE	2.93	0.47
1:E:294:LEU:HD11	1:E:345:CYS:CA	2.30	0.47
1:F:129:ALA:CB	1:F:222:TRP:NE1	2.76	0.47
1:F:136:PHE:O	1:F:139:LEU:HD11	2.15	0.47
1:F:233:LEU:CD1	1:F:233:LEU:N	2.68	0.47
1:F:294:LEU:HD13	1:F:345:CYS:HA	1.92	0.47
1:F:350:ARG:HB3	1:F:351:PRO:HD3	1.97	0.47
1:G:148:PHE:CG	1:H:120:TYR:CE1	3.02	0.47
1:G:249:SER:HA	1:G:262:ARG:NH2	2.29	0.47
1:H:157:ILE:O	1:H:157:ILE:CD1	2.47	0.47
1:H:343:LEU:HD12	1:H:343:LEU:HA	1.74	0.47
1:H:371:TYR:HE1	2:H:402:CMP:C5	2.31	0.47
1:A:182:VAL:HG23	1:A:189:ALA:HB3	1.97	0.47
1:A:245:GLU:OE1	1:A:246:GLU:OE1	2.33	0.47
1:B:127:ALA:O	1:B:130:ILE:HG22	2.15	0.47
1:B:186:ASN:N	1:B:186:ASN:OD1	2.48	0.47
1:B:293:ILE:HG21	1:B:317:GLY:C	2.35	0.47
1:C:116:ILE:CG2	1:C:118:LYS:HZ2	2.28	0.47
1:D:153:PRO:HA	1:D:222:TRP:CZ3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:311:VAL:O	1:D:311:VAL:HG22	2.14	0.47
1:E:153:PRO:HA	1:E:222:TRP:CE3	2.49	0.47
1:G:204:ILE:CG2	1:G:205:TYR:CE2	2.97	0.47
1:G:279:LYS:O	1:G:279:LYS:HG3	2.14	0.47
1:H:113:ARG:CB	1:H:231:ARG:HH12	2.28	0.47
1:A:260:TRP:CD1	2:A:401:CMP:N7	2.81	0.47
1:B:204:ILE:CG2	1:B:205:TYR:CD2	2.98	0.47
1:C:215:ALA:HB1	1:C:217:THR:O	2.14	0.47
1:C:291:PHE:CD2	1:C:322:PHE:CZ	3.02	0.47
1:D:119:ASP:O	1:D:120:TYR:C	2.53	0.47
1:E:204:ILE:HD13	1:E:238:LEU:HD11	1.96	0.47
1:E:233:LEU:CD1	1:E:233:LEU:N	2.68	0.47
1:E:253:ILE:HG13	1:E:254:LEU:CD2	2.45	0.47
1:E:260:TRP:NE1	2:E:401:CMP:C4	2.82	0.47
1:F:130:ILE:HD12	1:F:136:PHE:CE2	2.50	0.47
1:F:198:PHE:HD1	1:F:198:PHE:H	1.62	0.47
1:F:324:GLU:HB2	1:F:364:LEU:CD1	2.39	0.47
1:G:143:GLU:HB3	1:G:232:ILE:HD11	1.97	0.47
1:G:157:ILE:HG13	1:G:160:GLU:OE1	2.15	0.47
1:G:290:PHE:HB2	1:G:327:LEU:CD2	2.45	0.47
1:A:114:LYS:O	1:A:115:VAL:HG13	2.15	0.47
1:A:308:GLU:O	1:A:309:GLU:HB2	2.15	0.47
1:B:310:PHE:N	1:B:310:PHE:CD2	2.77	0.47
1:C:130:ILE:CD1	1:C:151:MET:CE	2.92	0.47
1:C:253:ILE:C	1:C:255:GLU:N	2.68	0.47
1:D:251:VAL:HG11	1:D:292:ILE:HD13	1.97	0.47
1:D:281:VAL:HG11	1:D:333:ARG:HD2	1.97	0.47
1:E:251:VAL:CG1	1:E:254:LEU:CD2	2.87	0.47
1:F:272:VAL:C	1:F:273:GLN:NE2	2.68	0.47
1:F:296:GLY:HA2	1:F:342:PRO:HG2	1.96	0.47
1:F:325:ILE:HG12	2:F:402:CMP:P	2.55	0.47
1:G:254:LEU:HB2	1:G:257:LEU:HD12	1.97	0.47
1:H:120:TYR:CD2	1:H:121:LYS:HA	2.46	0.47
1:H:281:VAL:HG13	1:H:333:ARG:CG	2.45	0.47
1:H:325:ILE:CD1	2:H:402:CMP:O1P	2.61	0.47
1:A:126:LEU:C	1:A:126:LEU:CD1	2.81	0.46
1:A:321:TYR:CD1	1:A:321:TYR:O	2.68	0.46
1:B:203:LEU:HD22	1:B:226:ARG:CG	2.44	0.46
1:B:255:GLU:O	1:B:256:SER:C	2.53	0.46
1:B:266:ALA:O	1:B:269:LEU:N	2.44	0.46
1:B:272:VAL:C	1:B:273:GLN:NE2	2.66	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:284:GLY:C	1:B:332:PRO:HB3	2.36	0.46
1:C:111:TYR:CG	1:C:112:VAL:N	2.82	0.46
1:C:232:ILE:HG23	1:C:233:LEU:HG	1.96	0.46
1:C:316:LEU:CA	1:C:320:ASP:OD2	2.60	0.46
1:D:158:ALA:N	1:D:218:ASN:OD1	2.41	0.46
1:D:232:ILE:HG23	1:D:233:LEU:CD1	2.45	0.46
1:D:327:LEU:HD23	1:D:353:PHE:CG	2.49	0.46
1:D:347:LYS:HE3	1:D:347:LYS:HB3	1.30	0.46
1:E:183:TYR:HE1	1:E:188:TRP:HB2	1.75	0.46
1:E:186:ASN:N	1:E:186:ASN:OD1	2.47	0.46
1:G:130:ILE:CD1	1:G:136:PHE:CD2	2.98	0.46
1:G:265:VAL:C	1:G:269:LEU:HD11	2.35	0.46
1:H:258:ASP:O	1:H:262:ARG:HG3	2.15	0.46
1:H:301:LEU:HA	1:H:312:GLU:HA	1.97	0.46
1:H:352:ARG:O	1:H:353:PHE:C	2.52	0.46
1:A:139:LEU:N	1:A:139:LEU:CD1	2.64	0.46
1:A:260:TRP:CD1	2:A:401:CMP:C4	3.04	0.46
1:A:280:ILE:CD1	1:A:281:VAL:HG23	2.43	0.46
1:B:163:ILE:O	1:B:213:VAL:N	2.39	0.46
1:B:285:GLU:OE1	1:B:285:GLU:CA	2.63	0.46
1:C:304:ARG:H	1:C:308:GLU:CB	2.29	0.46
1:D:204:ILE:CG2	1:D:205:TYR:HD2	2.23	0.46
1:D:272:VAL:HA	1:D:273:GLN:NE2	2.31	0.46
1:E:116:ILE:HB	1:E:118:LYS:NZ	2.31	0.46
1:F:203:LEU:CD1	1:F:226:ARG:HB3	2.38	0.46
1:F:273:GLN:NE2	1:F:273:GLN:H	1.89	0.46
1:G:174:VAL:HA	1:G:196:GLY:O	2.16	0.46
1:H:301:LEU:CA	1:H:311:VAL:O	2.63	0.46
1:H:357:LEU:CD1	1:H:357:LEU:N	2.72	0.46
1:A:113:ARG:CG	1:D:113:ARG:CB	2.93	0.46
1:B:123:MET:C	1:B:125:ALA:N	2.68	0.46
1:B:153:PRO:HA	1:B:222:TRP:CZ3	2.46	0.46
1:B:331:ARG:HH21	1:B:376:SER:HB3	1.80	0.46
1:C:157:ILE:O	1:C:158:ALA:C	2.51	0.46
1:C:175:ILE:HG22	1:C:221:LEU:HD21	1.97	0.46
1:C:230:ARG:O	1:C:234:MET:CB	2.58	0.46
1:D:131:GLU:N	1:D:131:GLU:CD	2.68	0.46
1:D:201:LEU:HB2	2:D:401:CMP:P	2.55	0.46
1:D:253:ILE:CG2	1:D:321:TYR:CE2	2.98	0.46
1:D:290:PHE:HB2	1:D:327:LEU:CD2	2.45	0.46
1:E:325:ILE:CG1	2:E:402:CMP:O2P	2.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:327:LEU:HD23	1:E:353:PHE:CD2	2.51	0.46
1:F:175:ILE:CD1	1:F:196:GLY:N	2.74	0.46
1:F:292:ILE:HB	1:F:346:VAL:HG13	1.96	0.46
1:F:366:ARG:O	1:F:369:GLN:CB	2.63	0.46
1:G:266:ALA:N	1:G:269:LEU:HD11	2.30	0.46
1:H:152:PHE:CD2	1:H:152:PHE:C	2.87	0.46
1:A:230:ARG:HH12	1:A:234:MET:HE3	1.74	0.46
1:A:266:ALA:O	1:A:268:ALA:N	2.49	0.46
1:B:173:TYR:HB3	1:B:222:TRP:O	2.15	0.46
1:C:148:PHE:CD1	1:D:120:TYR:CE1	3.03	0.46
1:C:251:VAL:CG2	1:C:319:SER:O	2.63	0.46
1:C:371:TYR:OH	2:C:402:CMP:C2'	2.64	0.46
1:D:162:VAL:HG23	1:D:163:ILE:H	1.79	0.46
1:E:152:PHE:CD2	1:E:223:GLY:O	2.69	0.46
1:F:143:GLU:HB3	1:F:232:ILE:HD11	1.98	0.46
1:F:175:ILE:CD1	1:F:194:GLU:HA	2.41	0.46
1:G:179:GLU:HB3	1:G:217:THR:HG23	1.97	0.46
1:G:296:GLY:CA	1:G:342:PRO:O	2.63	0.46
1:H:204:ILE:HG21	1:H:238:LEU:HD21	1.97	0.46
1:H:284:GLY:HA2	1:H:332:PRO:HB3	1.97	0.46
1:A:184:VAL:HG22	1:A:185:ASN:OD1	2.16	0.46
1:B:253:ILE:HD13	1:B:321:TYR:CD2	2.51	0.46
1:B:327:LEU:HD23	1:B:353:PHE:CG	2.49	0.46
1:B:352:ARG:HA	1:B:355:ARG:HB2	1.97	0.46
1:C:362:ASP:O	1:C:365:LYS:N	2.46	0.46
1:D:325:ILE:CD1	1:D:334:ALA:CB	2.94	0.46
1:E:151:MET:HA	1:E:224:ILE:CG2	2.45	0.46
1:E:203:LEU:CD1	1:E:229:TYR:HD2	2.28	0.46
1:E:298:ALA:HB1	1:E:338:VAL:O	2.14	0.46
1:F:234:MET:CG	1:F:238:LEU:HD12	2.45	0.46
1:F:260:TRP:NE1	2:F:401:CMP:N9	2.64	0.46
1:G:204:ILE:CG2	1:G:205:TYR:HD2	2.23	0.46
1:H:151:MET:HA	1:H:224:ILE:HG22	1.96	0.46
1:H:262:ARG:O	1:H:265:VAL:CB	2.54	0.46
1:H:276:ASP:HA	1:H:339:ALA:O	2.16	0.46
1:A:293:ILE:HG21	1:A:317:GLY:C	2.36	0.46
1:B:135:LEU:HD13	1:B:136:PHE:CE1	2.51	0.46
1:B:226:ARG:HA	1:B:229:TYR:HB3	1.97	0.46
1:B:325:ILE:HD11	1:B:334:ALA:H	1.79	0.46
1:C:272:VAL:CG2	1:C:273:GLN:H	2.24	0.46
1:D:129:ALA:HB3	1:D:222:TRP:HE1	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:157:ILE:O	1:D:157:ILE:HD12	2.16	0.46
1:E:144:ARG:O	1:E:145:SER:C	2.54	0.46
1:F:140:ASP:N	1:F:143:GLU:OE1	2.46	0.46
1:F:153:PRO:HA	1:F:222:TRP:CZ3	2.49	0.46
1:F:170:ASP:O	1:F:171:ASN:OD1	2.34	0.46
1:H:153:PRO:HA	1:H:222:TRP:CZ3	2.51	0.46
1:H:272:VAL:HG22	1:H:273:GLN:N	2.31	0.46
1:A:152:PHE:CE2	1:A:223:GLY:CA	2.96	0.46
1:A:152:PHE:HB2	1:A:153:PRO:HD2	1.97	0.46
1:B:131:GLU:O	1:B:133:ASN:N	2.49	0.46
1:B:239:ARG:C	1:B:241:ARG:H	2.19	0.46
1:B:269:LEU:CB	1:B:346:VAL:CG2	2.73	0.46
1:B:270:GLU:O	1:B:346:VAL:HA	2.15	0.46
1:B:299:ALA:O	1:B:337:VAL:HA	2.15	0.46
1:C:130:ILE:HG13	1:C:136:PHE:CB	2.46	0.46
1:C:220:LYS:C	1:C:221:LEU:HD23	2.35	0.46
1:D:253:ILE:C	1:D:255:GLU:H	2.19	0.46
1:D:366:ARG:HG2	1:D:367:ASN:H	1.80	0.46
1:E:174:VAL:CG1	1:E:222:TRP:HB2	2.46	0.46
1:E:279:LYS:O	1:E:279:LYS:HG3	2.15	0.46
1:E:325:ILE:HG12	2:E:402:CMP:O3'	2.16	0.46
1:F:328:LEU:HD11	1:F:364:LEU:HD11	1.96	0.46
1:G:155:SER:O	1:G:156:PHE:CD1	2.69	0.46
1:G:211:ASP:OD1	2:G:401:CMP:H5'1	2.14	0.46
1:G:265:VAL:C	1:G:269:LEU:CD1	2.84	0.46
1:H:175:ILE:HD11	1:H:194:GLU:C	2.35	0.46
1:A:113:ARG:NE	1:D:113:ARG:O	2.49	0.46
1:A:249:SER:CA	1:A:262:ARG:NH2	2.68	0.46
1:A:279:LYS:HB3	1:A:338:VAL:CG2	2.43	0.46
1:B:171:ASN:HB2	1:B:173:TYR:CE1	2.51	0.46
1:B:273:GLN:CB	1:B:343:LEU:O	2.59	0.46
1:B:292:ILE:HB	1:B:346:VAL:CG1	2.45	0.46
1:C:110:SER:C	1:F:114:LYS:HZ3	2.19	0.46
1:C:120:TYR:CD2	1:C:121:LYS:N	2.84	0.46
1:C:188:TRP:HZ3	1:C:190:THR:C	2.16	0.46
1:C:375:VAL:HG23	1:C:376:SER:N	2.25	0.46
1:D:126:LEU:O	1:D:127:ALA:C	2.52	0.46
1:D:200:GLU:CD	1:D:201:LEU:HD12	2.36	0.46
1:E:175:ILE:CD1	1:E:194:GLU:HA	2.41	0.46
1:E:178:GLY:CA	1:E:219:VAL:HG12	2.32	0.46
1:E:209:ARG:HD2	2:E:401:CMP:O5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:152:PHE:HD2	1:F:152:PHE:H	1.63	0.46
1:F:290:PHE:C	1:F:291:PHE:CD1	2.79	0.46
1:G:164:GLN:O	1:G:167:ASP:HB2	2.16	0.46
1:G:221:LEU:HA	1:G:221:LEU:HD23	1.42	0.46
1:G:251:VAL:HG12	1:G:254:LEU:HD21	1.90	0.46
1:H:302:GLN:O	1:H:309:GLU:O	2.33	0.46
1:A:111:TYR:O	1:A:112:VAL:CG1	2.64	0.46
1:A:111:TYR:CA	1:D:115:VAL:CG2	2.90	0.46
1:A:133:ASN:O	1:A:135:LEU:HD12	2.16	0.46
1:A:136:PHE:HE1	1:A:233:LEU:CD2	2.28	0.46
1:A:154:VAL:HG12	1:A:221:LEU:CB	2.32	0.46
1:A:247:PHE:HE1	1:A:294:LEU:HB3	1.81	0.46
1:B:260:TRP:CZ2	2:B:401:CMP:H8	2.51	0.46
1:B:302:GLN:O	1:B:310:PHE:CA	2.62	0.46
1:C:176:ASP:N	1:C:220:LYS:O	2.48	0.46
1:C:208:PRO:O	1:C:209:ARG:C	2.52	0.46
1:C:253:ILE:HD13	1:C:321:TYR:CE2	2.51	0.46
1:C:301:LEU:HD13	1:C:336:THR:HB	1.97	0.46
1:C:328:LEU:HD22	1:C:365:LYS:HE3	1.98	0.46
1:D:241:ARG:O	1:D:242:LYS:C	2.52	0.46
1:D:348:LEU:HD21	1:D:356:VAL:CG2	2.46	0.46
1:E:116:ILE:HG22	1:E:118:LYS:CG	2.43	0.46
1:E:164:GLN:CA	1:E:212:THR:HG22	2.37	0.46
1:E:363:ILE:O	1:E:366:ARG:HG2	2.16	0.46
1:F:113:ARG:CD	1:F:146:ASP:OD2	2.64	0.46
1:F:130:ILE:HG13	1:F:136:PHE:CB	2.45	0.46
1:F:274:PHE:N	1:F:343:LEU:O	2.40	0.46
1:G:147:ILE:HD13	1:G:147:ILE:HG21	1.54	0.46
1:G:162:VAL:CG2	1:G:213:VAL:O	2.63	0.46
1:H:158:ALA:HA	1:H:215:ALA:HB1	1.98	0.46
1:H:285:GLU:HB2	1:H:333:ARG:CG	2.46	0.46
1:H:297:SER:HA	1:H:316:LEU:O	2.16	0.46
1:H:313:VAL:HG12	1:H:314:GLY:N	2.31	0.46
1:H:341:GLY:HA3	1:H:342:PRO:HD2	1.67	0.46
1:B:203:LEU:CD1	1:B:229:TYR:HD2	2.28	0.46
1:B:211:ASP:OD1	2:B:401:CMP:O1P	2.34	0.46
1:B:241:ARG:O	1:B:245:GLU:HB2	2.16	0.46
1:C:259:LYS:O	1:C:262:ARG:N	2.49	0.46
1:C:261:GLU:O	1:C:264:THR:N	2.49	0.46
1:C:268:ALA:O	1:C:352:ARG:NH1	2.49	0.46
1:C:343:LEU:HD12	1:C:343:LEU:HA	1.77	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:152:PHE:HE1	1:D:223:GLY:HA3	1.81	0.46
1:E:143:GLU:O	1:E:144:ARG:C	2.54	0.46
1:E:273:GLN:HE21	1:E:273:GLN:CA	2.20	0.46
1:E:325:ILE:CD1	1:E:334:ALA:HB3	2.46	0.46
1:F:226:ARG:O	1:F:227:ASP:C	2.53	0.46
1:F:232:ILE:HG23	1:F:233:LEU:HG	1.98	0.46
1:G:270:GLU:O	1:G:346:VAL:HA	2.15	0.46
1:G:300:VAL:CG2	1:G:316:LEU:HD11	2.46	0.46
1:H:131:GLU:OE1	1:H:131:GLU:CA	2.62	0.46
1:H:164:GLN:O	1:H:167:ASP:HB2	2.16	0.46
1:H:208:PRO:O	1:H:209:ARG:C	2.54	0.46
1:A:253:ILE:HG13	1:A:254:LEU:HG	1.97	0.45
1:A:343:LEU:HD12	1:A:343:LEU:HA	1.70	0.45
1:B:325:ILE:HD13	1:B:334:ALA:HB3	1.98	0.45
1:C:154:VAL:O	1:C:154:VAL:CG1	2.63	0.45
1:C:158:ALA:HB2	1:C:218:ASN:N	2.29	0.45
1:C:300:VAL:CG2	1:C:312:GLU:OE2	2.64	0.45
1:D:113:ARG:NH1	1:D:146:ASP:OD1	2.49	0.45
1:F:114:LYS:HD2	1:F:114:LYS:HA	1.33	0.45
1:F:127:ALA:O	1:F:128:LYS:C	2.52	0.45
1:F:201:LEU:O	1:F:204:ILE:N	2.49	0.45
1:F:221:LEU:HD23	1:F:221:LEU:HA	1.48	0.45
1:G:152:PHE:HE2	1:G:223:GLY:CA	2.29	0.45
1:G:292:ILE:O	1:G:345:CYS:HB3	2.17	0.45
1:H:221:LEU:HD23	1:H:221:LEU:HA	1.36	0.45
1:H:281:VAL:HG13	1:H:333:ARG:HG3	1.96	0.45
1:H:325:ILE:HG12	2:H:402:CMP:O3'	2.17	0.45
1:B:365:LYS:O	1:B:368:ILE:N	2.35	0.45
1:C:144:ARG:NH1	1:C:144:ARG:HB2	2.30	0.45
1:D:362:ASP:O	1:D:365:LYS:HG3	2.16	0.45
1:E:230:ARG:HG2	1:E:230:ARG:NH1	2.31	0.45
1:E:255:GLU:OE1	1:E:255:GLU:CA	2.41	0.45
1:E:292:ILE:HB	1:E:346:VAL:CG1	2.38	0.45
1:E:328:LEU:HD11	1:E:364:LEU:HD11	1.98	0.45
1:F:160:GLU:O	1:F:214:LYS:HA	2.16	0.45
1:F:278:GLN:HG2	1:F:279:LYS:H	1.77	0.45
1:G:165:GLN:HG2	1:G:166:GLY:N	2.30	0.45
1:G:198:PHE:HD1	1:G:198:PHE:N	2.14	0.45
1:G:247:PHE:HE1	1:G:294:LEU:CB	2.29	0.45
1:H:188:TRP:CH2	1:H:190:THR:CA	2.97	0.45
1:H:362:ASP:O	1:H:363:ILE:C	2.54	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:LYS:O	1:A:122:THR:C	2.54	0.45
1:A:157:ILE:CB	1:A:218:ASN:OD1	2.65	0.45
1:A:280:ILE:HB	1:A:291:PHE:CE2	2.46	0.45
1:B:226:ARG:O	1:B:227:ASP:O	2.35	0.45
1:B:245:GLU:OE1	1:B:246:GLU:OE1	2.35	0.45
1:C:130:ILE:HD12	1:C:136:PHE:CD2	2.51	0.45
1:C:162:VAL:HG22	1:C:213:VAL:O	2.16	0.45
1:C:163:ILE:HD12	1:C:213:VAL:CG2	2.46	0.45
1:C:313:VAL:HG21	2:C:402:CMP:N6	2.32	0.45
1:D:123:MET:O	1:D:126:LEU:N	2.50	0.45
1:D:274:PHE:HD2	1:D:343:LEU:HD23	1.81	0.45
1:D:366:ARG:CG	1:D:367:ASN:N	2.79	0.45
1:E:175:ILE:HA	1:E:221:LEU:HD23	1.88	0.45
1:E:254:LEU:HB2	1:E:257:LEU:HD12	1.99	0.45
1:F:175:ILE:HG21	1:F:180:MET:HG3	1.98	0.45
1:F:366:ARG:HG2	1:F:367:ASN:N	2.31	0.45
1:H:371:TYR:CD1	2:H:402:CMP:C6	3.05	0.45
1:A:120:TYR:CD2	1:A:121:LYS:N	2.81	0.45
1:B:162:VAL:HG22	1:B:213:VAL:O	2.15	0.45
1:B:165:GLN:HE22	1:B:185:ASN:HD21	1.64	0.45
1:B:280:ILE:HD12	1:B:281:VAL:HG23	1.98	0.45
1:C:154:VAL:O	1:C:221:LEU:N	2.37	0.45
1:D:154:VAL:HG12	1:D:221:LEU:HB2	1.99	0.45
1:D:157:ILE:CD1	1:F:243:MET:HE1	2.46	0.45
1:D:268:ALA:C	1:D:269:LEU:O	2.45	0.45
1:D:316:LEU:O	1:D:316:LEU:CD2	2.64	0.45
1:F:153:PRO:HB3	1:F:222:TRP:CH2	2.51	0.45
1:F:254:LEU:C	1:F:254:LEU:CD1	2.84	0.45
1:F:325:ILE:CG1	2:F:402:CMP:O1P	2.65	0.45
1:G:123:MET:HE2	1:G:123:MET:HB2	1.95	0.45
1:G:325:ILE:O	1:G:328:LEU:N	2.49	0.45
1:G:368:ILE:HA	1:G:371:TYR:HD2	1.81	0.45
1:H:120:TYR:O	1:H:121:LYS:C	2.52	0.45
1:H:121:LYS:O	1:H:122:THR:C	2.54	0.45
1:H:173:TYR:CB	1:H:198:PHE:HE1	2.29	0.45
1:H:254:LEU:O	1:H:257:LEU:HG	2.17	0.45
1:H:260:TRP:HZ2	2:H:401:CMP:O2'	1.98	0.45
1:A:157:ILE:O	1:A:160:GLU:HB2	2.16	0.45
1:A:183:TYR:CE1	1:A:188:TRP:HB3	2.51	0.45
1:A:183:TYR:HE1	1:A:188:TRP:CB	2.28	0.45
1:A:221:LEU:HD23	1:A:221:LEU:HA	1.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:LYS:CE	1:B:148:PHE:O	2.54	0.45
1:B:302:GLN:O	1:B:310:PHE:CB	2.64	0.45
1:C:157:ILE:HB	1:C:218:ASN:OD1	2.17	0.45
1:C:283:GLN:CG	1:C:333:ARG:O	2.64	0.45
1:D:114:LYS:O	1:D:114:LYS:CG	2.62	0.45
1:D:174:VAL:HG13	1:D:222:TRP:HB2	1.98	0.45
1:E:239:ARG:HD3	1:G:157:ILE:CG1	2.47	0.45
1:F:139:LEU:N	1:F:139:LEU:CD1	2.67	0.45
1:F:211:ASP:OD2	2:F:401:CMP:C3'	2.63	0.45
1:G:139:LEU:HD21	1:G:147:ILE:HD13	1.99	0.45
1:G:153:PRO:HA	1:G:222:TRP:CE3	2.51	0.45
1:G:183:TYR:HD1	1:G:188:TRP:CA	2.29	0.45
1:G:230:ARG:HG2	1:G:230:ARG:HH11	1.82	0.45
1:G:366:ARG:O	1:G:369:GLN:CB	2.63	0.45
1:G:371:TYR:OH	2:G:402:CMP:H2'	2.16	0.45
1:H:123:MET:HB2	1:H:123:MET:HE2	1.65	0.45
1:H:130:ILE:HD13	1:H:151:MET:HE2	1.98	0.45
1:H:158:ALA:CA	1:H:217:THR:O	2.65	0.45
1:H:283:GLN:CA	1:H:333:ARG:O	2.63	0.45
1:A:230:ARG:CZ	1:A:234:MET:CE	2.94	0.45
1:B:259:LYS:CG	1:B:260:TRP:N	2.61	0.45
1:B:262:ARG:HE	1:B:262:ARG:HB3	1.42	0.45
1:C:221:LEU:HD23	1:C:221:LEU:HA	1.43	0.45
1:D:232:ILE:HG23	1:D:233:LEU:CG	2.45	0.45
1:D:268:ALA:O	1:D:352:ARG:NH1	2.50	0.45
1:D:283:GLN:HG2	1:D:284:GLY:N	2.30	0.45
1:E:123:MET:C	1:E:125:ALA:N	2.68	0.45
1:E:194:GLU:O	1:E:355:ARG:HD2	2.17	0.45
1:E:224:ILE:HD13	1:E:224:ILE:C	2.36	0.45
1:E:265:VAL:CG1	1:E:269:LEU:CD2	2.65	0.45
1:E:293:ILE:CD1	1:E:343:LEU:HD11	2.46	0.45
1:F:120:TYR:O	1:F:121:LYS:C	2.51	0.45
1:F:291:PHE:CD1	1:F:347:LYS:NZ	2.78	0.45
1:G:269:LEU:HB3	1:G:346:VAL:HG22	1.95	0.45
1:H:230:ARG:HB3	1:H:234:MET:CE	2.47	0.45
1:H:352:ARG:HA	1:H:355:ARG:HB2	1.98	0.45
1:A:113:ARG:HH12	1:D:150:ALA:HB2	1.81	0.45
1:B:130:ILE:HD11	1:B:151:MET:CE	2.46	0.45
1:C:153:PRO:HA	1:C:222:TRP:CE3	2.51	0.45
1:D:200:GLU:CG	1:D:201:LEU:HD12	2.46	0.45
1:D:300:VAL:HG13	1:D:313:VAL:HG13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:118:LYS:CE	1:E:148:PHE:O	2.56	0.45
1:E:131:GLU:O	1:E:132:LYS:C	2.54	0.45
1:E:270:GLU:O	1:E:346:VAL:HA	2.17	0.45
1:F:130:ILE:HD12	1:F:151:MET:CE	2.47	0.45
1:G:171:ASN:OD1	1:G:225:ASP:HA	2.16	0.45
1:H:226:ARG:HA	1:H:229:TYR:HB3	1.99	0.45
1:H:254:LEU:HB2	1:H:257:LEU:HD12	1.98	0.45
1:H:262:ARG:HA	1:H:265:VAL:HG21	1.98	0.45
1:H:282:VAL:O	1:H:333:ARG:HB2	2.16	0.45
1:A:253:ILE:HG13	1:A:254:LEU:CG	2.45	0.45
1:C:120:TYR:CE2	1:C:124:ALA:HB2	2.51	0.45
1:C:188:TRP:CZ3	1:C:190:THR:CA	2.99	0.45
1:C:188:TRP:HZ3	1:C:190:THR:O	2.00	0.45
1:C:259:LYS:C	1:C:262:ARG:HG3	2.38	0.45
1:E:116:ILE:HG22	1:E:118:LYS:HZ2	1.80	0.45
1:F:129:ALA:HA	1:F:132:LYS:HE3	1.99	0.45
1:F:209:ARG:HD2	2:F:401:CMP:O5'	2.16	0.45
1:G:234:MET:O	1:G:238:LEU:HD12	2.17	0.45
1:G:265:VAL:HG12	1:G:269:LEU:CD2	2.41	0.45
1:G:278:GLN:HG3	1:G:279:LYS:H	1.79	0.45
1:H:229:TYR:O	1:H:233:LEU:HD12	2.17	0.45
1:B:262:ARG:HA	1:B:265:VAL:HG21	1.97	0.45
1:C:176:ASP:O	1:C:194:GLU:HG2	2.17	0.45
1:C:190:THR:CG2	1:C:191:SER:N	2.76	0.45
1:C:201:LEU:O	1:C:204:ILE:N	2.50	0.45
1:C:203:LEU:HD22	1:C:226:ARG:CG	2.46	0.45
1:C:293:ILE:CG1	1:C:345:CYS:SG	3.01	0.45
1:D:160:GLU:C	1:D:214:LYS:HE3	2.37	0.45
1:D:304:ARG:CB	1:D:308:GLU:CB	2.95	0.45
1:E:110:SER:HB2	1:H:115:VAL:HG22	1.99	0.45
1:E:118:LYS:NZ	1:E:151:MET:O	2.43	0.45
1:E:147:ILE:O	1:E:150:ALA:N	2.50	0.45
1:E:180:MET:O	1:E:191:SER:HA	2.16	0.45
1:E:183:TYR:CD1	1:E:188:TRP:CB	3.00	0.45
1:E:203:LEU:CD1	1:E:229:TYR:CD2	2.95	0.45
1:E:232:ILE:HG23	1:E:233:LEU:HG	1.98	0.45
1:E:239:ARG:HH22	1:G:156:PHE:HD1	1.61	0.45
1:F:289:GLU:CG	1:F:347:LYS:HZ1	2.27	0.45
1:F:301:LEU:HD13	1:F:311:VAL:N	2.32	0.45
1:G:151:MET:HA	1:G:224:ILE:CG2	2.46	0.45
1:G:347:LYS:O	1:G:348:LEU:CD1	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:350:ARG:O	1:G:353:PHE:CB	2.57	0.45
1:H:302:GLN:O	1:H:310:PHE:CE1	2.69	0.45
1:A:249:SER:HA	1:A:262:ARG:NH2	2.32	0.45
1:B:157:ILE:HD12	1:B:157:ILE:C	2.36	0.45
1:B:261:GLU:O	1:B:264:THR:N	2.50	0.45
1:B:357:LEU:O	1:B:360:CYS:HB2	2.17	0.45
1:C:270:GLU:CB	1:C:271:PRO:CD	2.94	0.45
1:C:300:VAL:CG2	1:C:313:VAL:HG12	2.37	0.45
1:C:325:ILE:HG12	2:C:402:CMP:P	2.57	0.45
1:C:328:LEU:HD23	1:C:365:LYS:HE3	1.98	0.45
1:E:234:MET:HG3	1:E:238:LEU:CD1	2.47	0.45
1:E:253:ILE:CG2	1:E:321:TYR:CE2	2.96	0.45
1:E:281:VAL:CG1	1:E:333:ARG:NE	2.80	0.45
1:F:115:VAL:HG12	1:F:149:ASP:HB3	1.99	0.45
1:G:152:PHE:CD2	1:G:152:PHE:N	2.80	0.45
1:G:247:PHE:HE1	1:G:294:LEU:HB3	1.81	0.45
1:A:316:LEU:HB2	1:A:320:ASP:OD2	2.16	0.44
1:B:126:LEU:O	1:B:126:LEU:CD1	2.47	0.44
