



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 11:03 am BST

PDB ID : 3BLW
Title : Yeast Isocitrate Dehydrogenase with Citrate and AMP Bound in the Regulatory Subunits
Authors : Taylor, A.B.; Hu, G.; Hart, P.J.; McAlister-Henn, L.
Deposited on : 2007-12-11
Resolution : 4.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

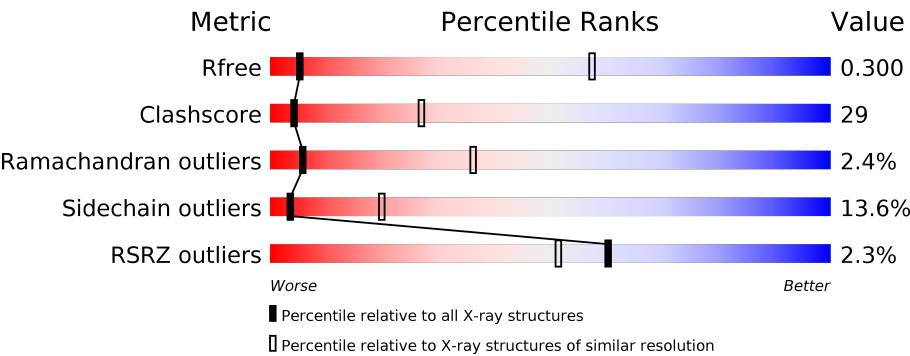
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.30 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.






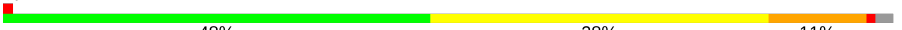
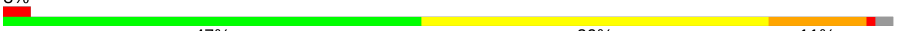
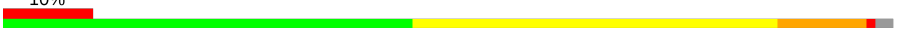




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1014 (4.80-3.80)
Clashscore	141614	1077 (4.80-3.80)
Ramachandran outliers	138981	1029 (4.80-3.80)
Sidechain outliers	138945	1012 (4.80-3.80)
RSRZ outliers	127900	1075 (4.90-3.70)

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

Mol	Chain	Length	Quality of chain
1	A	349	
1	C	349	
1	E	349	
1	G	349	
1	I	349	
1	K	349	

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Mol	Chain	Length	Quality of chain
1	M	349	
1	O	349	
2	B	354	
2	D	354	
2	F	354	
2	H	354	
2	J	354	
2	L	354	
2	N	354	
2	P	354	

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
3	FLC	A	1001	-	-	X	-
3	FLC	C	1002	-	-	X	-
3	FLC	E	1003	-	-	X	-
3	FLC	G	1004	-	-	X	-
3	FLC	I	1005	-	-	X	-
3	FLC	K	1006	-	-	X	-
3	FLC	M	1007	-	-	X	-
3	FLC	O	1008	-	-	X	-
4	AMP	G	2004	-	-	-	X
4	AMP	K	2006	-	-	X	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 41694 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 Isocitrate dehydrogenase [NAD] subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	329	Total	C	N	O	S	0	0	0
			2523	1594	440	482	7			
1	C	338	Total	C	N	O	S	0	0	0
			2599	1643	454	495	7			
1	E	338	Total	C	N	O	S	0	0	0
			2599	1643	454	495	7			
1	G	329	Total	C	N	O	S	0	0	0
			2523	1594	440	482	7			
1	I	329	Total	C	N	O	S	0	0	0
			2523	1594	440	482	7			
1	K	337	Total	C	N	O	S	0	0	0
			2590	1638	453	492	7			
1	M	339	Total	C	N	O	S	0	0	0
			2604	1646	455	496	7			
1	O	330	Total	C	N	O	S	0	0	0
			2527	1596	441	483	7			

- Molecule 2 is a protein called Isocitrate dehydrogenase [NAD] subunit 2.

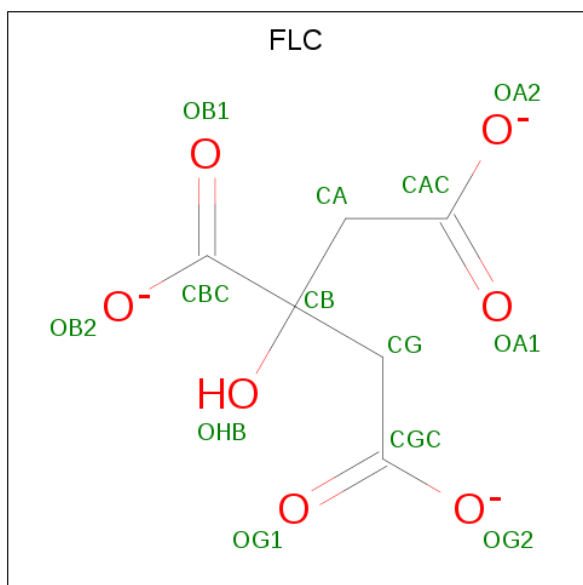
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	347	Total	C	N	O	S	0	0	0
			2617	1652	449	510	6			
2	D	347	Total	C	N	O	S	0	0	0
			2617	1652	449	510	6			
2	F	347	Total	C	N	O	S	0	0	0
			2617	1652	449	510	6			
2	H	346	Total	C	N	O	S	0	0	0
			2608	1646	447	509	6			
2	J	347	Total	C	N	O	S	0	0	0
			2617	1652	449	510	6			
2	L	346	Total	C	N	O	S	0	0	0
			2608	1646	447	509	6			

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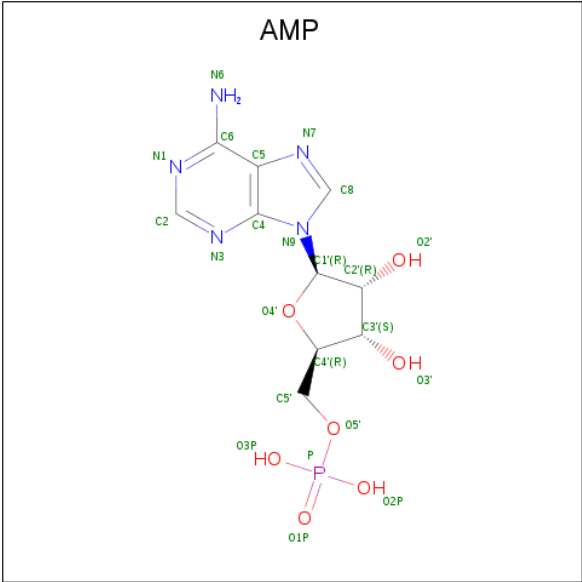
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	347	Total	C	N	O	S	0	0	0
			2617	1652	449	510	6			
2	P	347	Total	C	N	O	S	0	0	0
			2617	1652	449	510	6			

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	C	1	Total	C	O	0	0
			13	6	7		
3	E	1	Total	C	O	0	0
			13	6	7		
3	G	1	Total	C	O	0	0
			13	6	7		
3	I	1	Total	C	O	0	0
			13	6	7		
3	K	1	Total	C	O	0	0
			13	6	7		
3	M	1	Total	C	O	0	0
			13	6	7		
3	O	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).

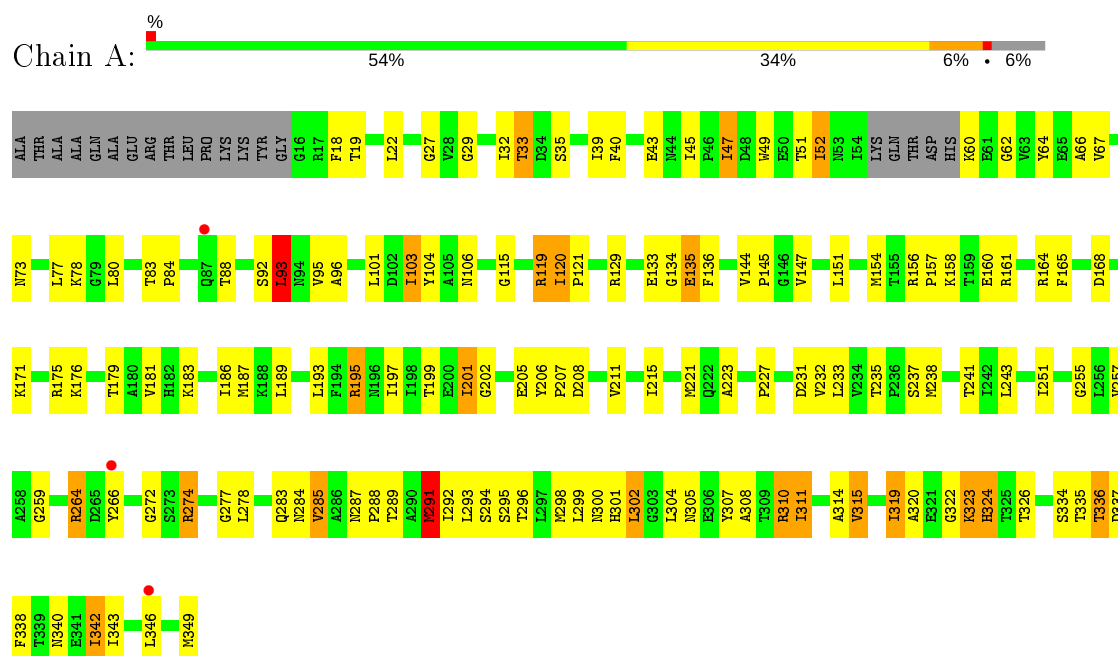


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	E	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	G	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	I	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	K	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	M	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	O	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

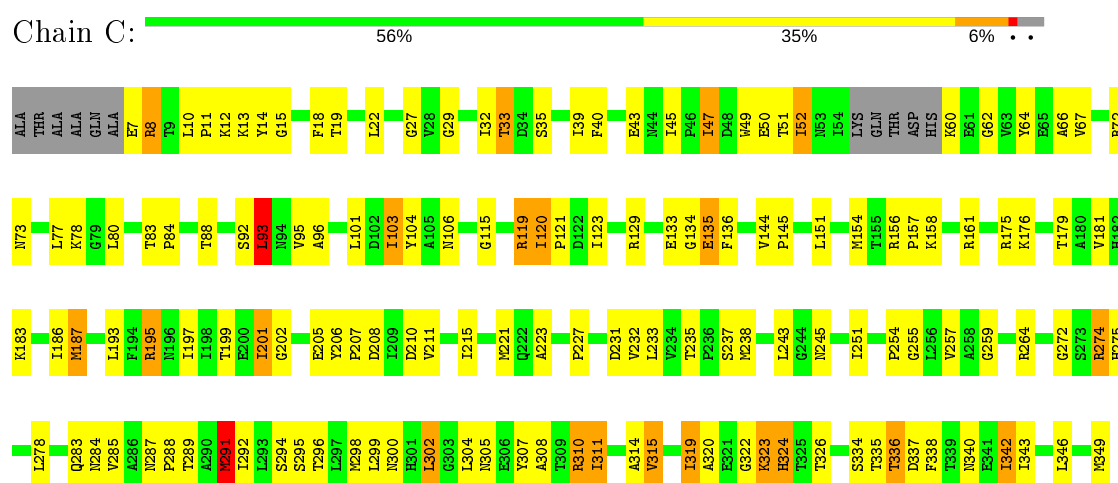
3 Residue-property plots [i](#)

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

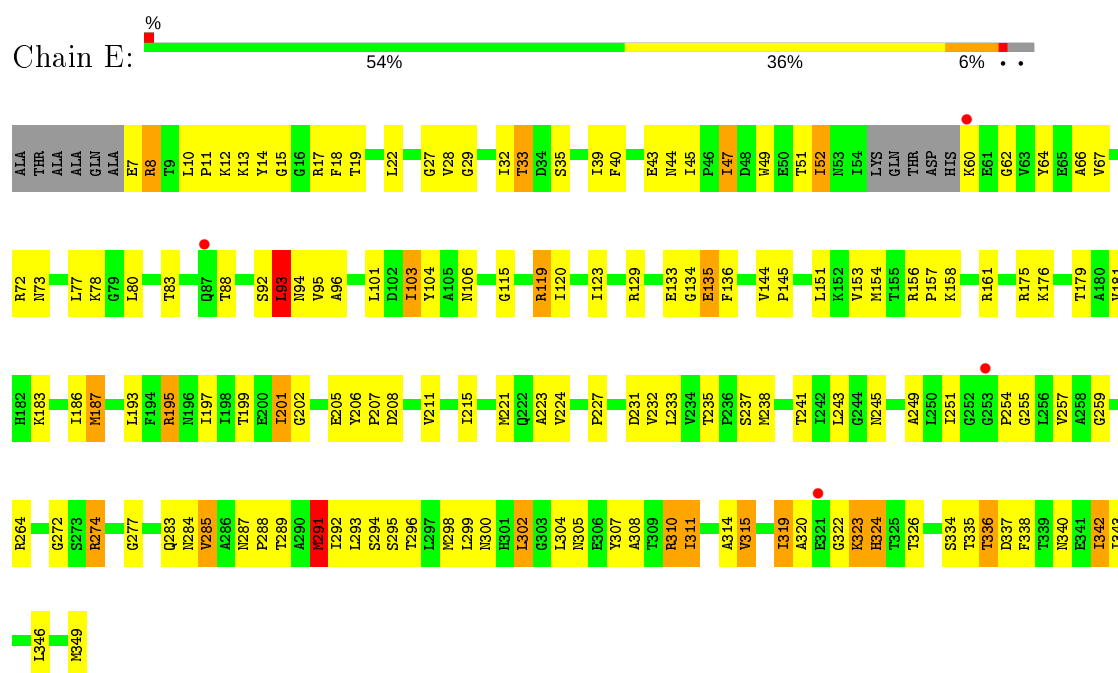
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1



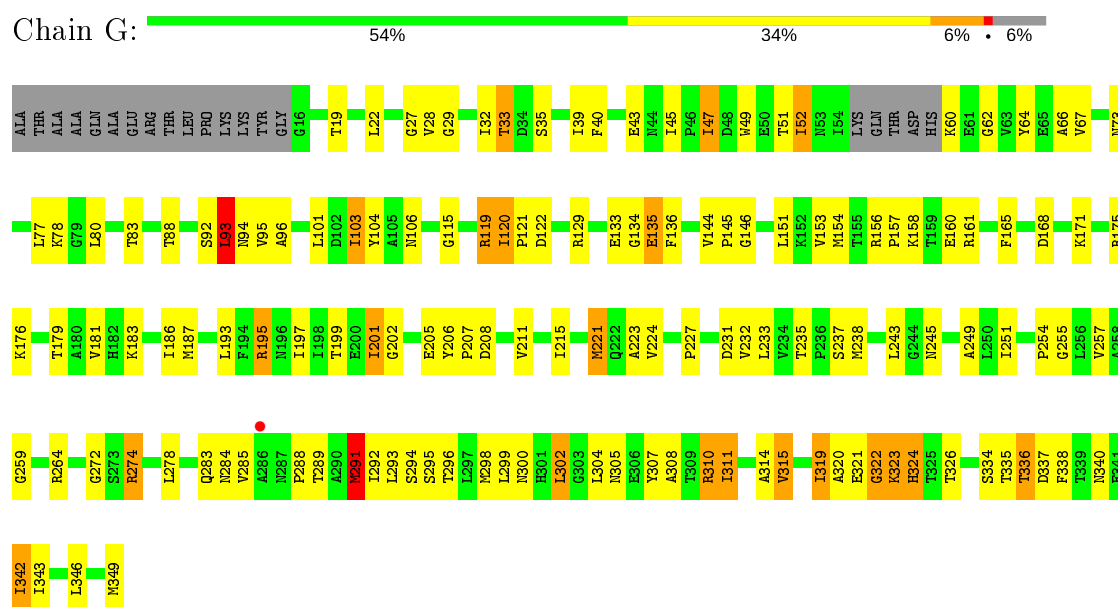
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1



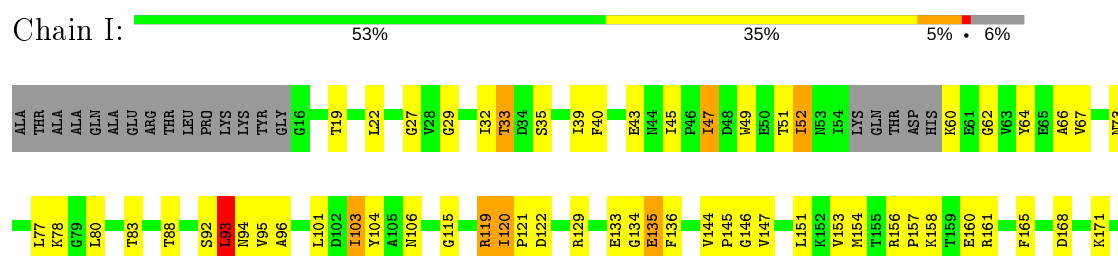
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

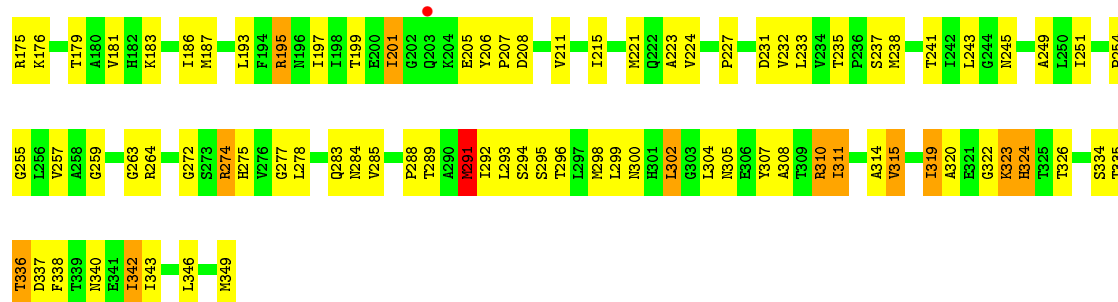


- Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

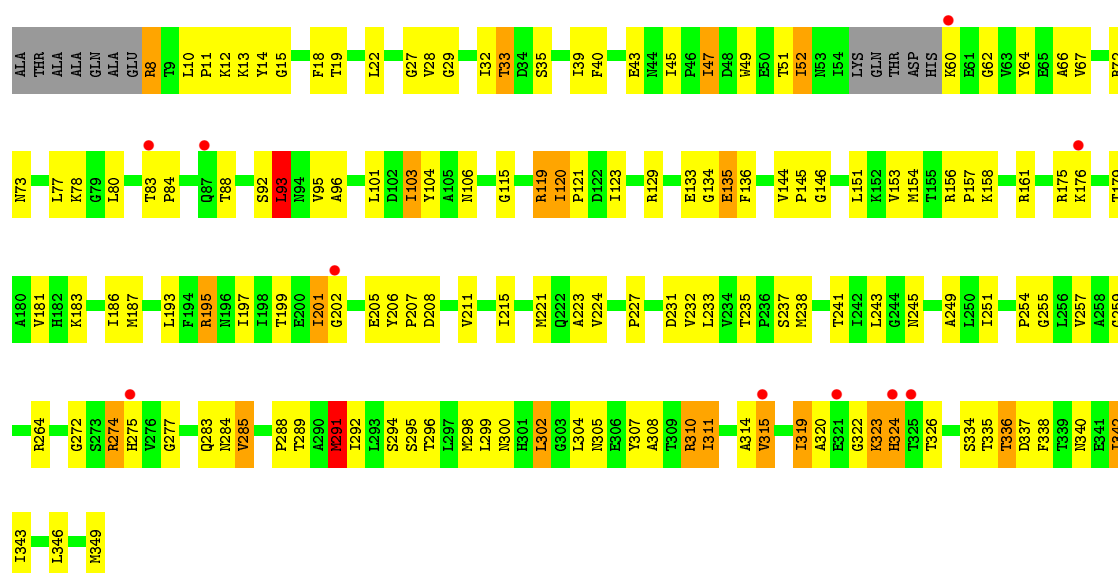


- Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

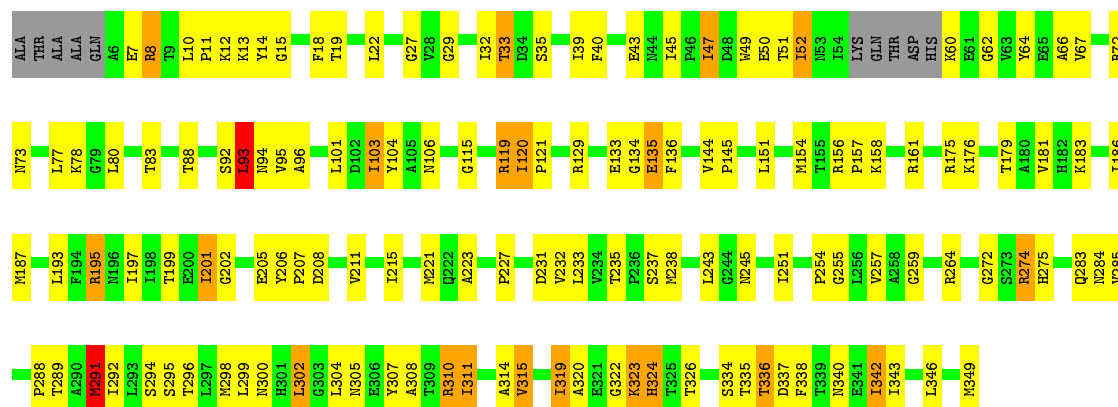




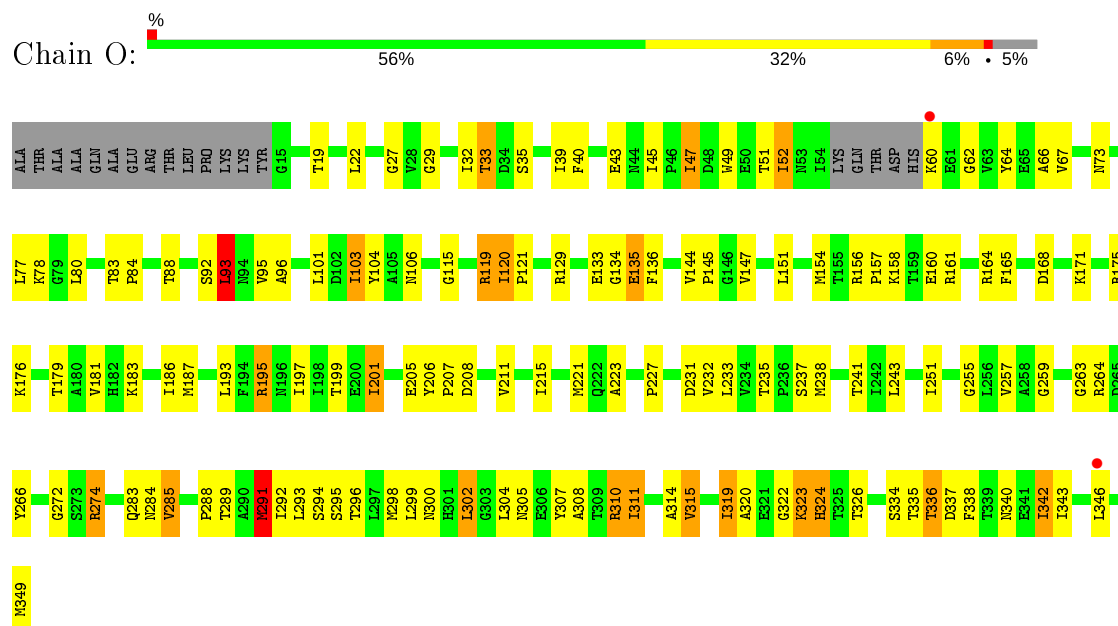
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1