1:C:143:GLU:O	1:C:144:ARG:C	2.54	0.44
1:D:121:LYS:O	1:D:122:THR:C	2.55	0.44
1:D:237:THR:O	1:D:241:ARG:HG3	2.16	0.44
1:D:300:VAL:HG13	1:D:300:VAL:O	2.16	0.44
1:D:300:VAL:HG23	1:D:335:ALA:HB1	1.96	0.44
1:E:297:SER:O	1:E:340:ARG:HB2	2.17	0.44
1:H:158:ALA:CB	1:H:217:THR:O	2.65	0.44
1:H:163:ILE:HD11	1:H:198:PHE:CZ	2.53	0.44
1:A:272:VAL:CG2	1:A:273:GLN:N	2.80	0.44
1:A:361:SER:HB2	1:A:365:LYS:HZ1	1.82	0.44
1:B:300:VAL:CG1	1:B:335:ALA:CB	2.94	0.44
1:C:366:ARG:O	1:C:369:GLN:CB	2.65	0.44
1:D:253:ILE:CD1	1:D:321:TYR:CD2	3.00	0.44
1:E:261:GLU:O	1:E:264:THR:N	2.50	0.44
1:E:278:GLN:O	1:E:338:VAL:HG22	2.18	0.44
1:F:113:ARG:CD	1:F:146:ASP:HA	2.47	0.44
1:F:121:LYS:O	1:F:123:MET:N	2.50	0.44
1:F:280:ILE:HB	1:F:291:PHE:CE2	2.51	0.44
1:G:175:ILE:HA	1:G:221:LEU:HD23	1.92	0.44
1:G:292:ILE:HB	1:G:346:VAL:CG1	2.44	0.44
1:G:295:GLU:CB	1:G:344:LYS:HB3	2.43	0.44
1:H:262:ARG:HE	1:H:262:ARG:HB3	1.48	0.44
1:H:328:LEU:HD12	1:H:328:LEU:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:LEU:CD2	1:A:147:ILE:CD1	2.96	0.44
1:A:201:LEU:O	1:A:204:ILE:N	2.51	0.44
1:A:271:PRO:O	1:A:272:VAL:HB	2.18	0.44
1:A:272:VAL:CG2	1:A:273:GLN:H	2.21	0.44
1:B:162:VAL:HG23	1:B:163:ILE:H	1.81	0.44
1:B:173:TYR:CD2	1:B:198:PHE:CZ	2.95	0.44
1:B:269:LEU:CD2	1:B:346:VAL:CG2	2.92	0.44
1:C:183:TYR:HD1	1:C:188:TRP:CA	2.28	0.44
1:C:259:LYS:O	1:C:262:ARG:CG	2.60	0.44
1:D:158:ALA:HB1	1:D:216:LYS:O	2.18	0.44
1:D:183:TYR:CD1	1:D:188:TRP:CB	3.01	0.44
1:E:121:LYS:O	1:E:122:THR:C	2.55	0.44
1:E:239:ARG:HH22	1:G:156:PHE:HA	1.82	0.44
1:E:265:VAL:C	1:E:269:LEU:HG	2.32	0.44
1:E:302:GLN:NE2	1:E:374:PHE:CB	2.80	0.44
1:F:139:LEU:HD21	1:F:147:ILE:HD13	1.98	0.44
1:G:172:PHE:CE1	1:G:200:GLU:HB3	2.53	0.44
1:G:309:GLU:OE1	1:G:309:GLU:HA	2.17	0.44
1:A:273:GLN:HE21	1:A:273:GLN:CA	2.23	0.44
1:B:124:ALA:O	1:B:127:ALA:HB3	2.17	0.44
1:C:111:TYR:CD1	1:C:112:VAL:N	2.85	0.44
1:D:198:PHE:HD1	1:D:198:PHE:H	1.66	0.44
1:D:335:ALA:HB3	2:D:402:CMP:H5'1	2.00	0.44
1:E:259:LYS:O	1:E:262:ARG:N	2.49	0.44
1:E:325:ILE:HD11	1:E:334:ALA:H	1.80	0.44
1:E:352:ARG:HA	1:E:355:ARG:HB2	2.00	0.44
1:F:121:LYS:O	1:F:122:THR:C	2.55	0.44
1:F:185:ASN:O	1:F:186:ASN:HB2	2.18	0.44
1:F:300:VAL:HG11	1:F:335:ALA:CB	2.47	0.44
1:G:274:PHE:CD2	1:G:343:LEU:HD23	2.52	0.44
1:A:293:ILE:CG1	1:A:343:LEU:HD11	2.48	0.44
1:B:152:PHE:HD2	1:B:152:PHE:N	2.14	0.44
1:B:202:ALA:HB1	1:B:207:THR:O	2.18	0.44
1:B:253:ILE:HG13	1:B:254:LEU:HD23	1.98	0.44
1:D:246:GLU:C	1:D:248:LEU:N	2.66	0.44
1:E:203:LEU:HD22	1:E:226:ARG:HD3	2.00	0.44
1:E:247:PHE:C	1:E:247:PHE:HD2	2.18	0.44
1:F:147:ILE:O	1:F:150:ALA:N	2.51	0.44
1:G:357:LEU:HD12	1:G:357:LEU:HA	1.67	0.44
1:H:153:PRO:CB	1:H:222:TRP:HZ3	2.28	0.44
1:A:149:ASP:OD1	1:B:120:TYR:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:LEU:O	1:A:295:GLU:CG	2.65	0.44
1:B:262:ARG:HA	1:B:265:VAL:HG23	1.99	0.44
1:C:265:VAL:C	1:C:269:LEU:CD1	2.86	0.44
1:C:362:ASP:N	1:C:365:LYS:HZ2	2.08	0.44
1:D:257:LEU:HD21	1:D:360:CYS:SG	2.58	0.44
1:E:266:ALA:N	1:E:269:LEU:HD11	2.33	0.44
1:F:183:TYR:HD1	1:F:188:TRP:CA	2.30	0.44
1:F:253:ILE:HG13	1:F:254:LEU:N	2.30	0.44
1:G:130:ILE:HG13	1:G:136:PHE:CD2	2.53	0.44
1:G:147:ILE:HG23	1:G:232:ILE:HD13	2.00	0.44
1:H:229:TYR:CD1	1:H:233:LEU:HD12	2.45	0.44
1:A:144:ARG:HB2	1:A:144:ARG:HH11	1.79	0.44
1:A:238:LEU:O	1:A:241:ARG:HB2	2.18	0.44
1:B:183:TYR:HE1	1:B:188:TRP:HB2	1.78	0.44
1:C:295:GLU:CG	1:C:318:PRO:HG3	2.48	0.44
1:D:247:PHE:CD2	1:D:247:PHE:O	2.70	0.44
1:D:278:GLN:HG2	1:D:279:LYS:N	2.32	0.44
1:D:280:ILE:HB	1:D:291:PHE:HE2	1.82	0.44
1:E:175:ILE:HD13	1:E:194:GLU:CA	2.43	0.44
1:E:357:LEU:HD12	1:E:357:LEU:N	2.28	0.44
1:E:366:ARG:O	1:E:369:GLN:HB2	2.18	0.44
1:F:113:ARG:NE	1:F:146:ASP:OD1	2.51	0.44
1:F:153:PRO:N	1:F:222:TRP:HZ3	2.16	0.44
1:F:178:GLY:N	1:F:194:GLU:HG3	2.30	0.44
1:F:185:ASN:OD1	1:F:185:ASN:N	2.46	0.44
1:G:157:ILE:CA	1:G:218:ASN:OD1	2.66	0.44
1:H:147:ILE:O	1:H:150:ALA:N	2.51	0.44
1:H:273:GLN:HB3	1:H:343:LEU:O	2.17	0.44
1:H:303:ARG:N	1:H:310:PHE:CE1	2.85	0.44
1:A:115:VAL:HG12	1:A:149:ASP:HB3	2.00	0.44
1:A:130:ILE:HG23	1:A:131:GLU:N	2.33	0.44
1:B:123:MET:O	1:B:124:ALA:C	2.56	0.44
1:B:164:GLN:O	1:B:167:ASP:HB2	2.18	0.44
1:B:329:MET:HA	1:B:329:MET:HE2	1.98	0.44
1:C:130:ILE:CG1	1:C:136:PHE:CD2	3.01	0.44
1:C:151:MET:HA	1:C:224:ILE:CG2	2.48	0.44
1:C:175:ILE:HD11	1:C:195:GLY:N	2.33	0.44
1:C:353:PHE:CD1	1:C:357:LEU:HD22	2.53	0.44
1:D:224:ILE:HD13	1:D:224:ILE:C	2.35	0.44
1:D:348:LEU:HD23	1:D:353:PHE:HA	1.99	0.44
1:F:211:ASP:OD1	2:F:401:CMP:H5'1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:278:GLN:HG2	1:F:279:LYS:N	2.27	0.44
1:F:331:ARG:HB3	1:F:332:PRO:CD	2.48	0.44
1:G:253:ILE:HG13	1:G:254:LEU:HD23	1.99	0.44
1:G:293:ILE:HG21	1:G:317:GLY:C	2.37	0.44
1:G:352:ARG:HA	1:G:355:ARG:HB2	1.99	0.44
1:G:357:LEU:CD1	1:G:357:LEU:N	2.74	0.44
1:H:165:GLN:CG	1:H:166:GLY:N	2.81	0.44
1:H:172:PHE:HB3	1:H:224:ILE:HD13	1.94	0.44
1:H:293:ILE:CG2	1:H:317:GLY:C	2.84	0.44
1:A:120:TYR:CD1	1:B:148:PHE:CB	2.97	0.44
1:A:152:PHE:HD2	1:A:152:PHE:H	1.65	0.44
1:A:294:LEU:O	1:A:318:PRO:HB3	2.18	0.44
1:A:317:GLY:O	1:A:320:ASP:HB2	2.18	0.44
1:B:175:ILE:HA	1:B:221:LEU:HD23	1.90	0.44
1:B:209:ARG:HD3	2:B:401:CMP:O2P	2.17	0.44
1:B:234:MET:HG3	1:B:238:LEU:CD1	2.42	0.44
1:B:263:LEU:O	1:B:266:ALA:CB	2.58	0.44
1:C:127:ALA:O	1:C:130:ILE:HG22	2.18	0.44
1:C:173:TYR:HB2	1:C:198:PHE:HE1	1.83	0.44
1:C:203:LEU:HD12	1:C:229:TYR:HD2	1.83	0.44
1:C:260:TRP:HA	1:C:263:LEU:HD23	1.99	0.44
1:D:121:LYS:O	1:D:123:MET:N	2.50	0.44
1:D:323:GLY:O	1:D:324:GLU:O	2.36	0.44
1:E:144:ARG:O	1:E:147:ILE:HG12	2.18	0.44
1:E:157:ILE:CB	1:E:218:ASN:OD1	2.66	0.44
1:E:163:ILE:O	1:E:213:VAL:N	2.39	0.44
1:F:269:LEU:CB	1:F:346:VAL:HG21	2.40	0.44
1:G:230:ARG:CZ	1:G:234:MET:HE1	2.48	0.44
1:H:138:HIS:HD1	1:H:138:HIS:H	1.65	0.44
1:H:173:TYR:O	1:H:197:SER:HA	2.17	0.44
1:H:283:GLN:OE1	1:H:302:GLN:HG2	2.18	0.44
1:H:360:CYS:O	1:H:364:LEU:HD23	2.18	0.44
1:A:183:TYR:HE1	1:A:188:TRP:HB2	1.79	0.43
1:A:325:ILE:O	1:A:328:LEU:N	2.51	0.43
1:B:294:LEU:N	1:B:294:LEU:CD1	2.52	0.43
1:C:325:ILE:HD11	1:C:334:ALA:HB3	1.99	0.43
1:D:126:LEU:CB	1:D:222:TRP:CZ2	2.91	0.43
1:D:226:ARG:HA	1:D:229:TYR:HB3	1.99	0.43
1:D:230:ARG:HG2	1:D:230:ARG:NH1	2.33	0.43
1:E:238:LEU:HD23	1:E:238:LEU:HA	1.71	0.43
1:E:252:SER:OG	1:E:253:ILE:N	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:293:ILE:HD12	1:E:343:LEU:HD11	1.99	0.43
1:E:324:GLU:OE2	1:E:371:TYR:HE2	2.00	0.43
1:F:114:LYS:CE	1:F:115:VAL:CG2	2.96	0.43
1:F:278:GLN:O	1:F:279:LYS:HB3	2.18	0.43
1:F:284:GLY:C	1:F:332:PRO:HB3	2.39	0.43
1:F:300:VAL:HG13	1:F:336:THR:O	2.18	0.43
1:F:348:LEU:CD2	1:F:356:VAL:CG2	2.96	0.43
1:F:362:ASP:HA	1:F:365:LYS:HZ3	1.83	0.43
1:G:180:MET:O	1:G:191:SER:HA	2.18	0.43
1:G:203:LEU:HD22	1:G:226:ARG:CG	2.48	0.43
1:G:283:GLN:N	1:G:336:THR:OG1	2.39	0.43
1:G:293:ILE:HG13	1:G:345:CYS:HG	1.75	0.43
1:H:158:ALA:HA	1:H:217:THR:O	2.16	0.43
1:H:173:TYR:HD1	1:H:223:GLY:HA3	1.83	0.43
1:A:322:PHE:CD2	1:A:337:VAL:HG21	2.53	0.43
1:B:115:VAL:HA	1:B:149:ASP:HB3	2.00	0.43
1:B:171:ASN:OD1	1:B:225:ASP:HA	2.18	0.43
1:B:262:ARG:O	1:B:265:VAL:CB	2.58	0.43
1:B:268:ALA:C	1:B:269:LEU:O	2.54	0.43
1:B:365:LYS:O	1:B:368:ILE:CG1	2.54	0.43
1:C:118:LYS:C	1:D:117:PRO:O	2.57	0.43
1:C:173:TYR:CB	1:C:198:PHE:HE1	2.31	0.43
1:D:175:ILE:HG22	1:D:221:LEU:CD2	2.48	0.43
1:D:204:ILE:HG22	1:D:205:TYR:CE2	2.51	0.43
1:D:299:ALA:N	1:D:338:VAL:O	2.42	0.43
1:D:361:SER:HB2	1:D:365:LYS:HZ1	1.82	0.43
1:E:152:PHE:CE2	1:E:223:GLY:CA	2.96	0.43
1:E:226:ARG:O	1:E:227:ASP:C	2.56	0.43
1:F:121:LYS:C	1:F:123:MET:N	2.70	0.43
1:F:203:LEU:CD1	1:F:229:TYR:CD2	2.96	0.43
1:H:291:PHE:CD1	1:H:347:LYS:NZ	2.86	0.43
1:A:111:TYR:C	1:D:115:VAL:HG23	2.38	0.43
1:A:173:TYR:HD1	1:A:223:GLY:CA	2.32	0.43
1:A:209:ARG:HA	2:A:401:CMP:O2P	2.18	0.43
1:A:325:ILE:CD1	1:A:334:ALA:HB2	2.48	0.43
1:C:111:TYR:O	1:C:112:VAL:HG12	2.13	0.43
1:C:163:ILE:HD11	1:C:198:PHE:CZ	2.53	0.43
1:C:226:ARG:O	1:C:227:ASP:C	2.57	0.43
1:C:262:ARG:HA	1:C:265:VAL:CG2	2.47	0.43
1:C:287:GLY:HA3	1:C:326:ALA:HB3	1.97	0.43
1:D:254:LEU:HB2	1:D:257:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:323:GLY:HA2	2:D:402:CMP:O2P	2.18	0.43
1:F:139:LEU:HD21	1:F:147:ILE:CD1	2.48	0.43
1:F:151:MET:HA	1:F:224:ILE:CG2	2.48	0.43
1:F:161:THR:HA	1:F:214:LYS:CD	2.34	0.43
1:F:247:PHE:CE2	1:F:292:ILE:HG21	2.53	0.43
1:F:352:ARG:O	1:F:353:PHE:C	2.56	0.43
1:G:204:ILE:HG22	1:G:205:TYR:CE2	2.52	0.43
1:H:135:LEU:CD1	1:H:136:PHE:N	2.78	0.43
1:H:253:ILE:C	1:H:255:GLU:N	2.71	0.43
1:A:112:VAL:O	1:A:231:ARG:NH2	2.51	0.43
1:A:135:LEU:CD1	1:A:136:PHE:CD2	3.02	0.43
1:A:226:ARG:O	1:A:227:ASP:O	2.37	0.43
1:B:139:LEU:CD2	1:B:147:ILE:CD1	2.95	0.43
1:B:153:PRO:CA	1:B:222:TRP:HZ3	2.27	0.43
1:B:276:ASP:OD2	1:B:341:GLY:N	2.39	0.43
1:C:280:ILE:HB	1:C:291:PHE:CE2	2.52	0.43
1:C:285:GLU:HB2	1:C:333:ARG:CG	2.48	0.43
1:D:201:LEU:O	1:D:205:TYR:N	2.49	0.43
1:E:249:SER:H	1:E:262:ARG:HH22	1.57	0.43
2:E:402:CMP:N3	2:E:402:CMP:H2'	2.32	0.43
1:F:152:PHE:CD2	1:F:152:PHE:N	2.83	0.43
1:G:120:TYR:CD2	1:G:120:TYR:O	2.72	0.43
1:G:129:ALA:CB	1:G:222:TRP:HE1	2.30	0.43
1:H:130:ILE:CD1	1:H:136:PHE:CE2	3.02	0.43
1:A:123:MET:C	1:A:125:ALA:N	2.71	0.43
1:B:115:VAL:O	1:B:115:VAL:CG2	2.65	0.43
1:C:148:PHE:CE1	1:D:120:TYR:CE1	3.06	0.43
1:C:293:ILE:CG2	1:C:317:GLY:C	2.84	0.43
1:C:322:PHE:CD1	1:C:322:PHE:N	2.85	0.43
1:D:285:GLU:HB3	1:D:286:PRO:CD	2.48	0.43
1:D:333:ARG:HA	2:D:402:CMP:O1P	2.19	0.43
1:D:371:TYR:OH	2:D:402:CMP:C8	2.66	0.43
1:E:178:GLY:N	1:E:194:GLU:HG3	2.29	0.43
1:G:253:ILE:H	1:G:253:ILE:HG12	1.49	0.43
1:G:283:GLN:HG2	1:G:284:GLY:N	2.32	0.43
1:G:365:LYS:O	1:G:368:ILE:N	2.42	0.43
1:H:204:ILE:HG21	1:H:205:TYR:CE2	2.54	0.43
1:H:258:ASP:O	1:H:262:ARG:CG	2.66	0.43
1:A:196:GLY:HA2	1:A:355:ARG:HH21	1.74	0.43
1:A:204:ILE:CG2	1:A:205:TYR:HD2	2.28	0.43
1:B:157:ILE:CA	1:B:218:ASN:OD1	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:MET:O	1:B:238:LEU:HD12	2.19	0.43
1:B:252:SER:O	1:B:253:ILE:HG12	2.16	0.43
1:B:289:GLU:HG2	1:B:333:ARG:HH22	1.83	0.43
1:B:317:GLY:O	1:B:320:ASP:HB2	2.19	0.43
1:C:162:VAL:HG23	1:C:213:VAL:O	2.18	0.43
1:E:113:ARG:O	1:H:112:VAL:CG1	2.67	0.43
1:E:160:GLU:O	1:E:214:LYS:HD2	2.19	0.43
1:E:200:GLU:HG2	1:E:201:LEU:N	2.33	0.43
1:E:224:ILE:HD12	1:E:224:ILE:H	1.78	0.43
1:E:269:LEU:CB	1:E:346:VAL:HG23	2.47	0.43
1:E:300:VAL:HG13	1:E:336:THR:O	2.17	0.43
1:E:324:GLU:HG2	1:E:325:ILE:N	2.34	0.43
1:F:183:TYR:CD1	1:F:188:TRP:CB	3.01	0.43
1:G:152:PHE:HD2	1:G:152:PHE:H	1.66	0.43
1:G:192:VAL:O	1:G:192:VAL:HG12	2.18	0.43
1:H:251:VAL:CG1	1:H:254:LEU:CD2	2.87	0.43
1:A:114:LYS:HB3	1:A:114:LYS:HE2	1.69	0.43
1:A:253:ILE:C	1:A:255:GLU:N	2.71	0.43
1:B:153:PRO:CA	1:B:222:TRP:CE3	2.98	0.43
1:B:220:LYS:O	1:B:221:LEU:HD23	2.19	0.43
1:B:316:LEU:HD12	1:B:316:LEU:HA	1.42	0.43
1:C:321:TYR:C	1:C:321:TYR:HD1	2.14	0.43
1:D:266:ALA:C	1:D:268:ALA:N	2.68	0.43
1:E:152:PHE:CE2	1:E:223:GLY:HA3	2.42	0.43
1:E:160:GLU:O	1:E:214:LYS:HA	2.18	0.43
1:E:165:GLN:CB	1:E:211:ASP:O	2.67	0.43
1:E:352:ARG:O	1:E:353:PHE:C	2.55	0.43
1:F:144:ARG:HG2	1:F:145:SER:H	1.82	0.43
1:F:184:VAL:O	1:F:185:ASN:HB2	2.19	0.43
1:F:324:GLU:HG2	1:F:325:ILE:N	2.33	0.43
1:F:329:MET:HA	1:F:329:MET:HE3	1.98	0.43
1:G:269:LEU:HB2	1:G:346:VAL:HG21	1.99	0.43
1:G:350:ARG:O	1:G:353:PHE:N	2.51	0.43
1:A:281:VAL:CG1	1:A:333:ARG:CG	2.92	0.43
1:B:118:LYS:NZ	1:B:151:MET:O	2.41	0.43
1:B:130:ILE:HD13	1:B:151:MET:CE	2.48	0.43
1:B:135:LEU:CD1	1:B:135:LEU:C	2.86	0.43
1:B:152:PHE:HE2	1:B:223:GLY:C	2.21	0.43
1:B:238:LEU:HD23	1:B:238:LEU:HA	1.76	0.43
1:B:283:GLN:HG2	1:B:284:GLY:N	2.33	0.43
1:C:241:ARG:NH2	1:C:263:LEU:HB3	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:280:ILE:HD11	1:C:337:VAL:CB	2.43	0.43
1:C:288:ASP:N	1:C:288:ASP:OD1	2.52	0.43
1:D:262:ARG:HA	1:D:265:VAL:HG23	2.00	0.43
1:E:158:ALA:HB2	1:E:218:ASN:N	2.34	0.43
1:E:201:LEU:H	1:E:201:LEU:HD12	1.83	0.43
1:F:204:ILE:CG2	1:F:238:LEU:HD11	2.49	0.43
1:F:289:GLU:HG2	1:F:291:PHE:CE1	2.53	0.43
1:H:174:VAL:HG23	1:H:196:GLY:O	2.19	0.43
1:H:282:VAL:O	1:H:283:GLN:C	2.56	0.43
1:H:303:ARG:CB	1:H:308:GLU:H	2.32	0.43
1:H:366:ARG:CG	1:H:367:ASN:N	2.81	0.43
1:A:203:LEU:CD1	1:A:229:TYR:HD2	2.32	0.43
1:B:123:MET:O	1:B:125:ALA:N	2.52	0.43
1:C:139:LEU:HD22	1:C:144:ARG:CA	2.49	0.43
1:C:148:PHE:CD1	1:D:120:TYR:HD1	2.34	0.43
1:D:154:VAL:HG13	1:D:155:SER:N	2.34	0.43
1:D:301:LEU:HD21	1:D:310:PHE:CG	2.52	0.43
1:D:328:LEU:H	1:D:328:LEU:HD12	1.83	0.43
1:E:173:TYR:HD1	1:E:223:GLY:CA	2.32	0.43
1:E:297:SER:O	1:E:340:ARG:N	2.46	0.43
1:F:204:ILE:CG2	1:F:205:TYR:CE2	3.02	0.43
1:F:229:TYR:HE1	1:F:233:LEU:HD13	1.78	0.43
1:F:342:PRO:O	1:F:342:PRO:CG	2.67	0.43
1:G:130:ILE:HD13	1:G:151:MET:CE	2.49	0.43
1:G:152:PHE:HD2	1:G:152:PHE:N	2.15	0.43
1:G:220:LYS:O	1:G:221:LEU:HD23	2.19	0.43
1:A:254:LEU:HB2	1:A:257:LEU:HD12	2.00	0.43
1:A:273:GLN:CB	1:A:343:LEU:O	2.57	0.43
1:A:321:TYR:C	1:A:321:TYR:HD1	2.18	0.43
1:B:309:GLU:CD	1:B:310:PHE:CD2	2.92	0.43
1:C:111:TYR:CE1	1:F:111:TYR:CD2	2.88	0.43
1:C:145:SER:O	1:C:146:ASP:C	2.56	0.43
1:C:273:GLN:C	1:C:274:PHE:CG	2.91	0.43
1:F:230:ARG:NH1	1:F:234:MET:HE1	2.33	0.43
1:F:266:ALA:C	1:F:268:ALA:N	2.69	0.43
1:G:300:VAL:HG13	1:G:335:ALA:HB1	1.99	0.43
1:H:172:PHE:HE1	1:H:200:GLU:HB3	1.84	0.43
1:H:260:TRP:CD1	2:H:401:CMP:C8	3.02	0.43
1:H:276:ASP:C	1:H:278:GLN:H	2.22	0.43
1:A:120:TYR:HE2	1:A:124:ALA:HB2	1.84	0.42
1:A:158:ALA:CB	1:A:216:LYS:O	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:ILE:HG21	1:A:180:MET:CG	2.49	0.42
1:A:232:ILE:HG23	1:A:233:LEU:HG	2.01	0.42
1:B:173:TYR:CB	1:B:198:PHE:HE1	2.32	0.42
1:B:178:GLY:HA3	1:B:219:VAL:HB	2.00	0.42
1:B:201:LEU:HB2	2:B:401:CMP:O3'	2.18	0.42
1:B:248:LEU:HD23	1:B:248:LEU:HA	1.72	0.42
1:B:251:VAL:C	1:B:252:SER:O	2.56	0.42
1:B:263:LEU:HD23	1:B:263:LEU:HA	1.61	0.42
1:C:139:LEU:HB3	1:C:143:GLU:HB2	2.00	0.42
1:C:182:VAL:HG23	1:C:190:THR:H	1.81	0.42
1:D:121:LYS:C	1:D:123:MET:N	2.69	0.42
1:E:110:SER:OG	1:H:115:VAL:CG2	2.67	0.42
1:E:131:GLU:OE1	1:E:132:LYS:N	2.51	0.42
1:E:273:GLN:NE2	1:E:273:GLN:H	1.88	0.42
1:F:347:LYS:HB3	1:F:347:LYS:HE3	1.16	0.42
1:F:368:ILE:O	1:F:371:TYR:HB2	2.19	0.42
1:G:112:VAL:HG12	1:G:231:ARG:NE	2.34	0.42
1:G:138:HIS:H	1:G:138:HIS:HD1	1.65	0.42
1:G:173:TYR:O	1:G:197:SER:HA	2.19	0.42
1:G:265:VAL:HG12	1:G:269:LEU:CG	2.48	0.42
1:H:170:ASP:H	1:H:209:ARG:CZ	2.32	0.42
1:A:120:TYR:HD2	1:A:121:LYS:CA	2.32	0.42
1:A:357:LEU:HB2	1:A:360:CYS:HB2	2.01	0.42
1:B:175:ILE:HD11	1:B:194:GLU:C	2.40	0.42
1:B:203:LEU:HD22	1:B:226:ARG:CB	2.47	0.42
1:C:113:ARG:CD	1:F:112:VAL:HB	2.27	0.42
1:C:157:ILE:C	1:C:157:ILE:CD1	2.83	0.42
1:D:165:GLN:CG	1:D:166:GLY:N	2.81	0.42
1:D:329:MET:HA	1:D:329:MET:HE2	1.99	0.42
1:D:362:ASP:O	1:D:365:LYS:N	2.52	0.42
1:E:203:LEU:HD22	1:E:226:ARG:CD	2.49	0.42
1:E:282:VAL:C	1:E:285:GLU:HG2	2.36	0.42
1:E:285:GLU:OE1	1:E:285:GLU:CA	2.66	0.42
1:E:308:GLU:O	1:E:309:GLU:HG2	2.19	0.42
1:E:325:ILE:CG1	2:E:402:CMP:P	3.07	0.42
1:E:329:MET:HB2	1:E:331:ARG:HG2	2.01	0.42
1:E:366:ARG:HH11	1:E:366:ARG:HD3	1.51	0.42
1:F:129:ALA:HB2	1:F:222:TRP:HE1	1.83	0.42
1:H:260:TRP:NE1	2:H:401:CMP:C8	2.81	0.42
1:A:113:ARG:HH22	1:D:114:LYS:C	2.18	0.42
1:A:115:VAL:CG2	1:D:112:VAL:N	2.61	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:ILE:CG2	1:A:238:LEU:HD11	2.49	0.42
1:A:226:ARG:HA	1:A:229:TYR:HB3	2.01	0.42
1:A:239:ARG:NH2	1:C:156:PHE:CD1	2.66	0.42
1:A:293:ILE:CG2	1:A:317:GLY:O	2.66	0.42
1:A:360:CYS:O	1:A:364:LEU:HD23	2.18	0.42
1:A:365:LYS:HA	1:A:368:ILE:HD11	2.01	0.42
1:B:260:TRP:CD1	2:B:401:CMP:N7	2.85	0.42
1:C:246:GLU:HA	1:C:249:SER:OG	2.18	0.42
1:C:264:THR:O	1:C:265:VAL:C	2.57	0.42
1:C:368:ILE:HG13	1:C:368:ILE:H	1.66	0.42
1:D:143:GLU:O	1:D:146:ASP:HB2	2.19	0.42
1:D:182:VAL:HG23	1:D:189:ALA:HB3	2.01	0.42
1:D:254:LEU:CD2	1:D:255:GLU:N	2.80	0.42
1:D:296:GLY:HA2	1:D:342:PRO:O	2.17	0.42
1:D:318:PRO:O	1:D:319:SER:CB	2.66	0.42
1:E:185:ASN:N	1:E:185:ASN:OD1	2.48	0.42
1:E:199:GLY:H	2:E:401:CMP:H4'	1.85	0.42
1:E:353:PHE:O	1:E:357:LEU:HB2	2.19	0.42
1:F:130:ILE:CD1	1:F:136:PHE:CE2	3.02	0.42
1:F:175:ILE:CD1	1:F:193:GLY:O	2.67	0.42
1:G:148:PHE:CG	1:H:120:TYR:HE1	2.35	0.42
1:H:116:ILE:HD13	1:H:116:ILE:HA	1.83	0.42
1:A:224:ILE:HD13	1:A:224:ILE:N	2.30	0.42
1:B:283:GLN:HG3	1:B:333:ARG:O	2.18	0.42
1:B:329:MET:HB2	1:B:331:ARG:HG2	2.00	0.42
1:C:291:PHE:CZ	1:C:347:LYS:NZ	2.86	0.42
1:D:269:LEU:CB	1:D:346:VAL:CG2	2.89	0.42
1:F:253:ILE:CG2	1:F:321:TYR:HE2	2.32	0.42
1:F:276:ASP:C	1:F:278:GLN:H	2.23	0.42
1:G:185:ASN:O	1:G:186:ASN:HB2	2.18	0.42
1:G:252:SER:OG	1:G:253:ILE:HG23	2.19	0.42
1:H:135:LEU:HD13	1:H:136:PHE:CE1	2.54	0.42
1:H:151:MET:HA	1:H:224:ILE:CG2	2.49	0.42
1:H:204:ILE:HG21	1:H:205:TYR:HE2	1.84	0.42
1:H:350:ARG:O	1:H:353:PHE:N	2.52	0.42
1:A:134:VAL:HG13	1:A:135:LEU:N	2.34	0.42
1:A:235:GLY:O	1:A:238:LEU:N	2.53	0.42
1:A:252:SER:O	1:A:253:ILE:C	2.58	0.42
1:A:272:VAL:CG2	1:A:273:GLN:NE2	2.83	0.42
1:A:278:GLN:O	1:A:279:LYS:HB3	2.18	0.42
1:B:213:VAL:C	1:B:214:LYS:HG2	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:253:ILE:C	1:D:255:GLU:N	2.73	0.42
1:D:259:LYS:O	1:D:260:TRP:C	2.56	0.42
1:D:263:LEU:O	1:D:266:ALA:CB	2.67	0.42
1:D:290:PHE:HB2	1:D:327:LEU:HD22	2.02	0.42
1:D:293:ILE:HD11	1:D:343:LEU:HD13	1.91	0.42
1:F:204:ILE:HD13	1:F:238:LEU:CD1	2.45	0.42
1:F:247:PHE:CE1	1:F:294:LEU:HB3	2.54	0.42
1:H:154:VAL:O	1:H:154:VAL:CG1	2.67	0.42
1:A:171:ASN:OD1	1:A:225:ASP:HA	2.20	0.42
1:A:309:GLU:HG3	1:A:310:PHE:O	2.19	0.42
1:A:325:ILE:HG13	2:A:402:CMP:O2P	2.18	0.42
1:A:329:MET:O	1:A:330:ASN:C	2.58	0.42
1:A:365:LYS:O	1:A:366:ARG:C	2.58	0.42
1:A:368:ILE:O	1:A:371:TYR:HB2	2.19	0.42
1:B:274:PHE:CE2	1:B:280:ILE:HG22	2.55	0.42
1:D:127:ALA:O	1:D:128:LYS:C	2.56	0.42
1:D:262:ARG:HG3	1:D:263:LEU:N	2.35	0.42
1:D:315:ARG:NH1	1:D:340:ARG:HH22	2.17	0.42
1:E:148:PHE:CE1	1:F:120:TYR:HE1	2.38	0.42
1:E:200:GLU:HG2	1:E:201:LEU:HG	2.02	0.42
1:F:239:ARG:HH11	1:F:239:ARG:HD2	1.63	0.42
1:F:266:ALA:HA	1:F:269:LEU:CD1	2.46	0.42
1:G:163:ILE:O	1:G:212:THR:HG22	2.19	0.42
1:G:184:VAL:O	1:G:185:ASN:HB2	2.19	0.42
1:G:248:LEU:C	1:G:262:ARG:NH2	2.73	0.42
1:G:260:TRP:NE1	2:G:401:CMP:C2'	2.76	0.42
1:G:263:LEU:O	1:G:266:ALA:N	2.53	0.42
1:H:139:LEU:CB	1:H:143:GLU:HB2	2.50	0.42
1:A:144:ARG:NH1	1:A:144:ARG:CB	2.80	0.42
1:A:263:LEU:O	1:A:266:ALA:N	2.53	0.42
1:A:302:GLN:O	1:A:310:PHE:HA	2.19	0.42
1:A:348:LEU:CD2	1:A:356:VAL:HG21	2.47	0.42
1:B:139:LEU:HB3	1:B:143:GLU:CB	2.49	0.42
1:B:154:VAL:O	1:B:154:VAL:CG1	2.62	0.42
1:B:199:GLY:H	2:B:401:CMP:H4'	1.84	0.42
1:C:158:ALA:HA	1:C:215:ALA:HB3	2.01	0.42
1:C:243:MET:HE1	1:E:157:ILE:O	2.20	0.42
1:C:260:TRP:NE1	2:C:401:CMP:C2'	2.80	0.42
1:D:342:PRO:O	1:D:342:PRO:HG2	2.20	0.42
1:D:349:ASP:C	1:D:349:ASP:OD1	2.58	0.42
1:E:130:ILE:CG2	1:E:131:GLU:N	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:135:LEU:HD13	1:E:136:PHE:CG	2.55	0.42
1:E:147:ILE:HD13	1:E:147:ILE:HG21	1.40	0.42
1:E:253:ILE:HG13	1:E:254:LEU:N	2.33	0.42
1:E:327:LEU:HD23	1:E:353:PHE:CZ	2.55	0.42
1:F:116:ILE:O	1:F:118:LYS:HG3	2.19	0.42
1:G:172:PHE:O	1:G:224:ILE:CD1	2.67	0.42
1:G:188:TRP:CH2	1:G:190:THR:CA	3.03	0.42
1:H:295:GLU:O	1:H:344:LYS:N	2.53	0.42
1:A:153:PRO:CA	1:A:222:TRP:CE3	3.01	0.42
1:A:203:LEU:CD1	1:A:229:TYR:CD2	3.00	0.42
1:A:247:PHE:CD2	1:A:247:PHE:O	2.73	0.42
1:A:363:ILE:H	1:A:363:ILE:HG13	1.51	0.42
1:B:134:VAL:O	1:B:134:VAL:CG2	2.64	0.42
1:B:211:ASP:OD2	2:B:401:CMP:N3	2.52	0.42
1:B:322:PHE:CE2	1:B:337:VAL:HG21	2.54	0.42
1:B:327:LEU:HD23	1:B:353:PHE:CE1	2.55	0.42
1:C:110:SER:CB	1:F:114:LYS:HZ3	2.32	0.42
1:D:135:LEU:HD13	1:D:136:PHE:CG	2.55	0.42
1:D:242:LYS:HD2	1:D:242:LYS:HA	1.66	0.42
1:D:260:TRP:CA	1:D:263:LEU:HD12	2.44	0.42
1:E:136:PHE:O	1:E:139:LEU:HD11	2.20	0.42
1:E:171:ASN:H	1:E:209:ARG:HH22	1.67	0.42
1:F:111:TYR:CD2	1:F:112:VAL:N	2.87	0.42
1:F:162:VAL:HG22	1:F:213:VAL:O	2.19	0.42
1:F:173:TYR:HD1	1:F:223:GLY:CA	2.33	0.42
1:F:200:GLU:HG2	1:F:201:LEU:N	2.35	0.42
1:F:203:LEU:HD22	1:F:226:ARG:HD3	2.01	0.42
1:F:253:ILE:HG13	1:F:254:LEU:HG	2.02	0.42
1:F:321:TYR:HD1	1:F:322:PHE:N	2.16	0.42
1:G:183:TYR:CD1	1:G:188:TRP:CB	3.03	0.42
1:G:244:TYR:O	1:G:245:GLU:C	2.58	0.42
1:G:266:ALA:O	1:G:269:LEU:N	2.51	0.42
1:H:116:ILE:HA	1:H:117:PRO:HD3	1.77	0.42
1:H:174:VAL:O	1:H:174:VAL:CG1	2.67	0.42
1:B:116:ILE:HA	1:B:117:PRO:HD3	1.78	0.42
1:B:126:LEU:O	1:B:129:ALA:HB3	2.20	0.42
1:C:245:GLU:OE1	1:C:246:GLU:N	2.53	0.42
1:D:163:ILE:CD1	1:D:213:VAL:HB	2.39	0.42
1:D:175:ILE:HG21	1:D:180:MET:CG	2.49	0.42
1:D:183:TYR:HA	1:D:188:TRP:HA	2.02	0.42
1:D:368:ILE:HD13	1:D:368:ILE:HG21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:111:TYR:CD2	1:H:111:TYR:OH	2.73	0.42
1:E:133:ASN:ND2	1:E:174:VAL:HG21	2.35	0.42
1:E:163:ILE:HD11	1:E:198:PHE:CE2	2.54	0.42
1:E:329:MET:HA	1:E:329:MET:HE2	1.99	0.42
1:E:348:LEU:HD23	1:E:353:PHE:HA	2.01	0.42
1:F:131:GLU:C	1:F:133:ASN:H	2.23	0.42
1:F:276:ASP:C	1:F:278:GLN:N	2.72	0.42
1:F:329:MET:CB	1:F:331:ARG:CG	2.91	0.42
1:H:119:ASP:O	1:H:120:TYR:C	2.58	0.42
1:H:163:ILE:HD12	1:H:213:VAL:HB	2.02	0.42
1:H:211:ASP:OD1	1:H:211:ASP:N	2.52	0.42
1:H:212:THR:C	1:H:213:VAL:HG23	2.40	0.42
1:H:294:LEU:CG	1:H:295:GLU:H	2.32	0.42
1:A:204:ILE:CG2	1:A:205:TYR:CE2	3.03	0.42
1:A:253:ILE:HG23	1:A:321:TYR:HE2	1.85	0.42
1:B:371:TYR:CZ	2:B:402:CMP:C8	3.00	0.42
1:C:278:GLN:C	1:C:338:VAL:HG22	2.40	0.42
1:F:114:LYS:CE	1:F:115:VAL:HG22	2.49	0.42
1:F:133:ASN:O	1:F:134:VAL:C	2.58	0.42
1:F:135:LEU:CD1	1:F:136:PHE:N	2.82	0.42
1:F:201:LEU:H	1:F:201:LEU:HD12	1.85	0.42
1:G:149:ASP:OD1	1:H:120:TYR:HB3	2.17	0.42
1:H:120:TYR:CD2	1:H:121:LYS:N	2.87	0.42
1:H:162:VAL:HG21	1:H:213:VAL:HG12	2.02	0.42
1:H:183:TYR:CD1	1:H:188:TRP:CB	3.02	0.42
1:H:188:TRP:CH2	1:H:190:THR:C	2.93	0.42
1:H:253:ILE:H	1:H:253:ILE:HG12	1.46	0.42
1:A:247:PHE:CZ	1:A:294:LEU:HA	2.53	0.41
1:B:130:ILE:CD1	1:B:151:MET:HE3	2.47	0.41
1:B:158:ALA:HB2	1:B:217:THR:CA	2.45	0.41
1:B:175:ILE:CG2	1:B:221:LEU:HD21	2.44	0.41
1:B:301:LEU:N	1:B:336:THR:O	2.51	0.41
1:C:135:LEU:HD13	1:C:136:PHE:CE1	2.55	0.41
1:C:172:PHE:CB	1:C:224:ILE:HD11	2.33	0.41
1:C:188:TRP:CH2	1:C:190:THR:C	2.94	0.41
1:C:254:LEU:O	1:C:257:LEU:HG	2.20	0.41
1:E:312:GLU:C	1:E:312:GLU:OE1	2.58	0.41
1:E:342:PRO:HG2	1:E:342:PRO:O	2.19	0.41
1:E:366:ARG:O	1:E:369:GLN:CB	2.68	0.41
1:F:123:MET:O	1:F:124:ALA:C	2.56	0.41
1:F:135:LEU:HD13	1:F:136:PHE:CD1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:159:GLY:C	1:H:243:MET:HE2	2.40	0.41
1:F:253:ILE:H	1:F:253:ILE:HG12	1.52	0.41
1:F:294:LEU:C	1:F:295:GLU:HG2	2.39	0.41
1:H:124:ALA:O	1:H:127:ALA:HB3	2.20	0.41
1:H:138:HIS:O	1:H:139:LEU:C	2.55	0.41
1:H:165:GLN:CA	1:H:211:ASP:O	2.67	0.41
1:H:174:VAL:CG1	1:H:222:TRP:HB2	2.50	0.41
1:H:273:GLN:C	1:H:274:PHE:CG	2.93	0.41
1:H:285:GLU:HB3	1:H:286:PRO:HD2	2.01	0.41
1:H:294:LEU:CG	1:H:295:GLU:N	2.82	0.41
1:H:321:TYR:CD1	1:H:321:TYR:O	2.73	0.41
1:A:158:ALA:HA	1:A:215:ALA:HB1	2.02	0.41
1:A:266:ALA:C	1:A:268:ALA:N	2.71	0.41
1:A:269:LEU:CG	1:A:346:VAL:HG21	2.49	0.41
1:A:352:ARG:O	1:A:355:ARG:HB2	2.21	0.41
1:B:116:ILE:HA	1:B:116:ILE:HD13	1.63	0.41
1:B:130:ILE:CD1	1:B:151:MET:HE2	2.50	0.41
1:B:158:ALA:HA	1:B:215:ALA:CB	2.50	0.41
1:B:201:LEU:HD13	2:B:401:CMP:C2'	2.50	0.41
1:B:263:LEU:H	1:B:263:LEU:HG	1.61	0.41
1:B:276:ASP:C	1:B:278:GLN:H	2.24	0.41
1:C:282:VAL:O	1:C:283:GLN:C	2.58	0.41
1:D:144:ARG:CZ	1:D:144:ARG:CB	2.98	0.41
1:D:251:VAL:HG11	1:D:292:ILE:CD1	2.50	0.41
1:D:263:LEU:HA	1:D:263:LEU:HD23	1.74	0.41
1:D:269:LEU:CD2	1:D:346:VAL:CG2	2.86	0.41
1:D:362:ASP:HA	1:D:365:LYS:NZ	2.35	0.41
1:F:129:ALA:CB	1:F:222:TRP:CD1	3.03	0.41
1:F:325:ILE:CG1	1:F:326:ALA:N	2.79	0.41
1:G:259:LYS:O	1:G:260:TRP:C	2.59	0.41
1:G:260:TRP:CG	2:G:401:CMP:N7	2.88	0.41
1:G:272:VAL:HG22	1:G:273:GLN:N	2.34	0.41
1:G:273:GLN:HB2	1:G:343:LEU:O	2.19	0.41
1:G:283:GLN:CB	1:G:336:THR:OG1	2.67	0.41
1:H:130:ILE:HG13	1:H:136:PHE:CD2	2.55	0.41
1:H:153:PRO:CA	1:H:222:TRP:HZ3	2.32	0.41
1:A:144:ARG:O	1:A:145:SER:C	2.54	0.41
1:B:112:VAL:HG12	1:B:231:ARG:CZ	2.48	0.41
1:B:142:ASN:O	1:B:143:GLU:C	2.56	0.41
1:B:269:LEU:HD23	1:B:348:LEU:HD13	2.02	0.41
1:C:175:ILE:CA	1:C:221:LEU:CD2	2.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:130:ILE:CG2	1:D:131:GLU:N	2.82	0.41
1:D:230:ARG:CB	1:D:234:MET:HE1	2.50	0.41
1:E:118:LYS:O	1:E:123:MET:HE2	2.20	0.41
1:E:119:ASP:O	1:E:120:TYR:C	2.59	0.41
1:E:160:GLU:C	1:E:214:LYS:HE3	2.41	0.41
1:E:249:SER:HA	1:E:262:ARG:NH2	2.35	0.41
1:E:260:TRP:NE1	2:E:401:CMP:C2'	2.79	0.41
1:E:262:ARG:HA	1:E:265:VAL:HG23	2.02	0.41
1:F:164:GLN:CA	1:F:212:THR:HG22	2.40	0.41
1:F:265:VAL:HG12	1:F:269:LEU:HD11	2.03	0.41
1:H:126:LEU:HD12	1:H:126:LEU:C	2.38	0.41
1:H:147:ILE:HD13	1:H:147:ILE:HG21	1.48	0.41
1:H:226:ARG:O	1:H:227:ASP:C	2.58	0.41
1:H:343:LEU:HG	1:H:344:LYS:N	2.34	0.41
1:H:365:LYS:O	1:H:366:ARG:C	2.57	0.41
1:A:156:PHE:HD1	1:A:156:PHE:HA	1.71	0.41
1:A:156:PHE:HE2	1:A:162:VAL:HG12	1.72	0.41
1:A:287:GLY:HA3	1:A:326:ALA:HB1	2.00	0.41
1:A:293:ILE:CG1	1:A:345:CYS:SG	2.96	0.41
1:A:362:ASP:CA	1:A:365:LYS:HZ2	2.33	0.41
1:C:262:ARG:HA	1:C:265:VAL:HG21	2.02	0.41
1:D:133:ASN:O	1:D:135:LEU:HD12	2.21	0.41
1:E:133:ASN:OD1	1:E:133:ASN:C	2.59	0.41
1:E:183:TYR:CD1	1:E:188:TRP:HA	2.51	0.41
1:E:221:LEU:HD23	1:E:221:LEU:HA	1.34	0.41
1:E:353:PHE:CD1	1:E:357:LEU:HD22	2.54	0.41
1:F:112:VAL:CG1	1:F:113:ARG:N	2.65	0.41
1:F:211:ASP:OD1	2:F:401:CMP:O1P	2.39	0.41
1:G:210:ALA:C	1:G:211:ASP:OD1	2.59	0.41
1:G:247:PHE:C	1:G:247:PHE:HD2	2.21	0.41
1:G:324:GLU:HB2	1:G:364:LEU:HD11	2.01	0.41
1:G:362:ASP:HA	1:G:365:LYS:HZ2	1.84	0.41
1:A:113:ARG:HE	1:D:113:ARG:CA	2.32	0.41
1:A:316:LEU:HD12	1:A:316:LEU:O	2.19	0.41
1:A:347:LYS:HE3	1:A:347:LYS:HB3	1.20	0.41
1:B:173:TYR:HB2	1:B:198:PHE:HE1	1.86	0.41
1:B:285:GLU:O	1:B:332:PRO:HA	2.20	0.41
1:B:322:PHE:N	1:B:322:PHE:HD1	2.18	0.41
1:C:120:TYR:O	1:C:123:MET:HB3	2.20	0.41
1:D:183:TYR:HD1	1:D:188:TRP:CA	2.30	0.41
1:D:297:SER:O	1:D:340:ARG:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:322:PHE:CD2	1:D:322:PHE:C	2.93	0.41
1:E:116:ILE:O	1:E:118:LYS:HG3	2.21	0.41
1:E:229:TYR:O	1:E:230:ARG:C	2.58	0.41
1:E:312:GLU:OE1	1:E:313:VAL:N	2.54	0.41
1:F:157:ILE:HG13	1:F:157:ILE:H	1.81	0.41
1:F:260:TRP:NE1	2:F:401:CMP:C4	2.88	0.41
1:F:289:GLU:CG	1:F:347:LYS:HZ3	2.07	0.41
1:G:341:GLY:HA3	1:G:342:PRO:HD2	1.70	0.41
1:H:283:GLN:HG2	1:H:333:ARG:O	2.20	0.41
1:A:263:LEU:HD23	1:A:263:LEU:HA	1.74	0.41
1:A:321:TYR:HD1	1:A:322:PHE:N	2.18	0.41
1:B:261:GLU:OE2	1:B:359:PRO:HG2	2.20	0.41
1:C:197:SER:O	1:C:198:PHE:HB3	2.21	0.41
1:C:290:PHE:CE2	1:C:357:LEU:HD21	2.56	0.41
1:C:362:ASP:O	1:C:363:ILE:C	2.58	0.41
1:D:153:PRO:HB3	1:D:222:TRP:CH2	2.49	0.41
1:D:157:ILE:CA	1:D:218:ASN:OD1	2.68	0.41
1:D:163:ILE:HD12	1:D:213:VAL:CB	2.39	0.41
1:D:200:GLU:CG	1:D:201:LEU:N	2.51	0.41
1:D:263:LEU:O	1:D:267:ASP:N	2.43	0.41
1:D:269:LEU:CG	1:D:346:VAL:HG21	2.50	0.41
1:E:260:TRP:NE1	2:E:401:CMP:N9	2.68	0.41
1:E:362:ASP:O	1:E:365:LYS:N	2.50	0.41
1:F:316:LEU:HD22	1:F:320:ASP:HB3	2.02	0.41
1:F:325:ILE:HD13	1:F:334:ALA:HB3	2.03	0.41
1:H:163:ILE:HD11	1:H:198:PHE:CE2	2.55	0.41
1:H:188:TRP:HZ3	1:H:190:THR:C	2.22	0.41
1:B:230:ARG:HG2	1:B:230:ARG:HH11	1.86	0.41
1:B:289:GLU:HG3	1:B:347:LYS:HZ3	1.86	0.41
1:B:313:VAL:CG2	2:B:402:CMP:HN61	2.22	0.41
1:C:162:VAL:CG2	1:C:163:ILE:HG13	2.49	0.41
1:C:183:TYR:CD1	1:C:188:TRP:CB	3.04	0.41
1:C:253:ILE:HG13	1:C:254:LEU:CG	2.50	0.41
1:C:290:PHE:HB2	1:C:327:LEU:HD21	2.02	0.41
1:D:154:VAL:HG12	1:D:154:VAL:O	2.20	0.41
1:D:201:LEU:HB2	2:D:401:CMP:O3'	2.19	0.41
1:D:313:VAL:HG21	2:D:402:CMP:N6	2.36	0.41
1:E:120:TYR:O	1:E:121:LYS:C	2.56	0.41
1:E:316:LEU:HD22	1:E:320:ASP:HB3	2.03	0.41
1:E:347:LYS:O	1:E:348:LEU:CD1	2.65	0.41
1:F:147:ILE:HD13	1:F:147:ILE:HG21	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:329:MET:HB3	1:F:331:ARG:CG	2.50	0.41
1:F:343:LEU:HD12	1:F:343:LEU:HA	1.73	0.41
1:G:202:ALA:HB1	1:G:207:THR:O	2.20	0.41
1:H:158:ALA:CB	1:H:217:THR:C	2.74	0.41
1:H:283:GLN:HG3	1:H:333:ARG:O	2.21	0.41
1:H:300:VAL:H	1:H:312:GLU:HB2	1.84	0.41
1:H:357:LEU:HD12	1:H:357:LEU:HA	1.49	0.41
1:A:113:ARG:CZ	1:D:114:LYS:CA	2.99	0.41
1:A:209:ARG:HD3	2:A:401:CMP:O1P	2.21	0.41
1:B:266:ALA:O	1:B:268:ALA:N	2.54	0.41
1:B:325:ILE:HG12	2:B:402:CMP:P	2.60	0.41
1:B:362:ASP:HA	1:B:365:LYS:HZ3	1.84	0.41
1:C:299:ALA:HA	1:C:314:GLY:O	2.21	0.41
1:D:269:LEU:CB	1:D:346:VAL:HG21	2.47	0.41
1:D:325:ILE:HD11	1:D:334:ALA:H	1.86	0.41
1:E:352:ARG:O	1:E:355:ARG:HB2	2.20	0.41
1:F:158:ALA:HB2	1:F:218:ASN:N	2.35	0.41
1:F:244:TYR:O	1:F:245:GLU:C	2.59	0.41
1:F:263:LEU:O	1:F:266:ALA:CB	2.56	0.41
1:G:123:MET:O	1:G:124:ALA:C	2.59	0.41
1:G:162:VAL:HG23	1:G:163:ILE:H	1.84	0.41
1:G:176:ASP:O	1:G:194:GLU:HG2	2.20	0.41
1:G:235:GLY:O	1:G:238:LEU:N	2.54	0.41
1:H:304:ARG:N	1:H:308:GLU:CB	2.75	0.41
1:A:116:ILE:HA	1:A:117:PRO:HD3	1.69	0.41
1:A:120:TYR:HE2	1:A:124:ALA:CB	2.33	0.41
1:A:144:ARG:CB	1:A:144:ARG:CZ	2.98	0.41
1:A:147:ILE:HD13	1:A:147:ILE:HG21	1.74	0.41
1:A:183:TYR:CD1	1:A:188:TRP:CA	3.03	0.41
1:A:260:TRP:HE1	2:A:401:CMP:C2'	2.31	0.41
1:A:350:ARG:CB	1:A:351:PRO:HD3	2.37	0.41
1:A:353:PHE:O	1:A:357:LEU:CD1	2.69	0.41
1:B:121:LYS:O	1:B:122:THR:C	2.59	0.41
1:B:173:TYR:CD2	1:B:198:PHE:HE1	2.39	0.41
1:B:203:LEU:CD1	1:B:226:ARG:HB3	2.43	0.41
1:B:230:ARG:HA	1:B:234:MET:HB2	2.03	0.41
1:B:239:ARG:O	1:B:243:MET:HB3	2.21	0.41
1:B:295:GLU:HA	1:B:318:PRO:HG3	2.02	0.41
1:C:110:SER:O	1:F:114:LYS:CD	2.64	0.41
1:C:132:LYS:HG3	1:C:133:ASN:N	2.36	0.41
1:C:260:TRP:NE1	2:C:401:CMP:C8	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:272:VAL:O	1:C:345:CYS:N	2.51	0.41
1:C:342:PRO:HG2	1:C:342:PRO:O	2.21	0.41
1:D:147:ILE:O	1:D:148:PHE:C	2.57	0.41
1:D:262:ARG:HA	1:D:265:VAL:HG21	2.03	0.41
1:D:343:LEU:HG	1:D:344:LYS:N	2.35	0.41
1:E:113:ARG:N	1:H:112:VAL:HG11	2.36	0.41
1:E:133:ASN:HD22	1:E:174:VAL:HG21	1.86	0.41
1:E:155:SER:HA	1:E:220:LYS:HA	2.03	0.41
1:E:174:VAL:HG13	1:E:222:TRP:HB2	2.02	0.41
1:E:181:ASP:OD1	1:E:191:SER:HB3	2.21	0.41
1:E:247:PHE:CE1	1:E:294:LEU:CA	2.97	0.41
1:E:261:GLU:OE2	1:E:359:PRO:HG2	2.21	0.41
1:E:266:ALA:C	1:E:268:ALA:N	2.72	0.41
1:E:321:TYR:HD1	1:E:322:PHE:N	2.18	0.41
1:G:173:TYR:HB2	1:G:198:PHE:CZ	2.52	0.41
1:G:173:TYR:HD1	1:G:223:GLY:CA	2.34	0.41
1:G:265:VAL:C	1:G:269:LEU:CG	2.89	0.41
1:G:343:LEU:HA	1:G:343:LEU:HD12	1.71	0.41
1:G:362:ASP:O	1:G:365:LYS:N	2.53	0.41
1:H:253:ILE:CD1	1:H:254:LEU:HD23	2.51	0.41
1:H:284:GLY:HA2	1:H:332:PRO:CB	2.51	0.41
1:H:328:LEU:HD12	1:H:328:LEU:N	2.35	0.41
1:H:362:ASP:HA	1:H:365:LYS:HZ2	1.85	0.41
1:A:117:PRO:HG2	1:D:110:SER:HB2	2.00	0.41
1:B:126:LEU:HD11	1:B:130:ILE:HD13	2.03	0.41
1:B:175:ILE:CG1	1:B:193:GLY:O	2.69	0.41
1:C:156:PHE:CD2	1:C:162:VAL:HG13	2.52	0.41
1:C:170:ASP:H	1:C:209:ARG:CZ	2.32	0.41
1:C:175:ILE:HG21	1:C:180:MET:HG3	2.03	0.41
1:C:234:MET:O	1:C:238:LEU:CD1	2.61	0.41
1:D:175:ILE:HD12	1:D:175:ILE:C	2.25	0.41
1:D:270:GLU:HA	1:D:271:PRO:HD3	1.57	0.41
1:E:139:LEU:HD22	1:E:144:ARG:CA	2.51	0.41
1:E:201:LEU:HD12	2:E:401:CMP:O2'	2.20	0.41
1:F:181:ASP:OD1	1:F:191:SER:HB3	2.21	0.41
1:F:247:PHE:CE1	1:F:294:LEU:CA	2.94	0.41
1:F:270:GLU:HB2	1:F:271:PRO:CD	2.50	0.41
1:F:365:LYS:O	1:F:368:ILE:CG1	2.58	0.41
1:G:174:VAL:HG13	1:G:174:VAL:O	2.20	0.41
1:G:365:LYS:HA	1:G:368:ILE:CD1	2.51	0.41
1:H:130:ILE:HG23	1:H:131:GLU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:162:VAL:CG2	1:H:213:VAL:HG12	2.51	0.41
1:H:342:PRO:HG2	1:H:342:PRO:O	2.21	0.41
1:B:147:ILE:HD13	1:B:147:ILE:HG21	1.70	0.40
1:B:280:ILE:CG1	1:B:337:VAL:HB	2.51	0.40
1:D:301:LEU:CD2	1:D:310:PHE:CB	2.81	0.40
1:E:126:LEU:O	1:E:127:ALA:C	2.57	0.40
1:F:175:ILE:HG22	1:F:221:LEU:CD2	2.49	0.40
1:F:353:PHE:O	1:F:357:LEU:HB2	2.21	0.40
1:F:365:LYS:O	1:F:368:ILE:N	2.38	0.40
1:G:245:GLU:OE1	1:G:246:GLU:N	2.54	0.40
1:G:301:LEU:HD13	1:G:310:PHE:CG	2.55	0.40
1:H:122:THR:C	1:H:125:ALA:HB3	2.39	0.40
1:H:171:ASN:OD1	1:H:225:ASP:HA	2.21	0.40
1:H:265:VAL:O	1:H:266:ALA:C	2.58	0.40
1:A:280:ILE:CD1	1:A:337:VAL:HB	2.46	0.40
1:A:282:VAL:HA	1:A:336:THR:HG23	2.02	0.40
1:B:252:SER:O	1:B:254:LEU:N	2.54	0.40
1:C:111:TYR:HD1	1:F:111:TYR:CE2	2.36	0.40
1:C:130:ILE:HD13	1:C:151:MET:CE	2.51	0.40
1:C:157:ILE:CA	1:C:218:ASN:OD1	2.68	0.40
1:C:270:GLU:HB3	1:C:271:PRO:CD	2.51	0.40
1:C:271:PRO:O	1:C:272:VAL:HB	2.20	0.40
1:C:279:LYS:HD2	1:C:336:THR:CG2	2.50	0.40
1:D:128:LYS:C	1:D:130:ILE:N	2.74	0.40
1:D:180:MET:HB2	1:D:192:VAL:CG1	2.51	0.40
1:E:129:ALA:CB	1:E:222:TRP:NE1	2.84	0.40
1:E:132:LYS:HG3	1:E:133:ASN:N	2.36	0.40
1:E:230:ARG:O	1:E:234:MET:HB2	2.20	0.40
1:E:268:ALA:O	1:E:352:ARG:NH1	2.54	0.40
1:E:282:VAL:HB	1:E:285:GLU:CG	2.51	0.40
1:E:365:LYS:O	1:E:368:ILE:N	2.40	0.40
1:G:197:SER:O	1:G:198:PHE:HB3	2.22	0.40
1:H:181:ASP:OD1	1:H:191:SER:HB3	2.21	0.40
1:H:198:PHE:HD1	1:H:198:PHE:N	2.17	0.40
1:H:266:ALA:C	1:H:268:ALA:N	2.71	0.40
1:A:153:PRO:N	1:A:222:TRP:CZ3	2.90	0.40
1:A:204:ILE:HG23	1:A:238:LEU:HD11	2.03	0.40
1:A:241:ARG:O	1:A:245:GLU:N	2.54	0.40
1:B:116:ILE:HD12	1:B:116:ILE:HG23	1.86	0.40
1:B:139:LEU:N	1:B:139:LEU:CD1	2.62	0.40
1:B:204:ILE:HG12	1:B:234:MET:SD	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:PHE:N	1:B:343:LEU:O	2.41	0.40
1:B:316:LEU:HD13	1:B:316:LEU:N	2.34	0.40
1:B:371:TYR:CD1	2:B:402:CMP:C5	3.08	0.40
1:C:247:PHE:CE1	1:C:294:LEU:CA	2.91	0.40
1:D:253:ILE:CD1	1:D:254:LEU:HD13	2.50	0.40
1:D:254:LEU:HD22	1:D:254:LEU:C	2.41	0.40
1:D:266:ALA:O	1:D:268:ALA:N	2.54	0.40
1:D:325:ILE:HG13	2:D:402:CMP:O1P	2.21	0.40
1:E:271:PRO:O	1:E:272:VAL:HB	2.21	0.40
1:F:174:VAL:O	1:F:222:TRP:HB2	2.21	0.40
1:F:182:VAL:HG23	1:F:189:ALA:HB3	2.04	0.40
1:F:230:ARG:CB	1:F:234:MET:CE	2.96	0.40
1:F:298:ALA:N	1:F:316:LEU:O	2.40	0.40
1:G:138:HIS:O	1:G:139:LEU:C	2.57	0.40
1:G:230:ARG:HA	1:G:234:MET:HB2	2.02	0.40
1:G:342:PRO:O	1:G:342:PRO:CG	2.70	0.40
1:A:325:ILE:CG1	1:A:326:ALA:N	2.80	0.40
1:B:130:ILE:HD12	1:B:130:ILE:HA	1.80	0.40
1:B:301:LEU:HD13	1:B:310:PHE:CB	2.37	0.40
1:C:173:TYR:HD1	1:C:223:GLY:CA	2.33	0.40
1:C:259:LYS:O	1:C:261:GLU:N	2.54	0.40
1:C:266:ALA:C	1:C:268:ALA:N	2.72	0.40
1:C:352:ARG:O	1:C:353:PHE:C	2.58	0.40
1:C:352:ARG:O	1:C:355:ARG:HB2	2.21	0.40
1:D:175:ILE:H	1:D:175:ILE:HG13	1.59	0.40
1:D:260:TRP:CG	2:D:401:CMP:N7	2.89	0.40
1:E:160:GLU:H	1:E:215:ALA:HB3	1.86	0.40
1:E:248:LEU:HB2	1:E:262:ARG:HH21	1.84	0.40
1:H:157:ILE:HB	1:H:218:ASN:OD1	2.21	0.40
1:A:162:VAL:HG23	1:A:163:ILE:H	1.86	0.40
1:B:139:LEU:HD22	1:B:144:ARG:HA	2.04	0.40
1:C:172:PHE:HE1	1:C:200:GLU:HG3	1.86	0.40
1:D:238:LEU:HD23	1:D:238:LEU:HA	1.96	0.40
1:E:116:ILE:HG21	1:E:118:LYS:HZ2	1.83	0.40
1:E:165:GLN:HG3	1:E:211:ASP:N	2.36	0.40
1:E:201:LEU:O	1:E:204:ILE:N	2.55	0.40
1:E:263:LEU:O	1:E:266:ALA:N	2.53	0.40
1:E:347:LYS:HB3	1:E:347:LYS:HE3	1.14	0.40
1:F:121:LYS:O	1:F:124:ALA:N	2.54	0.40
1:F:290:PHE:HB2	1:F:327:LEU:HD22	2.03	0.40
1:G:174:VAL:HG23	1:G:196:GLY:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:175:ILE:HD12	1:G:175:ILE:C	2.24	0.40
1:H:242:LYS:HD2	1:H:242:LYS:HA	1.60	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	266/269 (99%)	225 (85%)	32 (12%)	9 (3%)	3	30
1	B	266/269 (99%)	218 (82%)	40 (15%)	8 (3%)	4	32
1	C	266/269 (99%)	221 (83%)	34 (13%)	11 (4%)	3	26
1	D	264/269 (98%)	226 (86%)	31 (12%)	7 (3%)	5	34
1	E	266/269 (99%)	219 (82%)	41 (15%)	6 (2%)	6	37
1	F	266/269 (99%)	224 (84%)	37 (14%)	5 (2%)	8	41
1	G	266/269 (99%)	224 (84%)	31 (12%)	11 (4%)	3	26
1	H	266/269 (99%)	225 (85%)	35 (13%)	6 (2%)	6	37
All	All	2126/2152 (99%)	1782 (84%)	281 (13%)	63 (3%)	4	32