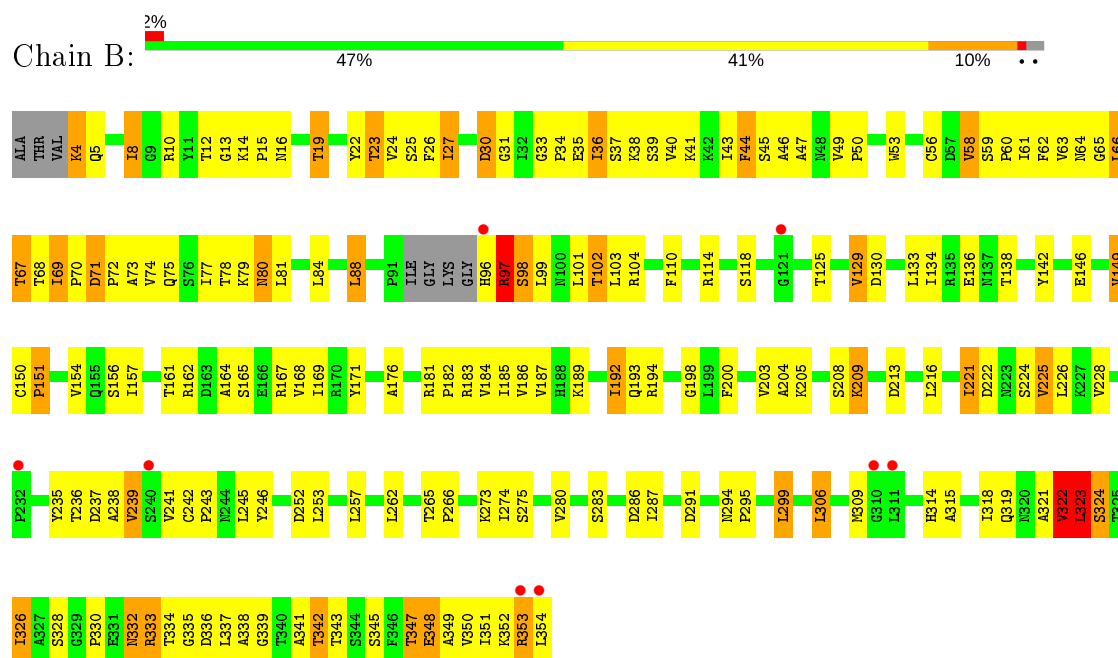
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1



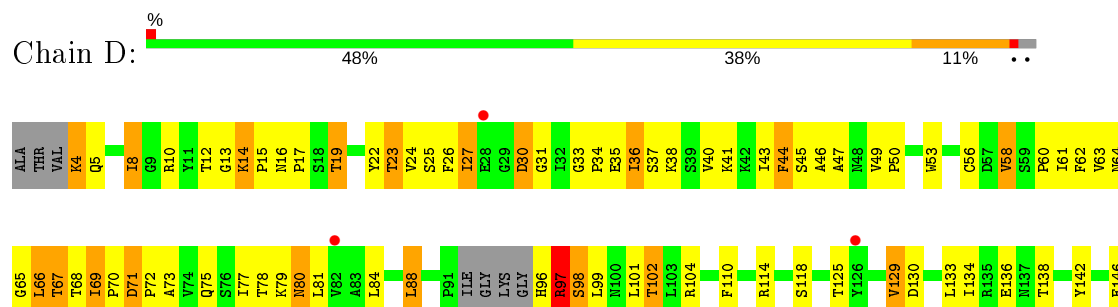
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

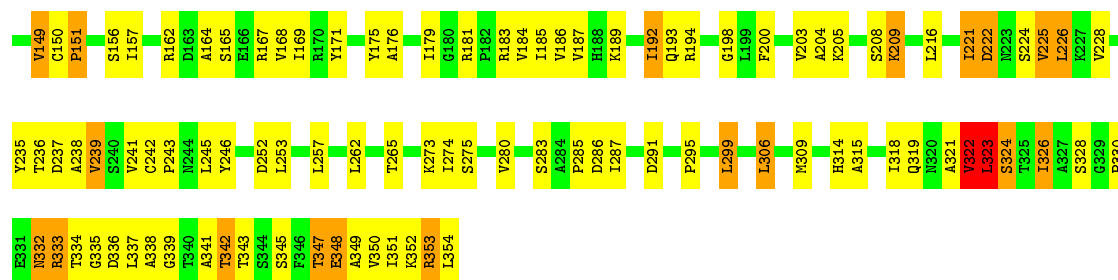


• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

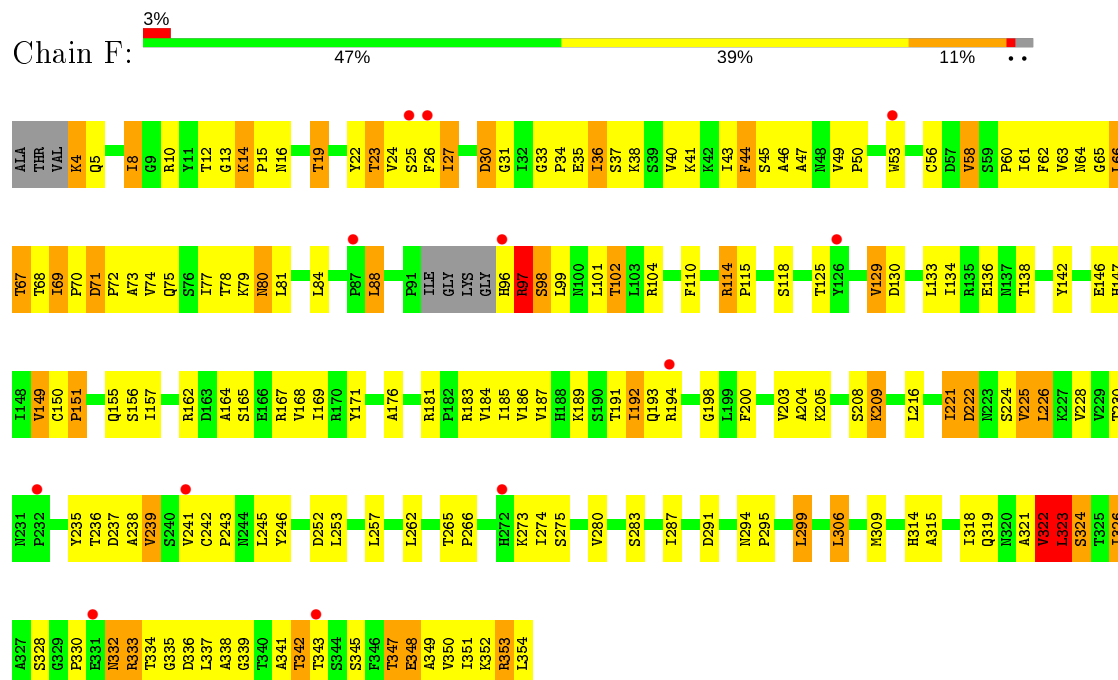


• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

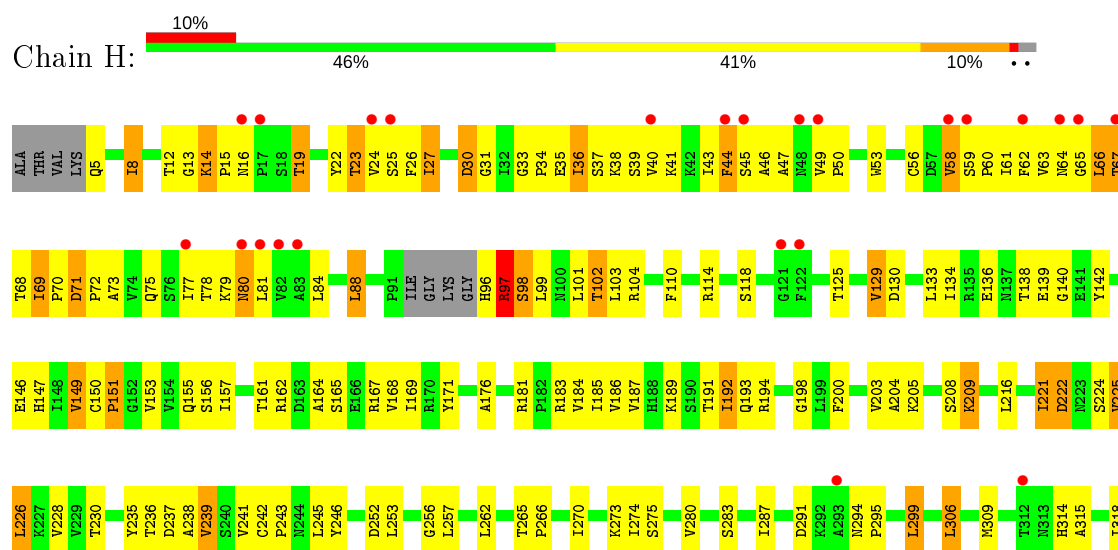


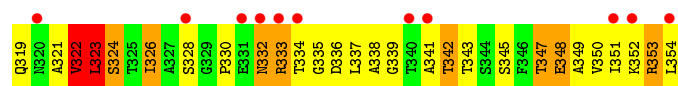


- Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

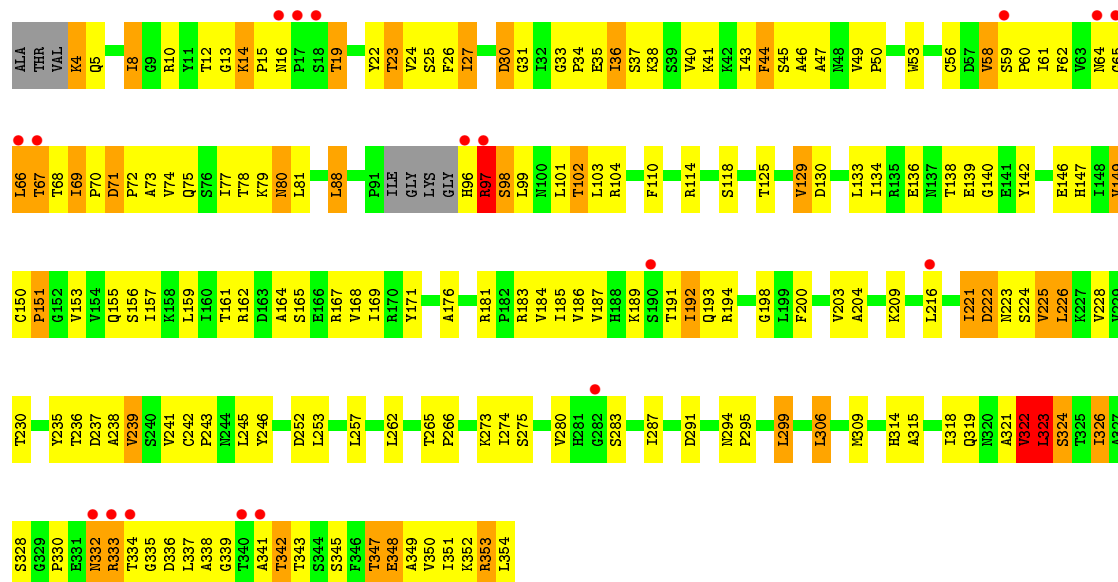


- Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

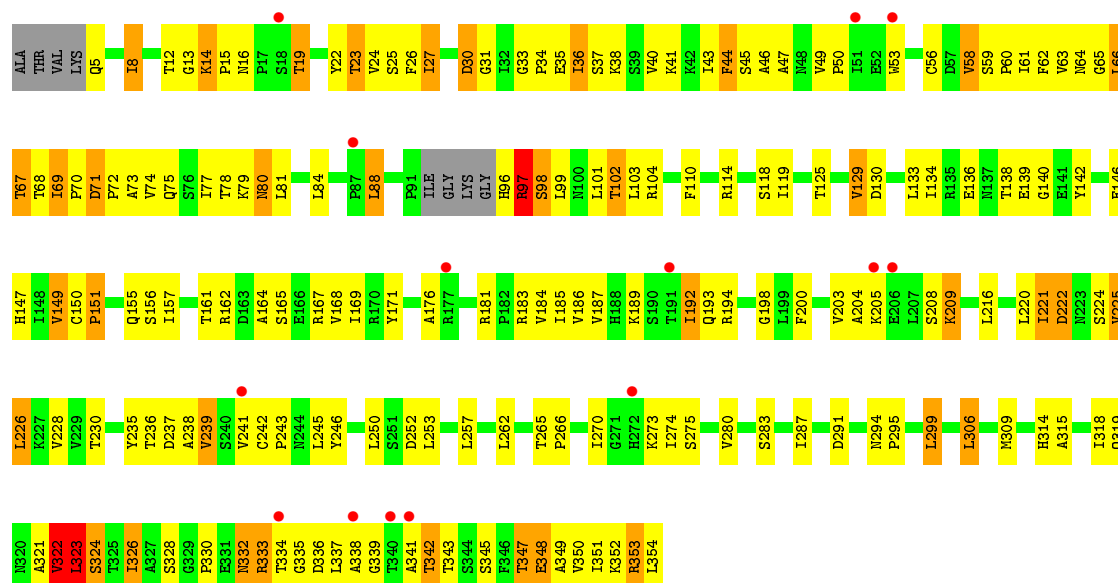




• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

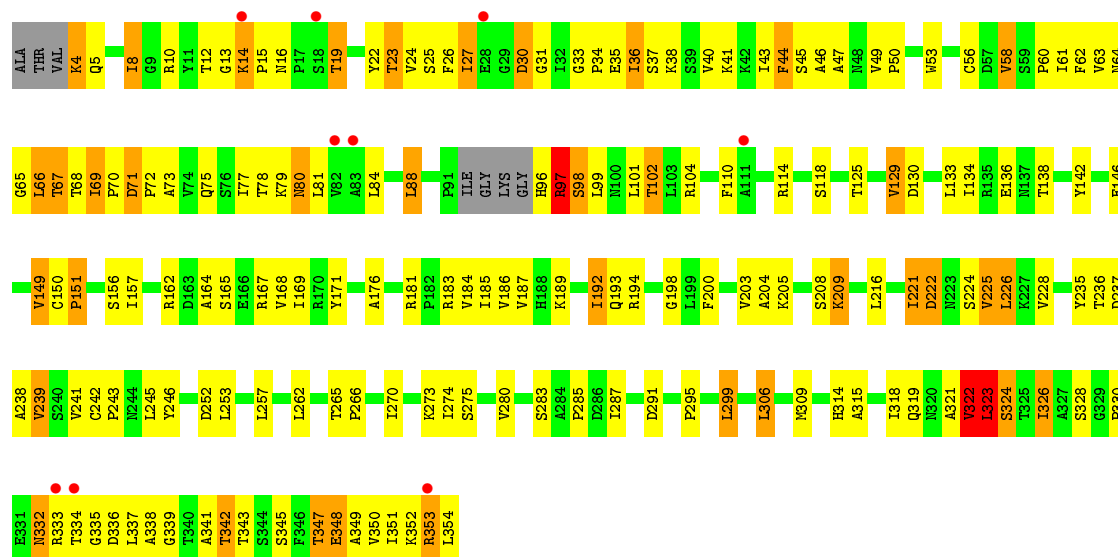


• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

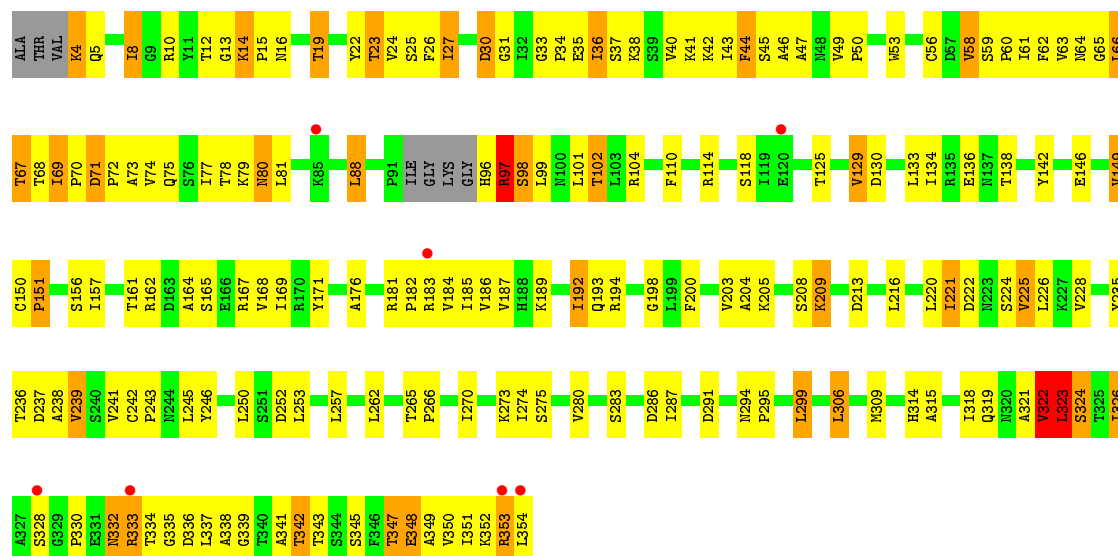


• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2





• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	113.16Å 116.35Å 163.62Å 98.96° 110.23° 106.63°	Depositor
Resolution (Å)	49.38 – 4.30 49.39 – 4.30	Depositor EDS
% Data completeness (in resolution range)	90.7 (49.38-4.30) 90.8 (49.39-4.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 4.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.274 , 0.311 0.261 , 0.300	Depositor DCC
R_{free} test set	2238 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	139.2	Xtriage
Anisotropy	0.281	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 124.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.000 for k,h,-h-k-l	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	41694	wwPDB-VP
Average B, all atoms (Å ²)	190.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.49	6/2565 (0.2%)	0.59	1/3467 (0.0%)
1	C	0.49	6/2643 (0.2%)	0.62	3/3571 (0.1%)
1	E	0.49	6/2643 (0.2%)	0.60	1/3571 (0.0%)
1	G	0.49	6/2565 (0.2%)	0.61	3/3467 (0.1%)
1	I	0.49	6/2565 (0.2%)	0.61	3/3467 (0.1%)
1	K	0.49	6/2634 (0.2%)	0.62	3/3559 (0.1%)
1	M	0.49	6/2648 (0.2%)	0.62	3/3578 (0.1%)
1	O	0.49	6/2569 (0.2%)	0.59	1/3472 (0.0%)
2	B	0.41	0/2663	0.57	0/3621
2	D	0.40	0/2663	0.57	0/3621
2	F	0.40	0/2663	0.57	0/3621
2	H	0.40	0/2654	0.57	0/3610
2	J	0.40	0/2663	0.57	0/3621
2	L	0.40	0/2654	0.57	0/3610
2	N	0.40	0/2663	0.57	0/3621
2	P	0.40	0/2663	0.57	0/3621
All	All	0.45	48/42118 (0.1%)	0.59	18/57098 (0.0%)

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	349	MET	CG-SD	5.84	1.96	1.81
1	E	349	MET	CG-SD	5.81	1.96	1.81
1	C	349	MET	CG-SD	5.80	1.96	1.81
1	K	349	MET	CG-SD	5.79	1.96	1.81
1	O	349	MET	CG-SD	5.78	1.96	1.81
1	M	349	MET	CG-SD	5.77	1.96	1.81
1	I	349	MET	CG-SD	5.73	1.96	1.81
1	A	349	MET	CG-SD	5.72	1.96	1.81
1	C	154	MET	CG-SD	5.61	1.95	1.81
1	I	154	MET	CG-SD	5.61	1.95	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	154	MET	CG-SD	5.57	1.95	1.81
1	E	154	MET	CG-SD	5.55	1.95	1.81
1	G	154	MET	CG-SD	5.54	1.95	1.81
1	O	154	MET	CG-SD	5.54	1.95	1.81
1	K	154	MET	CG-SD	5.53	1.95	1.81
1	M	154	MET	CG-SD	5.52	1.95	1.81
1	G	291	MET	CG-SD	5.39	1.95	1.81
1	A	291	MET	CG-SD	5.37	1.95	1.81
1	E	291	MET	CG-SD	5.35	1.95	1.81
1	C	291	MET	CG-SD	5.34	1.95	1.81
1	I	291	MET	CG-SD	5.34	1.95	1.81
1	K	291	MET	CG-SD	5.34	1.95	1.81
1	M	187	MET	CG-SD	5.34	1.95	1.81
1	K	187	MET	CG-SD	5.33	1.95	1.81
1	M	291	MET	CG-SD	5.31	1.95	1.81
1	A	187	MET	CG-SD	5.31	1.95	1.81
1	I	187	MET	CG-SD	5.31	1.95	1.81
1	C	187	MET	CG-SD	5.30	1.95	1.81
1	O	291	MET	CG-SD	5.28	1.94	1.81
1	O	187	MET	CG-SD	5.28	1.94	1.81
1	E	187	MET	CG-SD	5.27	1.94	1.81
1	G	187	MET	CG-SD	5.25	1.94	1.81
1	O	298	MET	CG-SD	5.20	1.94	1.81
1	M	221	MET	CG-SD	5.18	1.94	1.81
1	C	298	MET	CG-SD	5.15	1.94	1.81
1	A	298	MET	CG-SD	5.15	1.94	1.81
1	G	221	MET	CG-SD	5.15	1.94	1.81
1	I	298	MET	CG-SD	5.15	1.94	1.81
1	I	221	MET	CG-SD	5.13	1.94	1.81
1	A	221	MET	CG-SD	5.13	1.94	1.81
1	E	298	MET	CG-SD	5.13	1.94	1.81
1	O	221	MET	CG-SD	5.13	1.94	1.81
1	C	221	MET	CG-SD	5.12	1.94	1.81
1	G	298	MET	CG-SD	5.12	1.94	1.81
1	E	221	MET	CG-SD	5.12	1.94	1.81
1	K	221	MET	CG-SD	5.11	1.94	1.81
1	M	298	MET	CG-SD	5.09	1.94	1.81
1	K	298	MET	CG-SD	5.09	1.94	1.81

All (18) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	264	ARG	NE-CZ-NH2	-5.95	117.32	120.30
1	M	264	ARG	NE-CZ-NH2	-5.95	117.32	120.30
1	I	264	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	K	264	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	G	264	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	C	264	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	O	93	LEU	CA-CB-CG	5.49	127.92	115.30
1	A	93	LEU	CA-CB-CG	5.47	127.88	115.30
1	E	93	LEU	CA-CB-CG	5.45	127.83	115.30
1	I	93	LEU	CA-CB-CG	5.45	127.82	115.30
1	C	93	LEU	CA-CB-CG	5.43	127.80	115.30
1	K	93	LEU	CA-CB-CG	5.43	127.78	115.30
1	G	93	LEU	CA-CB-CG	5.40	127.72	115.30
1	M	93	LEU	CA-CB-CG	5.38	127.67	115.30
1	I	264	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	M	264	ARG	NE-CZ-NH1	5.33	122.96	120.30
1	G	264	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	K	264	ARG	NE-CZ-NH1	5.28	122.94	120.30

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	2523	0	2559	151	0
1	C	2599	0	2641	142	0
1	E	2599	0	2641	158	0
1	G	2523	0	2559	134	1
1	I	2523	0	2559	141	0
1	K	2590	0	2635	155	0
1	M	2604	0	2646	142	0
1	O	2527	0	2562	133	0
2	B	2617	0	2662	180	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2617	0	2662	193	0
2	F	2617	0	2662	186	0
2	H	2608	0	2649	185	0
2	J	2617	0	2662	192	0
2	L	2608	0	2649	194	0
2	N	2617	0	2662	171	2
2	P	2617	0	2662	200	1
3	A	13	0	5	5	0
3	C	13	0	5	4	0
3	E	13	0	5	4	0
3	G	13	0	5	5	0
3	I	13	0	5	5	0
3	K	13	0	5	4	0
3	M	13	0	5	6	0
3	O	13	0	5	5	0
4	A	23	0	12	2	0
4	C	23	0	12	2	0
4	E	23	0	12	6	0
4	G	23	0	12	1	0
4	I	23	0	12	3	0
4	K	23	0	12	9	0
4	M	23	0	12	3	0
4	O	23	0	12	0	0
All	All	41694	0	42208	2462	3

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 29.

All (2462) 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:171:LYS:HZ2	1:E:72:ARG:NH2	1.27	1.32
2:B:213:ASP:HB3	1:I:122:ASP:OD2	1.23	1.27
2:D:285:PRO:HG3	2:P:286:ASP:OD2	1.42	1.20
2:D:285:PRO:CB	2:P:286:ASP:OD2	1.89	1.19
2:D:285:PRO:CG	2:P:286:ASP:OD2	1.91	1.19
1:A:64:TYR:CE1	2:P:63:VAL:HG13	1.76	1.18
1:A:171:LYS:NZ	1:E:72:ARG:NH2	1.94	1.14
1:K:135:GLU:HG3	1:K:238:MET:HB2	1.31	1.11
1:C:135:GLU:HG3	1:C:238:MET:HB2	1.32	1.10
1:M:135:GLU:HG3	1:M:238:MET:HB2	1.32	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:135:GLU:HG3	1:G:238:MET:HB2	1.32	1.09
1:O:135:GLU:HG3	1:O:238:MET:HB2	1.32	1.08
1:I:135:GLU:HG3	1:I:238:MET:HB2	1.32	1.06
1:A:135:GLU:HG3	1:A:238:MET:HB2	1.31	1.06
1:E:135:GLU:HG3	1:E:238:MET:HB2	1.32	1.05
1:K:72:ARG:CZ	1:O:171:LYS:HZ2	1.71	1.03
1:C:7:GLU:HB3	1:C:10:LEU:HD11	1.37	1.03
1:K:28:VAL:HG21	4:K:2006:AMP:HN61	1.17	1.02
2:B:213:ASP:CB	1:I:122:ASP:OD2	2.08	1.02
1:E:7:GLU:HB3	1:E:10:LEU:HD11	1.37	1.02
1:M:7:GLU:HB3	1:M:10:LEU:HD11	1.37	1.01
2:D:286:ASP:OD1	2:P:287:ILE:HD11	1.60	1.00
1:A:171:LYS:NZ	1:E:72:ARG:HH22	1.60	0.99
2:P:342:THR:HG23	2:P:345:SER:H	1.27	0.98
2:B:342:THR:HG23	2:B:345:SER:H	1.27	0.98
2:H:342:THR:HG23	2:H:345:SER:H	1.27	0.98
2:N:342:THR:HG23	2:N:345:SER:H	1.27	0.98
1:A:64:TYR:CE1	2:P:63:VAL:CG1	2.46	0.98
2:L:342:THR:HG23	2:L:345:SER:H	1.27	0.98
1:K:274:ARG:HG2	3:K:1006:FLC:OB1	1.65	0.97
2:J:342:THR:HG23	2:J:345:SER:H	1.28	0.96
1:K:12:LYS:HE3	1:O:168:ASP:OD2	1.66	0.96
2:D:342:THR:HG23	2:D:345:SER:H	1.27	0.96
1:C:119:ARG:HG2	2:D:125:THR:HG22	1.48	0.95
1:K:72:ARG:NH2	1:O:171:LYS:HZ2	1.64	0.94
1:A:171:LYS:HZ2	1:E:72:ARG:CZ	1.80	0.94
2:F:342:THR:HG23	2:F:345:SER:H	1.27	0.94
1:E:274:ARG:HG2	3:E:1003:FLC:OB1	1.68	0.94
1:K:277:GLY:HA2	4:K:2006:AMP:C8	2.03	0.93
1:K:72:ARG:NH2	1:O:171:LYS:NZ	2.17	0.93
1:K:277:GLY:CA	4:K:2006:AMP:C8	2.52	0.93
2:H:322:VAL:HG12	2:H:350:VAL:HG13	1.52	0.92
2:J:322:VAL:HG12	2:J:350:VAL:HG13	1.52	0.92
2:N:322:VAL:HG12	2:N:350:VAL:HG13	1.52	0.91
2:D:136:GLU:HG2	2:D:168:VAL:HG21	1.53	0.91
2:B:136:GLU:HG2	2:B:168:VAL:HG21	1.53	0.91
2:N:136:GLU:HG2	2:N:168:VAL:HG21	1.53	0.91
2:F:322:VAL:HG12	2:F:350:VAL:HG13	1.52	0.90
2:J:136:GLU:HG2	2:J:168:VAL:HG21	1.53	0.90
2:D:322:VAL:HG12	2:D:350:VAL:HG13	1.52	0.90
1:I:168:ASP:OD2	1:M:12:LYS:HE3	1.70	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:275:HIS:HB3	4:C:2002:AMP:O2P	1.70	0.90
1:G:151:LEU:HD23	2:H:157:ILE:HG12	1.53	0.90
2:H:69:ILE:HD12	2:H:70:PRO:HD2	1.54	0.90
2:P:136:GLU:HG2	2:P:168:VAL:HG21	1.53	0.90
2:L:136:GLU:HG2	2:L:168:VAL:HG21	1.53	0.90
2:P:322:VAL:HG12	2:P:350:VAL:HG13	1.52	0.90
2:D:69:ILE:HD12	2:D:70:PRO:HD2	1.54	0.89
2:F:69:ILE:HD12	2:F:70:PRO:HD2	1.54	0.89
2:D:285:PRO:HB3	2:P:286:ASP:OD2	1.69	0.89
2:F:150:CYS:HB2	2:F:151:PRO:HD2	1.55	0.89
2:P:69:ILE:HD12	2:P:70:PRO:HD2	1.54	0.89
2:P:150:CYS:HB2	2:P:151:PRO:HD2	1.55	0.89
2:J:150:CYS:HB2	2:J:151:PRO:HD2	1.54	0.89
1:A:168:ASP:OD2	1:E:12:LYS:HE3	1.72	0.89
2:N:150:CYS:HB2	2:N:151:PRO:HD2	1.55	0.89
2:H:150:CYS:HB2	2:H:151:PRO:HD2	1.55	0.89
1:E:135:GLU:CG	1:E:238:MET:HB2	2.04	0.88
2:F:136:GLU:HG2	2:F:168:VAL:HG21	1.53	0.88
2:B:322:VAL:HG12	2:B:350:VAL:HG13	1.51	0.88
2:J:69:ILE:HD12	2:J:70:PRO:HD2	1.54	0.88
2:B:150:CYS:HB2	2:B:151:PRO:HD2	1.55	0.88
1:A:119:ARG:HG2	2:B:125:THR:HG22	1.56	0.88
2:L:322:VAL:HG12	2:L:350:VAL:HG13	1.52	0.88
1:K:135:GLU:CG	1:K:238:MET:HB2	2.03	0.88
2:D:285:PRO:HG3	2:P:286:ASP:CG	1.94	0.88
1:C:135:GLU:CG	1:C:238:MET:HB2	2.04	0.88
1:I:135:GLU:CG	1:I:238:MET:HB2	2.04	0.88
1:A:135:GLU:CG	1:A:238:MET:HB2	2.03	0.88
2:N:69:ILE:HD12	2:N:70:PRO:HD2	1.54	0.88
2:N:58:VAL:HG12	2:N:69:ILE:HD13	1.56	0.87
2:L:150:CYS:HB2	2:L:151:PRO:HD2	1.55	0.87
2:L:69:ILE:HD12	2:L:70:PRO:HD2	1.54	0.87
2:D:58:VAL:HG12	2:D:69:ILE:HD13	1.56	0.87
2:H:136:GLU:HG2	2:H:168:VAL:HG21	1.53	0.87
2:J:58:VAL:HG12	2:J:69:ILE:HD13	1.56	0.87
2:H:58:VAL:HG12	2:H:69:ILE:HD13	1.56	0.87
2:L:58:VAL:HG12	2:L:69:ILE:HD13	1.56	0.87
2:B:69:ILE:HD12	2:B:70:PRO:HD2	1.54	0.87
1:G:300:ASN:HA	1:G:305:ASN:HB3	1.57	0.87
1:E:300:ASN:HA	1:E:305:ASN:HB3	1.57	0.87
1:C:12:LYS:HE3	1:G:168:ASP:OD2	1.73	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:221:ILE:O	2:B:225:VAL:HG12	1.75	0.87
1:I:300:ASN:HA	1:I:305:ASN:HB3	1.57	0.87
1:G:135:GLU:CG	1:G:238:MET:HB2	2.04	0.86
1:C:300:ASN:HA	1:C:305:ASN:HB3	1.57	0.86
2:D:150:CYS:HB2	2:D:151:PRO:HD2	1.55	0.86
1:G:195:ARG:HG2	1:G:195:ARG:HH11	1.40	0.86
1:O:119:ARG:HG2	2:P:125:THR:HG22	1.56	0.86
1:A:195:ARG:HH11	1:A:195:ARG:HG2	1.40	0.86
2:L:221:ILE:O	2:L:225:VAL:HG12	1.75	0.86
1:M:135:GLU:CG	1:M:238:MET:HB2	2.03	0.86
1:O:195:ARG:HH11	1:O:195:ARG:HG2	1.40	0.86
1:M:300:ASN:HA	1:M:305:ASN:HB3	1.57	0.86
1:O:135:GLU:CG	1:O:238:MET:HB2	2.04	0.86
1:A:300:ASN:HA	1:A:305:ASN:HB3	1.57	0.86
2:B:58:VAL:HG12	2:B:69:ILE:HD13	1.56	0.86
2:F:58:VAL:HG12	2:F:69:ILE:HD13	1.56	0.86
1:K:195:ARG:HG2	1:K:195:ARG:HH11	1.40	0.86
1:K:300:ASN:HA	1:K:305:ASN:HB3	1.57	0.86
2:P:58:VAL:HG12	2:P:69:ILE:HD13	1.56	0.86
1:O:241:THR:OG1	3:O:1008:FLC:OA2	1.94	0.86
1:C:195:ARG:HH11	1:C:195:ARG:HG2	1.40	0.85
2:F:221:ILE:O	2:F:225:VAL:HG12	1.75	0.85
2:H:221:ILE:O	2:H:225:VAL:HG12	1.75	0.85
1:I:195:ARG:HH11	1:I:195:ARG:HG2	1.41	0.85
2:J:221:ILE:O	2:J:225:VAL:HG12	1.75	0.85
2:D:221:ILE:O	2:D:225:VAL:HG12	1.75	0.85
1:M:83:THR:OG1	3:M:1007:FLC:OG2	1.95	0.84
2:P:221:ILE:O	2:P:225:VAL:HG12	1.75	0.84
1:O:300:ASN:HA	1:O:305:ASN:HB3	1.57	0.84
1:M:195:ARG:HG2	1:M:195:ARG:HH11	1.41	0.84
1:E:195:ARG:HH11	1:E:195:ARG:HG2	1.40	0.84
2:N:221:ILE:O	2:N:225:VAL:HG12	1.75	0.84
1:E:7:GLU:HB3	1:E:10:LEU:CD1	2.08	0.83
1:I:314:ALA:HB2	1:I:346:LEU:HD13	1.62	0.82
1:M:195:ARG:HH11	1:M:195:ARG:CG	1.93	0.82
1:C:314:ALA:HB2	1:C:346:LEU:HD13	1.62	0.82
1:K:195:ARG:CG	1:K:195:ARG:HH11	1.93	0.82
1:M:7:GLU:HB3	1:M:10:LEU:CD1	2.08	0.82
1:G:195:ARG:CG	1:G:195:ARG:HH11	1.93	0.82
1:C:195:ARG:HH11	1:C:195:ARG:CG	1.93	0.81
1:E:195:ARG:HH11	1:E:195:ARG:CG	1.93	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:195:ARG:CG	1:O:195:ARG:HH11	1.93	0.81
1:O:314:ALA:HB2	1:O:346:LEU:HD13	1.62	0.81
1:A:64:TYR:CZ	2:P:63:VAL:CG1	2.64	0.81
1:C:7:GLU:HB3	1:C:10:LEU:CD1	2.08	0.81
1:I:195:ARG:CG	1:I:195:ARG:HH11	1.93	0.81
1:A:195:ARG:HH11	1:A:195:ARG:CG	1.93	0.81
2:H:67:THR:HG21	2:H:96:HIS:N	1.96	0.81
1:K:277:GLY:HA2	4:K:2006:AMP:H8	1.44	0.81
2:B:67:THR:HG21	2:B:96:HIS:N	1.96	0.81
1:C:72:ARG:NH2	1:G:171:LYS:HZ2	1.78	0.81
1:A:314:ALA:HB2	1:A:346:LEU:HD13	1.62	0.80
2:J:318:ILE:HA	2:J:322:VAL:HG21	1.64	0.80
2:L:67:THR:HG21	2:L:96:HIS:N	1.96	0.80
2:N:333:ARG:HB2	2:N:339:GLY:HA3	1.63	0.80
2:B:333:ARG:HB2	2:B:339:GLY:HA3	1.63	0.80
1:K:314:ALA:HB2	1:K:346:LEU:HD13	1.62	0.80
1:G:314:ALA:HB2	1:G:346:LEU:HD13	1.62	0.80
1:I:92:SER:HB3	1:I:95:VAL:HG22	1.63	0.80
2:J:67:THR:HG21	2:J:96:HIS:N	1.96	0.80
1:C:92:SER:HB3	1:C:95:VAL:HG22	1.63	0.80
2:H:333:ARG:HB2	2:H:339:GLY:HA3	1.63	0.80
1:K:92:SER:HB3	1:K:95:VAL:HG22	1.63	0.80
1:M:119:ARG:HG2	2:N:125:THR:HG22	1.63	0.80
2:P:318:ILE:HA	2:P:322:VAL:HG21	1.64	0.80
2:P:67:THR:HG21	2:P:96:HIS:N	1.96	0.80
1:M:314:ALA:HB2	1:M:346:LEU:HD13	1.62	0.80
2:N:67:THR:HG21	2:N:96:HIS:N	1.96	0.80
1:G:92:SER:HB3	1:G:95:VAL:HG22	1.63	0.80
1:E:92:SER:HB3	1:E:95:VAL:HG22	1.63	0.80
1:M:92:SER:HB3	1:M:95:VAL:HG22	1.63	0.80
2:N:318:ILE:HA	2:N:322:VAL:HG21	1.64	0.80
1:O:93:LEU:HA	1:O:96:ALA:HB3	1.64	0.80
1:I:93:LEU:HA	1:I:96:ALA:HB3	1.64	0.79
2:L:333:ARG:HB2	2:L:339:GLY:HA3	1.63	0.79
2:D:67:THR:HG21	2:D:96:HIS:N	1.96	0.79
2:N:61:ILE:HG22	2:N:62:PHE:H	1.47	0.79
2:B:61:ILE:HG22	2:B:62:PHE:H	1.47	0.79
1:G:93:LEU:HA	1:G:96:ALA:HB3	1.64	0.79
2:J:333:ARG:HB2	2:J:339:GLY:HA3	1.63	0.79
2:J:71:ASP:O	2:J:75:GLN:HG2	1.83	0.79
2:P:333:ARG:HB2	2:P:339:GLY:HA3	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:61:ILE:HG22	2:P:62:PHE:H	1.47	0.79
1:C:93:LEU:HA	1:C:96:ALA:HB3	1.64	0.79
2:F:333:ARG:HB2	2:F:339:GLY:HA3	1.63	0.79
2:F:67:THR:HG21	2:F:96:HIS:N	1.96	0.79
1:K:151:LEU:HD23	2:L:157:ILE:HG12	1.64	0.79
1:O:92:SER:HB3	1:O:95:VAL:HG22	1.63	0.79
1:A:92:SER:HB3	1:A:95:VAL:HG22	1.63	0.79
2:D:71:ASP:O	2:D:75:GLN:HG2	1.82	0.79
2:H:318:ILE:HA	2:H:322:VAL:HG21	1.64	0.79
2:L:71:ASP:O	2:L:75:GLN:HG2	1.83	0.79
2:D:286:ASP:OD1	2:P:287:ILE:CD1	2.29	0.79
1:E:314:ALA:HB2	1:E:346:LEU:HD13	1.62	0.79
2:D:61:ILE:HG22	2:D:62:PHE:H	1.48	0.79
2:P:71:ASP:O	2:P:75:GLN:HG2	1.83	0.79
2:F:61:ILE:HG22	2:F:62:PHE:H	1.48	0.79
2:N:71:ASP:O	2:N:75:GLN:HG2	1.82	0.79
2:D:318:ILE:HA	2:D:322:VAL:HG21	1.64	0.78
2:D:333:ARG:HB2	2:D:339:GLY:HA3	1.63	0.78
2:L:318:ILE:HA	2:L:322:VAL:HG21	1.64	0.78
1:M:93:LEU:HA	1:M:96:ALA:HB3	1.64	0.78
2:H:71:ASP:O	2:H:75:GLN:HG2	1.82	0.78
2:J:61:ILE:HG22	2:J:62:PHE:H	1.48	0.78
1:K:12:LYS:CE	1:O:168:ASP:OD2	2.31	0.78
2:B:71:ASP:O	2:B:75:GLN:HG2	1.82	0.78
2:H:61:ILE:HG22	2:H:62:PHE:H	1.48	0.78
2:F:318:ILE:HA	2:F:322:VAL:HG21	1.64	0.78
1:C:72:ARG:CZ	1:G:171:LYS:HZ2	1.96	0.78
1:I:151:LEU:HD23	2:J:157:ILE:HG12	1.66	0.78
1:C:119:ARG:CG	2:D:125:THR:HG22	2.13	0.78
2:B:318:ILE:HA	2:B:322:VAL:HG21	1.64	0.77
2:F:71:ASP:O	2:F:75:GLN:HG2	1.82	0.77
2:L:61:ILE:HG22	2:L:62:PHE:H	1.48	0.77
1:M:323:LYS:HE3	1:M:323:LYS:H	1.49	0.77
1:E:93:LEU:HA	1:E:96:ALA:HB3	1.64	0.77
1:K:93:LEU:HA	1:K:96:ALA:HB3	1.64	0.77
1:A:93:LEU:HA	1:A:96:ALA:HB3	1.64	0.77
1:E:323:LYS:HE3	1:E:323:LYS:H	1.50	0.77
2:F:130:ASP:HB3	2:F:236:THR:HG23	1.67	0.76
1:G:323:LYS:HE3	1:G:323:LYS:H	1.50	0.76
2:L:130:ASP:HB3	2:L:236:THR:HG23	1.67	0.76
1:O:323:LYS:HE3	1:O:323:LYS:H	1.49	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:130:ASP:HB3	2:J:236:THR:HG23	1.67	0.76
1:I:323:LYS:HE3	1:I:323:LYS:H	1.49	0.76
2:B:97:ARG:HG3	2:B:102:THR:HG23	1.68	0.76
1:K:12:LYS:HE3	1:O:168:ASP:CG	2.06	0.76
2:P:130:ASP:HB3	2:P:236:THR:HG23	1.67	0.76
2:D:97:ARG:HG3	2:D:102:THR:HG23	1.68	0.76
1:A:168:ASP:OD2	1:E:12:LYS:CE	2.33	0.76
2:N:97:ARG:HG3	2:N:102:THR:HG23	1.68	0.76
1:K:14:TYR:OH	1:O:165:PHE:HA	1.85	0.75
2:P:97:ARG:HG3	2:P:102:THR:HG23	1.68	0.75
1:K:323:LYS:HE3	1:K:323:LYS:H	1.49	0.75
2:H:97:ARG:HG3	2:H:102:THR:HG23	1.68	0.75
2:D:285:PRO:HG2	2:P:287:ILE:HD13	1.66	0.75
2:D:130:ASP:HB3	2:D:236:THR:HG23	1.68	0.75
2:J:351:ILE:O	2:J:354:LEU:HB3	1.87	0.75
1:A:323:LYS:H	1:A:323:LYS:HE3	1.50	0.74
1:C:323:LYS:H	1:C:323:LYS:HE3	1.49	0.74
2:H:130:ASP:HB3	2:H:236:THR:HG23	1.68	0.74
2:B:351:ILE:O	2:B:354:LEU:HB3	1.87	0.74
2:N:130:ASP:HB3	2:N:236:THR:HG23	1.67	0.74
2:F:97:ARG:HG3	2:F:102:THR:HG23	1.68	0.74
1:K:277:GLY:HA3	4:K:2006:AMP:N7	2.02	0.74
2:B:130:ASP:HB3	2:B:236:THR:HG23	1.67	0.74
2:J:97:ARG:HG3	2:J:102:THR:HG23	1.68	0.74
1:K:28:VAL:HG21	4:K:2006:AMP:N6	1.99	0.74
2:L:351:ILE:O	2:L:354:LEU:HB3	1.87	0.74
2:J:41:LYS:HG2	2:J:53:TRP:CD1	2.23	0.74
2:L:97:ARG:HG3	2:L:102:THR:HG23	1.68	0.74
2:P:41:LYS:HG2	2:P:53:TRP:CD1	2.23	0.74
1:A:64:TYR:CZ	2:P:63:VAL:HG13	2.22	0.74
2:F:41:LYS:HG2	2:F:53:TRP:CD1	2.23	0.74
2:H:41:LYS:HG2	2:H:53:TRP:CD1	2.23	0.74
2:B:41:LYS:HG2	2:B:53:TRP:CD1	2.23	0.73
2:D:351:ILE:O	2:D:354:LEU:HB3	1.87	0.73
2:D:41:LYS:HG2	2:D:53:TRP:CD1	2.23	0.73
2:H:351:ILE:O	2:H:354:LEU:HB3	1.87	0.73
1:E:151:LEU:HD23	2:F:157:ILE:HG12	1.71	0.73
2:P:351:ILE:O	2:P:354:LEU:HB3	1.87	0.73
1:K:72:ARG:CZ	1:O:171:LYS:NZ	2.52	0.73
2:N:351:ILE:O	2:N:354:LEU:HB3	1.87	0.73
2:L:41:LYS:HG2	2:L:53:TRP:CD1	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:119:ARG:HG2	2:L:125:THR:HG22	1.70	0.73