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	VAL
1	A	252	SER
1	A	253	ILE
1	B	112	VAL
1	B	252	SER
1	C	361	SER
1	C	362	ASP
1	D	252	SER

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Mol	Chain	Res	Type
1	D	324	GLU
1	E	112	VAL
1	F	112	VAL
1	G	113	ARG
1	G	252	SER
1	H	306	GLU
1	A	115	VAL
1	B	111	TYR
1	B	253	ILE
1	C	113	ARG
1	C	311	VAL
1	D	253	ILE
1	D	325	ILE
1	F	252	SER
1	G	114	LYS
1	G	375	VAL
1	H	272	VAL
1	B	304	ARG
1	C	131	GLU
1	C	252	SER
1	D	254	LEU
1	E	252	SER
1	F	304	ARG
1	G	118	LYS
1	G	325	ILE
1	H	252	SER
1	A	111	TYR
1	A	254	LEU
1	B	130	ILE
1	C	272	VAL
1	C	300	VAL
1	D	201	LEU
1	F	272	VAL
1	H	112	VAL
1	B	254	LEU
1	C	111	TYR
1	E	123	MET
1	G	117	PRO
1	G	247	PHE
1	H	119	ASP
1	H	304	ARG
1	A	304	ARG

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Mol	Chain	Res	Type
1	C	201	LEU
1	F	201	LEU
1	G	112	VAL
1	G	123	MET
1	G	350	ARG
1	A	325	ILE
1	B	272	VAL
1	C	130	ILE
1	E	130	ILE
1	E	318	PRO
1	A	272	VAL
1	E	272	VAL
1	D	272	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	222/229 (97%)	165 (74%)	57 (26%)	0 4
1	B	222/229 (97%)	158 (71%)	64 (29%)	0 3
1	C	222/229 (97%)	155 (70%)	67 (30%)	0 2
1	D	220/229 (96%)	156 (71%)	64 (29%)	0 2
1	E	222/229 (97%)	169 (76%)	53 (24%)	0 5
1	F	222/229 (97%)	168 (76%)	54 (24%)	0 4
1	G	222/229 (97%)	179 (81%)	43 (19%)	1 9
1	H	222/229 (97%)	164 (74%)	58 (26%)	0 4
All	All	1774/1832 (97%)	1314 (74%)	460 (26%)	0 4

All (460) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	111	TYR
1	A	113	ARG

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Mol	Chain	Res	Type
1	A	114	LYS
1	A	115	VAL
1	A	119	ASP
1	A	120	TYR
1	A	121	LYS
1	A	122	THR
1	A	126	LEU
1	A	128	LYS
1	A	131	GLU
1	A	135	LEU
1	A	137	SER
1	A	139	LEU
1	A	144	ARG
1	A	145	SER
1	A	151	MET
1	A	152	PHE
1	A	154	VAL
1	A	156	PHE
1	A	168	GLU
1	A	177	GLN
1	A	186	ASN
1	A	188	TRP
1	A	198	PHE
1	A	205	TYR
1	A	207	THR
1	A	211	ASP
1	A	212	THR
1	A	222	TRP
1	A	224	ILE
1	A	226	ARG
1	A	233	LEU
1	A	236	SER
1	A	242	LYS
1	A	246	GLU
1	A	254	LEU
1	A	256	SER
1	A	262	ARG
1	A	264	THR
1	A	270	GLU
1	A	273	GLN
1	A	279	LYS
1	A	291	PHE

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Mol	Chain	Res	Type
1	A	293	ILE
1	A	294	LEU
1	A	310	PHE
1	A	313	VAL
1	A	315	ARG
1	A	329	MET
1	A	338	VAL
1	A	348	LEU
1	A	357	LEU
1	A	364	LEU
1	A	366	ARG
1	A	372	ASN
1	A	376	SER
1	B	112	VAL
1	B	115	VAL
1	B	120	TYR
1	B	121	LYS
1	B	122	THR
1	B	126	LEU
1	B	128	LYS
1	B	131	GLU
1	B	134	VAL
1	B	135	LEU
1	B	139	LEU
1	B	144	ARG
1	B	145	SER
1	B	151	MET
1	B	152	PHE
1	B	154	VAL
1	B	156	PHE
1	B	168	GLU
1	B	170	ASP
1	B	177	GLN
1	B	186	ASN
1	B	188	TRP
1	B	191	SER
1	B	198	PHE
1	B	200	GLU
1	B	201	LEU
1	B	205	TYR
1	B	207	THR
1	B	211	ASP

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Mol	Chain	Res	Type
1	B	212	THR
1	B	222	TRP
1	B	224	ILE
1	B	226	ARG
1	B	231	ARG
1	B	233	LEU
1	B	234	MET
1	B	236	SER
1	B	241	ARG
1	B	242	LYS
1	B	254	LEU
1	B	262	ARG
1	B	264	THR
1	B	273	GLN
1	B	279	LYS
1	B	288	ASP
1	B	291	PHE
1	B	292	ILE
1	B	293	ILE
1	B	294	LEU
1	B	301	LEU
1	B	310	PHE
1	B	312	GLU
1	B	313	VAL
1	B	315	ARG
1	B	316	LEU
1	B	321	TYR
1	B	322	PHE
1	B	329	MET
1	B	331	ARG
1	B	338	VAL
1	B	348	LEU
1	B	364	LEU
1	B	366	ARG
1	B	375	VAL
1	C	110	SER
1	C	113	ARG
1	C	115	VAL
1	C	120	TYR
1	C	121	LYS
1	C	122	THR
1	C	126	LEU