2:F:351:ILE:O	2:F:354:LEU:HB3	1.87	0.72
1:K:72:ARG:HH22	1:O:171:LYS:NZ	1.84	0.72
2:N:41:LYS:HG2	2:N:53:TRP:CD1	2.23	0.72
1:C:72:ARG:NH2	1:G:171:LYS:NZ	2.38	0.71
1:E:277:GLY:CA	4:E:2003:AMP:C8	2.74	0.71
2:D:286:ASP:CG	2:P:287:ILE:HD11	2.10	0.71
2:L:348:GLU:O	2:L:352:LYS:HG2	1.91	0.71
2:F:348:GLU:O	2:F:352:LYS:HG2	1.91	0.71
2:D:348:GLU:O	2:D:352:LYS:HG2	1.90	0.71
1:G:28:VAL:HG21	4:G:2004:AMP:HN61	1.55	0.71
2:H:348:GLU:O	2:H:352:LYS:HG2	1.90	0.71
1:E:28:VAL:HG21	4:E:2003:AMP:HN61	1.55	0.70
2:P:348:GLU:O	2:P:352:LYS:HG2	1.90	0.70
2:B:235:TYR:O	2:B:238:ALA:HB2	1.91	0.70
2:D:235:TYR:O	2:D:238:ALA:HB2	1.91	0.70
2:B:348:GLU:O	2:B:352:LYS:HG2	1.91	0.70
2:J:235:TYR:O	2:J:238:ALA:HB2	1.91	0.70
2:J:348:GLU:O	2:J:352:LYS:HG2	1.90	0.70
2:L:235:TYR:O	2:L:238:ALA:HB2	1.91	0.70
1:E:277:GLY:HA2	4:E:2003:AMP:H8	1.57	0.70
2:N:348:GLU:O	2:N:352:LYS:HG2	1.90	0.70
2:H:235:TYR:O	2:H:238:ALA:HB2	1.92	0.70
2:H:322:VAL:HB	2:H:323:LEU:HD23	1.74	0.70
1:C:52:ILE:HD12	1:C:66:ALA:HA	1.74	0.69
2:D:322:VAL:HB	2:D:323:LEU:HD23	1.74	0.69
2:N:322:VAL:HB	2:N:323:LEU:HD23	1.74	0.69
2:P:235:TYR:O	2:P:238:ALA:HB2	1.92	0.69
1:K:52:ILE:HD12	1:K:66:ALA:HA	1.75	0.69
1:O:52:ILE:HD12	1:O:66:ALA:HA	1.75	0.69
2:J:322:VAL:HB	2:J:323:LEU:HD23	1.74	0.69
1:E:195:ARG:HG2	1:E:195:ARG:NH1	2.07	0.69
1:G:52:ILE:HD12	1:G:66:ALA:HA	1.75	0.69
2:F:235:TYR:O	2:F:238:ALA:HB2	1.91	0.69
1:G:305:ASN:HA	1:G:308:ALA:HB3	1.75	0.69
1:I:259:GLY:H	1:I:294:SER:HB3	1.58	0.69
2:N:235:TYR:O	2:N:238:ALA:HB2	1.91	0.69
1:A:64:TYR:CD1	2:P:63:VAL:HG13	2.28	0.69
1:E:305:ASN:HA	1:E:308:ALA:HB3	1.75	0.69
2:L:322:VAL:HB	2:L:323:LEU:HD23	1.74	0.69
1:M:195:ARG:HG2	1:M:195:ARG:NH1	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:TYR:CZ	2:P:63:VAL:HG11	2.28	0.68
1:C:259:GLY:H	1:C:294:SER:HB3	1.58	0.68
1:E:52:ILE:HD12	1:E:66:ALA:HA	1.74	0.68
1:O:305:ASN:HA	1:O:308:ALA:HB3	1.76	0.68
2:P:322:VAL:HB	2:P:323:LEU:HD23	1.74	0.68
2:B:322:VAL:HB	2:B:323:LEU:HD23	1.74	0.68
1:M:52:ILE:HD12	1:M:66:ALA:HA	1.75	0.68
1:M:259:GLY:H	1:M:294:SER:HB3	1.58	0.68
2:P:274:ILE:HG22	2:P:275:SER:N	2.09	0.68
1:C:305:ASN:HA	1:C:308:ALA:HB3	1.76	0.68
2:J:274:ILE:HG22	2:J:275:SER:N	2.09	0.68
1:A:52:ILE:HD12	1:A:66:ALA:HA	1.74	0.68
1:I:305:ASN:HA	1:I:308:ALA:HB3	1.75	0.68
1:E:259:GLY:H	1:E:294:SER:HB3	1.58	0.68
1:G:259:GLY:H	1:G:294:SER:HB3	1.58	0.68
1:I:151:LEU:CD1	2:L:147:HIS:CD2	2.77	0.68
1:K:195:ARG:NH1	1:K:195:ARG:HG2	2.07	0.68
1:M:305:ASN:HA	1:M:308:ALA:HB3	1.76	0.68
1:O:259:GLY:H	1:O:294:SER:HB3	1.58	0.68
2:H:274:ILE:HG22	2:H:275:SER:N	2.09	0.68
1:K:259:GLY:H	1:K:294:SER:HB3	1.58	0.68
2:D:274:ILE:HG22	2:D:275:SER:N	2.09	0.67
2:F:322:VAL:HB	2:F:323:LEU:HD23	1.74	0.67
1:E:323:LYS:N	1:E:323:LYS:HE3	2.09	0.67
1:K:305:ASN:HA	1:K:308:ALA:HB3	1.76	0.67
1:M:323:LYS:HE3	1:M:323:LYS:N	2.09	0.67
1:C:323:LYS:HE3	1:C:323:LYS:N	2.09	0.67
2:F:274:ILE:HG22	2:F:275:SER:N	2.09	0.67
1:I:52:ILE:HD12	1:I:66:ALA:HA	1.74	0.67
2:D:351:ILE:HG23	2:D:354:LEU:HD23	1.77	0.67
1:A:160:GLU:OE1	1:E:8:ARG:NH2	2.27	0.67
2:H:322:VAL:CG1	2:H:350:VAL:HG13	2.24	0.67
2:J:351:ILE:HG23	2:J:354:LEU:HD23	1.77	0.67
2:L:274:ILE:HG22	2:L:275:SER:N	2.09	0.67
2:P:351:ILE:HG23	2:P:354:LEU:HD23	1.77	0.67
1:A:305:ASN:HA	1:A:308:ALA:HB3	1.76	0.67
1:C:195:ARG:HG2	1:C:195:ARG:NH1	2.07	0.67
2:H:150:CYS:CB	2:H:151:PRO:HD2	2.25	0.67
1:O:323:LYS:N	1:O:323:LYS:HE3	2.09	0.67
1:A:259:GLY:H	1:A:294:SER:HB3	1.58	0.67
1:G:323:LYS:HE3	1:G:323:LYS:N	2.10	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:326:ILE:HG21	2:P:350:VAL:HA	1.77	0.67
2:B:351:ILE:HG23	2:B:354:LEU:HD23	1.77	0.67
1:I:119:ARG:HG2	2:J:125:THR:HG22	1.77	0.67
1:I:195:ARG:HG2	1:I:195:ARG:NH1	2.07	0.67
2:L:351:ILE:HG23	2:L:354:LEU:HD23	1.77	0.67
1:A:323:LYS:N	1:A:323:LYS:HE3	2.10	0.67
2:B:150:CYS:CB	2:B:151:PRO:HD2	2.25	0.67
2:D:322:VAL:CG1	2:D:350:VAL:HG13	2.24	0.67
2:H:164:ALA:O	2:H:168:VAL:HG23	1.95	0.67
2:L:40:VAL:HG22	2:L:299:LEU:HD13	1.77	0.67
2:D:164:ALA:O	2:D:168:VAL:HG23	1.95	0.66
2:F:150:CYS:CB	2:F:151:PRO:HD2	2.25	0.66
2:F:322:VAL:CG1	2:F:350:VAL:HG13	2.24	0.66
1:G:195:ARG:HG2	1:G:195:ARG:NH1	2.07	0.66
1:I:323:LYS:N	1:I:323:LYS:HE3	2.09	0.66
2:J:326:ILE:HG21	2:J:350:VAL:HA	1.77	0.66
1:K:323:LYS:HE3	1:K:323:LYS:N	2.09	0.66
2:D:40:VAL:HG22	2:D:299:LEU:HD13	1.77	0.66
1:E:277:GLY:CA	4:E:2003:AMP:H8	2.07	0.66
2:N:274:ILE:HG22	2:N:275:SER:N	2.09	0.66
2:N:326:ILE:HG21	2:N:350:VAL:HA	1.77	0.66
2:P:164:ALA:O	2:P:168:VAL:HG23	1.95	0.66
2:B:164:ALA:O	2:B:168:VAL:HG23	1.95	0.66
2:H:326:ILE:HG21	2:H:350:VAL:HA	1.77	0.66
2:B:274:ILE:HG22	2:B:275:SER:N	2.09	0.66
2:F:40:VAL:HG22	2:F:299:LEU:HD13	1.77	0.66
2:N:351:ILE:HG23	2:N:354:LEU:HD23	1.77	0.66
1:O:323:LYS:O	1:O:324:HIS:HB2	1.96	0.66
2:D:17:PRO:HB2	2:J:62:PHE:CD2	2.30	0.66
2:N:164:ALA:O	2:N:168:VAL:HG23	1.95	0.66
1:O:151:LEU:HD23	2:P:157:ILE:HG12	1.78	0.66
2:D:150:CYS:CB	2:D:151:PRO:HD2	2.25	0.66
2:L:326:ILE:HG21	2:L:350:VAL:HA	1.77	0.66
2:F:164:ALA:O	2:F:168:VAL:HG23	1.95	0.66
2:H:351:ILE:HG23	2:H:354:LEU:HD23	1.77	0.66
2:B:333:ARG:O	2:B:341:ALA:HB3	1.96	0.66
1:E:323:LYS:O	1:E:324:HIS:HB2	1.95	0.66
2:F:326:ILE:HG21	2:F:350:VAL:HA	1.77	0.66
2:P:40:VAL:HG22	2:P:299:LEU:HD13	1.77	0.66
2:B:326:ILE:HG21	2:B:350:VAL:HA	1.77	0.65
2:B:322:VAL:CG1	2:B:350:VAL:HG13	2.24	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:323:LYS:O	1:K:324:HIS:HB2	1.96	0.65
2:D:326:ILE:HG21	2:D:350:VAL:HA	1.77	0.65
1:G:323:LYS:O	1:G:324:HIS:HB2	1.96	0.65
2:H:40:VAL:HG22	2:H:299:LEU:HD13	1.77	0.65
2:B:291:ASP:OD2	2:B:343:THR:HB	1.97	0.65
1:C:323:LYS:O	1:C:324:HIS:HB2	1.96	0.65
2:N:40:VAL:HG22	2:N:299:LEU:HD13	1.77	0.65
1:A:195:ARG:NH1	1:A:195:ARG:HG2	2.07	0.65
2:D:291:ASP:OD2	2:D:343:THR:HB	1.97	0.65
2:J:40:VAL:HG22	2:J:299:LEU:HD13	1.77	0.65
1:M:323:LYS:O	1:M:324:HIS:HB2	1.96	0.65
2:B:40:VAL:HG22	2:B:299:LEU:HD13	1.77	0.65
2:F:333:ARG:O	2:F:341:ALA:HB3	1.96	0.65
2:F:351:ILE:HG23	2:F:354:LEU:HD23	1.77	0.65
2:J:164:ALA:O	2:J:168:VAL:HG23	1.95	0.65
1:A:168:ASP:OD2	1:E:12:LYS:NZ	2.29	0.65
1:A:323:LYS:O	1:A:324:HIS:HB2	1.95	0.65
2:D:333:ARG:O	2:D:341:ALA:HB3	1.96	0.65
2:H:333:ARG:O	2:H:341:ALA:HB3	1.96	0.65
2:L:164:ALA:O	2:L:168:VAL:HG23	1.95	0.65
2:J:322:VAL:CG1	2:J:350:VAL:HG13	2.24	0.65
2:P:333:ARG:O	2:P:341:ALA:HB3	1.96	0.65
2:N:322:VAL:CG1	2:N:350:VAL:HG13	2.24	0.65
2:J:333:ARG:O	2:J:341:ALA:HB3	1.96	0.64
2:N:333:ARG:O	2:N:341:ALA:HB3	1.96	0.64
2:P:150:CYS:CB	2:P:151:PRO:HD2	2.25	0.64
1:A:171:LYS:NZ	1:E:72:ARG:CZ	2.50	0.64
1:I:323:LYS:O	1:I:324:HIS:HB2	1.96	0.64
2:L:291:ASP:OD2	2:L:343:THR:HB	1.97	0.64
1:O:119:ARG:CG	2:P:125:THR:HG22	2.25	0.64
1:E:277:GLY:HA2	4:E:2003:AMP:C8	2.31	0.64
2:F:97:ARG:HE	2:F:97:ARG:HA	1.62	0.64
2:P:322:VAL:CG1	2:P:350:VAL:HG13	2.24	0.64
1:A:119:ARG:CG	2:B:125:THR:HG22	2.26	0.64
1:C:12:LYS:CE	1:G:168:ASP:OD2	2.44	0.64
2:L:333:ARG:O	2:L:341:ALA:HB3	1.96	0.64
2:P:291:ASP:OD2	2:P:343:THR:HB	1.97	0.64
2:H:291:ASP:OD2	2:H:343:THR:HB	1.97	0.64
2:J:291:ASP:OD2	2:J:343:THR:HB	1.97	0.64
2:J:97:ARG:HE	2:J:97:ARG:HA	1.62	0.64
1:K:14:TYR:CE2	1:O:165:PHE:HD1	2.16	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:97:ARG:HE	2:D:97:ARG:HA	1.62	0.64
2:L:150:CYS:CB	2:L:151:PRO:HD2	2.25	0.64
2:P:97:ARG:HA	2:P:97:ARG:HE	1.62	0.64
1:A:181:VAL:HB	1:A:235:THR:HG22	1.80	0.64
2:L:97:ARG:HA	2:L:97:ARG:HE	1.62	0.64
2:N:291:ASP:OD2	2:N:343:THR:HB	1.97	0.64
2:N:97:ARG:HE	2:N:97:ARG:HA	1.62	0.64
2:B:97:ARG:HA	2:B:97:ARG:HE	1.62	0.64
2:F:291:ASP:OD2	2:F:343:THR:HB	1.97	0.64
1:K:72:ARG:HH22	1:O:171:LYS:HZ1	1.46	0.64
1:E:181:VAL:HB	1:E:235:THR:HG22	1.80	0.63
1:G:181:VAL:HB	1:G:235:THR:HG22	1.80	0.63
2:N:150:CYS:CB	2:N:151:PRO:HD2	2.25	0.63
2:P:67:THR:CG2	2:P:96:HIS:N	2.61	0.63
1:I:181:VAL:HB	1:I:235:THR:HG22	1.80	0.63
2:J:67:THR:CG2	2:J:96:HIS:N	2.62	0.63
2:L:322:VAL:CG1	2:L:350:VAL:HG13	2.24	0.63
2:H:97:ARG:HA	2:H:97:ARG:HE	1.62	0.63
2:L:67:THR:CG2	2:L:96:HIS:N	2.61	0.63
2:J:43:ILE:HD13	2:J:350:VAL:HG11	1.81	0.63
2:N:67:THR:CG2	2:N:96:HIS:N	2.62	0.63
2:P:60:PRO:HG3	2:P:99:LEU:HD13	1.81	0.63
1:E:315:VAL:O	1:E:319:ILE:HG23	1.99	0.63
1:M:315:VAL:O	1:M:319:ILE:HG23	1.99	0.63
2:D:58:VAL:HG12	2:D:69:ILE:CD1	2.29	0.63
2:B:58:VAL:HG12	2:B:69:ILE:CD1	2.29	0.63
2:H:67:THR:CG2	2:H:96:HIS:N	2.62	0.63
2:N:60:PRO:HG3	2:N:99:LEU:HD13	1.81	0.63
2:N:58:VAL:HG12	2:N:69:ILE:CD1	2.29	0.63
1:O:181:VAL:HB	1:O:235:THR:HG22	1.80	0.62
2:F:43:ILE:HD13	2:F:350:VAL:HG11	1.81	0.62
2:L:43:ILE:HD13	2:L:350:VAL:HG11	1.81	0.62
2:F:60:PRO:HG3	2:F:99:LEU:HD13	1.81	0.62
1:K:315:VAL:O	1:K:319:ILE:HG23	1.99	0.62
1:K:72:ARG:NH1	1:O:171:LYS:HZ2	1.97	0.62
1:O:315:VAL:O	1:O:319:ILE:HG23	1.99	0.62
1:I:315:VAL:O	1:I:319:ILE:HG23	1.99	0.62
2:P:334:THR:HG22	2:P:335:GLY:H	1.64	0.62
2:B:67:THR:CG2	2:B:96:HIS:N	2.62	0.62
1:C:315:VAL:O	1:C:319:ILE:HG23	1.99	0.62
1:K:277:GLY:CA	4:K:2006:AMP:N7	2.62	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:195:ARG:NH1	1:O:195:ARG:HG2	2.07	0.62
2:B:60:PRO:HG3	2:B:99:LEU:HD13	1.81	0.62
1:K:181:VAL:HB	1:K:235:THR:HG22	1.80	0.62
2:L:60:PRO:HG3	2:L:99:LEU:HD13	1.81	0.62
2:B:43:ILE:HD13	2:B:350:VAL:HG11	1.81	0.62
2:D:43:ILE:HD13	2:D:350:VAL:HG11	1.81	0.62
2:F:67:THR:CG2	2:F:96:HIS:N	2.62	0.62
2:J:58:VAL:HG12	2:J:69:ILE:CD1	2.29	0.62
1:M:181:VAL:HB	1:M:235:THR:HG22	1.80	0.62
1:A:315:VAL:O	1:A:319:ILE:HG23	1.99	0.62
1:C:181:VAL:HB	1:C:235:THR:HG22	1.80	0.62
1:I:92:SER:OG	3:I:1005:FLC:OG2	2.15	0.62
2:J:60:PRO:HG3	2:J:99:LEU:HD13	1.81	0.62
2:P:43:ILE:HD13	2:P:350:VAL:HG11	1.81	0.62
1:A:64:TYR:CE2	2:P:63:VAL:HG22	2.34	0.62
2:D:67:THR:CG2	2:D:96:HIS:N	2.62	0.61
2:L:58:VAL:HG12	2:L:69:ILE:CD1	2.29	0.61
2:N:334:THR:HG22	2:N:335:GLY:H	1.65	0.61
1:C:119:ARG:HD2	2:D:125:THR:O	2.00	0.61
2:H:186:VAL:HG23	2:H:216:LEU:HD11	1.83	0.61
2:J:150:CYS:CB	2:J:151:PRO:HD2	2.25	0.61
2:D:334:THR:HG22	2:D:335:GLY:H	1.65	0.61
2:D:60:PRO:HG3	2:D:99:LEU:HD13	1.81	0.61
1:G:92:SER:OG	3:G:1004:FLC:OG2	2.17	0.61
2:H:60:PRO:HG3	2:H:99:LEU:HD13	1.81	0.61
1:I:307:TYR:O	1:I:311:ILE:HG23	2.01	0.61
1:A:307:TYR:O	1:A:311:ILE:HG23	2.01	0.61
2:F:334:THR:HG22	2:F:335:GLY:H	1.65	0.61
2:L:334:THR:HG22	2:L:335:GLY:H	1.65	0.61
1:O:307:TYR:O	1:O:311:ILE:HG23	2.01	0.61
2:D:186:VAL:HG23	2:D:216:LEU:HD11	1.83	0.61
1:M:151:LEU:HD23	2:N:157:ILE:HG12	1.82	0.61
1:M:307:TYR:O	1:M:311:ILE:HG23	2.00	0.61
2:F:58:VAL:HG12	2:F:69:ILE:CD1	2.29	0.61
2:B:334:THR:HG22	2:B:335:GLY:H	1.65	0.61
1:G:315:VAL:O	1:G:319:ILE:HG23	1.99	0.61
1:K:115:GLY:HA3	1:K:320:ALA:HA	1.83	0.61
1:I:168:ASP:OD2	1:M:12:LYS:CE	2.47	0.61
2:F:186:VAL:HG23	2:F:216:LEU:HD11	1.83	0.61
1:I:115:GLY:HA3	1:I:320:ALA:HA	1.83	0.61
2:J:186:VAL:HG23	2:J:216:LEU:HD11	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:307:TYR:O	1:K:311:ILE:HG23	2.00	0.61
2:N:36:ILE:HG12	2:N:295:PRO:HA	1.83	0.61
2:B:186:VAL:HG23	2:B:216:LEU:HD11	1.83	0.61
1:G:307:TYR:O	1:G:311:ILE:HG23	2.01	0.61
1:G:115:GLY:HA3	1:G:320:ALA:HA	1.83	0.61
1:I:171:LYS:HZ2	1:M:72:ARG:NH2	1.98	0.61
2:P:12:THR:HB	2:P:81:LEU:HD12	1.83	0.61
1:K:277:GLY:CA	4:K:2006:AMP:H8	2.02	0.60
1:A:115:GLY:HA3	1:A:320:ALA:HA	1.83	0.60
1:A:171:LYS:HZ1	1:E:72:ARG:HH22	1.48	0.60
2:H:306:LEU:HD12	2:H:309:MET:CE	2.31	0.60
2:H:43:ILE:HD13	2:H:350:VAL:HG11	1.81	0.60
2:J:334:THR:HG22	2:J:335:GLY:H	1.65	0.60
1:M:115:GLY:HA3	1:M:320:ALA:HA	1.83	0.60
2:B:306:LEU:HD12	2:B:309:MET:CE	2.32	0.60
1:C:35:SER:O	1:C:39:ILE:HG13	2.01	0.60
2:D:306:LEU:HD12	2:D:309:MET:CE	2.31	0.60
2:P:58:VAL:HG12	2:P:69:ILE:CD1	2.29	0.60
1:C:307:TYR:O	1:C:311:ILE:HG23	2.01	0.60
1:G:35:SER:O	1:G:39:ILE:HG13	2.02	0.60
1:M:35:SER:O	1:M:39:ILE:HG13	2.02	0.60
2:N:67:THR:HG23	2:N:97:ARG:HB3	1.83	0.60
2:B:351:ILE:HA	2:B:354:LEU:HB2	1.84	0.60
2:B:12:THR:HB	2:B:81:LEU:HD12	1.83	0.60
2:F:351:ILE:HA	2:F:354:LEU:HB2	1.84	0.60
2:H:351:ILE:HA	2:H:354:LEU:HB2	1.84	0.60
2:N:306:LEU:HD12	2:N:309:MET:CE	2.31	0.60
2:P:36:ILE:HG12	2:P:295:PRO:HA	1.83	0.60
2:D:36:ILE:HG12	2:D:295:PRO:HA	1.83	0.60
1:E:245:ASN:ND2	2:F:222:ASP:HA	2.16	0.60
1:I:35:SER:O	1:I:39:ILE:HG13	2.02	0.60
2:J:36:ILE:HG12	2:J:295:PRO:HA	1.83	0.60
2:J:306:LEU:HD12	2:J:309:MET:CE	2.32	0.60
2:L:351:ILE:HA	2:L:354:LEU:HB2	1.84	0.60
2:N:186:VAL:HG23	2:N:216:LEU:HD11	1.83	0.60
2:P:295:PRO:HB2	2:P:299:LEU:HD22	1.84	0.60
2:P:306:LEU:HD12	2:P:309:MET:CE	2.32	0.60
1:E:119:ARG:HG2	2:F:125:THR:HG22	1.84	0.60
1:E:307:TYR:O	1:E:311:ILE:HG23	2.00	0.60
1:K:300:ASN:OD1	1:K:305:ASN:HB2	2.02	0.60
1:E:151:LEU:CD1	2:H:147:HIS:CD2	2.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:306:LEU:HD12	2:F:309:MET:CE	2.32	0.60
2:H:295:PRO:HB2	2:H:299:LEU:HD22	1.84	0.60
2:H:58:VAL:HG12	2:H:69:ILE:CD1	2.29	0.60
2:J:351:ILE:HA	2:J:354:LEU:HB2	1.84	0.60
2:N:43:ILE:HD13	2:N:350:VAL:HG11	1.81	0.60
2:D:351:ILE:HA	2:D:354:LEU:HB2	1.83	0.60
1:E:115:GLY:HA3	1:E:320:ALA:HA	1.83	0.60
2:F:149:VAL:HG21	2:H:149:VAL:HG21	1.83	0.60
2:F:36:ILE:HG12	2:F:295:PRO:HA	1.83	0.60
2:L:12:THR:HB	2:L:81:LEU:HD12	1.83	0.60
1:I:171:LYS:HZ2	1:M:72:ARG:CZ	2.15	0.60
1:G:197:ILE:O	1:G:201:ILE:HG23	2.02	0.60
1:I:300:ASN:OD1	1:I:305:ASN:HB2	2.02	0.60
1:K:35:SER:O	1:K:39:ILE:HG13	2.02	0.60
1:M:300:ASN:OD1	1:M:305:ASN:HB2	2.02	0.60
1:O:115:GLY:HA3	1:O:320:ALA:HA	1.83	0.60
2:P:186:VAL:HG23	2:P:216:LEU:HD11	1.83	0.60
1:A:197:ILE:O	1:A:201:ILE:HG23	2.02	0.59
1:C:115:GLY:HA3	1:C:320:ALA:HA	1.83	0.59
1:E:300:ASN:OD1	1:E:305:ASN:HB2	2.02	0.59
2:H:314:HIS:O	2:H:318:ILE:HG13	2.02	0.59
2:J:12:THR:HB	2:J:81:LEU:HD12	1.83	0.59
2:L:306:LEU:HD12	2:L:309:MET:CE	2.32	0.59
2:L:314:HIS:O	2:L:318:ILE:HG13	2.02	0.59
2:P:44:PHE:CD2	2:P:49:VAL:HG21	2.37	0.59
2:B:295:PRO:HB2	2:B:299:LEU:HD22	1.84	0.59
1:G:92:SER:CB	3:G:1004:FLC:OG2	2.50	0.59
2:J:155:GLN:NE2	2:L:155:GLN:OE1	2.33	0.59
2:L:186:VAL:HG23	2:L:216:LEU:HD11	1.83	0.59
2:L:67:THR:HG23	2:L:97:ARG:HB3	1.84	0.59
2:N:314:HIS:O	2:N:318:ILE:HG13	2.02	0.59
2:N:12:THR:HB	2:N:81:LEU:HD12	1.83	0.59
1:A:300:ASN:OD1	1:A:305:ASN:HB2	2.02	0.59
1:C:197:ILE:O	1:C:201:ILE:HG23	2.02	0.59
2:D:44:PHE:CD2	2:D:49:VAL:HG21	2.37	0.59
2:D:12:THR:HB	2:D:81:LEU:HD12	1.83	0.59
2:F:314:HIS:O	2:F:318:ILE:HG13	2.02	0.59
2:B:67:THR:HG23	2:B:97:ARG:HB3	1.83	0.59
2:B:322:VAL:O	2:B:324:SER:N	2.36	0.59
1:E:35:SER:O	1:E:39:ILE:HG13	2.02	0.59
2:F:322:VAL:O	2:F:324:SER:N	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:67:THR:HG23	2:F:97:ARG:HB3	1.83	0.59
2:H:12:THR:HB	2:H:81:LEU:HD12	1.83	0.59
1:M:83:THR:OG1	3:M:1007:FLC:CGC	2.49	0.59
2:N:322:VAL:O	2:N:324:SER:N	2.36	0.59
1:O:300:ASN:OD1	1:O:305:ASN:HB2	2.02	0.59
2:B:44:PHE:CD2	2:B:49:VAL:HG21	2.38	0.59
1:C:300:ASN:OD1	1:C:305:ASN:HB2	2.02	0.59
1:I:153:VAL:HG11	2:L:149:VAL:O	2.02	0.59
1:C:12:LYS:HE3	1:G:168:ASP:CG	2.23	0.59
2:D:314:HIS:O	2:D:318:ILE:HG13	2.02	0.59
1:E:197:ILE:O	1:E:201:ILE:HG23	2.02	0.59
2:N:44:PHE:CD2	2:N:49:VAL:HG21	2.38	0.59
2:P:351:ILE:HA	2:P:354:LEU:HB2	1.84	0.59
1:A:183:LYS:HE2	2:B:142:TYR:OH	2.02	0.59
2:F:44:PHE:CD2	2:F:49:VAL:HG21	2.37	0.59
2:F:12:THR:HB	2:F:81:LEU:HD12	1.83	0.59
2:H:36:ILE:HG12	2:H:295:PRO:HA	1.83	0.59
2:J:44:PHE:CD2	2:J:49:VAL:HG21	2.37	0.59
2:L:323:LEU:HD23	2:L:323:LEU:H	1.68	0.59
2:L:322:VAL:O	2:L:324:SER:N	2.36	0.59
1:M:183:LYS:HE2	2:N:142:TYR:OH	2.03	0.59
1:M:197:ILE:O	1:M:201:ILE:HG23	2.02	0.59
2:N:295:PRO:HB2	2:N:299:LEU:HD22	1.84	0.59
2:D:322:VAL:O	2:D:324:SER:N	2.36	0.59
1:G:300:ASN:OD1	1:G:305:ASN:HB2	2.02	0.59
2:H:334:THR:HG22	2:H:335:GLY:H	1.65	0.59
2:J:322:VAL:O	2:J:324:SER:N	2.36	0.59
2:L:36:ILE:HG12	2:L:295:PRO:HA	1.83	0.59
2:N:351:ILE:HA	2:N:354:LEU:HB2	1.84	0.59
1:O:183:LYS:HE2	2:P:142:TYR:OH	2.03	0.59
2:F:295:PRO:HB2	2:F:299:LEU:HD22	1.84	0.59
2:B:36:ILE:HG12	2:B:295:PRO:HA	1.83	0.58
2:D:67:THR:HG23	2:D:97:ARG:HB3	1.83	0.58
2:L:44:PHE:CD2	2:L:49:VAL:HG21	2.37	0.58
2:P:322:VAL:O	2:P:324:SER:N	2.36	0.58
1:C:151:LEU:HD23	2:D:157:ILE:HG12	1.85	0.58
2:F:189:LYS:HB2	2:F:221:ILE:HD11	1.86	0.58
1:I:338:PHE:O	1:I:342:ILE:HG12	2.04	0.58
1:O:35:SER:O	1:O:39:ILE:HG13	2.02	0.58
2:P:67:THR:HG23	2:P:97:ARG:HB3	1.84	0.58
1:A:35:SER:O	1:A:39:ILE:HG13	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:189:LYS:HB2	2:D:221:ILE:HD11	1.85	0.58
1:E:338:PHE:O	1:E:342:ILE:HG12	2.04	0.58
2:J:295:PRO:HB2	2:J:299:LEU:HD22	1.84	0.58
1:C:338:PHE:O	1:C:342:ILE:HG12	2.04	0.58
2:D:295:PRO:HB2	2:D:299:LEU:HD22	1.84	0.58
1:K:338:PHE:O	1:K:342:ILE:HG12	2.04	0.58
1:M:338:PHE:O	1:M:342:ILE:HG12	2.03	0.58
2:P:314:HIS:O	2:P:318:ILE:HG13	2.02	0.58
2:J:314:HIS:O	2:J:318:ILE:HG13	2.02	0.58
2:N:189:LYS:HB2	2:N:221:ILE:HD11	1.85	0.58
1:O:338:PHE:O	1:O:342:ILE:HG12	2.04	0.58
2:B:314:HIS:O	2:B:318:ILE:HG13	2.03	0.58
1:G:338:PHE:O	1:G:342:ILE:HG12	2.04	0.58
2:H:44:PHE:CD2	2:H:49:VAL:HG21	2.38	0.58
2:J:67:THR:HG23	2:J:97:ARG:HB3	1.83	0.58
1:K:197:ILE:O	1:K:201:ILE:HG23	2.02	0.58
1:O:197:ILE:O	1:O:201:ILE:HG23	2.02	0.58
1:A:338:PHE:O	1:A:342:ILE:HG12	2.04	0.58
2:D:187:VAL:HB	2:D:242:CYS:HB3	1.86	0.58
2:H:187:VAL:HB	2:H:242:CYS:HB3	1.86	0.58
2:H:67:THR:HG23	2:H:97:ARG:HB3	1.83	0.58
1:I:197:ILE:O	1:I:201:ILE:HG23	2.02	0.58
2:P:323:LEU:HD23	2:P:323:LEU:H	1.68	0.58
2:B:101:LEU:HD23	2:B:104:ARG:HH12	1.69	0.58
2:B:189:LYS:HB2	2:B:221:ILE:HD11	1.85	0.58
2:B:187:VAL:HB	2:B:242:CYS:HB3	1.86	0.58
1:E:93:LEU:HA	1:E:96:ALA:CB	2.34	0.58
1:C:72:ARG:HH22	1:G:171:LYS:NZ	2.01	0.58
1:G:80:LEU:HD11	1:G:274:ARG:HG3	1.86	0.57
2:J:187:VAL:HB	2:J:242:CYS:HB3	1.86	0.57
1:M:119:ARG:CG	2:N:125:THR:HG22	2.32	0.57
2:H:322:VAL:O	2:H:324:SER:N	2.36	0.57
1:A:151:LEU:HD23	2:B:157:ILE:HG12	1.85	0.57
2:H:101:LEU:HD23	2:H:104:ARG:HH12	1.69	0.57
1:K:93:LEU:HA	1:K:96:ALA:CB	2.34	0.57
2:L:295:PRO:HB2	2:L:299:LEU:HD22	1.84	0.57
2:P:187:VAL:HB	2:P:242:CYS:HB3	1.86	0.57
1:A:80:LEU:HD11	1:A:274:ARG:HG3	1.86	0.57
1:E:183:LYS:HE2	2:F:142:TYR:OH	2.05	0.57
2:H:189:LYS:HB2	2:H:221:ILE:HD11	1.85	0.57
2:L:189:LYS:HB2	2:L:221:ILE:HD11	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:23:THR:O	2:L:80:ASN:HB3	2.05	0.57
2:N:101:LEU:HD23	2:N:104:ARG:HH12	1.70	0.57
2:N:323:LEU:HD23	2:N:323:LEU:H	1.68	0.57
2:B:165:SER:HG	2:B:200:PHE:HD1	1.51	0.57
2:B:323:LEU:H	2:B:323:LEU:HD23	1.68	0.57
2:D:101:LEU:HD23	2:D:104:ARG:HH12	1.69	0.57
2:F:147:HIS:CD2	1:G:151:LEU:CD1	2.87	0.57
2:J:323:LEU:HD23	2:J:323:LEU:H	1.68	0.57
2:L:187:VAL:HB	2:L:242:CYS:HB3	1.86	0.57
2:B:23:THR:O	2:B:80:ASN:HB3	2.05	0.57
2:H:23:THR:O	2:H:80:ASN:HB3	2.05	0.57
2:J:101:LEU:HD23	2:J:104:ARG:HH12	1.70	0.57
2:N:68:THR:HG22	2:N:69:ILE:N	2.20	0.57
2:P:61:ILE:HG22	2:P:62:PHE:N	2.19	0.57
1:C:80:LEU:HD11	1:C:274:ARG:HG3	1.86	0.57
2:D:323:LEU:HD23	2:D:323:LEU:H	1.68	0.57
2:D:23:THR:O	2:D:80:ASN:HB3	2.05	0.57
2:F:187:VAL:HB	2:F:242:CYS:HB3	1.86	0.57
2:F:68:THR:HG22	2:F:69:ILE:N	2.20	0.57
2:L:189:LYS:HD3	2:L:221:ILE:HD11	1.87	0.57
1:M:255:GLY:HA3	4:M:2007:AMP:N1	2.20	0.57
1:M:80:LEU:HD11	1:M:274:ARG:HG3	1.87	0.57
2:F:189:LYS:HD3	2:F:221:ILE:HD11	1.87	0.57
2:J:23:THR:O	2:J:80:ASN:HB3	2.05	0.57
2:P:23:THR:O	2:P:80:ASN:HB3	2.05	0.57
1:C:83:THR:OG1	3:C:1002:FLC:OG2	2.22	0.57
1:G:129:ARG:CZ	1:G:274:ARG:HH12	2.18	0.57
1:O:129:ARG:CZ	1:O:274:ARG:HH12	2.18	0.57
2:P:189:LYS:HB2	2:P:221:ILE:HD11	1.85	0.57
2:B:68:THR:HG22	2:B:69:ILE:N	2.20	0.57
1:C:14:TYR:OH	1:G:165:PHE:HA	2.04	0.57
1:A:165:PHE:HA	1:E:14:TYR:OH	2.05	0.57
2:H:189:LYS:HD3	2:H:221:ILE:HD11	1.87	0.57
1:I:93:LEU:HA	1:I:96:ALA:CB	2.34	0.57
2:J:165:SER:HG	2:J:200:PHE:HD1	1.52	0.57
2:J:189:LYS:HB2	2:J:221:ILE:HD11	1.85	0.57
2:L:101:LEU:HD23	2:L:104:ARG:HH12	1.69	0.57
1:A:164:ARG:HH22	1:E:8:ARG:NH2	2.03	0.56
1:A:160:GLU:CD	1:E:8:ARG:NH2	2.58	0.56
2:F:323:LEU:HD23	2:F:323:LEU:H	1.68	0.56
2:N:187:VAL:HB	2:N:242:CYS:HB3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:165:SER:HG	2:D:200:PHE:HD1	1.51	0.56
1:E:129:ARG:CZ	1:E:274:ARG:HH12	2.18	0.56
1:I:263:GLY:O	1:M:15:GLY:N	2.31	0.56
2:L:68:THR:HG22	2:L:69:ILE:N	2.20	0.56
1:M:129:ARG:CZ	1:M:274:ARG:HH12	2.18	0.56
1:O:80:LEU:HD11	1:O:274:ARG:HG3	1.87	0.56
2:P:101:LEU:HD23	2:P:104:ARG:HH12	1.69	0.56
2:D:285:PRO:HG3	2:P:286:ASP:CB	2.35	0.56
2:B:16:ASN:O	2:B:19:THR:O	2.24	0.56
1:I:151:LEU:HD11	2:L:147:HIS:CD2	2.40	0.56
2:J:68:THR:HG22	2:J:69:ILE:N	2.20	0.56
1:K:45:ILE:HG12	1:K:307:TYR:CD2	2.41	0.56
2:L:181:ARG:HD3	2:L:238:ALA:N	2.21	0.56
1:I:171:LYS:NZ	1:M:50:GLU:OE1	2.36	0.56
1:O:183:LYS:HE3	1:O:186:ILE:HD12	1.87	0.56
2:P:181:ARG:HD3	2:P:238:ALA:N	2.21	0.56
1:A:168:ASP:CG	1:E:12:LYS:HE3	2.25	0.56
2:H:181:ARG:HD3	2:H:238:ALA:N	2.20	0.56
1:I:45:ILE:HG12	1:I:307:TYR:CD2	2.41	0.56
2:N:181:ARG:HD3	2:N:238:ALA:N	2.21	0.56
2:N:189:LYS:HD3	2:N:221:ILE:HD11	1.87	0.56
2:N:23:THR:O	2:N:80:ASN:HB3	2.05	0.56
2:P:16:ASN:O	2:P:19:THR:O	2.24	0.56
2:P:189:LYS:HD3	2:P:221:ILE:HD11	1.87	0.56
2:B:189:LYS:HD3	2:B:221:ILE:HD11	1.87	0.56
1:C:210:ASP:OD2	2:P:42:LYS:NZ	2.26	0.56
1:G:45:ILE:HG12	1:G:307:TYR:CD2	2.41	0.56
2:J:189:LYS:HD3	2:J:221:ILE:HD11	1.87	0.56
2:N:16:ASN:O	2:N:19:THR:O	2.24	0.56
1:A:183:LYS:HE3	1:A:186:ILE:HD12	1.87	0.56
2:D:16:ASN:O	2:D:19:THR:O	2.24	0.56
2:F:181:ARG:HD3	2:F:238:ALA:N	2.21	0.56
1:I:144:VAL:HB	1:I:145:PRO:HD2	1.88	0.56
1:K:129:ARG:CZ	1:K:274:ARG:HH12	2.18	0.56
2:P:68:THR:HG22	2:P:69:ILE:N	2.20	0.56
1:C:45:ILE:HG12	1:C:307:TYR:CD2	2.41	0.56
1:G:183:LYS:HE3	1:G:186:ILE:HD12	1.87	0.56
1:I:80:LEU:HD11	1:I:274:ARG:HG3	1.87	0.56
2:L:69:ILE:HD12	2:L:70:PRO:CD	2.34	0.56
1:M:45:ILE:HG12	1:M:307:TYR:CD2	2.41	0.56
1:C:183:LYS:HE3	1:C:186:ILE:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:183:LYS:HE3	1:E:186:ILE:HD12	1.87	0.56
2:F:23:THR:O	2:F:80:ASN:HB3	2.05	0.56
1:K:80:LEU:HD11	1:K:274:ARG:HG3	1.87	0.56
1:O:144:VAL:HB	1:O:145:PRO:HD2	1.88	0.56
1:C:183:LYS:HE2	2:D:142:TYR:OH	2.06	0.56
1:E:45:ILE:HG12	1:E:307:TYR:CD2	2.41	0.56
1:O:93:LEU:HA	1:O:96:ALA:CB	2.34	0.56
2:P:14:LYS:O	2:P:14:LYS:HD3	2.06	0.56
1:A:129:ARG:CZ	1:A:274:ARG:HH12	2.18	0.56
2:D:68:THR:HG22	2:D:69:ILE:N	2.20	0.56
2:F:101:LEU:HD23	2:F:104:ARG:HH12	1.70	0.56
2:H:323:LEU:H	2:H:323:LEU:HD23	1.68	0.56
1:I:314:ALA:CB	1:I:346:LEU:HD13	2.35	0.56
2:J:306:LEU:HB3	2:J:315:ALA:HB2	1.88	0.56
1:K:144:VAL:HB	1:K:145:PRO:HD2	1.88	0.56
1:M:195:ARG:CB	1:M:195:ARG:HH11	2.19	0.56
2:N:61:ILE:HG22	2:N:62:PHE:N	2.19	0.56
1:O:274:ARG:NH1	3:O:1008:FLC:OB1	2.39	0.56
2:B:181:ARG:HD3	2:B:238:ALA:N	2.21	0.56
2:B:326:ILE:HG12	2:B:350:VAL:HG23	1.88	0.56
2:D:14:LYS:HD3	2:D:14:LYS:O	2.06	0.56
1:A:301:HIS:O	1:E:17:ARG:NH1	2.39	0.56
2:F:165:SER:HG	2:F:200:PHE:HD1	1.53	0.56
2:H:14:LYS:HD3	2:H:14:LYS:O	2.06	0.56
2:H:68:THR:HG22	2:H:69:ILE:N	2.20	0.56
2:J:274:ILE:HG22	2:J:275:SER:H	1.71	0.56
2:L:14:LYS:O	2:L:14:LYS:HD3	2.06	0.56
1:M:183:LYS:HE3	1:M:186:ILE:HD12	1.87	0.56
1:A:52:ILE:CD1	1:A:66:ALA:HA	2.36	0.55