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Mol	Chain	Res	Type
1	C	128	LYS
1	C	131	GLU
1	C	134	VAL
1	C	135	LEU
1	C	137	SER
1	C	139	LEU
1	C	144	ARG
1	C	145	SER
1	C	151	MET
1	C	152	PHE
1	C	154	VAL
1	C	156	PHE
1	C	161	THR
1	C	162	VAL
1	C	168	GLU
1	C	177	GLN
1	C	186	ASN
1	C	188	TRP
1	C	198	PHE
1	C	200	GLU
1	C	205	TYR
1	C	207	THR
1	C	211	ASP
1	C	212	THR
1	C	213	VAL
1	C	222	TRP
1	C	224	ILE
1	C	226	ARG
1	C	233	LEU
1	C	234	MET
1	C	236	SER
1	C	242	LYS
1	C	246	GLU
1	C	247	PHE
1	C	248	LEU
1	C	249	SER
1	C	251	VAL
1	C	254	LEU
1	C	262	ARG
1	C	263	LEU
1	C	264	THR
1	C	269	LEU

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Mol	Chain	Res	Type
1	C	270	GLU
1	C	273	GLN
1	C	291	PHE
1	C	293	ILE
1	C	294	LEU
1	C	297	SER
1	C	301	LEU
1	C	309	GLU
1	C	313	VAL
1	C	315	ARG
1	C	316	LEU
1	C	329	MET
1	C	332	PRO
1	C	338	VAL
1	C	364	LEU
1	C	365	LYS
1	C	366	ARG
1	C	368	ILE
1	D	112	VAL
1	D	116	ILE
1	D	120	TYR
1	D	121	LYS
1	D	122	THR
1	D	126	LEU
1	D	128	LYS
1	D	131	GLU
1	D	134	VAL
1	D	135	LEU
1	D	139	LEU
1	D	144	ARG
1	D	145	SER
1	D	147	ILE
1	D	151	MET
1	D	152	PHE
1	D	154	VAL
1	D	157	ILE
1	D	161	THR
1	D	168	GLU
1	D	177	GLN
1	D	186	ASN
1	D	188	TRP
1	D	191	SER

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Mol	Chain	Res	Type
1	D	192	VAL
1	D	198	PHE
1	D	201	LEU
1	D	205	TYR
1	D	207	THR
1	D	211	ASP
1	D	212	THR
1	D	222	TRP
1	D	224	ILE
1	D	226	ARG
1	D	233	LEU
1	D	234	MET
1	D	236	SER
1	D	242	LYS
1	D	246	GLU
1	D	247	PHE
1	D	249	SER
1	D	250	LYS
1	D	251	VAL
1	D	254	LEU
1	D	256	SER
1	D	264	THR
1	D	270	GLU
1	D	273	GLN
1	D	279	LYS
1	D	291	PHE
1	D	293	ILE
1	D	294	LEU
1	D	309	GLU
1	D	311	VAL
1	D	312	GLU
1	D	313	VAL
1	D	315	ARG
1	D	316	LEU
1	D	325	ILE
1	D	329	MET
1	D	331	ARG
1	D	338	VAL
1	D	344	LYS
1	D	366	ARG
1	E	110	SER
1	E	112	VAL

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Mol	Chain	Res	Type
1	E	114	LYS
1	E	115	VAL
1	E	116	ILE
1	E	120	TYR
1	E	121	LYS
1	E	122	THR
1	E	126	LEU
1	E	131	GLU
1	E	135	LEU
1	E	139	LEU
1	E	144	ARG
1	E	145	SER
1	E	151	MET
1	E	152	PHE
1	E	154	VAL
1	E	156	PHE
1	E	168	GLU
1	E	177	GLN
1	E	188	TRP
1	E	198	PHE
1	E	205	TYR
1	E	207	THR
1	E	211	ASP
1	E	212	THR
1	E	222	TRP
1	E	224	ILE
1	E	226	ARG
1	E	233	LEU
1	E	236	SER
1	E	242	LYS
1	E	246	GLU
1	E	249	SER
1	E	254	LEU
1	E	264	THR
1	E	269	LEU
1	E	270	GLU
1	E	273	GLN
1	E	279	LYS
1	E	281	VAL
1	E	291	PHE
1	E	294	LEU
1	E	301	LEU

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Mol	Chain	Res	Type
1	E	309	GLU
1	E	312	GLU
1	E	329	MET
1	E	338	VAL
1	E	344	LYS
1	E	364	LEU
1	E	366	ARG
1	E	368	ILE
1	E	375	VAL
1	F	113	ARG
1	F	114	LYS
1	F	115	VAL
1	F	116	ILE
1	F	121	LYS
1	F	122	THR
1	F	126	LEU
1	F	128	LYS
1	F	130	ILE
1	F	131	GLU
1	F	135	LEU
1	F	139	LEU
1	F	144	ARG
1	F	145	SER
1	F	146	ASP
1	F	151	MET
1	F	152	PHE
1	F	154	VAL
1	F	156	PHE
1	F	168	GLU
1	F	177	GLN
1	F	186	ASN
1	F	188	TRP
1	F	190	THR
1	F	191	SER
1	F	198	PHE
1	F	205	TYR
1	F	207	THR
1	F	211	ASP
1	F	212	THR
1	F	222	TRP
1	F	224	ILE
1	F	226	ARG

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Mol	Chain	Res	Type
1	F	233	LEU
1	F	236	SER
1	F	242	LYS
1	F	246	GLU
1	F	247	PHE
1	F	249	SER
1	F	251	VAL
1	F	254	LEU
1	F	262	ARG
1	F	264	THR
1	F	273	GLN
1	F	279	LYS
1	F	291	PHE
1	F	294	LEU
1	F	301	LEU
1	F	302	GLN
1	F	321	TYR
1	F	329	MET
1	F	338	VAL
1	F	364	LEU
1	F	366	ARG
1	G	112	VAL
1	G	120	TYR
1	G	122	THR
1	G	126	LEU
1	G	135	LEU
1	G	139	LEU
1	G	144	ARG
1	G	145	SER
1	G	151	MET
1	G	152	PHE
1	G	154	VAL
1	G	161	THR
1	G	177	GLN
1	G	188	TRP
1	G	198	PHE
1	G	207	THR
1	G	211	ASP
1	G	212	THR
1	G	222	TRP
1	G	224	ILE
1	G	226	ARG

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Mol	Chain	Res	Type
1	G	233	LEU
1	G	236	SER
1	G	242	LYS
1	G	246	GLU
1	G	247	PHE
1	G	249	SER
1	G	251	VAL
1	G	254	LEU
1	G	262	ARG
1	G	264	THR
1	G	269	LEU
1	G	273	GLN
1	G	279	LYS
1	G	291	PHE
1	G	293	ILE
1	G	294	LEU
1	G	309	GLU
1	G	311	VAL
1	G	329	MET
1	G	338	VAL
1	G	364	LEU
1	G	366	ARG
1	H	110	SER
1	H	113	ARG
1	H	120	TYR
1	H	121	LYS
1	H	122	THR
1	H	126	LEU
1	H	128	LYS
1	H	131	GLU
1	H	135	LEU
1	H	137	SER
1	H	139	LEU
1	H	144	ARG
1	H	145	SER
1	H	151	MET
1	H	152	PHE
1	H	154	VAL
1	H	156	PHE
1	H	168	GLU
1	H	177	GLN
1	H	186	ASN

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Mol	Chain	Res	Type
1	H	188	TRP
1	H	198	PHE
1	H	205	TYR
1	H	207	THR
1	H	211	ASP
1	H	212	THR
1	H	222	TRP
1	H	224	ILE
1	H	226	ARG
1	H	233	LEU
1	H	236	SER
1	H	242	LYS
1	H	246	GLU
1	H	247	PHE
1	H	249	SER
1	H	251	VAL
1	H	254	LEU
1	H	256	SER
1	H	262	ARG
1	H	264	THR
1	H	270	GLU
1	H	273	GLN
1	H	279	LYS
1	H	285	GLU
1	H	291	PHE
1	H	292	ILE
1	H	293	ILE
1	H	300	VAL
1	H	301	LEU
1	H	309	GLU
1	H	311	VAL
1	H	313	VAL
1	H	329	MET
1	H	331	ARG
1	H	332	PRO
1	H	338	VAL
1	H	364	LEU
1	H	376	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	273	GLN
1	B	185	ASN
1	B	273	GLN
1	C	273	GLN
1	D	142	ASN
1	D	273	GLN
1	E	142	ASN
1	E	273	GLN
1	F	142	ASN
1	F	273	GLN
1	F	302	GLN
1	G	273	GLN
1	H	273	GLN
1	H	302	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

16 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	CMP	F	401	-	22,25,25	1.76	3 (13%)	24,39,39	1.71	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	CMP	D	402	-	22,25,25	1.80	6 (27%)	24,39,39	1.60	4 (16%)
2	CMP	C	402	-	22,25,25	1.89	6 (27%)	24,39,39	2.15	5 (20%)
2	CMP	H	401	-	22,25,25	2.15	5 (22%)	24,39,39	2.52	6 (25%)
2	CMP	C	401	-	22,25,25	1.72	4 (18%)	24,39,39	2.14	6 (25%)
2	CMP	G	401	-	22,25,25	1.93	6 (27%)	24,39,39	1.65	5 (20%)
2	CMP	H	402	-	22,25,25	1.81	5 (22%)	24,39,39	1.90	6 (25%)
2	CMP	E	402	-	22,25,25	1.92	5 (22%)	24,39,39	1.65	5 (20%)
2	CMP	A	401	-	22,25,25	1.68	3 (13%)	24,39,39	2.27	9 (37%)
2	CMP	B	402	-	22,25,25	2.22	6 (27%)	24,39,39	2.03	8 (33%)
2	CMP	D	401	-	22,25,25	1.89	4 (18%)	24,39,39	1.70	7 (29%)
2	CMP	F	402	-	22,25,25	1.91	5 (22%)	24,39,39	1.82	5 (20%)
2	CMP	E	401	-	22,25,25	1.76	7 (31%)	24,39,39	1.96	7 (29%)
2	CMP	G	402	-	22,25,25	1.63	6 (27%)	24,39,39	2.46	7 (29%)
2	CMP	B	401	-	22,25,25	1.77	4 (18%)	24,39,39	2.57	8 (33%)
2	CMP	A	402	-	22,25,25	2.07	7 (31%)	24,39,39	2.44	7 (29%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CMP	F	401	-	-	0/0/31/31	0/4/4/4
2	CMP	D	402	-	-	0/0/31/31	0/4/4/4
2	CMP	C	402	-	-	0/0/31/31	0/4/4/4
2	CMP	H	401	-	-	0/0/31/31	0/4/4/4
2	CMP	C	401	-	-	0/0/31/31	0/4/4/4
2	CMP	G	401	-	-	0/0/31/31	0/4/4/4
2	CMP	H	402	-	-	0/0/31/31	0/4/4/4
2	CMP	E	402	-	-	0/0/31/31	0/4/4/4
2	CMP	A	401	-	-	0/0/31/31	0/4/4/4
2	CMP	B	402	-	-	0/0/31/31	0/4/4/4
2	CMP	D	401	-	-	0/0/31/31	0/4/4/4
2	CMP	F	402	-	-	0/0/31/31	0/4/4/4
2	CMP	E	401	-	-	0/0/31/31	0/4/4/4
2	CMP	G	402	-	-	0/0/31/31	0/4/4/4
2	CMP	B	401	-	-	0/0/31/31	0/4/4/4
2	CMP	A	402	-	-	0/0/31/31	0/4/4/4

All (82) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	402	CMP	P-O3'	6.88	1.69	1.57
2	H	401	CMP	P-O3'	6.86	1.69	1.57
2	D	401	CMP	P-O3'	5.93	1.67	1.57
2	A	402	CMP	P-O5'	5.43	1.63	1.57
2	A	401	CMP	P-O3'	5.41	1.66	1.57
2	B	401	CMP	P-O3'	5.40	1.66	1.57
2	B	402	CMP	P-O5'	5.32	1.63	1.57
2	G	401	CMP	P-O3'	5.24	1.66	1.57
2	F	402	CMP	P-O5'	5.06	1.63	1.57
2	H	402	CMP	P-O5'	4.96	1.63	1.57
2	E	402	CMP	P-O5'	4.88	1.63	1.57
2	E	402	CMP	P-O3'	4.87	1.65	1.57
2	F	401	CMP	P-O3'	4.85	1.65	1.57
2	C	401	CMP	P-O3'	4.83	1.65	1.57
2	A	402	CMP	P-O3'	4.82	1.65	1.57
2	D	402	CMP	P-O3'	4.81	1.65	1.57
2	H	402	CMP	P-O3'	4.53	1.65	1.57
2	F	402	CMP	P-O3'	4.44	1.65	1.57
2	E	401	CMP	P-O3'	4.23	1.64	1.57
2	C	402	CMP	P-O5'	4.15	1.62	1.57
2	C	402	CMP	P-O3'	3.95	1.64	1.57
2	G	401	CMP	C5-C4	3.43	1.50	1.40
2	D	401	CMP	P-O5'	3.33	1.61	1.57
2	G	402	CMP	P-O3'	3.26	1.63	1.57
2	F	401	CMP	O5'-C5'	-3.24	1.41	1.46
2	G	401	CMP	P-O5'	3.23	1.61	1.57
2	E	401	CMP	O5'-C5'	-3.15	1.41	1.46
2	E	402	CMP	C5-C4	3.13	1.49	1.40
2	F	402	CMP	C5-C4	3.08	1.49	1.40
2	C	402	CMP	C2-N3	3.04	1.37	1.32
2	H	401	CMP	C5-C4	3.02	1.48	1.40
2	G	402	CMP	C5-C4	3.00	1.48	1.40
2	C	402	CMP	C5-C4	2.93	1.48	1.40
2	H	401	CMP	C2-N3	2.90	1.36	1.32
2	D	402	CMP	P-O5'	2.89	1.61	1.57
2	G	402	CMP	O3'-C3'	-2.89	1.40	1.44
2	E	401	CMP	O3'-C3'	-2.88	1.40	1.44
2	A	402	CMP	C2-N3	2.87	1.36	1.32
2	B	401	CMP	O5'-C5'	-2.85	1.42	1.46
2	C	401	CMP	C2-N3	2.81	1.36	1.32
2	F	401	CMP	O3'-C3'	-2.80	1.40	1.44
2	H	401	CMP	C6-C5	2.79	1.53	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	CMP	O5'-C5'	-2.76	1.42	1.46
2	H	401	CMP	O5'-C5'	-2.74	1.42	1.46
2	D	402	CMP	O3'-C3'	-2.73	1.40	1.44
2	D	401	CMP	C5-C4	2.73	1.48	1.40
2	G	401	CMP	O3'-C3'	-2.68	1.40	1.44
2	C	401	CMP	C5-C4	2.65	1.47	1.40
2	A	402	CMP	C5-C4	2.62	1.47	1.40
2	F	402	CMP	C2-N3	2.62	1.36	1.32
2	F	402	CMP	C6-C5	2.54	1.52	1.43
2	E	401	CMP	C2-N3	2.54	1.36	1.32
2	C	401	CMP	O3'-C3'	-2.53	1.40	1.44
2	D	401	CMP	C2-N3	2.52	1.36	1.32
2	B	401	CMP	C2-N3	2.50	1.36	1.32
2	G	402	CMP	C5'-C4'	-2.50	1.47	1.51
2	G	401	CMP	C2-N3	2.48	1.36	1.32
2	G	401	CMP	O5'-C5'	-2.48	1.42	1.46
2	D	402	CMP	C2-N3	2.44	1.36	1.32
2	A	402	CMP	C2'-C1'	2.41	1.57	1.53
2	C	402	CMP	O5'-C5'	-2.40	1.42	1.46
2	B	402	CMP	C2'-C1'	2.39	1.57	1.53
2	H	402	CMP	C5-C4	2.35	1.47	1.40
2	D	402	CMP	C5-C4	2.33	1.47	1.40
2	G	402	CMP	O5'-C5'	-2.32	1.42	1.46
2	H	402	CMP	O3'-C3'	-2.31	1.40	1.44
2	B	402	CMP	C2-N3	2.30	1.35	1.32
2	E	402	CMP	C2-N3	2.25	1.35	1.32
2	H	402	CMP	O5'-C5'	-2.24	1.43	1.46
2	C	402	CMP	O3'-C3'	-2.19	1.41	1.44
2	G	402	CMP	P-O5'	2.16	1.60	1.57
2	A	401	CMP	P-O5'	2.14	1.60	1.57
2	B	401	CMP	C5-C4	2.14	1.46	1.40
2	B	402	CMP	C5-C4	2.12	1.46	1.40
2	D	402	CMP	O5'-C5'	-2.12	1.43	1.46
2	E	401	CMP	P-O5'	2.12	1.60	1.57
2	A	402	CMP	C4-N3	2.11	1.38	1.35
2	E	402	CMP	C6-C5	2.10	1.51	1.43
2	A	402	CMP	O5'-C5'	-2.09	1.43	1.46
2	E	401	CMP	C5-C4	2.05	1.46	1.40
2	E	401	CMP	C6-C5	2.04	1.50	1.43
2	B	402	CMP	C5'-C4'	-2.00	1.48	1.51

All (100) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	402	CMP	C1'-N9-C4	8.60	141.76	126.64
2	H	401	CMP	C4-C5-N7	-7.18	101.92	109.40
2	A	402	CMP	O3'-P-O1P	-6.46	96.56	110.39
2	B	401	CMP	N3-C2-N1	-6.19	119.01	128.68
2	A	401	CMP	N3-C2-N1	-6.05	119.22	128.68
2	B	401	CMP	C5-C6-N6	-6.01	111.22	120.35
2	E	401	CMP	C4-C5-N7	-5.87	103.28	109.40
2	C	401	CMP	C1'-N9-C4	5.84	136.90	126.64
2	H	402	CMP	O5'-P-O3'	5.72	113.56	105.68
2	C	402	CMP	O5'-P-O3'	5.59	113.37	105.68
2	C	402	CMP	O3'-P-O1P	-5.52	98.57	110.39
2	H	401	CMP	C5-C6-N6	5.52	128.74	120.35
2	A	402	CMP	C1'-N9-C4	5.25	135.86	126.64
2	F	402	CMP	O3'-P-O1P	-4.90	99.90	110.39
2	B	402	CMP	O2P-P-O3'	-4.80	95.85	107.04
2	H	401	CMP	C1'-N9-C4	4.71	134.91	126.64
2	B	401	CMP	O3'-P-O1P	-4.66	100.42	110.39
2	C	401	CMP	C4-C5-N7	-4.64	104.56	109.40
2	G	402	CMP	O3'-P-O1P	-4.58	100.57	110.39
2	B	401	CMP	N6-C6-N1	4.51	127.94	118.57
2	F	401	CMP	C4-C5-N7	-4.27	104.95	109.40
2	A	401	CMP	C5-C6-N6	-4.26	113.88	120.35
2	A	402	CMP	O5'-P-O3'	4.23	111.50	105.68
2	D	401	CMP	C1'-N9-C4	4.13	133.89	126.64
2	A	402	CMP	N3-C2-N1	-3.97	122.47	128.68
2	A	401	CMP	N6-C6-N1	3.96	126.79	118.57
2	F	402	CMP	C4-C5-N7	-3.96	105.28	109.40
2	D	402	CMP	O2P-P-O3'	-3.94	97.86	107.04
2	G	401	CMP	C1'-N9-C4	3.81	133.33	126.64
2	C	402	CMP	N3-C2-N1	-3.70	122.90	128.68
2	G	402	CMP	O2P-P-O1P	3.67	120.22	108.73
2	B	402	CMP	O5'-P-O3'	3.65	110.70	105.68
2	E	402	CMP	C4-C5-N7	-3.57	105.68	109.40
2	F	401	CMP	O2P-P-O1P	3.49	119.66	108.73
2	C	402	CMP	C1'-N9-C4	3.47	132.74	126.64
2	G	401	CMP	O2P-P-O1P	3.43	119.46	108.73
2	H	401	CMP	N6-C6-N1	-3.42	111.47	118.57
2	G	401	CMP	O3'-C3'-C4'	-3.39	108.15	110.71
2	B	402	CMP	O3'-C3'-C4'	-3.35	108.18	110.71
2	E	401	CMP	O2P-P-O1P	3.33	119.15	108.73
2	D	402	CMP	C4-C5-N7	-3.27	106.00	109.40
2	D	401	CMP	C4-C5-N7	-3.24	106.03	109.40
2	D	402	CMP	N3-C2-N1	-3.23	123.63	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	401	CMP	O3'-P-O1P	-3.21	103.51	110.39
2	C	401	CMP	O2P-P-O1P	3.15	118.60	108.73
2	E	402	CMP	O2P-P-O3'	-3.12	99.77	107.04
2	C	401	CMP	O3'-P-O1P	-3.12	103.70	110.39
2	B	401	CMP	O2P-P-O1P	3.12	118.49	108.73
2	D	402	CMP	O2P-P-O1P	3.11	118.46	108.73
2	E	402	CMP	O2P-P-O1P	3.10	118.45	108.73
2	C	402	CMP	O2P-P-O1P	3.10	118.44	108.73
2	B	402	CMP	C1'-N9-C4	3.07	132.04	126.64
2	H	402	CMP	O2P-P-O1P	3.07	118.35	108.73
2	D	401	CMP	O2P-P-O1P	3.06	118.31	108.73
2	F	402	CMP	O2P-P-O1P	3.06	118.31	108.73
2	A	402	CMP	O2P-P-O1P	3.05	118.30	108.73
2	A	401	CMP	O2P-P-O1P	3.05	118.27	108.73
2	A	402	CMP	C4-C5-N7	-3.03	106.24	109.40
2	H	401	CMP	O2P-P-O1P	3.00	118.13	108.73
2	E	402	CMP	N3-C2-N1	-2.95	124.06	128.68
2	G	402	CMP	N3-C2-N1	-2.94	124.08	128.68
2	B	402	CMP	O2P-P-O1P	2.87	117.72	108.73
2	B	402	CMP	N3-C2-N1	-2.86	124.20	128.68
2	G	401	CMP	C4-C5-N7	-2.84	106.44	109.40
2	H	402	CMP	O3'-P-O1P	-2.83	104.33	110.39
2	C	401	CMP	C5-C6-N6	2.75	124.53	120.35
2	B	402	CMP	O3'-C3'-C2'	-2.73	112.93	115.61
2	A	402	CMP	O3'-C3'-C4'	2.72	112.76	110.71
2	A	401	CMP	C2-N1-C6	2.71	123.40	118.75
2	G	401	CMP	O3'-P-O1P	-2.70	104.60	110.39
2	F	402	CMP	N3-C2-N1	-2.68	124.48	128.68
2	H	402	CMP	O2P-P-O3'	-2.65	100.86	107.04
2	F	401	CMP	N3-C2-N1	-2.64	124.55	128.68
2	D	401	CMP	N3-C2-N1	-2.62	124.58	128.68
2	A	401	CMP	C1'-N9-C4	2.60	131.22	126.64
2	F	402	CMP	C5-C6-N6	2.54	124.21	120.35
2	H	402	CMP	N3-C2-N1	-2.45	124.85	128.68
2	B	401	CMP	O3'-C3'-C2'	2.42	117.98	115.61
2	G	402	CMP	N6-C6-N1	2.42	123.59	118.57
2	A	401	CMP	O3'-P-O1P	-2.42	105.22	110.39
2	F	401	CMP	O4'-C4'-C3'	-2.37	99.79	104.87
2	G	402	CMP	O3'-C3'-C4'	-2.32	108.96	110.71
2	H	401	CMP	O3'-C3'-C2'	2.32	117.88	115.61
2	A	401	CMP	O3'-C3'-C2'	2.31	117.87	115.61
2	C	401	CMP	O5'-C5'-C4'	2.30	111.07	105.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	401	CMP	O5'-P-O3'	2.29	108.83	105.68
2	D	401	CMP	O3'-C3'-C2'	2.24	117.80	115.61
2	D	401	CMP	O5'-P-O3'	-2.20	102.65	105.68
2	F	401	CMP	O2P-P-O3'	-2.20	101.92	107.04
2	E	402	CMP	O3'-C3'-C4'	2.20	112.37	110.71
2	H	402	CMP	C4-C5-N7	-2.19	107.12	109.40
2	B	401	CMP	O4'-C4'-C3'	-2.18	100.20	104.87
2	E	401	CMP	N3-C2-N1	-2.16	125.31	128.68
2	D	401	CMP	O5'-C5'-C4'	2.11	110.62	105.71
2	E	401	CMP	C1'-N9-C4	-2.10	122.94	126.64
2	E	401	CMP	O4'-C4'-C3'	-2.10	100.36	104.87
2	A	401	CMP	O4'-C4'-C3'	-2.07	100.43	104.87
2	G	402	CMP	C2-N1-C6	2.07	122.29	118.75
2	B	401	CMP	C2-N1-C6	2.05	122.25	118.75
2	B	402	CMP	C4-C5-N7	-2.04	107.28	109.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

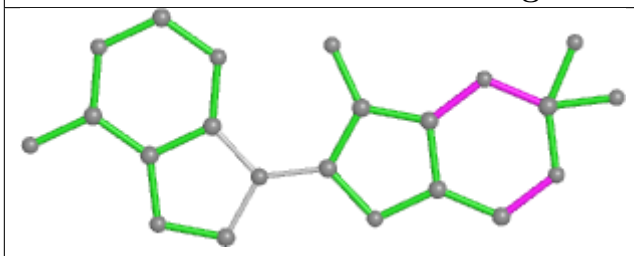
16 monomers are involved in 300 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	401	CMP	22	0
2	D	402	CMP	21	0
2	C	402	CMP	19	0
2	H	401	CMP	22	0
2	C	401	CMP	17	0
2	G	401	CMP	19	0
2	H	402	CMP	16	0
2	E	402	CMP	11	0
2	A	401	CMP	25	0
2	B	402	CMP	21	0
2	D	401	CMP	16	0
2	F	402	CMP	7	0
2	E	401	CMP	24	0
2	G	402	CMP	11	0
2	B	401	CMP	34	0
2	A	402	CMP	15	0

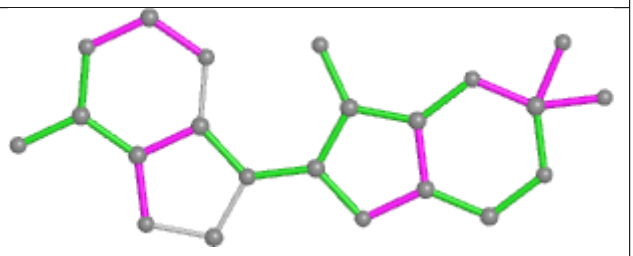
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