2:B:14:LYS:O	2:B:14:LYS:HD3	2.06	0.55
1:C:144:VAL:HB	1:C:145:PRO:HD2	1.88	0.55
1:C:8:ARG:NH2	1:G:160:GLU:OE1	2.38	0.55
2:F:326:ILE:HG12	2:F:350:VAL:HG23	1.88	0.55
2:H:16:ASN:O	2:H:19:THR:O	2.24	0.55
1:I:52:ILE:CD1	1:I:66:ALA:HA	2.36	0.55
2:J:61:ILE:HG22	2:J:62:PHE:N	2.19	0.55
2:D:17:PRO:HB2	2:J:62:PHE:HD2	1.72	0.55
2:F:16:ASN:O	2:F:19:THR:O	2.24	0.55
1:I:254:PRO:HG3	2:J:226:LEU:HD11	1.87	0.55
1:K:314:ALA:CB	1:K:346:LEU:HD13	2.35	0.55
2:L:306:LEU:HB3	2:L:315:ALA:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:181:ARG:HD3	2:D:238:ALA:N	2.21	0.55
2:D:189:LYS:HD3	2:D:221:ILE:HD11	1.87	0.55
1:G:195:ARG:CB	1:G:195:ARG:HH11	2.19	0.55
2:H:306:LEU:HB3	2:H:315:ALA:HB2	1.88	0.55
1:I:129:ARG:CZ	1:I:274:ARG:HH12	2.18	0.55
1:I:183:LYS:HE3	1:I:186:ILE:HD12	1.87	0.55
2:J:181:ARG:HD3	2:J:238:ALA:N	2.21	0.55
1:I:104:TYR:HH	1:M:14:TYR:HE2	1.54	0.55
1:C:129:ARG:CZ	1:C:274:ARG:HH12	2.18	0.55
1:E:314:ALA:CB	1:E:346:LEU:HD13	2.35	0.55
1:E:52:ILE:CD1	1:E:66:ALA:HA	2.36	0.55
2:F:306:LEU:HB3	2:F:315:ALA:HB2	1.88	0.55
1:O:274:ARG:HG2	3:O:1008:FLC:OB1	2.06	0.55
1:O:45:ILE:HG12	1:O:307:TYR:CD2	2.41	0.55
1:A:45:ILE:HG12	1:A:307:TYR:CD2	2.41	0.55
2:B:274:ILE:HG22	2:B:275:SER:H	1.71	0.55
1:A:165:PHE:HD1	1:E:14:TYR:CE2	2.25	0.55
2:F:14:LYS:HD3	2:F:14:LYS:O	2.06	0.55
1:G:52:ILE:CD1	1:G:66:ALA:HA	2.37	0.55
2:H:61:ILE:HG22	2:H:62:PHE:N	2.19	0.55
1:K:195:ARG:CB	1:K:195:ARG:HH11	2.19	0.55
2:N:326:ILE:HG12	2:N:350:VAL:HG23	1.88	0.55
2:P:306:LEU:HB3	2:P:315:ALA:HB2	1.88	0.55
2:D:69:ILE:HD12	2:D:70:PRO:CD	2.34	0.55
1:E:144:VAL:HB	1:E:145:PRO:HD2	1.88	0.55
1:E:80:LEU:HD11	1:E:274:ARG:HG3	1.87	0.55
1:G:144:VAL:HB	1:G:145:PRO:HD2	1.88	0.55
1:K:183:LYS:HE3	1:K:186:ILE:HD12	1.87	0.55
2:N:14:LYS:HD3	2:N:14:LYS:O	2.06	0.55
1:C:195:ARG:HH11	1:C:195:ARG:CB	2.19	0.55
1:C:93:LEU:HA	1:C:96:ALA:CB	2.34	0.55
1:M:144:VAL:HB	1:M:145:PRO:HD2	1.88	0.55
1:I:195:ARG:CB	1:I:195:ARG:HH11	2.19	0.55
2:J:16:ASN:O	2:J:19:THR:O	2.24	0.55
1:M:52:ILE:CD1	1:M:66:ALA:HA	2.37	0.55
1:I:160:GLU:OE1	1:M:8:ARG:NH2	2.40	0.55
1:A:195:ARG:HH11	1:A:195:ARG:CB	2.19	0.55
2:F:274:ILE:HG22	2:F:275:SER:H	1.71	0.55
2:L:16:ASN:O	2:L:19:THR:O	2.24	0.55
1:O:52:ILE:CD1	1:O:66:ALA:HA	2.37	0.55
2:N:306:LEU:HB3	2:N:315:ALA:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:195:ARG:HH11	1:E:195:ARG:CB	2.19	0.54
1:E:32:ILE:CG1	1:E:288:PRO:HA	2.38	0.54
2:H:326:ILE:HG22	2:H:353:ARG:HG3	1.90	0.54
1:M:314:ALA:CB	1:M:346:LEU:HD13	2.35	0.54
2:N:253:LEU:HD23	2:N:253:LEU:C	2.28	0.54
2:B:326:ILE:HG22	2:B:353:ARG:HG3	1.89	0.54
1:C:52:ILE:CD1	1:C:66:ALA:HA	2.36	0.54
2:D:306:LEU:HB3	2:D:315:ALA:HB2	1.88	0.54
2:D:61:ILE:HG22	2:D:62:PHE:N	2.20	0.54
1:E:241:THR:OG1	3:E:1003:FLC:OA2	2.16	0.54
1:G:224:VAL:HG11	2:H:257:LEU:HG	1.90	0.54
2:H:326:ILE:HG12	2:H:350:VAL:HG23	1.88	0.54
2:J:14:LYS:O	2:J:14:LYS:HD3	2.06	0.54
1:O:195:ARG:HH11	1:O:195:ARG:CB	2.19	0.54
2:B:253:LEU:HD23	2:B:253:LEU:C	2.28	0.54
1:C:32:ILE:CG1	1:C:288:PRO:HA	2.38	0.54
1:I:45:ILE:HG22	1:I:47:ILE:HG22	1.90	0.54
2:J:253:LEU:C	2:J:253:LEU:HD23	2.28	0.54
2:L:326:ILE:HG12	2:L:350:VAL:HG23	1.88	0.54
1:I:168:ASP:CG	1:M:12:LYS:HE3	2.28	0.54
1:M:45:ILE:HG22	1:M:47:ILE:HG22	1.90	0.54
2:P:274:ILE:HG22	2:P:275:SER:H	1.71	0.54
2:B:306:LEU:HB3	2:B:315:ALA:HB2	1.88	0.54
1:C:43:GLU:OE1	1:C:310:ARG:HD3	2.08	0.54
2:D:253:LEU:C	2:D:253:LEU:HD23	2.28	0.54
2:F:326:ILE:HG22	2:F:353:ARG:HG3	1.89	0.54
1:K:43:GLU:OE1	1:K:310:ARG:HD3	2.08	0.54
2:P:326:ILE:HG12	2:P:350:VAL:HG23	1.88	0.54
1:A:32:ILE:CG1	1:A:288:PRO:HA	2.38	0.54
1:C:314:ALA:CB	1:C:346:LEU:HD13	2.35	0.54
2:H:133:LEU:C	2:H:133:LEU:HD23	2.28	0.54
1:M:32:ILE:CG1	1:M:288:PRO:HA	2.38	0.54
1:E:45:ILE:HG22	1:E:47:ILE:HG22	1.90	0.54
2:J:326:ILE:HG12	2:J:350:VAL:HG23	1.88	0.54
2:P:323:LEU:N	2:P:326:ILE:HG23	2.23	0.54
1:A:43:GLU:OE1	1:A:310:ARG:HD3	2.08	0.54
1:C:45:ILE:HG22	1:C:47:ILE:HG22	1.90	0.54
1:G:32:ILE:CG1	1:G:288:PRO:HA	2.38	0.54
1:I:120:ILE:HG13	2:J:125:THR:HG21	1.90	0.54
2:J:323:LEU:N	2:J:326:ILE:HG23	2.23	0.54
2:L:133:LEU:HD23	2:L:133:LEU:C	2.28	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:93:LEU:HA	1:M:96:ALA:CB	2.35	0.54
1:O:32:ILE:CG1	1:O:288:PRO:HA	2.37	0.54
2:P:253:LEU:HD23	2:P:253:LEU:C	2.28	0.54
1:G:305:ASN:HA	1:G:308:ALA:CB	2.38	0.54
2:J:133:LEU:HD23	2:J:133:LEU:C	2.28	0.54
2:L:323:LEU:N	2:L:326:ILE:HG23	2.23	0.54
2:L:326:ILE:HG22	2:L:353:ARG:HG3	1.90	0.54
2:N:274:ILE:HG22	2:N:275:SER:H	1.71	0.54
2:N:326:ILE:HG22	2:N:353:ARG:HG3	1.89	0.54
1:A:45:ILE:HG22	1:A:47:ILE:HG22	1.90	0.54
2:D:273:LYS:HG3	2:D:274:ILE:HD12	1.90	0.54
2:D:326:ILE:HG12	2:D:350:VAL:HG23	1.88	0.54
2:H:253:LEU:C	2:H:253:LEU:HD23	2.28	0.54
1:K:72:ARG:NH1	1:O:171:LYS:NZ	2.55	0.54
2:L:253:LEU:C	2:L:253:LEU:HD23	2.28	0.54
1:A:314:ALA:CB	1:A:346:LEU:HD13	2.35	0.54
2:D:133:LEU:C	2:D:133:LEU:HD23	2.28	0.54
2:H:323:LEU:N	2:H:326:ILE:HG23	2.23	0.54
2:J:326:ILE:HG12	2:J:350:VAL:CG2	2.38	0.54
1:O:45:ILE:HG22	1:O:47:ILE:HG22	1.90	0.54
1:A:93:LEU:HA	1:A:96:ALA:CB	2.34	0.53
1:K:52:ILE:CD1	1:K:66:ALA:HA	2.37	0.53
2:F:133:LEU:HD23	2:F:133:LEU:C	2.28	0.53
2:F:323:LEU:N	2:F:326:ILE:HG23	2.23	0.53
2:N:64:ASN:C	2:N:66:LEU:H	2.12	0.53
2:B:133:LEU:HD23	2:B:133:LEU:C	2.28	0.53
2:D:323:LEU:N	2:D:326:ILE:HG23	2.23	0.53
1:E:43:GLU:OE1	1:E:310:ARG:HD3	2.08	0.53
2:F:273:LYS:HG3	2:F:274:ILE:HD12	1.91	0.53
1:G:314:ALA:CB	1:G:346:LEU:HD13	2.35	0.53
2:H:273:LYS:HG3	2:H:274:ILE:HD12	1.91	0.53
2:J:31:GLY:O	2:J:34:PRO:HD2	2.09	0.53
2:J:4:LYS:HE3	2:J:10:ARG:HH22	1.73	0.53
2:J:69:ILE:HD12	2:J:70:PRO:CD	2.34	0.53
2:L:273:LYS:HG3	2:L:274:ILE:HD12	1.90	0.53
2:N:323:LEU:N	2:N:326:ILE:HG23	2.23	0.53
1:A:144:VAL:HB	1:A:145:PRO:HD2	1.88	0.53
1:A:305:ASN:HA	1:A:308:ALA:CB	2.38	0.53
2:D:318:ILE:HA	2:D:322:VAL:CG2	2.38	0.53
2:F:253:LEU:C	2:F:253:LEU:HD23	2.28	0.53
2:H:31:GLY:O	2:H:34:PRO:HD2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:64:ASN:C	2:H:66:LEU:H	2.12	0.53
1:O:106:ASN:HB3	1:O:129:ARG:HG2	1.91	0.53
2:P:318:ILE:HA	2:P:322:VAL:CG2	2.38	0.53
2:P:326:ILE:HG22	2:P:353:ARG:HG3	1.89	0.53
2:B:273:LYS:HG3	2:B:274:ILE:HD12	1.90	0.53
2:F:4:LYS:HE3	2:F:10:ARG:HH22	1.74	0.53
2:F:31:GLY:O	2:F:34:PRO:HD2	2.09	0.53
1:G:45:ILE:HG22	1:G:47:ILE:HG22	1.90	0.53
2:J:147:HIS:CD2	1:K:151:LEU:CD1	2.91	0.53
1:K:32:ILE:CG1	1:K:288:PRO:HA	2.38	0.53
2:P:4:LYS:HE3	2:P:10:ARG:HH22	1.74	0.53
1:C:106:ASN:HB3	1:C:129:ARG:HG2	1.91	0.53
2:D:4:LYS:HE3	2:D:10:ARG:HH22	1.74	0.53
2:D:326:ILE:HG22	2:D:353:ARG:HG3	1.90	0.53
2:F:64:ASN:C	2:F:66:LEU:H	2.12	0.53
2:F:69:ILE:HD12	2:F:70:PRO:CD	2.34	0.53
1:G:119:ARG:HG2	2:H:125:THR:HG22	1.90	0.53
1:O:43:GLU:OE1	1:O:310:ARG:HD3	2.08	0.53
2:P:133:LEU:C	2:P:133:LEU:HD23	2.28	0.53
2:P:165:SER:HG	2:P:200:PHE:HD1	1.55	0.53
2:F:326:ILE:HG12	2:F:350:VAL:CG2	2.39	0.53
2:F:330:PRO:HA	2:F:333:ARG:HG3	1.91	0.53
2:H:318:ILE:HA	2:H:322:VAL:CG2	2.37	0.53
1:I:32:ILE:CG1	1:I:288:PRO:HA	2.38	0.53
1:M:305:ASN:HA	1:M:308:ALA:CB	2.38	0.53
2:N:326:ILE:HG12	2:N:350:VAL:CG2	2.38	0.53
2:P:64:ASN:C	2:P:66:LEU:H	2.11	0.53
2:B:61:ILE:HG22	2:B:62:PHE:N	2.19	0.53
2:D:274:ILE:HG22	2:D:275:SER:H	1.71	0.53
2:H:274:ILE:HG22	2:H:275:SER:H	1.71	0.53
2:L:31:GLY:O	2:L:34:PRO:HD2	2.09	0.53
1:M:43:GLU:OE1	1:M:310:ARG:HD3	2.08	0.53
2:N:133:LEU:C	2:N:133:LEU:HD23	2.28	0.53
1:O:305:ASN:HA	1:O:308:ALA:CB	2.38	0.53
2:P:31:GLY:O	2:P:34:PRO:HD2	2.09	0.53
2:B:323:LEU:N	2:B:326:ILE:HG23	2.23	0.53
2:B:64:ASN:C	2:B:66:LEU:H	2.12	0.53
1:C:206:TYR:N	1:C:207:PRO:HD3	2.24	0.53
2:F:97:ARG:CG	2:F:102:THR:HG23	2.39	0.53
1:G:206:TYR:N	1:G:207:PRO:HD3	2.24	0.53
1:K:45:ILE:HG22	1:K:47:ILE:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:31:GLY:O	2:N:34:PRO:HD2	2.09	0.53
2:N:69:ILE:HD12	2:N:70:PRO:CD	2.34	0.53
2:B:326:ILE:HG12	2:B:350:VAL:CG2	2.39	0.53
2:B:31:GLY:O	2:B:34:PRO:HD2	2.09	0.53
1:C:305:ASN:HA	1:C:308:ALA:CB	2.38	0.53
1:E:254:PRO:HG3	2:F:226:LEU:HD11	1.91	0.53
1:G:43:GLU:OE1	1:G:310:ARG:HD3	2.08	0.53
1:G:93:LEU:HA	1:G:96:ALA:CB	2.34	0.53
2:J:318:ILE:HA	2:J:322:VAL:CG2	2.38	0.53
2:N:330:PRO:HA	2:N:333:ARG:HG3	1.91	0.53
1:E:206:TYR:N	1:E:207:PRO:HD3	2.25	0.52
2:H:326:ILE:HG12	2:H:350:VAL:CG2	2.39	0.52
2:H:330:PRO:HA	2:H:333:ARG:HG3	1.91	0.52
2:J:64:ASN:C	2:J:66:LEU:H	2.12	0.52
2:L:64:ASN:C	2:L:66:LEU:H	2.12	0.52
1:A:287:ASN:H	4:A:2001:AMP:HN62	1.57	0.52
2:B:4:LYS:HE3	2:B:10:ARG:HH22	1.74	0.52
2:H:97:ARG:CG	2:H:102:THR:HG23	2.39	0.52
1:I:43:GLU:OE1	1:I:310:ARG:HD3	2.08	0.52
2:J:273:LYS:HG3	2:J:274:ILE:HD12	1.91	0.52
1:M:106:ASN:HB3	1:M:129:ARG:HG2	1.91	0.52
2:D:31:GLY:O	2:D:34:PRO:HD2	2.09	0.52
1:G:106:ASN:HB3	1:G:129:ARG:HG2	1.91	0.52
1:I:206:TYR:N	1:I:207:PRO:HD3	2.25	0.52
2:L:118:SER:OG	2:L:129:VAL:HG13	2.10	0.52
2:N:273:LYS:HG3	2:N:274:ILE:HD12	1.91	0.52
1:A:106:ASN:HB3	1:A:129:ARG:HG2	1.91	0.52
1:A:206:TYR:N	1:A:207:PRO:HD3	2.25	0.52
2:D:64:ASN:C	2:D:66:LEU:H	2.12	0.52
2:H:165:SER:HG	2:H:200:PHE:HD1	1.58	0.52
2:J:326:ILE:HG22	2:J:353:ARG:HG3	1.89	0.52
2:N:118:SER:OG	2:N:129:VAL:HG13	2.10	0.52
2:P:326:ILE:HG12	2:P:350:VAL:CG2	2.39	0.52
2:B:330:PRO:HA	2:B:333:ARG:HG3	1.91	0.52
2:D:118:SER:OG	2:D:129:VAL:HG13	2.10	0.52
2:H:69:ILE:HD12	2:H:70:PRO:CD	2.33	0.52
1:K:12:LYS:NZ	1:O:168:ASP:OD2	2.42	0.52
1:O:206:TYR:N	1:O:207:PRO:HD3	2.25	0.52
2:B:36:ILE:CG1	2:B:295:PRO:HA	2.40	0.52
2:D:330:PRO:HA	2:D:333:ARG:HG3	1.91	0.52
1:K:206:TYR:N	1:K:207:PRO:HD3	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:330:PRO:HA	2:L:333:ARG:HG3	1.91	0.52
2:N:4:LYS:HE3	2:N:10:ARG:HH22	1.74	0.52
1:E:305:ASN:HA	1:E:308:ALA:CB	2.38	0.52
2:L:318:ILE:HA	2:L:322:VAL:CG2	2.38	0.52
2:L:326:ILE:HG12	2:L:350:VAL:CG2	2.39	0.52
1:I:224:VAL:HG11	2:J:257:LEU:HG	1.91	0.52
2:J:97:ARG:CG	2:J:102:THR:HG23	2.39	0.52
2:B:118:SER:OG	2:B:129:VAL:HG13	2.10	0.52
2:D:326:ILE:HG12	2:D:350:VAL:CG2	2.39	0.52
2:P:36:ILE:CG1	2:P:295:PRO:HA	2.40	0.52
1:E:106:ASN:HB3	1:E:129:ARG:HG2	1.91	0.52
1:E:153:VAL:HG11	2:H:149:VAL:O	2.10	0.52
2:J:330:PRO:HA	2:J:333:ARG:HG3	1.91	0.52
2:L:274:ILE:HG22	2:L:275:SER:H	1.71	0.52
2:L:61:ILE:HG22	2:L:62:PHE:N	2.20	0.52
1:O:314:ALA:CB	1:O:346:LEU:HD13	2.35	0.52
1:A:195:ARG:NH1	1:A:195:ARG:CG	2.63	0.51
2:H:118:SER:OG	2:H:129:VAL:HG13	2.10	0.51
1:I:305:ASN:HA	1:I:308:ALA:CB	2.38	0.51
1:E:323:LYS:H	1:E:323:LYS:CE	2.23	0.51
4:I:2005:AMP:H4'	4:I:2005:AMP:O3P	2.10	0.51
1:K:193:LEU:HD11	1:K:197:ILE:HD11	1.92	0.51
1:K:305:ASN:HA	1:K:308:ALA:CB	2.38	0.51
1:M:206:TYR:N	1:M:207:PRO:HD3	2.25	0.51
2:P:330:PRO:HA	2:P:333:ARG:HG3	1.91	0.51
2:J:155:GLN:OE1	2:L:155:GLN:NE2	2.42	0.51
2:P:273:LYS:HG3	2:P:274:ILE:HD12	1.90	0.51
1:C:210:ASP:CG	2:P:42:LYS:HZ3	2.10	0.51
1:A:193:LEU:HD11	1:A:197:ILE:HD11	1.92	0.51
1:E:193:LEU:HD11	1:E:197:ILE:HD11	1.92	0.51
2:F:61:ILE:HG22	2:F:62:PHE:N	2.20	0.51
2:H:36:ILE:CG1	2:H:295:PRO:HA	2.40	0.51
2:L:36:ILE:CG1	2:L:295:PRO:HA	2.40	0.51
2:N:36:ILE:CG1	2:N:295:PRO:HA	2.40	0.51
2:P:118:SER:OG	2:P:129:VAL:HG13	2.10	0.51
1:C:33:THR:HG23	1:C:291:MET:HE2	1.93	0.51
1:I:106:ASN:HB3	1:I:129:ARG:HG2	1.91	0.51
1:M:193:LEU:HD11	1:M:197:ILE:HD11	1.92	0.51
1:C:119:ARG:CD	2:D:125:THR:O	2.58	0.51
1:C:254:PRO:HG3	2:D:226:LEU:HD11	1.91	0.51
2:F:323:LEU:N	2:F:323:LEU:HD23	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:277:GLY:HA2	4:I:2005:AMP:H5'2	1.93	0.51
2:J:118:SER:OG	2:J:129:VAL:HG13	2.10	0.51
2:F:36:ILE:CG1	2:F:295:PRO:HA	2.40	0.51
2:P:69:ILE:HD12	2:P:70:PRO:CD	2.34	0.51
1:C:7:GLU:HA	1:C:7:GLU:OE1	2.10	0.51
2:D:189:LYS:HD3	2:D:221:ILE:CD1	2.41	0.51
1:E:7:GLU:HA	1:E:7:GLU:OE1	2.10	0.51
1:K:106:ASN:HB3	1:K:129:ARG:HG2	1.91	0.51
1:O:323:LYS:CE	1:O:323:LYS:H	2.23	0.51
2:P:189:LYS:HD3	2:P:221:ILE:CD1	2.41	0.51
2:P:323:LEU:HD23	2:P:323:LEU:N	2.26	0.51
2:D:97:ARG:CG	2:D:102:THR:HG23	2.39	0.51
2:L:323:LEU:N	2:L:323:LEU:HD23	2.26	0.51
2:P:97:ARG:CG	2:P:102:THR:HG23	2.39	0.51
2:B:323:LEU:N	2:B:323:LEU:HD23	2.26	0.51
2:D:36:ILE:CG1	2:D:295:PRO:HA	2.40	0.51
2:F:118:SER:OG	2:F:129:VAL:HG13	2.10	0.51
1:K:72:ARG:NH2	1:O:171:LYS:HZ1	2.01	0.51
1:A:64:TYR:OH	2:P:63:VAL:HG11	2.11	0.50
2:B:97:ARG:CG	2:B:102:THR:HG23	2.39	0.50
1:E:245:ASN:HD22	2:F:222:ASP:HA	1.75	0.50
2:H:189:LYS:HD3	2:H:221:ILE:CD1	2.41	0.50
1:I:171:LYS:NZ	1:M:72:ARG:NH2	2.58	0.50
2:L:189:LYS:HD3	2:L:221:ILE:CD1	2.41	0.50
1:O:119:ARG:HD2	2:P:125:THR:O	2.12	0.50
1:A:33:THR:HG23	1:A:291:MET:HE2	1.93	0.50
2:B:97:ARG:O	2:B:98:SER:C	2.50	0.50
1:C:323:LYS:H	1:C:323:LYS:CE	2.23	0.50
2:F:189:LYS:HD3	2:F:221:ILE:CD1	2.41	0.50
1:I:249:ALA:CB	2:J:230:THR:HG23	2.40	0.50
1:I:323:LYS:H	1:I:323:LYS:CE	2.23	0.50
2:L:165:SER:HG	2:L:200:PHE:HD1	1.59	0.50
2:L:243:PRO:HD2	2:L:246:TYR:HD2	1.77	0.50
2:L:61:ILE:HD11	2:L:70:PRO:HA	1.94	0.50
2:L:97:ARG:O	2:L:98:SER:C	2.50	0.50
2:D:97:ARG:O	2:D:98:SER:C	2.50	0.50
1:K:254:PRO:HG3	2:L:226:LEU:HD11	1.93	0.50
2:N:97:ARG:O	2:N:98:SER:C	2.50	0.50
2:B:213:ASP:CA	1:I:122:ASP:OD2	2.58	0.50
2:H:323:LEU:N	2:H:323:LEU:HD23	2.26	0.50
2:H:61:ILE:HD11	2:H:70:PRO:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:189:LYS:HD3	2:J:221:ILE:CD1	2.41	0.50
2:J:323:LEU:N	2:J:323:LEU:HD23	2.26	0.50
2:J:69:ILE:HD11	2:J:73:ALA:HB3	1.94	0.50
2:L:349:ALA:O	2:L:353:ARG:HD3	2.12	0.50
2:N:334:THR:HB	2:N:336:ASP:OD1	2.12	0.50
1:O:193:LEU:HD11	1:O:197:ILE:HD11	1.92	0.50
2:D:243:PRO:HD2	2:D:246:TYR:HD2	1.77	0.50
2:D:69:ILE:HD11	2:D:73:ALA:HB3	1.94	0.50
1:E:283:GLN:HB3	1:E:285:VAL:HG13	1.94	0.50
2:F:61:ILE:HD11	2:F:70:PRO:HA	1.94	0.50
4:I:2005:AMP:O3P	2:J:223:ASN:ND2	2.45	0.50
2:J:36:ILE:CG1	2:J:295:PRO:HA	2.40	0.50
1:K:299:LEU:HB2	1:K:308:ALA:HB2	1.94	0.50
1:K:62:GLY:C	1:K:64:TYR:N	2.65	0.50
1:M:257:VAL:HG12	1:M:272:GLY:HA3	1.94	0.50
1:O:299:LEU:HB2	1:O:308:ALA:HB2	1.94	0.50
1:O:186:ILE:HD13	2:P:142:TYR:CD2	2.47	0.50
1:A:241:THR:OG1	3:A:1001:FLC:OA2	2.24	0.50
1:A:283:GLN:HB3	1:A:285:VAL:HG13	1.94	0.50
2:D:323:LEU:HD23	2:D:323:LEU:N	2.26	0.50
1:E:255:GLY:O	1:E:289:THR:HB	2.12	0.50
2:F:349:ALA:O	2:F:353:ARG:HD3	2.11	0.50
1:G:342:ILE:O	1:G:346:LEU:HB2	2.12	0.50
1:I:33:THR:HG23	1:I:291:MET:HE2	1.92	0.50
1:M:299:LEU:HB2	1:M:308:ALA:HB2	1.94	0.50
2:N:323:LEU:HD23	2:N:323:LEU:N	2.26	0.50
2:P:69:ILE:HD11	2:P:73:ALA:HB3	1.94	0.50
2:B:349:ALA:O	2:B:353:ARG:HD3	2.12	0.50
1:C:14:TYR:CE2	1:G:165:PHE:HD1	2.30	0.50
1:C:257:VAL:HG12	1:C:272:GLY:HA3	1.94	0.50
1:E:257:VAL:HG12	1:E:272:GLY:HA3	1.94	0.50
1:G:62:GLY:C	1:G:64:TYR:N	2.65	0.50
1:I:193:LEU:HD11	1:I:197:ILE:HD11	1.93	0.50
2:J:274:ILE:CG2	2:J:275:SER:N	2.75	0.50
2:J:71:ASP:N	2:J:72:PRO:HD2	2.27	0.50
3:K:1006:FLC:OG1	3:K:1006:FLC:OHB	2.30	0.50
1:K:283:GLN:HB3	1:K:285:VAL:HG13	1.94	0.50
2:L:69:ILE:HD11	2:L:73:ALA:HB3	1.94	0.50
1:M:7:GLU:OE1	1:M:7:GLU:HA	2.11	0.50
1:O:176:LYS:HE3	1:O:208:ASP:O	2.12	0.50
2:P:274:ILE:CG2	2:P:275:SER:N	2.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:334:THR:HB	2:P:336:ASP:OD1	2.12	0.50
2:P:61:ILE:HD11	2:P:70:PRO:HA	1.94	0.50
1:A:342:ILE:O	1:A:346:LEU:HB2	2.12	0.50
2:B:243:PRO:HD2	2:B:246:TYR:HD2	1.77	0.50
1:C:104:TYR:CE2	1:C:161:ARG:HG2	2.47	0.50
1:C:283:GLN:HB3	1:C:285:VAL:HG13	1.94	0.50
1:C:62:GLY:C	1:C:64:TYR:N	2.65	0.50
2:D:334:THR:HB	2:D:336:ASP:OD1	2.12	0.50
2:D:46:ALA:HB2	2:D:351:ILE:HD13	1.94	0.50
2:F:274:ILE:CG2	2:F:275:SER:N	2.75	0.50
2:J:349:ALA:O	2:J:353:ARG:HD3	2.11	0.50
1:M:176:LYS:HE3	1:M:208:ASP:O	2.12	0.50
2:N:349:ALA:O	2:N:353:ARG:HD3	2.12	0.50
1:O:104:TYR:CE2	1:O:161:ARG:HG2	2.47	0.50
2:P:243:PRO:HD2	2:P:246:TYR:HD2	1.77	0.50
2:B:189:LYS:HD3	2:B:221:ILE:CD1	2.41	0.50
2:F:134:ILE:HD13	2:F:239:VAL:HG13	1.94	0.50
2:F:334:THR:HB	2:F:336:ASP:OD1	2.12	0.50
1:G:193:LEU:HD11	1:G:197:ILE:HD11	1.92	0.50
2:H:243:PRO:HD2	2:H:246:TYR:HD2	1.77	0.50
1:K:255:GLY:O	1:K:289:THR:HB	2.12	0.50
2:L:134:ILE:HD13	2:L:239:VAL:HG13	1.94	0.50
2:P:97:ARG:O	2:P:98:SER:C	2.50	0.50
1:A:160:GLU:CD	1:E:8:ARG:HH21	2.15	0.49
1:A:257:VAL:HG12	1:A:272:GLY:HA3	1.94	0.49
1:C:176:LYS:HE3	1:C:208:ASP:O	2.12	0.49
2:D:71:ASP:N	2:D:72:PRO:HD2	2.27	0.49
1:G:255:GLY:O	1:G:289:THR:HB	2.12	0.49
1:G:151:LEU:CD2	2:H:157:ILE:HG12	2.34	0.49
2:J:97:ARG:O	2:J:98:SER:C	2.50	0.49
1:K:104:TYR:CE2	1:K:161:ARG:HG2	2.47	0.49
2:L:334:THR:HB	2:L:336:ASP:OD1	2.12	0.49
1:O:62:GLY:C	1:O:64:TYR:N	2.65	0.49
2:P:46:ALA:HB2	2:P:351:ILE:HD13	1.94	0.49
2:B:134:ILE:HD13	2:B:239:VAL:HG13	1.94	0.49
2:B:46:ALA:HB2	2:B:351:ILE:HD13	1.94	0.49
1:C:255:GLY:O	1:C:289:THR:HB	2.12	0.49
1:C:342:ILE:O	1:C:346:LEU:HB2	2.12	0.49
1:E:342:ILE:O	1:E:346:LEU:HB2	2.12	0.49
2:H:134:ILE:HD13	2:H:239:VAL:HG13	1.94	0.49
2:H:69:ILE:HD11	2:H:73:ALA:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:283:GLN:HB3	1:I:285:VAL:HG13	1.94	0.49
2:L:71:ASP:N	2:L:72:PRO:HD2	2.27	0.49
1:M:195:ARG:NH1	1:M:195:ARG:CG	2.63	0.49
2:N:101:LEU:HD23	2:N:104:ARG:NH1	2.27	0.49
2:N:97:ARG:CG	2:N:102:THR:HG23	2.39	0.49
2:N:69:ILE:HD11	2:N:73:ALA:HB3	1.94	0.49
1:O:283:GLN:HB3	1:O:285:VAL:HG13	1.94	0.49
2:P:349:ALA:O	2:P:353:ARG:HD3	2.12	0.49
1:A:186:ILE:HD13	2:B:142:TYR:CD2	2.47	0.49
2:B:69:ILE:HD11	2:B:73:ALA:HB3	1.94	0.49
1:C:274:ARG:HG2	3:C:1002:FLC:OB1	2.11	0.49
1:C:193:LEU:HD11	1:C:197:ILE:HD11	1.92	0.49
1:C:245:ASN:ND2	2:D:222:ASP:HA	2.27	0.49
1:C:22:LEU:HD11	1:C:33:THR:HG22	1.95	0.49
2:D:4:LYS:CE	2:D:10:ARG:HH22	2.25	0.49
1:G:257:VAL:HG12	1:G:272:GLY:HA3	1.94	0.49
1:G:33:THR:HG23	1:G:291:MET:HE2	1.95	0.49
1:G:299:LEU:HB2	1:G:308:ALA:HB2	1.94	0.49
1:K:176:LYS:HE3	1:K:208:ASP:O	2.12	0.49
1:M:22:LEU:HD11	1:M:33:THR:HG22	1.95	0.49
1:M:255:GLY:O	1:M:289:THR:HB	2.12	0.49
1:M:342:ILE:O	1:M:346:LEU:HB2	2.12	0.49
1:M:62:GLY:C	1:M:64:TYR:N	2.65	0.49
2:N:71:ASP:N	2:N:72:PRO:HD2	2.27	0.49
1:K:15:GLY:N	1:O:263:GLY:O	2.34	0.49
2:P:4:LYS:CE	2:P:10:ARG:HH22	2.25	0.49
1:A:119:ARG:HD2	2:B:125:THR:O	2.11	0.49
2:B:4:LYS:CE	2:B:10:ARG:HH22	2.25	0.49
2:B:71:ASP:N	2:B:72:PRO:HD2	2.27	0.49
2:D:136:GLU:OE2	2:D:138:THR:HB	2.13	0.49
1:G:176:LYS:HE3	1:G:208:ASP:O	2.12	0.49
2:H:97:ARG:O	2:H:98:SER:C	2.50	0.49
2:J:334:THR:HB	2:J:336:ASP:OD1	2.12	0.49
2:J:4:LYS:CE	2:J:10:ARG:HH22	2.25	0.49
1:K:241:THR:OG1	3:K:1006:FLC:OA2	2.16	0.49
1:I:165:PHE:HA	1:M:14:TYR:OH	2.12	0.49
1:O:67:VAL:HG13	1:O:101:LEU:HD21	1.94	0.49
1:A:62:GLY:C	1:A:64:TYR:N	2.65	0.49
2:B:334:THR:HB	2:B:336:ASP:OD1	2.12	0.49
1:C:67:VAL:HG13	1:C:101:LEU:HD21	1.94	0.49
2:D:101:LEU:HD23	2:D:104:ARG:NH1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:62:GLY:C	1:E:64:TYR:N	2.65	0.49
2:F:97:ARG:O	2:F:98:SER:C	2.50	0.49
1:G:249:ALA:CB	2:H:230:THR:HG23	2.42	0.49
2:L:97:ARG:CG	2:L:102:THR:HG23	2.39	0.49
2:N:169:ILE:HD13	2:N:204:ALA:HB2	1.95	0.49
1:O:342:ILE:O	1:O:346:LEU:HB2	2.12	0.49
1:A:22:LEU:HD11	1:A:33:THR:HG22	1.95	0.49
2:B:318:ILE:HA	2:B:322:VAL:CG2	2.38	0.49
2:D:61:ILE:HD11	2:D:70:PRO:HA	1.94	0.49
2:F:243:PRO:HD2	2:F:246:TYR:HD2	1.77	0.49
2:F:46:ALA:HB2	2:F:351:ILE:HD13	1.94	0.49
2:H:349:ALA:O	2:H:353:ARG:HD3	2.11	0.49
1:I:104:TYR:CE2	1:I:161:ARG:HG2	2.47	0.49
1:I:255:GLY:O	1:I:289:THR:HB	2.12	0.49
2:J:243:PRO:HD2	2:J:246:TYR:HD2	1.77	0.49
1:K:257:VAL:HG12	1:K:272:GLY:HA3	1.94	0.49
2:N:189:LYS:HD3	2:N:221:ILE:CD1	2.41	0.49
1:A:104:TYR:CE2	1:A:161:ARG:HG2	2.47	0.49
2:D:349:ALA:O	2:D:353:ARG:HD3	2.12	0.49
1:E:67:VAL:HG13	1:E:101:LEU:HD21	1.94	0.49
2:H:274:ILE:CG2	2:H:275:SER:N	2.75	0.49
2:H:334:THR:HB	2:H:336:ASP:OD1	2.12	0.49
1:I:67:VAL:HG13	1:I:101:LEU:HD21	1.94	0.49
2:J:101:LEU:HD23	2:J:104:ARG:NH1	2.27	0.49
1:K:22:LEU:HD11	1:K:33:THR:HG22	1.95	0.49
2:L:46:ALA:HB2	2:L:351:ILE:HD13	1.94	0.49
2:N:46:ALA:HB2	2:N:351:ILE:HD13	1.94	0.49
1:A:176:LYS:HE3	1:A:208:ASP:O	2.12	0.49
1:A:255:GLY:O	1:A:289:THR:HB	2.12	0.49
2:H:103:LEU:HD12	2:H:103:LEU:HA	1.68	0.49
2:H:136:GLU:OE2	2:H:138:THR:HB	2.13	0.49
2:H:71:ASP:N	2:H:72:PRO:HD2	2.27	0.49
1:I:151:LEU:HD12	2:L:147:HIS:CD2	2.48	0.49
1:I:257:VAL:HG12	1:I:272:GLY:HA3	1.94	0.49
1:I:299:LEU:HB2	1:I:308:ALA:HB2	1.94	0.49
1:K:342:ILE:O	1:K:346:LEU:HB2	2.12	0.49
1:M:104:TYR:CE2	1:M:161:ARG:HG2	2.47	0.49
2:N:134:ILE:HD13	2:N:239:VAL:HG13	1.94	0.49
2:P:101:LEU:HD23	2:P:104:ARG:NH1	2.27	0.49
2:P:71:ASP:N	2:P:72:PRO:HD2	2.27	0.49
1:A:195:ARG:HB3	1:A:195:ARG:HH11	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:299:LEU:HB2	1:C:308:ALA:HB2	1.94	0.49
2:D:134:ILE:HD13	2:D:239:VAL:HG13	1.94	0.49
2:F:71:ASP:N	2:F:72:PRO:HD2	2.27	0.49
2:J:149:VAL:HG21	2:L:149:VAL:HG21	1.94	0.49
2:J:61:ILE:HD11	2:J:70:PRO:HA	1.94	0.49
1:M:283:GLN:HB3	1:M:285:VAL:HG13	1.94	0.49
2:N:4:LYS:CE	2:N:10:ARG:HH22	2.25	0.49
2:P:136:GLU:OE2	2:P:138:THR:HB	2.13	0.49
2:B:274:ILE:CG2	2:B:275:SER:N	2.75	0.49
2:B:61:ILE:HD11	2:B:70:PRO:HA	1.94	0.49
2:D:274:ILE:CG2	2:D:275:SER:N	2.75	0.49
2:H:101:LEU:HD23	2:H:104:ARG:NH1	2.27	0.49
2:J:33:GLY:O	2:J:36:ILE:HG22	2.13	0.49
2:N:243:PRO:HD2	2:N:246:TYR:HD2	1.77	0.49
2:N:61:ILE:HD11	2:N:70:PRO:HA	1.94	0.49
1:O:257:VAL:HG12	1:O:272:GLY:HA3	1.94	0.49
1:A:323:LYS:CE	1:A:323:LYS:H	2.23	0.48
1:A:64:TYR:CE1	2:P:63:VAL:HG11	2.41	0.48
2:D:169:ILE:HD13	2:D:204:ALA:HB2	1.95	0.48
1:E:292:ILE:O	1:E:296:THR:HG23	2.13	0.48
2:F:101:LEU:HD23	2:F:104:ARG:NH1	2.27	0.48
2:F:318:ILE:HA	2:F:322:VAL:CG2	2.38	0.48
2:F:33:GLY:O	2:F:36:ILE:HG22	2.13	0.48
1:I:146:GLY:O	2:J:161:THR:HA	2.13	0.48
1:I:195:ARG:HB3	1:I:195:ARG:HH11	1.78	0.48
1:I:176:LYS:HE3	1:I:208:ASP:O	2.12	0.48
2:J:136:GLU:OE2	2:J:138:THR:HB	2.13	0.48
2:J:337:LEU:O	2:J:338:ALA:HB3	2.13	0.48
2:J:153:VAL:HG11	2:L:149:VAL:CG2	2.43	0.48
1:M:104:TYR:CZ	1:M:161:ARG:HG2	2.49	0.48
1:M:292:ILE:O	1:M:296:THR:HG23	2.13	0.48
2:B:189:LYS:HE2	2:B:192:ILE:HD12	1.95	0.48
2:B:33:GLY:O	2:B:36:ILE:HG22	2.13	0.48
1:C:10:LEU:HB3	1:C:11:PRO:CD	2.43	0.48
1:A:164:ARG:HH22	1:E:8:ARG:HH21	1.61	0.48
2:F:4:LYS:CE	2:F:10:ARG:HH22	2.25	0.48
1:K:67:VAL:HG13	1:K:101:LEU:HD21	1.94	0.48
1:M:67:VAL:HG13	1:M:101:LEU:HD21	1.94	0.48
2:N:136:GLU:OE2	2:N:138:THR:HB	2.13	0.48
3:O:1008:FLC:OG1	3:O:1008:FLC:OHB	2.30	0.48
1:O:104:TYR:CZ	1:O:161:ARG:HG2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:189:LYS:HE2	2:D:192:ILE:HD12	1.95	0.48
1:E:299:LEU:HB2	1:E:308:ALA:HB2	1.94	0.48
2:F:69:ILE:HD11	2:F:73:ALA:HB3	1.94	0.48
2:H:189:LYS:HE2	2:H:192:ILE:HD12	1.95	0.48
2:H:46:ALA:HB2	2:H:351:ILE:HD13	1.94	0.48
2:J:46:ALA:HB2	2:J:351:ILE:HD13	1.94	0.48
1:M:10:LEU:HB3	1:M:11:PRO:CD	2.43	0.48
1:O:133:GLU:OE1	1:O:158:LYS:HD2	2.13	0.48
1:O:255:GLY:O	1:O:289:THR:HB	2.12	0.48
1:A:175:ARG:NH1	1:A:231:ASP:OD1	2.47	0.48
2:B:101:LEU:HD23	2:B:104:ARG:NH1	2.27	0.48
2:B:189:LYS:CG	2:B:192:ILE:HD13	2.44	0.48
2:B:169:ILE:HD12	2:B:203:VAL:HG12	1.96	0.48
1:C:199:THR:HA	1:C:211:VAL:HG11	1.96	0.48
1:C:292:ILE:O	1:C:296:THR:HG23	2.13	0.48
1:E:104:TYR:CZ	1:E:161:ARG:HG2	2.49	0.48
1:E:10:LEU:HB3	1:E:11:PRO:CD	2.43	0.48
1:E:104:TYR:CE2	1:E:161:ARG:HG2	2.47	0.48