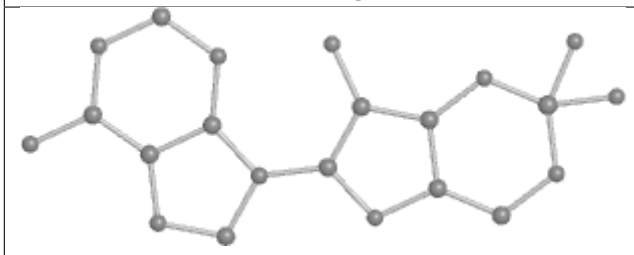
Ligand CMP F 401



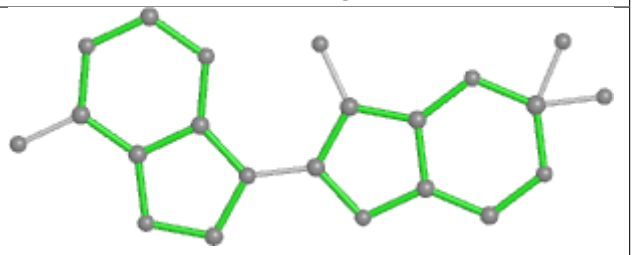
Bond lengths



Bond angles

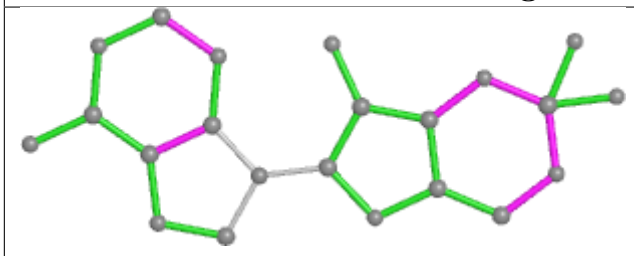


Torsions

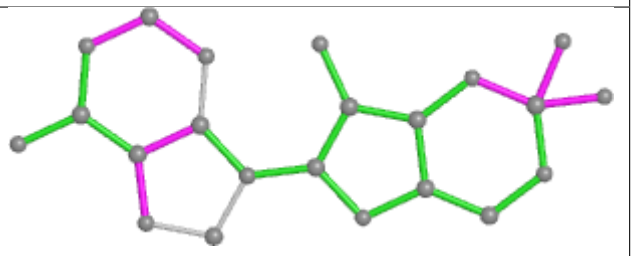


Rings

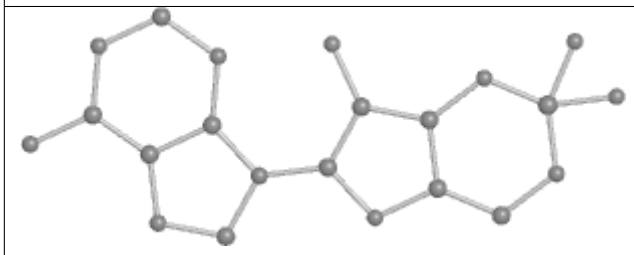
Ligand CMP D 402



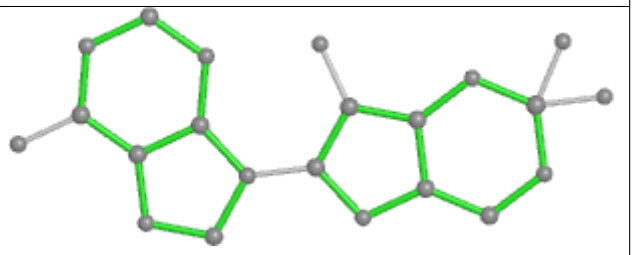
Bond lengths



Bond angles

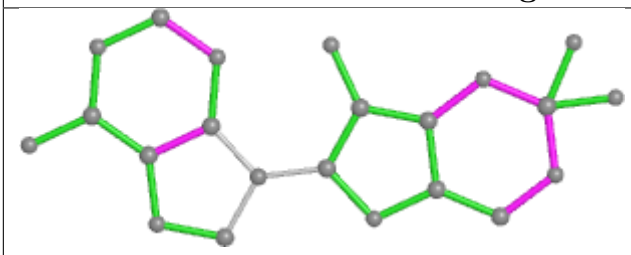


Torsions

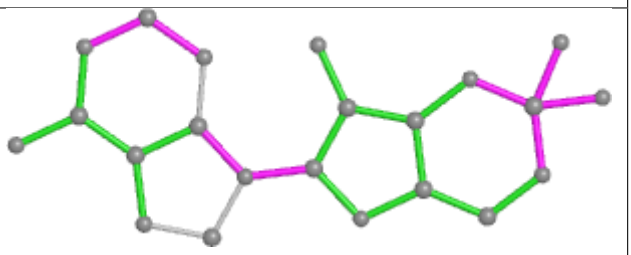


Rings

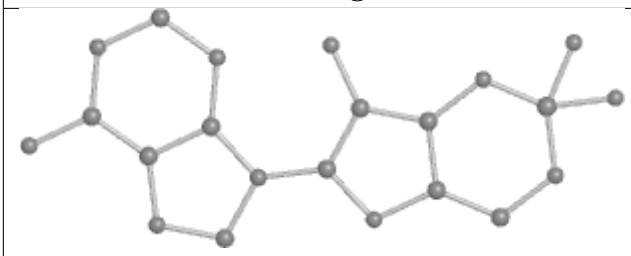
Ligand CMP C 402



Bond lengths



Bond angles



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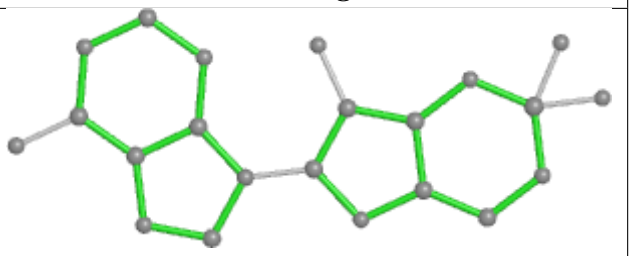
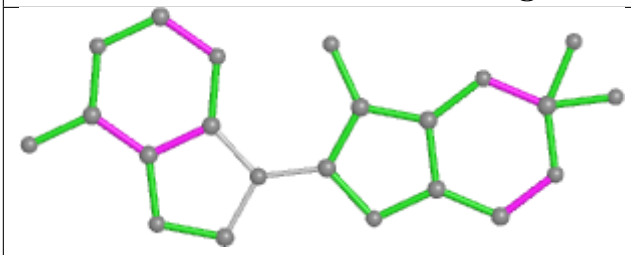


Rings

Ligand CMP H 401



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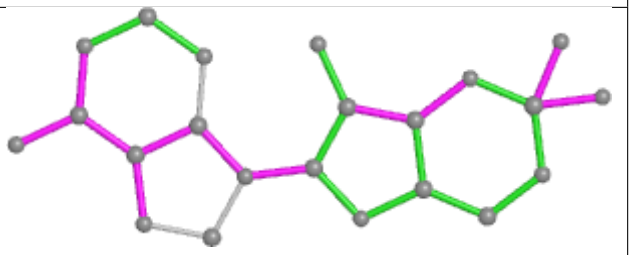
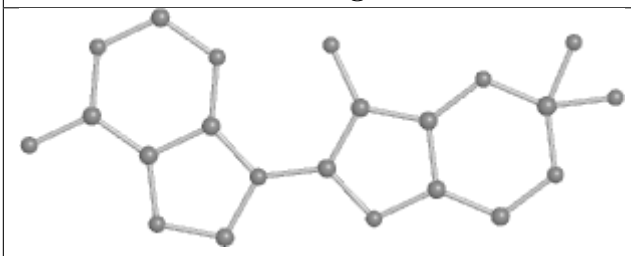
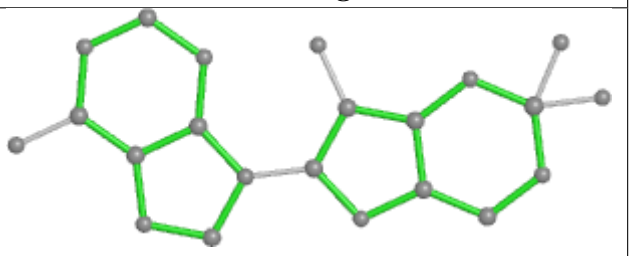


Bond angles

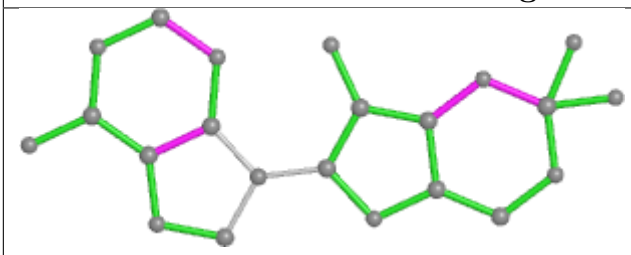


Torsions

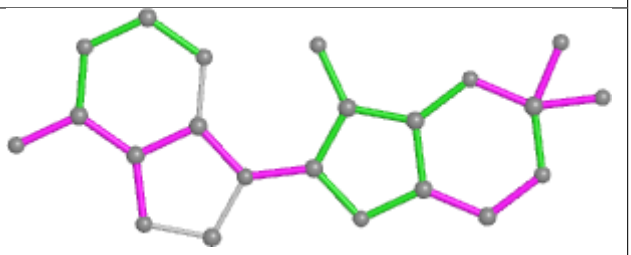


Rings

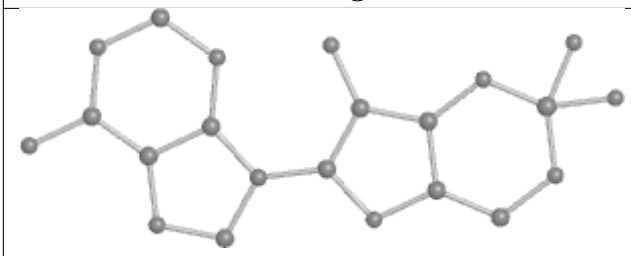
Ligand CMP C 401



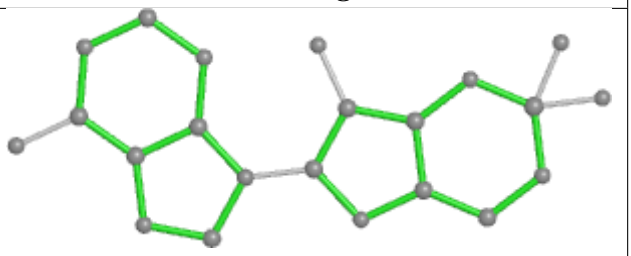
Bond lengths



Bond angles

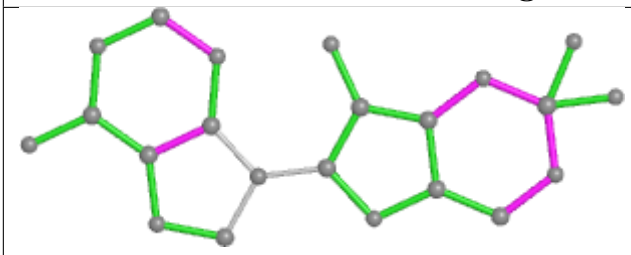


Torsions

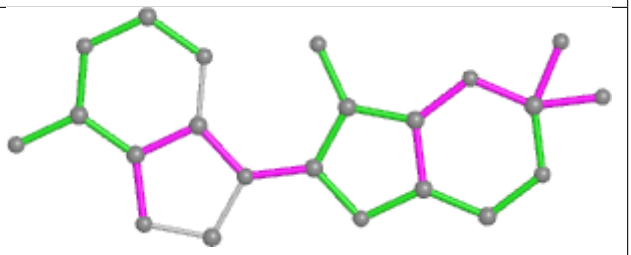


Rings

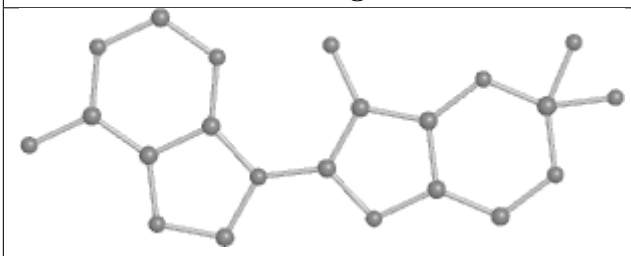
Ligand CMP G 401



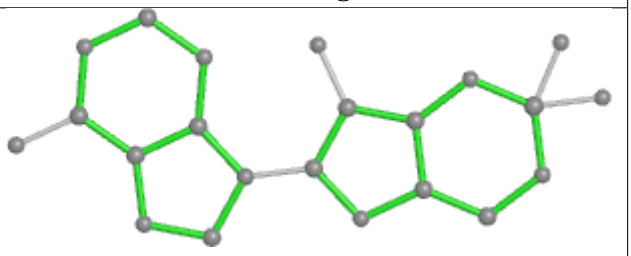
Bond lengths



Bond angles

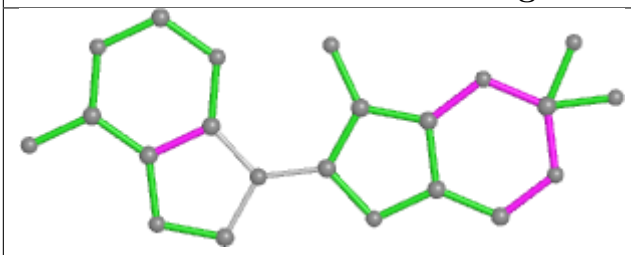


Torsions

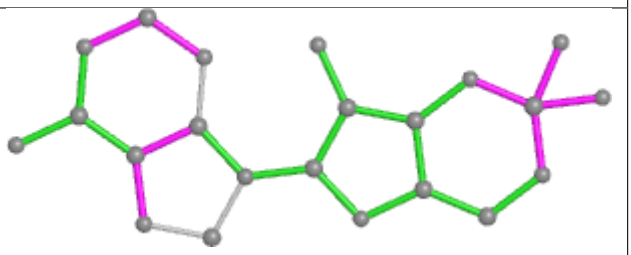


Rings

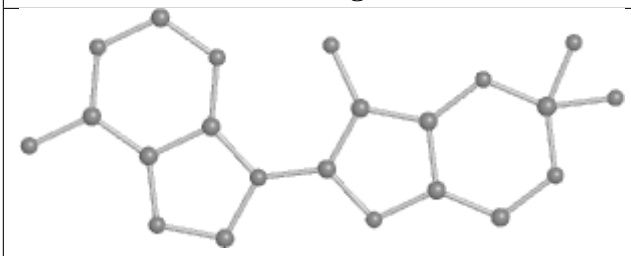
Ligand CMP H 402



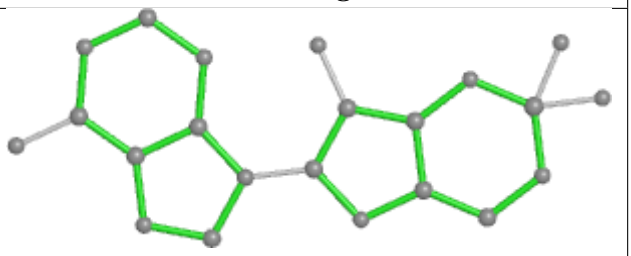
Bond lengths



Bond angles

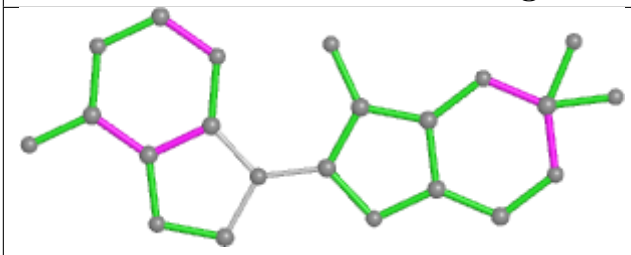


Torsions

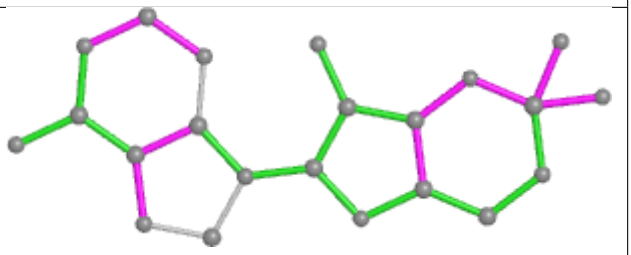


Rings

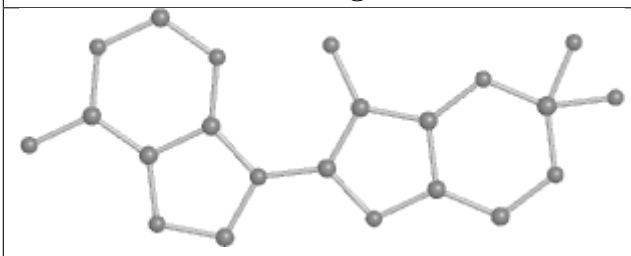
Ligand CMP E 402



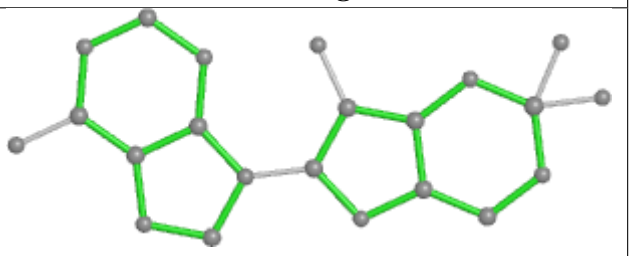
Bond lengths



Bond angles

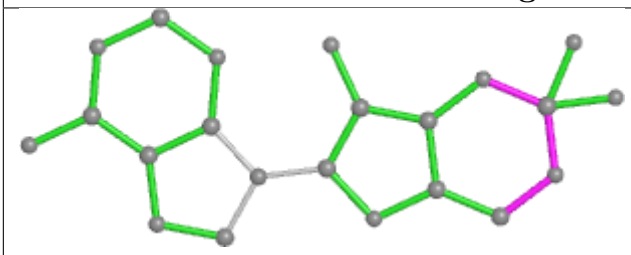


Torsions

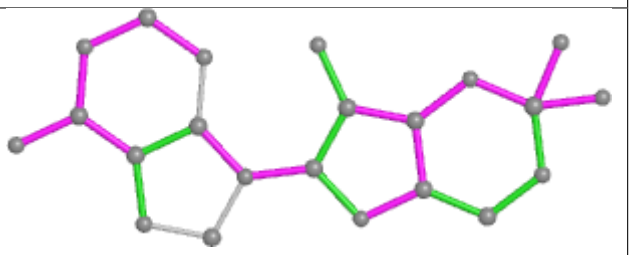


Rings

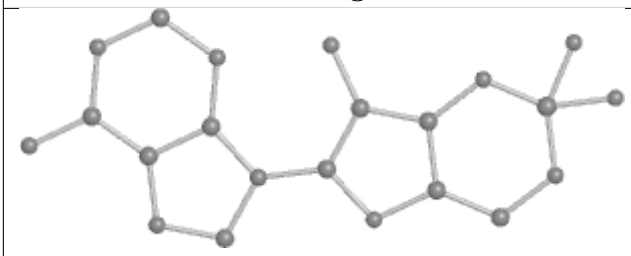
Ligand CMP A 401



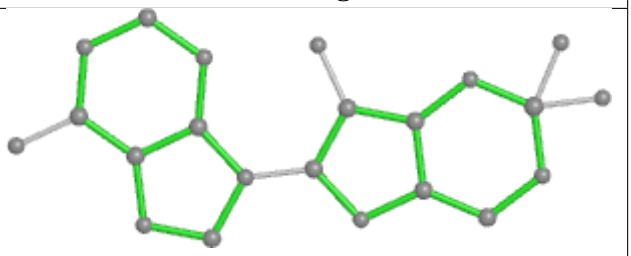
Bond lengths



Bond angles

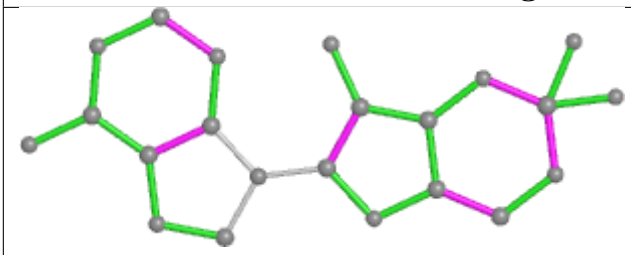


Torsions

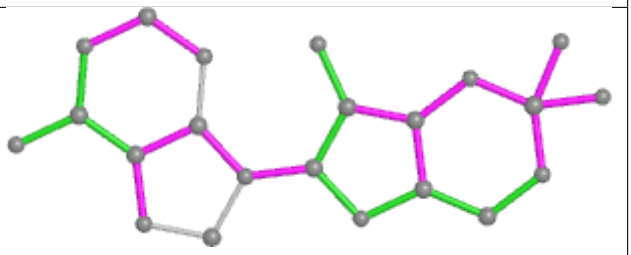


Rings

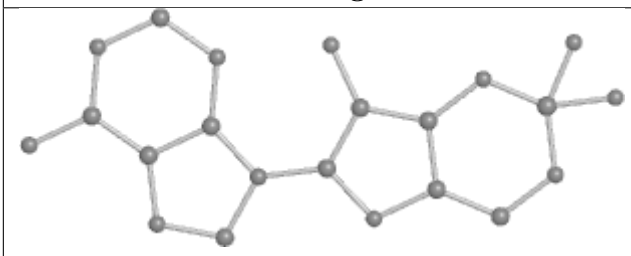
Ligand CMP B 402



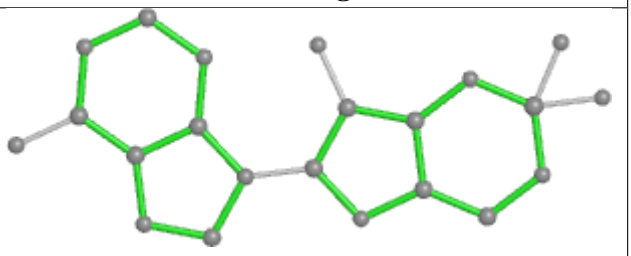
Bond lengths



Bond angles

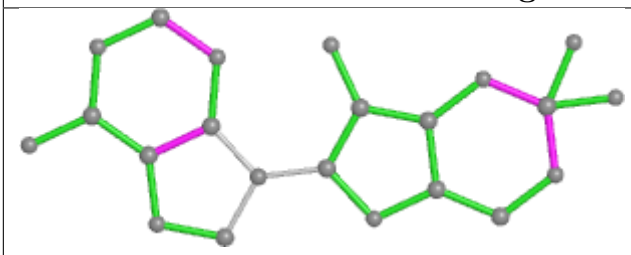


Torsions

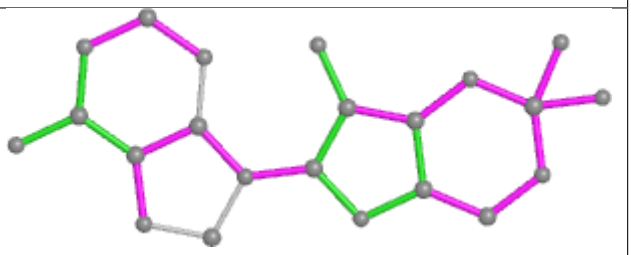


Rings

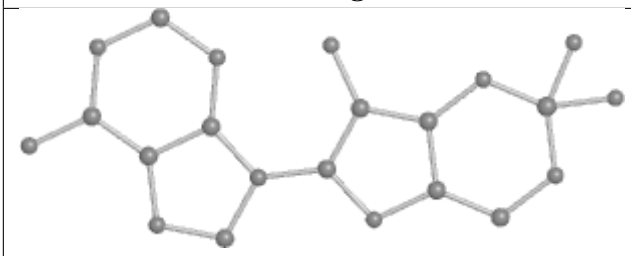
Ligand CMP D 401



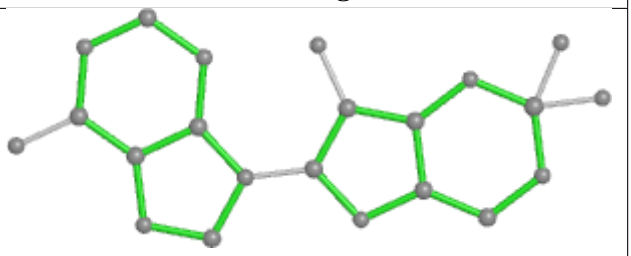
Bond lengths



Bond angles

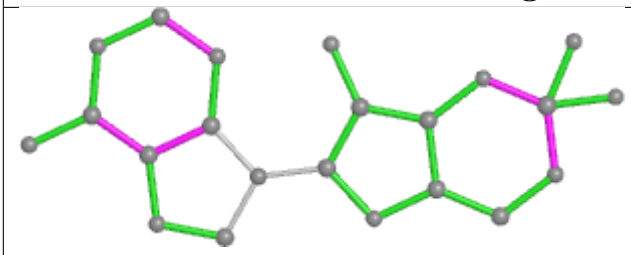


Torsions

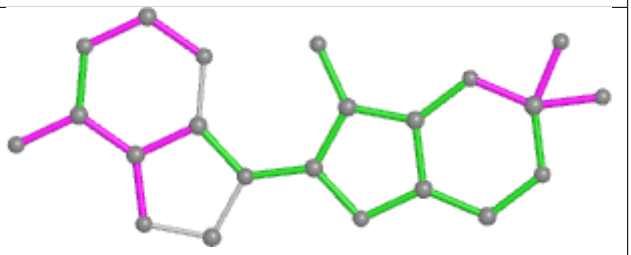


Rings

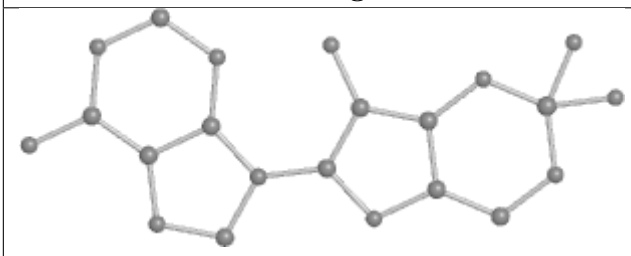
Ligand CMP F 402



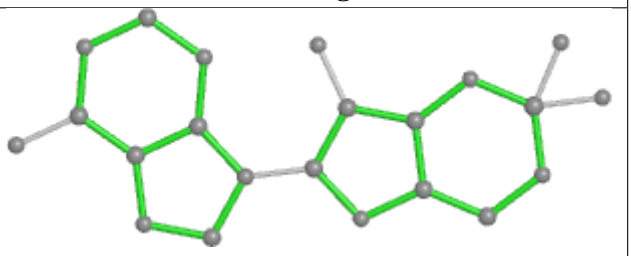
Bond lengths



Bond angles

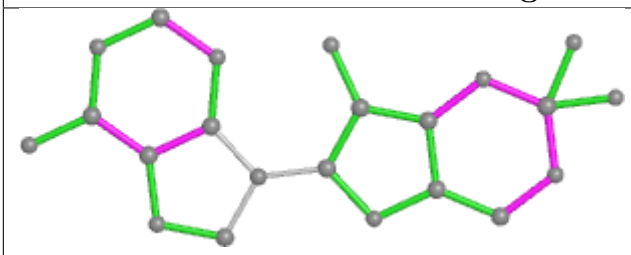


Torsions

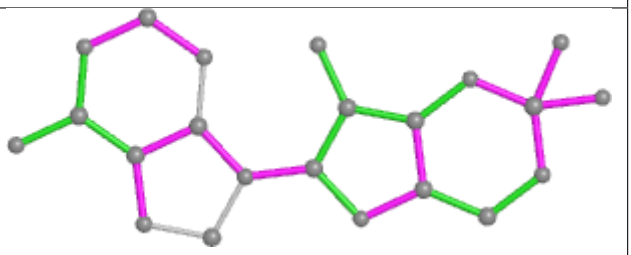


Rings

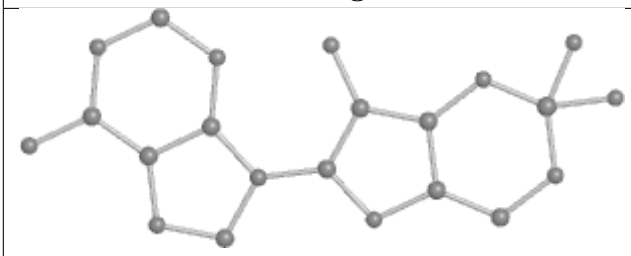
Ligand CMP E 401



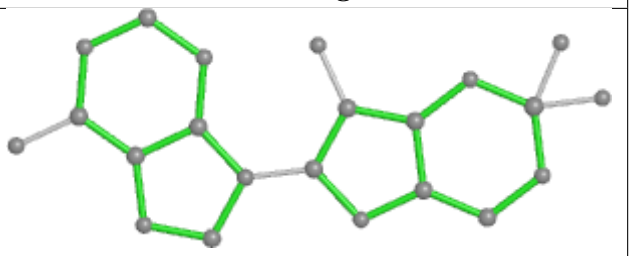
Bond lengths



Bond angles

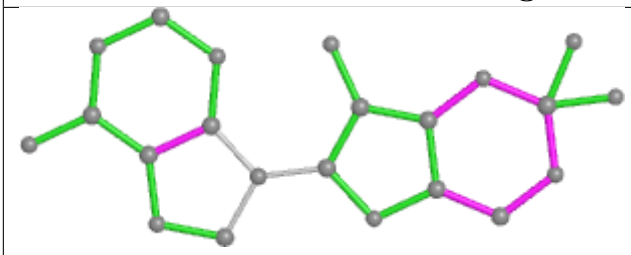


Torsions

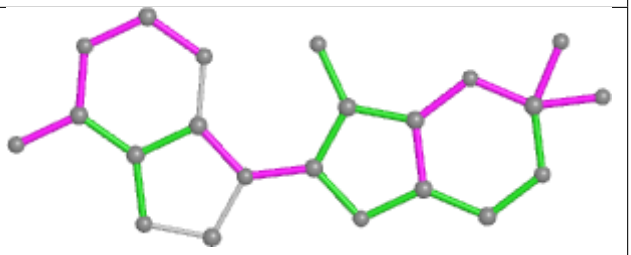


Rings

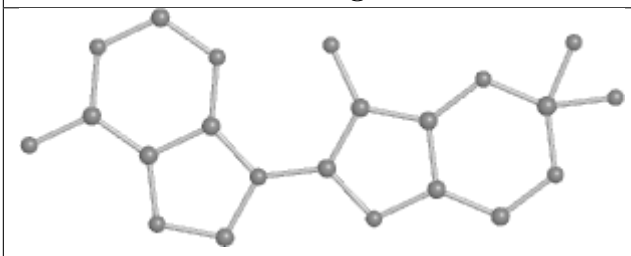
Ligand CMP G 402



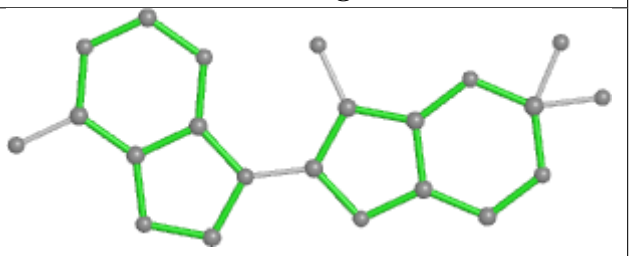
Bond lengths



Bond angles

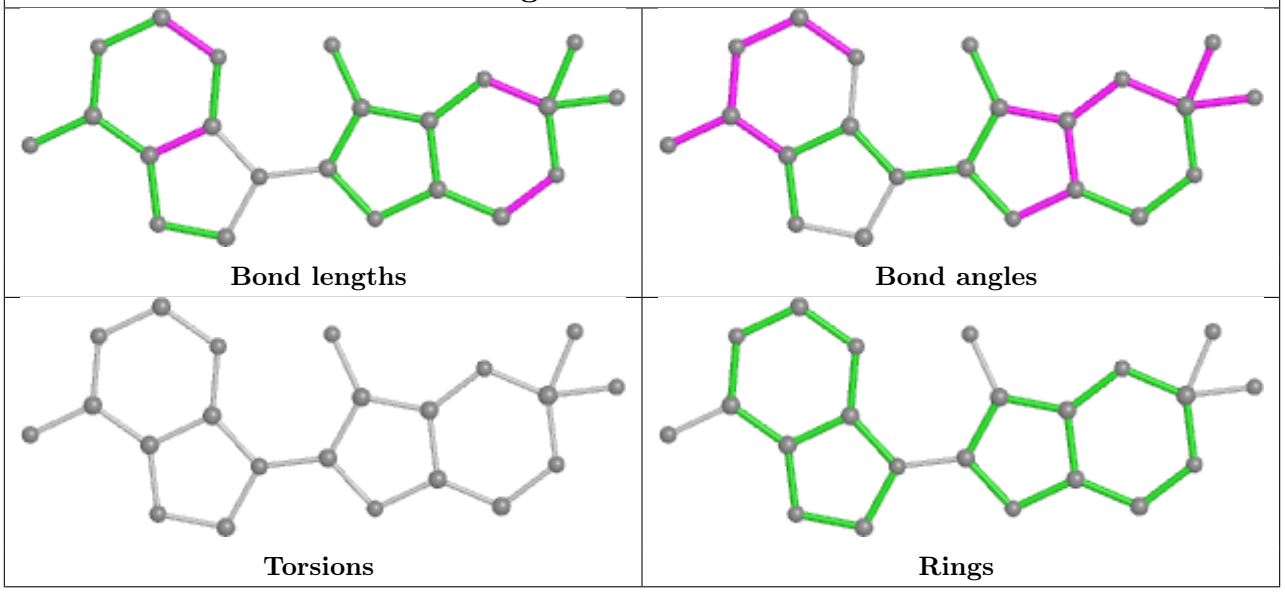


Torsions

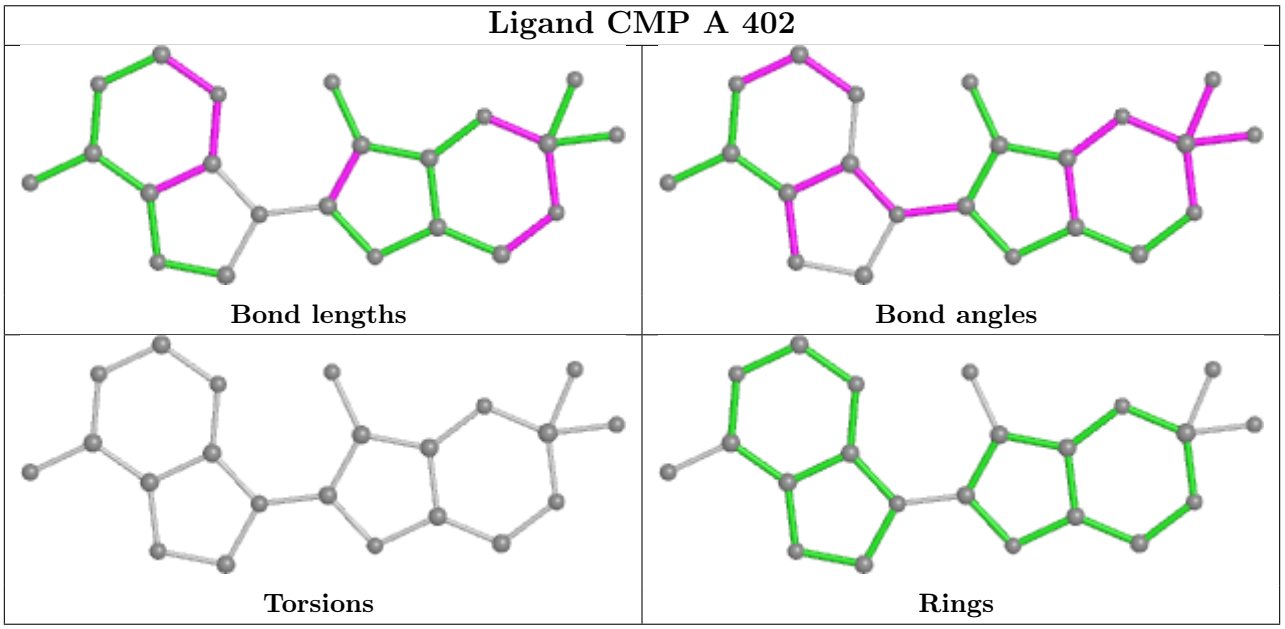


Rings

Ligand CMP B 401



Ligand CMP A 402



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	268/269 (99%)	0.03	13 (4%)	29	25	70, 133, 202, 260	0
1	B	268/269 (99%)	-0.04	11 (4%)	37	30	70, 133, 202, 266	0
1	C	268/269 (99%)	-0.09	8 (2%)	50	39	71, 131, 201, 286	0
1	D	266/269 (98%)	-0.05	10 (3%)	40	32	75, 133, 194, 246	0
1	E	268/269 (99%)	0.02	10 (3%)	41	33	75, 139, 215, 259	0
1	F	268/269 (99%)	0.04	8 (2%)	50	39	75, 138, 212, 261	0
1	G	268/269 (99%)	-0.06	10 (3%)	41	33	77, 135, 201, 268	0
1	H	268/269 (99%)	-0.05	7 (2%)	56	45	71, 132, 199, 274	0
All	All	2142/2152 (99%)	-0.03	77 (3%)	42	34	70, 134, 205, 286	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	306	GLU	7.7
1	B	304	ARG	6.4
1	B	305	SER	6.4
1	A	306	GLU	5.1
1	H	169	GLY	5.0
1	A	305	SER	4.9
1	A	304	ARG	4.7
1	E	307	ASN	4.6
1	C	287	GLY	4.5
1	F	375	VAL	4.4
1	E	305	SER	4.4
1	D	305	SER	4.3
1	D	306	GLU	3.9
1	A	168	GLU	3.8
1	B	307	ASN	3.7
1	H	168	GLU	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	168	GLU	3.6
1	C	169	GLY	3.5
1	A	340	ARG	3.5
1	D	304	ARG	3.4
1	E	306	GLU	3.4
1	D	302	GLN	3.3
1	E	304	ARG	3.3
1	A	370	GLN	3.3
1	D	307	ASN	3.3
1	A	109	ALA	3.3
1	B	179	GLU	3.2
1	G	167	ASP	3.0
1	G	305	SER	2.9
1	E	368	ILE	2.9
1	C	187	GLU	2.9
1	G	374	PHE	2.9
1	G	166	GLY	2.9
1	D	275	GLU	2.8
1	B	164	GLN	2.7
1	C	168	GLU	2.7
1	D	286	PRO	2.7
1	H	226	ARG	2.7
1	C	331	ARG	2.6
1	F	368	ILE	2.6
1	E	169	GLY	2.6
1	A	179	GLU	2.5
1	G	286	PRO	2.5
1	E	308	GLU	2.5
1	F	305	SER	2.4
1	B	178	GLY	2.4
1	H	334	ALA	2.4
1	H	170	ASP	2.4
1	H	376	SER	2.4
1	A	339	ALA	2.4
1	F	304	ARG	2.3
1	G	275	GLU	2.3
1	F	185	ASN	2.3
1	F	372	ASN	2.3
1	B	308	GLU	2.3
1	C	334	ALA	2.3
1	D	370	GLN	2.3
1	G	183	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	369	GLN	2.2
1	E	282	VAL	2.2
1	G	168	GLU	2.2
1	E	370	GLN	2.2
1	A	307	ASN	2.2
1	B	286	PRO	2.2
1	H	164	GLN	2.2
1	F	168	GLU	2.2
1	A	186	ASN	2.1
1	D	168	GLU	2.1
1	F	307	ASN	2.1
1	G	164	GLN	2.1
1	C	277	GLY	2.1
1	A	185	ASN	2.1
1	D	187	GLU	2.1
1	E	177	GLN	2.1
1	C	307	ASN	2.0
1	B	370	GLN	2.0
1	G	184	VAL	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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CMP	A	402	22/22	0.92	0.33	79,151,186,198	0
2	CMP	B	402	22/22	0.92	0.26	86,150,175,194	0
2	CMP	C	401	22/22	0.94	0.29	77,107,140,155	0
2	CMP	E	402	22/22	0.94	0.15	118,201,228,242	0

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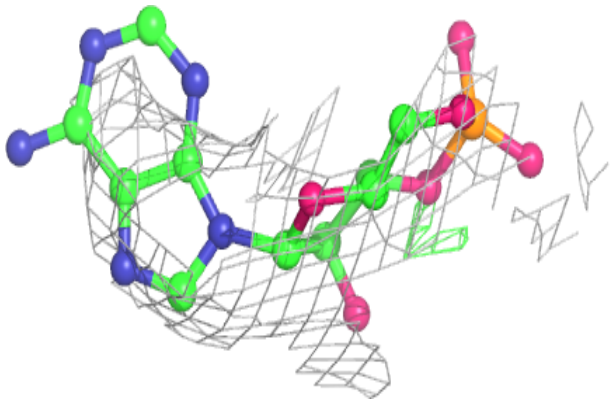
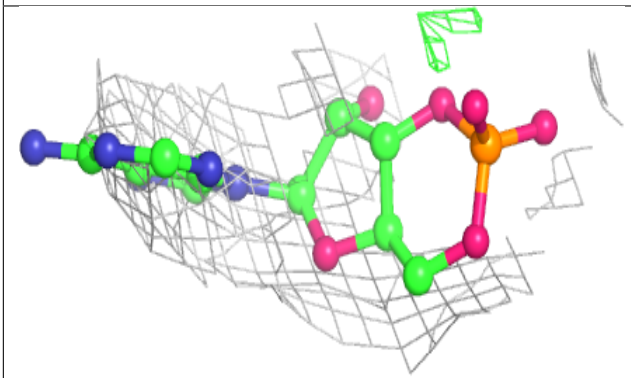
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CMP	G	402	22/22	0.94	0.32	101,148,200,208	0
2	CMP	H	401	22/22	0.94	0.30	74,105,125,133	0
2	CMP	F	402	22/22	0.95	0.18	137,185,218,227	0
2	CMP	G	401	22/22	0.95	0.23	79,112,144,145	0
2	CMP	D	402	22/22	0.95	0.28	112,143,193,210	0
2	CMP	D	401	22/22	0.95	0.21	84,111,128,131	0
2	CMP	B	401	22/22	0.96	0.22	70,102,127,132	0
2	CMP	C	402	22/22	0.96	0.28	79,130,177,213	0
2	CMP	A	401	22/22	0.96	0.28	77,102,123,128	0
2	CMP	E	401	22/22	0.97	0.28	73,108,130,140	0
2	CMP	F	401	22/22	0.97	0.28	69,96,132,143	0
2	CMP	H	402	22/22	0.97	0.27	81,139,165,200	0

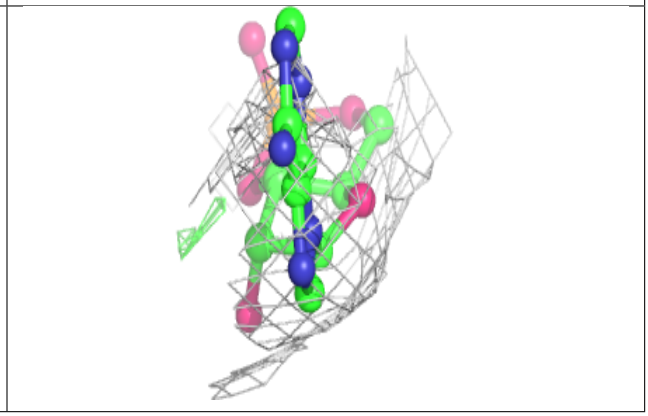
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around CMP A 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

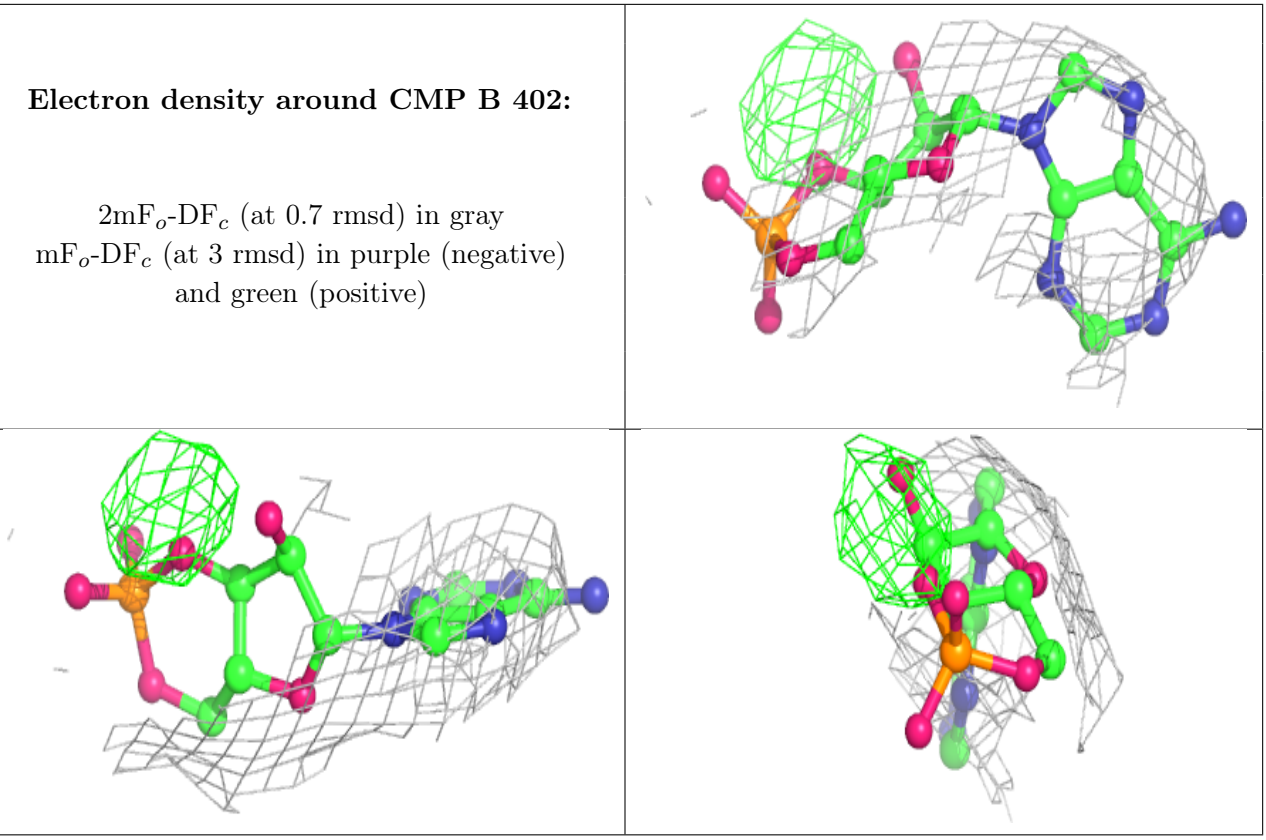






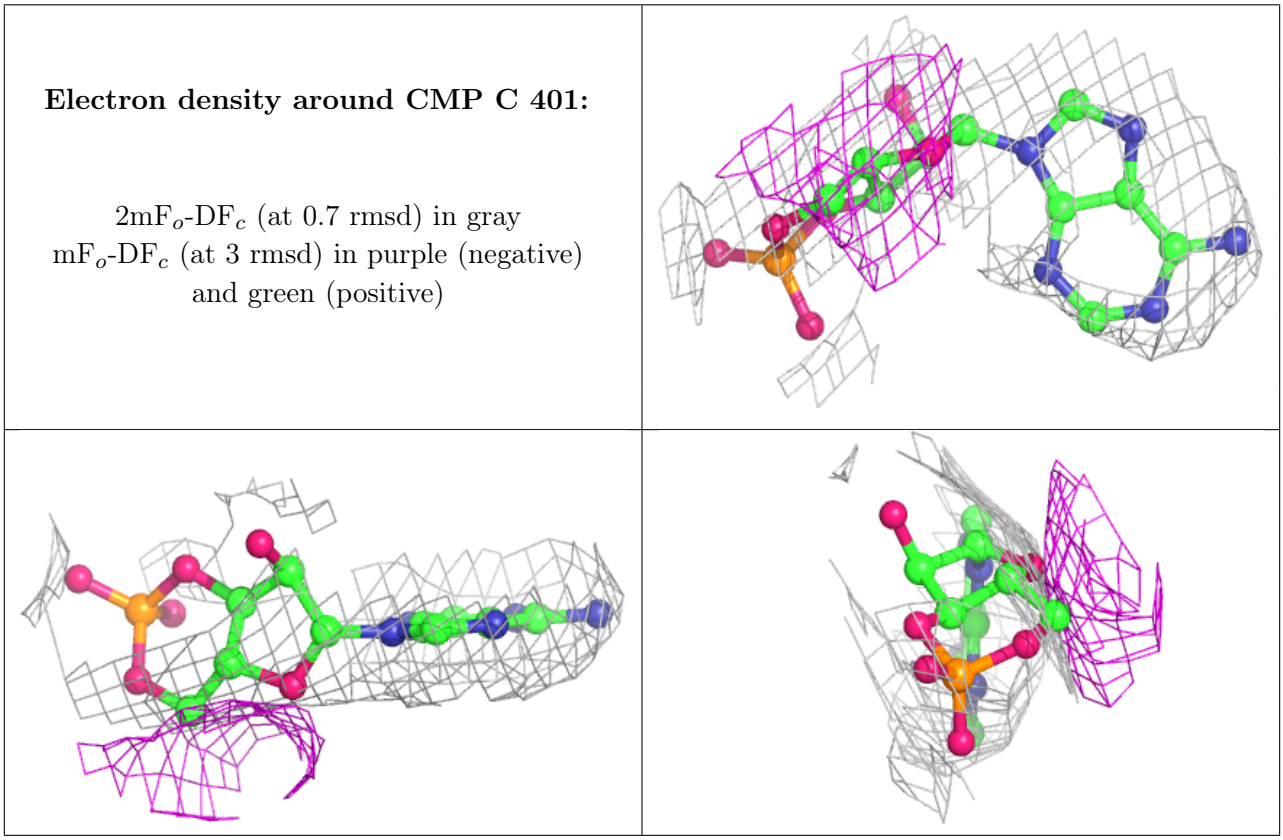
Electron density around CMP B 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



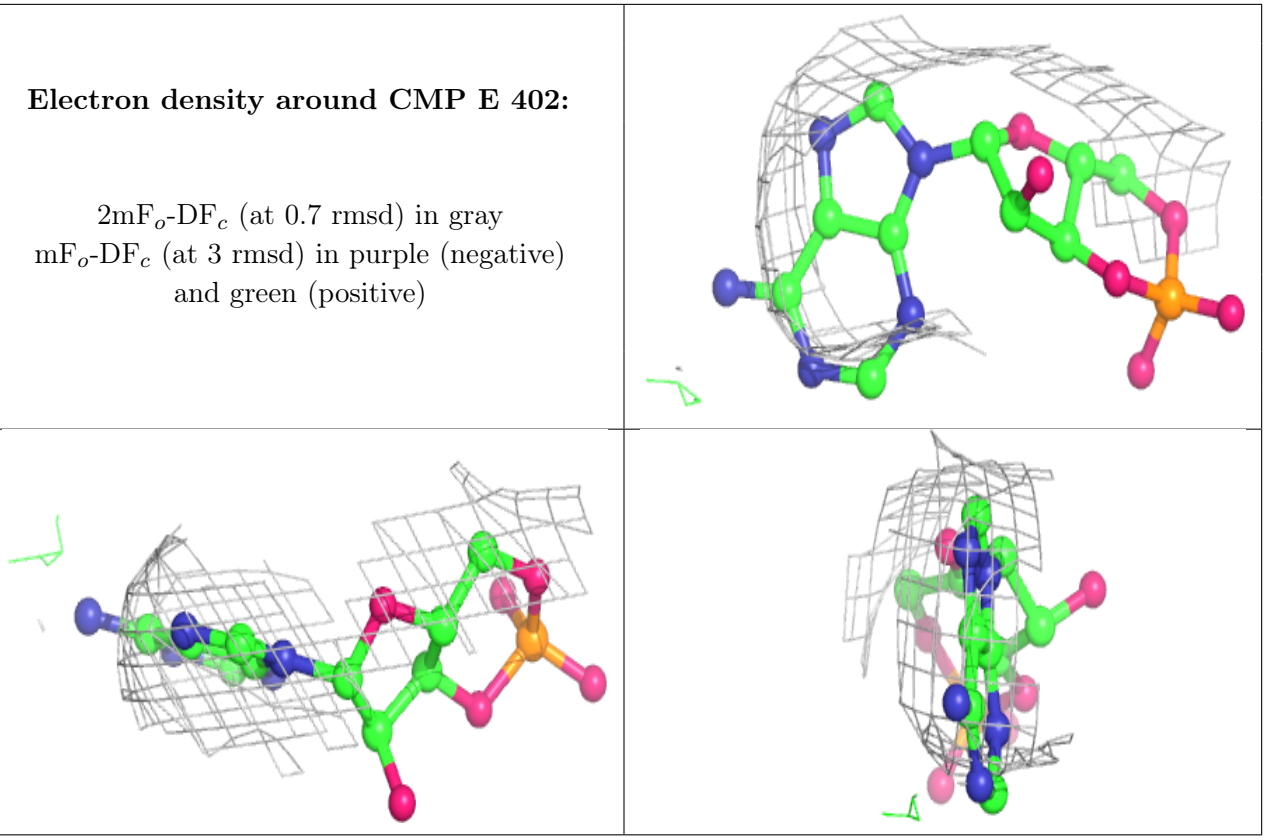
Electron density around CMP C 401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



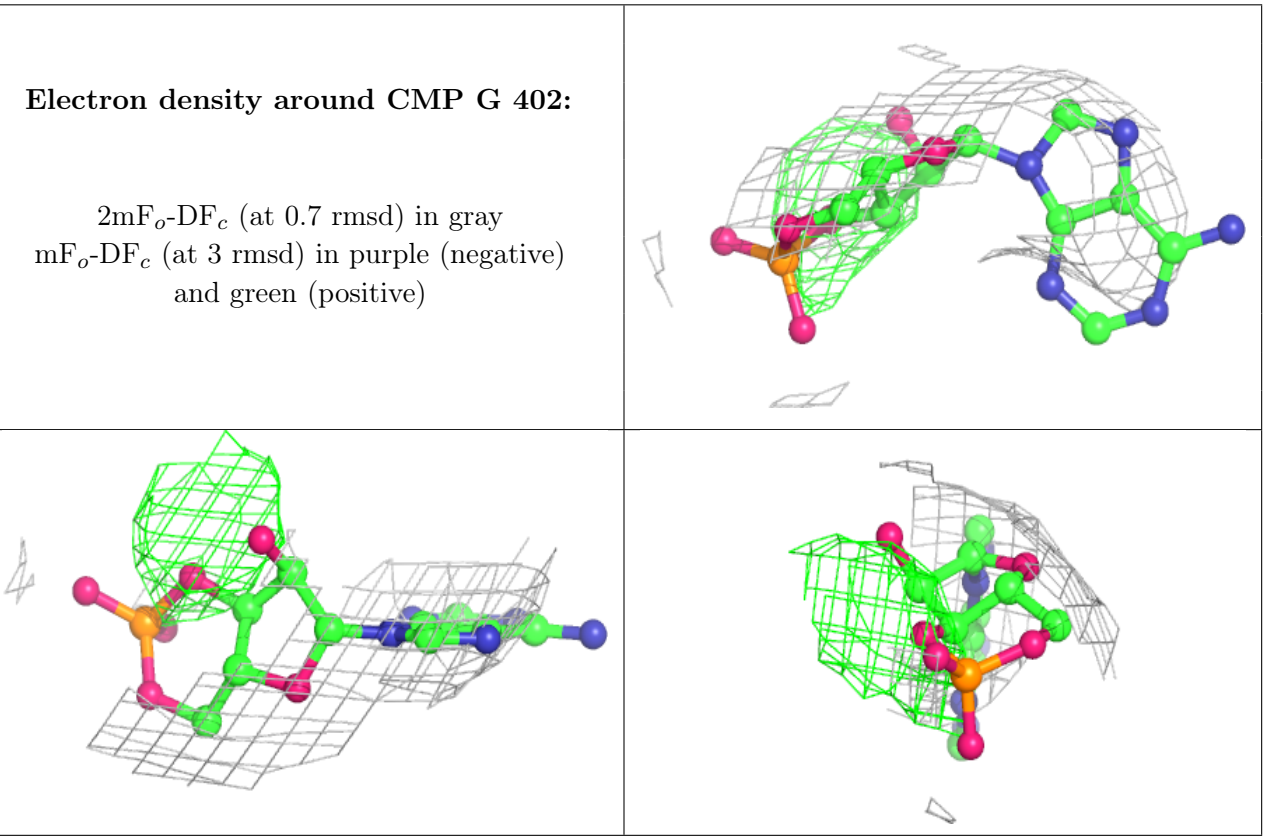
Electron density around CMP E 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



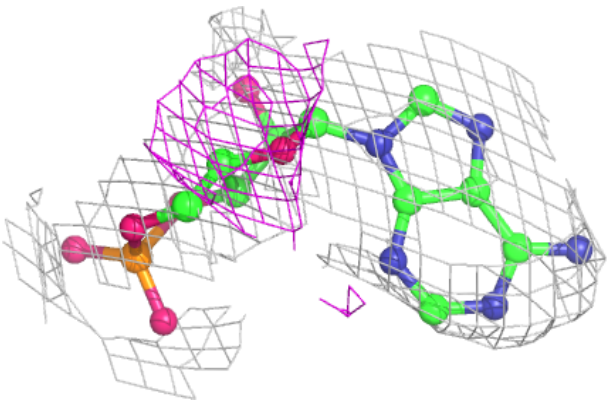
Electron density around CMP G 402:

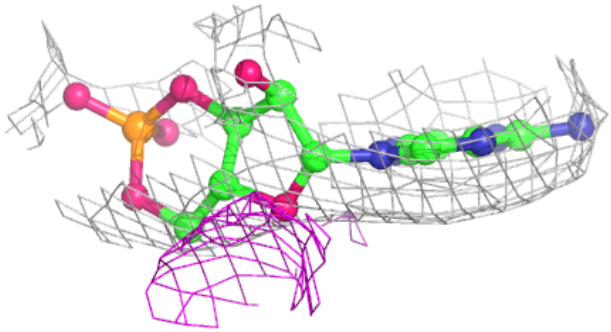
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

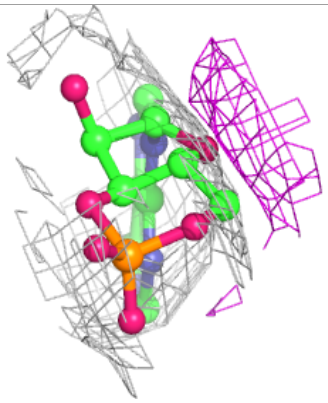


Electron density around CMP H 401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

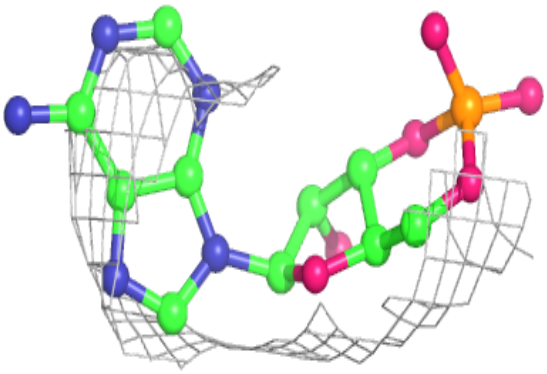


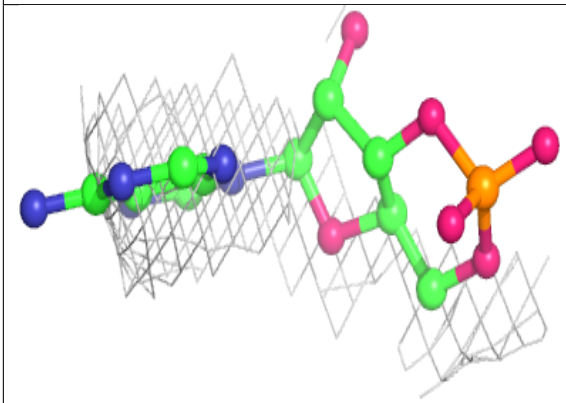


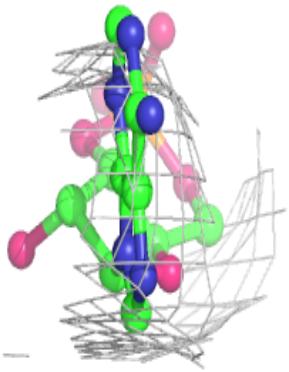


Electron density around CMP F 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

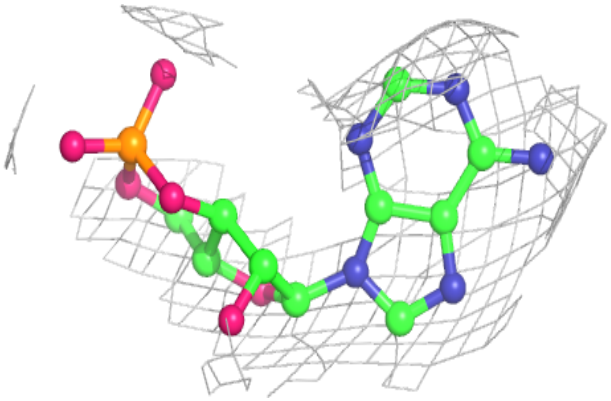


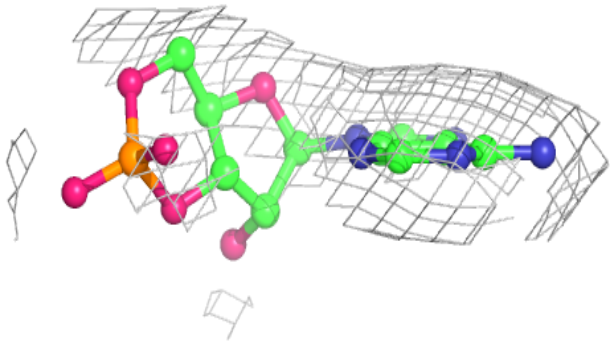


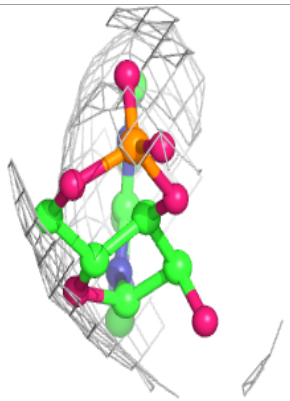


Electron density around CMP G 401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

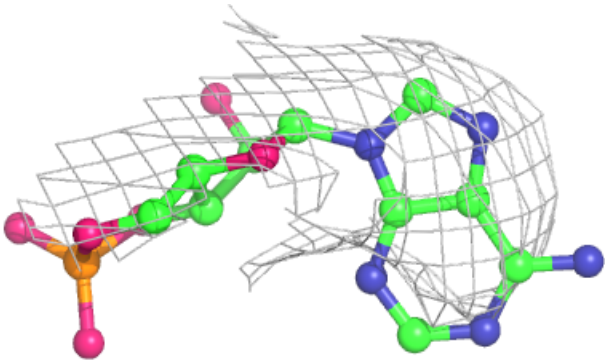


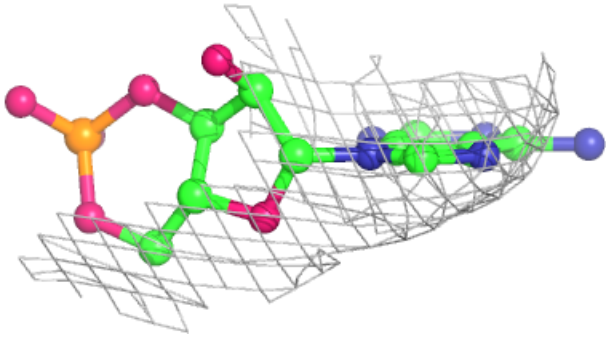


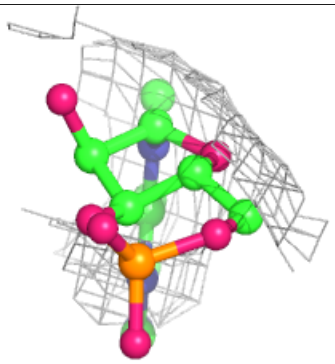


Electron density around CMP D 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

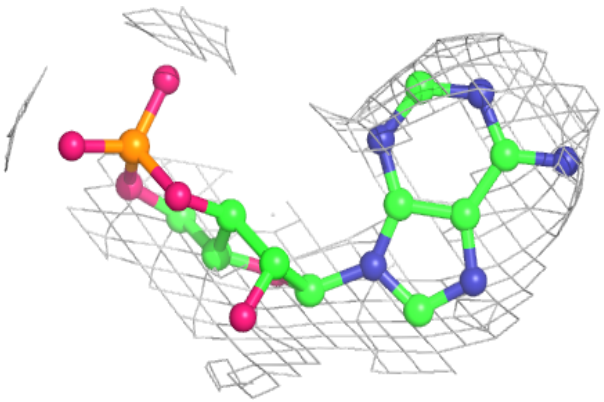


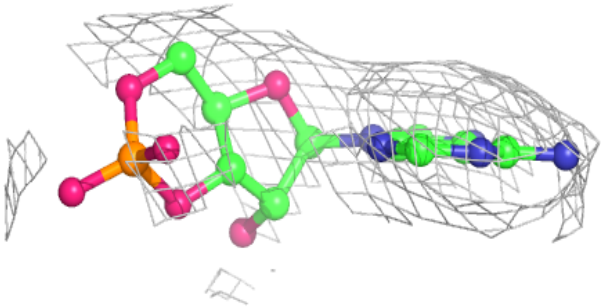


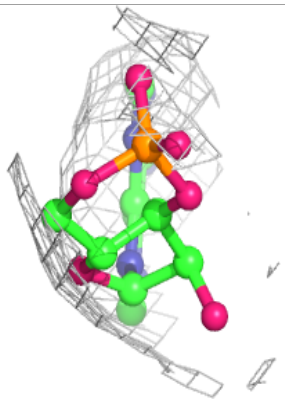


Electron density around CMP D 401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

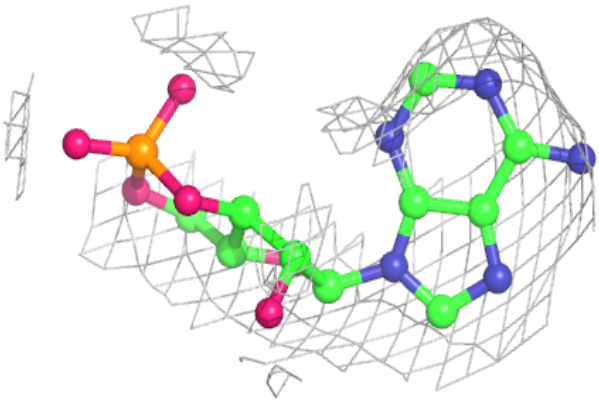


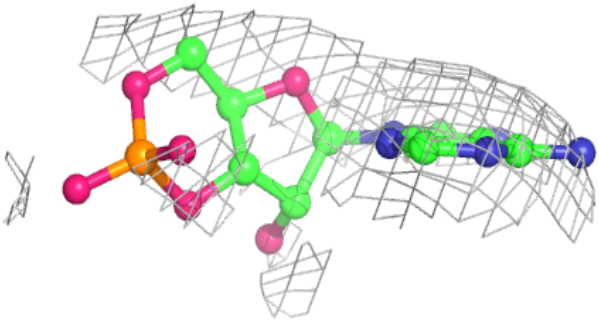


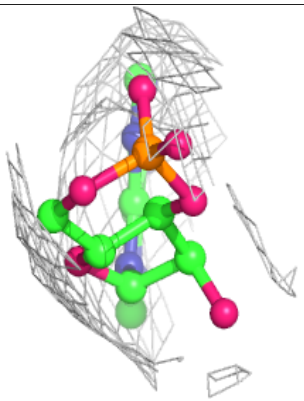


Electron density around CMP B 401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

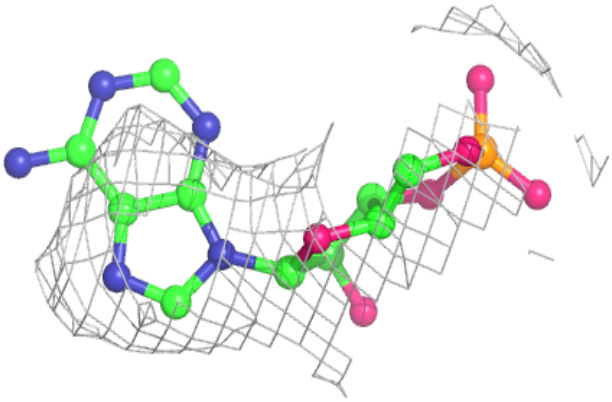


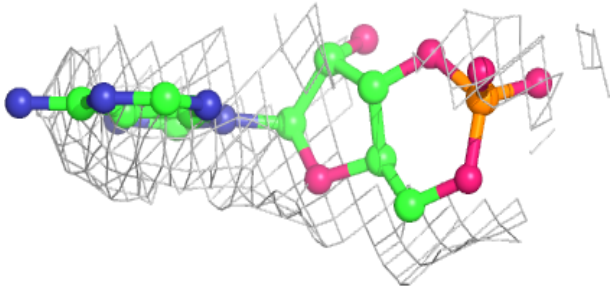


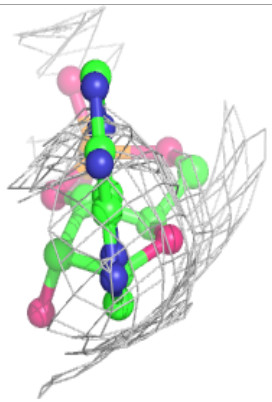


Electron density around CMP C 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

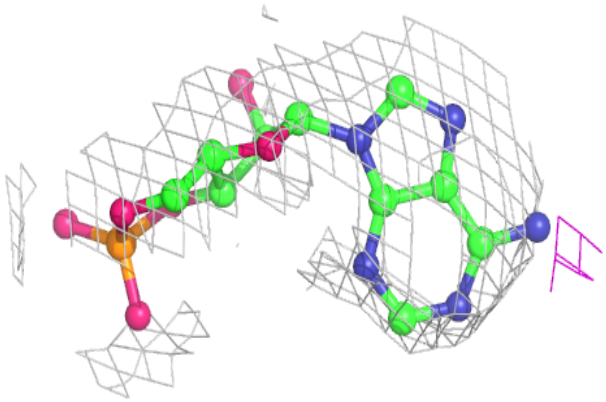


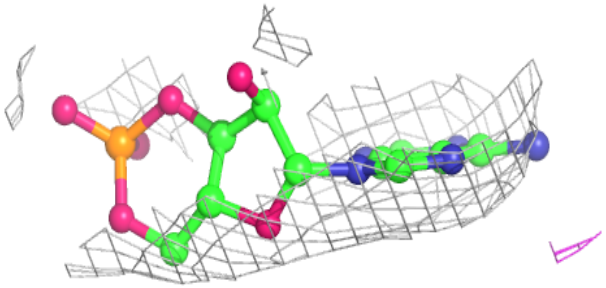


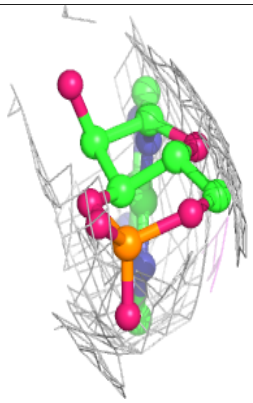


Electron density around CMP A 401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

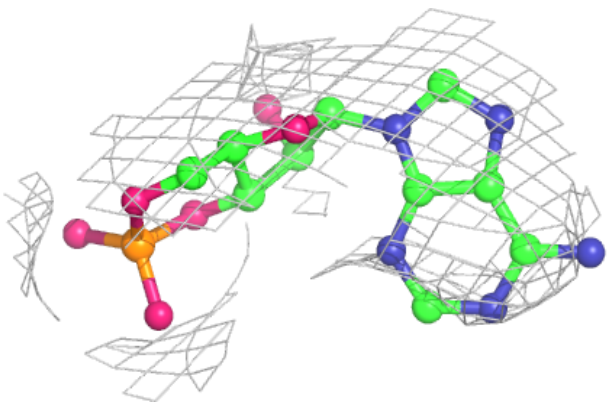


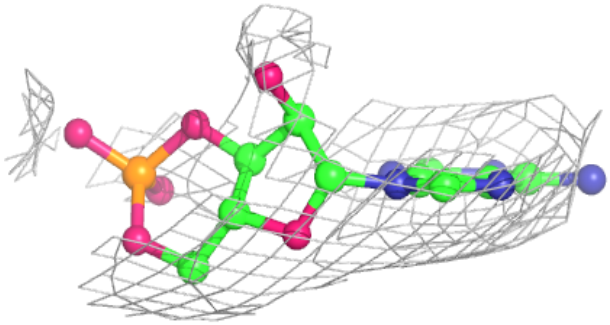


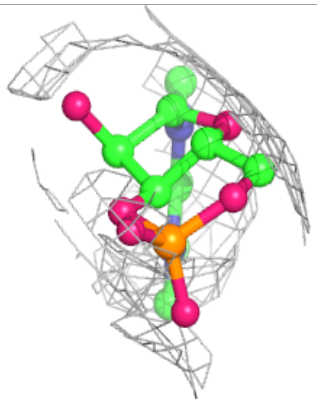


Electron density around CMP E 401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

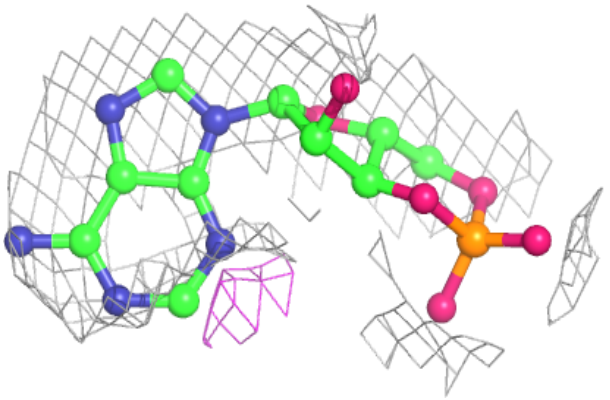


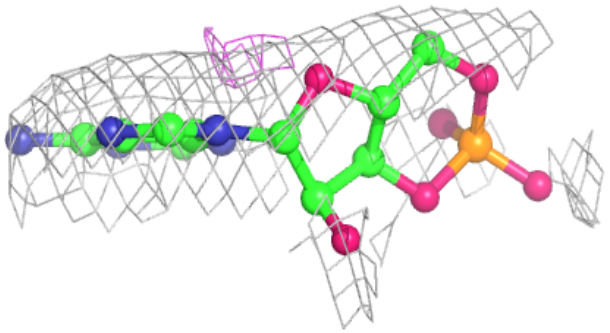


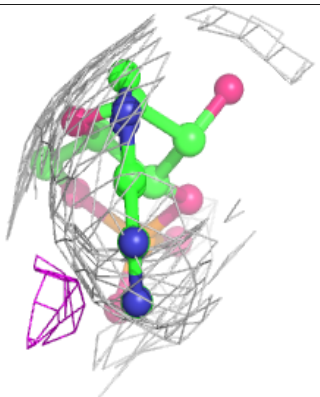


Electron density around CMP F 401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

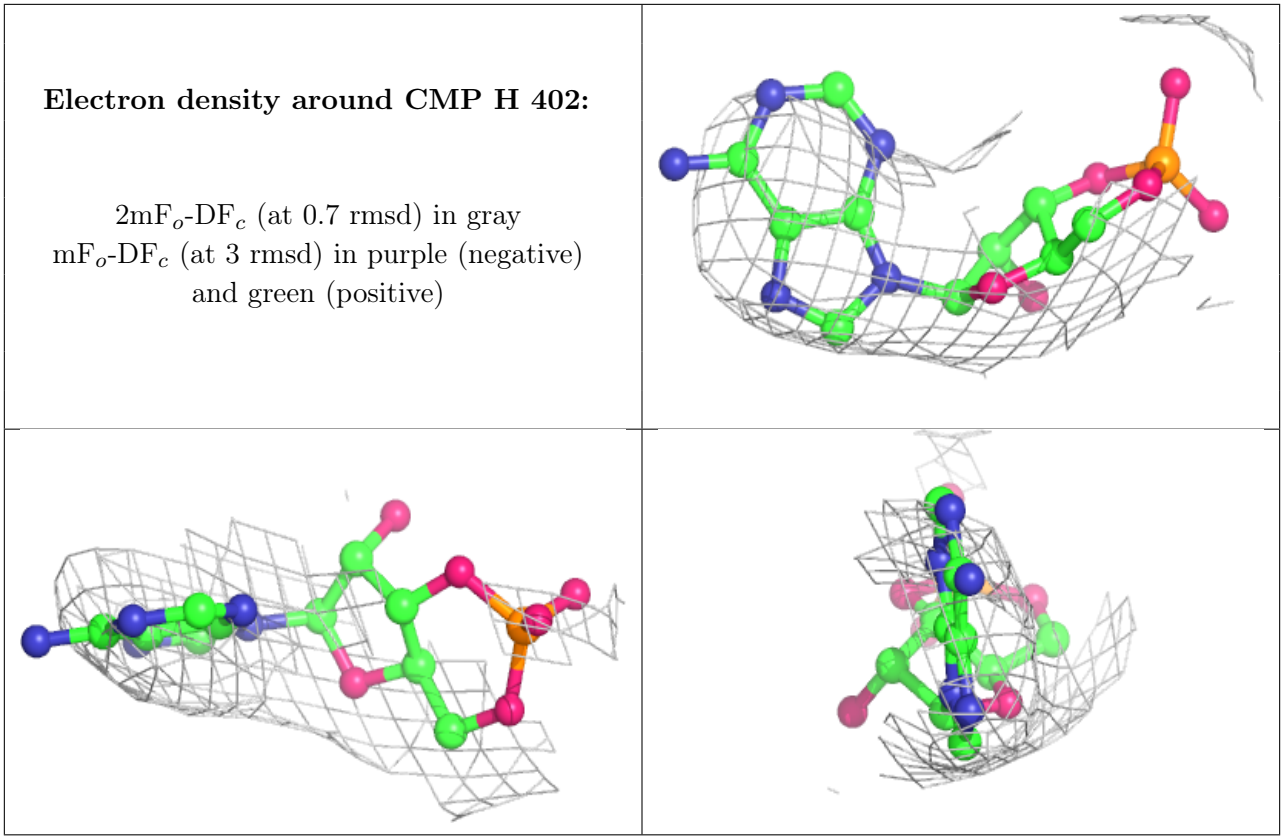






Electron density around CMP H 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.