1:G:67:VAL:HG13	1:G:101:LEU:HD21	1.94	0.48
1:G:104:TYR:CE2	1:G:161:ARG:HG2	2.47	0.48
1:I:199:THR:HA	1:I:211:VAL:HG11	1.96	0.48
2:J:189:LYS:CG	2:J:192:ILE:HD13	2.44	0.48
2:L:337:LEU:O	2:L:338:ALA:HB3	2.14	0.48
2:L:33:GLY:O	2:L:36:ILE:HG22	2.13	0.48
2:N:274:ILE:CG2	2:N:275:SER:N	2.75	0.48
1:O:292:ILE:O	1:O:296:THR:HG23	2.14	0.48
2:F:136:GLU:OE2	2:F:138:THR:HB	2.13	0.48
2:F:189:LYS:HE2	2:F:192:ILE:HD12	1.95	0.48
2:F:169:ILE:HD13	2:F:204:ALA:HB2	1.95	0.48
1:G:292:ILE:O	1:G:296:THR:HG23	2.13	0.48
1:G:22:LEU:HD11	1:G:33:THR:HG22	1.95	0.48
1:I:133:GLU:HG2	1:I:134:GLY:H	1.78	0.48
1:I:175:ARG:NH1	1:I:231:ASP:OD1	2.47	0.48
2:J:134:ILE:HD13	2:J:239:VAL:HG13	1.94	0.48
2:J:319:GLN:O	2:J:321:ALA:O	2.32	0.48
2:L:101:LEU:HD23	2:L:104:ARG:NH1	2.27	0.48
2:L:189:LYS:HE2	2:L:192:ILE:HD12	1.95	0.48
2:N:189:LYS:HE2	2:N:192:ILE:HD12	1.95	0.48
2:N:318:ILE:HA	2:N:322:VAL:CG2	2.37	0.48
2:N:319:GLN:O	2:N:321:ALA:O	2.32	0.48
2:P:169:ILE:HD13	2:P:204:ALA:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:GLY:C	1:A:29:GLY:H	2.17	0.48
2:B:319:GLN:O	2:B:324:SER:HB2	2.14	0.48
1:G:104:TYR:CZ	1:G:161:ARG:HG2	2.49	0.48
1:M:19:THR:O	1:M:73:ASN:HB3	2.14	0.48
2:N:165:SER:HG	2:N:200:PHE:HD1	1.60	0.48
2:N:337:LEU:O	2:N:338:ALA:HB3	2.14	0.48
2:N:33:GLY:O	2:N:36:ILE:HG22	2.13	0.48
1:O:22:LEU:HD11	1:O:33:THR:HG22	1.95	0.48
2:P:134:ILE:HD13	2:P:239:VAL:HG13	1.94	0.48
2:P:319:GLN:O	2:P:324:SER:HB2	2.14	0.48
1:A:133:GLU:HG2	1:A:134:GLY:H	1.79	0.48
1:A:133:GLU:OE1	1:A:158:LYS:HD2	2.13	0.48
1:C:175:ARG:NH1	1:C:231:ASP:OD1	2.47	0.48
1:C:19:THR:O	1:C:73:ASN:HB3	2.14	0.48
2:D:189:LYS:CG	2:D:192:ILE:HD13	2.44	0.48
1:G:283:GLN:HB3	1:G:285:VAL:HG13	1.94	0.48
1:I:104:TYR:CZ	1:I:161:ARG:HG2	2.49	0.48
1:I:342:ILE:O	1:I:346:LEU:HB2	2.12	0.48
2:J:189:LYS:HE2	2:J:192:ILE:HD12	1.95	0.48
1:K:133:GLU:OE1	1:K:158:LYS:HD2	2.13	0.48
1:K:224:VAL:HG11	2:L:257:LEU:HG	1.96	0.48
1:K:323:LYS:CE	1:K:323:LYS:H	2.23	0.48
1:M:133:GLU:HG2	1:M:134:GLY:H	1.78	0.48
2:N:189:LYS:CG	2:N:192:ILE:HD13	2.44	0.48
2:P:189:LYS:HE2	2:P:192:ILE:HD12	1.95	0.48
1:A:104:TYR:CZ	1:A:161:ARG:HG2	2.49	0.48
1:A:199:THR:HA	1:A:211:VAL:HG11	1.96	0.48
1:A:292:ILE:O	1:A:296:THR:HG23	2.13	0.48
1:A:299:LEU:HB2	1:A:308:ALA:HB2	1.94	0.48
2:B:228:VAL:HG12	2:B:257:LEU:HD11	1.96	0.48
2:B:181:ARG:HH11	2:B:238:ALA:H	1.62	0.48
2:D:319:GLN:O	2:D:324:SER:HB2	2.14	0.48
1:E:176:LYS:HE3	1:E:208:ASP:O	2.12	0.48
1:E:199:THR:HA	1:E:211:VAL:HG11	1.96	0.48
1:E:27:GLY:C	1:E:29:GLY:H	2.17	0.48
2:F:169:ILE:HD12	2:F:203:VAL:HG12	1.96	0.48
2:H:169:ILE:HD13	2:H:204:ALA:HB2	1.95	0.48
1:I:133:GLU:OE1	1:I:158:LYS:HD2	2.13	0.48
1:I:292:ILE:O	1:I:296:THR:HG23	2.13	0.48
1:K:133:GLU:HG2	1:K:134:GLY:H	1.78	0.48
1:K:195:ARG:HB3	1:K:195:ARG:HH11	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:27:GLY:C	1:K:29:GLY:H	2.17	0.48
2:L:319:GLN:O	2:L:321:ALA:O	2.32	0.48
1:M:33:THR:HG23	1:M:291:MET:HE2	1.96	0.48
2:N:169:ILE:HD12	2:N:203:VAL:HG12	1.96	0.48
1:O:33:THR:HG23	1:O:291:MET:HE2	1.94	0.48
2:P:319:GLN:O	2:P:321:ALA:O	2.32	0.48
2:B:69:ILE:HD12	2:B:70:PRO:CD	2.34	0.48
1:C:133:GLU:HG2	1:C:134:GLY:H	1.78	0.48
1:G:133:GLU:OE1	1:G:158:LYS:HD2	2.13	0.48
2:H:169:ILE:HD12	2:H:203:VAL:HG12	1.96	0.48
2:H:228:VAL:HG12	2:H:257:LEU:CD1	2.44	0.48
2:J:253:LEU:O	2:J:253:LEU:HD23	2.14	0.48
1:K:104:TYR:CZ	1:K:161:ARG:HG2	2.49	0.48
2:L:169:ILE:HD13	2:L:204:ALA:HB2	1.95	0.48
2:L:228:VAL:HG12	2:L:257:LEU:CD1	2.44	0.48
1:O:199:THR:HA	1:O:211:VAL:HG11	1.96	0.48
2:P:189:LYS:CG	2:P:192:ILE:HD13	2.44	0.48
2:P:169:ILE:HD12	2:P:203:VAL:HG12	1.96	0.48
2:P:253:LEU:O	2:P:253:LEU:HD23	2.14	0.48
2:P:326:ILE:C	2:P:328:SER:H	2.17	0.48
1:A:67:VAL:HG13	1:A:101:LEU:HD21	1.94	0.48
2:B:169:ILE:HD13	2:B:204:ALA:HB2	1.95	0.48
2:B:295:PRO:O	2:B:299:LEU:HB2	2.14	0.48
2:B:319:GLN:O	2:B:321:ALA:O	2.32	0.48
2:D:228:VAL:HG12	2:D:257:LEU:HD11	1.96	0.48
1:E:224:VAL:HG11	2:F:257:LEU:HG	1.95	0.48
1:E:175:ARG:NH1	1:E:231:ASP:OD1	2.47	0.48
2:F:149:VAL:O	1:G:153:VAL:HG11	2.13	0.48
2:F:228:VAL:HG12	2:F:257:LEU:CD1	2.44	0.48
1:G:133:GLU:HG2	1:G:134:GLY:H	1.78	0.48
1:G:195:ARG:HB3	1:G:195:ARG:HH11	1.78	0.48
2:H:319:GLN:O	2:H:321:ALA:O	2.32	0.48
1:I:22:LEU:HD11	1:I:33:THR:HG22	1.95	0.48
2:J:228:VAL:HG12	2:J:257:LEU:CD1	2.44	0.48
1:K:205:GLU:HB2	1:K:206:TYR:CD1	2.49	0.48
2:L:136:GLU:OE2	2:L:138:THR:HB	2.13	0.48
2:L:189:LYS:CG	2:L:192:ILE:HD13	2.44	0.48
1:M:205:GLU:HB2	1:M:206:TYR:CD1	2.49	0.48
2:N:228:VAL:HG12	2:N:257:LEU:CD1	2.44	0.48
2:N:181:ARG:HH11	2:N:238:ALA:H	1.62	0.48
2:N:319:GLN:O	2:N:324:SER:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:326:ILE:C	2:N:328:SER:H	2.17	0.48
1:K:8:ARG:NH2	1:O:164:ARG:HH22	2.12	0.48
1:O:205:GLU:HB2	1:O:206:TYR:CD1	2.49	0.48
1:O:27:GLY:C	1:O:29:GLY:H	2.17	0.48
1:C:27:GLY:C	1:C:29:GLY:H	2.17	0.47
1:I:19:THR:O	1:I:73:ASN:HB3	2.14	0.47
1:I:62:GLY:C	1:I:64:TYR:N	2.65	0.47
2:J:169:ILE:HD13	2:J:204:ALA:HB2	1.95	0.47
1:K:183:LYS:HE2	2:L:142:TYR:OH	2.14	0.47
1:M:27:GLY:C	1:M:29:GLY:H	2.17	0.47
2:N:295:PRO:O	2:N:299:LEU:HB2	2.14	0.47
1:O:133:GLU:HG2	1:O:134:GLY:H	1.78	0.47
2:P:228:VAL:HG12	2:P:257:LEU:CD1	2.44	0.47
2:P:337:LEU:O	2:P:338:ALA:HB3	2.14	0.47
2:D:319:GLN:O	2:D:321:ALA:O	2.32	0.47
1:E:133:GLU:OE1	1:E:158:LYS:HD2	2.13	0.47
2:F:326:ILE:C	2:F:328:SER:H	2.17	0.47
1:K:292:ILE:O	1:K:296:THR:HG23	2.13	0.47
1:K:8:ARG:NH2	1:O:160:GLU:OE1	2.47	0.47
2:L:319:GLN:O	2:L:324:SER:HB2	2.14	0.47
1:M:133:GLU:OE1	1:M:158:LYS:HD2	2.13	0.47
1:M:199:THR:HA	1:M:211:VAL:HG11	1.96	0.47
1:O:19:THR:O	1:O:73:ASN:HB3	2.14	0.47
1:C:104:TYR:CZ	1:C:161:ARG:HG2	2.49	0.47
1:C:205:GLU:HB2	1:C:206:TYR:CD1	2.49	0.47
2:D:253:LEU:HD23	2:D:253:LEU:O	2.14	0.47
2:F:253:LEU:HD23	2:F:253:LEU:O	2.14	0.47
2:H:319:GLN:O	2:H:324:SER:HB2	2.14	0.47
2:H:326:ILE:C	2:H:328:SER:H	2.17	0.47
2:J:26:PHE:O	2:J:27:ILE:HB	2.15	0.47
1:K:10:LEU:HB3	1:K:11:PRO:CD	2.43	0.47
1:K:175:ARG:NH1	1:K:231:ASP:OD1	2.47	0.47
1:K:33:THR:HG23	1:K:291:MET:HE2	1.95	0.47
1:M:195:ARG:HH11	1:M:195:ARG:HB3	1.78	0.47
1:M:175:ARG:NH1	1:M:231:ASP:OD1	2.47	0.47
1:O:175:ARG:NH1	1:O:231:ASP:OD1	2.47	0.47
2:D:209:LYS:HE3	2:D:209:LYS:HB3	1.36	0.47
2:F:189:LYS:O	2:F:189:LYS:HG3	2.15	0.47
2:F:26:PHE:O	2:F:27:ILE:HB	2.15	0.47
2:H:33:GLY:O	2:H:36:ILE:HG22	2.13	0.47
2:L:326:ILE:C	2:L:328:SER:H	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:255:GLY:CA	4:M:2007:AMP:N1	2.77	0.47
2:P:33:GLY:O	2:P:36:ILE:HG22	2.13	0.47
2:B:136:GLU:OE2	2:B:138:THR:HB	2.13	0.47
1:C:133:GLU:OE1	1:C:158:LYS:HD2	2.13	0.47
2:D:33:GLY:O	2:D:36:ILE:HG22	2.13	0.47
1:E:133:GLU:HG2	1:E:134:GLY:H	1.78	0.47
1:E:205:GLU:HB2	1:E:206:TYR:CD1	2.49	0.47
1:E:12:LYS:HB2	1:E:73:ASN:HA	1.97	0.47
1:G:183:LYS:HE2	2:H:142:TYR:OH	2.13	0.47
1:G:199:THR:HA	1:G:211:VAL:HG11	1.96	0.47
1:G:323:LYS:CE	1:G:323:LYS:H	2.23	0.47
2:H:189:LYS:CG	2:H:192:ILE:HD13	2.44	0.47
2:N:228:VAL:HG12	2:N:257:LEU:HD11	1.96	0.47
2:N:26:PHE:O	2:N:27:ILE:HB	2.15	0.47
2:N:322:VAL:O	2:N:323:LEU:C	2.53	0.47
2:P:228:VAL:HG12	2:P:257:LEU:HD11	1.96	0.47
1:A:64:TYR:CE2	2:P:63:VAL:CG2	2.97	0.47
2:F:189:LYS:CG	2:F:192:ILE:HD13	2.44	0.47
2:F:228:VAL:HG12	2:F:257:LEU:HD11	1.96	0.47
2:H:322:VAL:O	2:H:323:LEU:C	2.53	0.47
2:H:337:LEU:O	2:H:338:ALA:HB3	2.14	0.47
2:J:326:ILE:C	2:J:328:SER:H	2.17	0.47
1:K:19:THR:O	1:K:73:ASN:HB3	2.14	0.47
1:K:29:GLY:O	1:K:33:THR:OG1	2.33	0.47
2:P:322:VAL:O	2:P:323:LEU:C	2.53	0.47
2:B:26:PHE:O	2:B:27:ILE:HB	2.15	0.47
2:B:341:ALA:HB1	2:B:345:SER:OG	2.15	0.47
2:D:228:VAL:HG12	2:D:257:LEU:CD1	2.44	0.47
2:D:326:ILE:C	2:D:328:SER:H	2.17	0.47
1:E:151:LEU:HD11	2:H:147:HIS:CD2	2.50	0.47
1:G:205:GLU:HB2	1:G:206:TYR:CD1	2.49	0.47
1:G:175:ARG:NH1	1:G:231:ASP:OD1	2.47	0.47
1:G:245:ASN:ND2	2:H:222:ASP:HA	2.30	0.47
2:H:189:LYS:HG3	2:H:189:LYS:O	2.15	0.47
1:I:153:VAL:HG21	2:L:149:VAL:O	2.14	0.47
2:L:181:ARG:HH11	2:L:238:ALA:H	1.62	0.47
2:L:274:ILE:CG2	2:L:275:SER:N	2.75	0.47
2:N:253:LEU:HD23	2:N:253:LEU:O	2.14	0.47
1:O:195:ARG:HH11	1:O:195:ARG:HB3	1.78	0.47
2:P:26:PHE:O	2:P:27:ILE:HB	2.15	0.47
1:A:19:THR:O	1:A:73:ASN:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:322:VAL:O	2:B:323:LEU:C	2.53	0.47
2:B:326:ILE:C	2:B:328:SER:H	2.17	0.47
2:B:337:LEU:O	2:B:338:ALA:HB3	2.14	0.47
1:C:29:GLY:O	1:C:33:THR:OG1	2.33	0.47
1:E:195:ARG:HH11	1:E:195:ARG:HB3	1.79	0.47
1:E:22:LEU:HD11	1:E:33:THR:HG22	1.95	0.47
2:F:319:GLN:O	2:F:321:ALA:O	2.32	0.47
2:F:337:LEU:O	2:F:338:ALA:HB3	2.14	0.47
2:H:295:PRO:O	2:H:299:LEU:HB2	2.14	0.47
2:H:341:ALA:HB1	2:H:345:SER:OG	2.15	0.47
2:J:169:ILE:HD12	2:J:203:VAL:HG12	1.96	0.47
2:L:26:PHE:O	2:L:27:ILE:HB	2.15	0.47
1:K:8:ARG:NH2	1:O:160:GLU:CD	2.68	0.47
1:A:293:LEU:HD23	1:A:293:LEU:HA	1.62	0.47
2:B:253:LEU:HD23	2:B:253:LEU:O	2.14	0.47
2:B:26:PHE:HE2	2:B:37:SER:OG	1.98	0.47
3:C:1002:FLC:OG1	3:C:1002:FLC:OHB	2.30	0.47
1:C:195:ARG:HH11	1:C:195:ARG:HB3	1.78	0.47
1:E:60:LYS:O	1:E:60:LYS:HG2	2.15	0.47
2:F:295:PRO:O	2:F:299:LEU:HB2	2.14	0.47
2:J:322:VAL:O	2:J:323:LEU:C	2.53	0.47
1:M:47:ILE:HD11	1:M:49:TRP:CE3	2.50	0.47
2:P:110:PHE:CE1	2:P:167:ARG:HG3	2.50	0.47
1:A:47:ILE:HD11	1:A:49:TRP:CE3	2.50	0.47
2:B:189:LYS:HG3	2:B:189:LYS:O	2.15	0.47
1:C:101:LEU:HB2	1:C:103:ILE:HG13	1.97	0.47
1:C:47:ILE:HD11	1:C:49:TRP:CE3	2.50	0.47
2:F:341:ALA:HB1	2:F:345:SER:OG	2.15	0.47
2:H:253:LEU:O	2:H:253:LEU:HD23	2.14	0.47
1:I:205:GLU:HB2	1:I:206:TYR:CD1	2.49	0.47
2:J:189:LYS:O	2:J:189:LYS:HG3	2.15	0.47
2:N:110:PHE:CE1	2:N:167:ARG:HG3	2.50	0.47
2:N:318:ILE:HG22	2:N:323:LEU:HD21	1.97	0.47
1:O:101:LEU:HB2	1:O:103:ILE:HG13	1.97	0.47
1:O:293:LEU:HD23	1:O:293:LEU:HA	1.62	0.47
2:P:181:ARG:HH11	2:P:238:ALA:H	1.62	0.47
2:D:341:ALA:HB1	2:D:345:SER:OG	2.15	0.47
1:G:27:GLY:C	1:G:29:GLY:H	2.17	0.47
1:I:27:GLY:C	1:I:29:GLY:H	2.17	0.47
2:J:147:HIS:CD2	1:K:151:LEU:HD11	2.50	0.47
2:J:319:GLN:O	2:J:324:SER:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:199:THR:HA	1:K:211:VAL:HG11	1.96	0.47
2:L:110:PHE:CE1	2:L:167:ARG:HG3	2.50	0.47
2:D:285:PRO:HD3	2:P:286:ASP:HB2	1.97	0.47
2:B:228:VAL:HG12	2:B:257:LEU:CD1	2.44	0.46
2:B:265:THR:HA	2:B:266:PRO:HD3	1.64	0.46
2:D:169:ILE:HD12	2:D:203:VAL:HG12	1.96	0.46
2:D:189:LYS:O	2:D:189:LYS:HG3	2.15	0.46
2:D:26:PHE:O	2:D:27:ILE:HB	2.15	0.46
2:F:319:GLN:O	2:F:324:SER:HB2	2.14	0.46
2:J:110:PHE:CE1	2:J:167:ARG:HG3	2.50	0.46
2:J:181:ARG:HH11	2:J:238:ALA:H	1.62	0.46
2:J:341:ALA:HB1	2:J:345:SER:OG	2.15	0.46
1:K:60:LYS:O	1:K:60:LYS:HG2	2.15	0.46
2:L:253:LEU:O	2:L:253:LEU:HD23	2.14	0.46
2:L:228:VAL:HG12	2:L:257:LEU:HD11	1.96	0.46
2:L:318:ILE:HG22	2:L:323:LEU:HD21	1.97	0.46
1:O:288:PRO:HG3	1:O:335:THR:HG23	1.97	0.46
1:A:288:PRO:HG3	1:A:335:THR:HG23	1.97	0.46
2:D:295:PRO:O	2:D:299:LEU:HB2	2.14	0.46
2:D:337:LEU:O	2:D:338:ALA:HB3	2.14	0.46
1:E:19:THR:O	1:E:73:ASN:HB3	2.14	0.46
1:G:60:LYS:O	1:G:60:LYS:HG2	2.15	0.46
1:G:221:MET:HG3	2:H:256:GLY:CA	2.45	0.46
2:H:26:PHE:HE2	2:H:37:SER:OG	1.98	0.46
2:L:169:ILE:HD12	2:L:203:VAL:HG12	1.96	0.46
2:L:26:PHE:HE2	2:L:37:SER:OG	1.98	0.46
1:O:47:ILE:HD11	1:O:49:TRP:CE3	2.50	0.46
2:P:189:LYS:HG3	2:P:189:LYS:O	2.15	0.46
2:H:26:PHE:O	2:H:27:ILE:HB	2.15	0.46
2:H:318:ILE:HG22	2:H:323:LEU:HD21	1.97	0.46
1:I:60:LYS:HG2	1:I:60:LYS:O	2.14	0.46
2:J:224:SER:O	2:J:228:VAL:HG23	2.15	0.46
2:L:224:SER:O	2:L:228:VAL:HG23	2.16	0.46
1:M:288:PRO:HG3	1:M:335:THR:HG23	1.97	0.46
2:N:224:SER:O	2:N:228:VAL:HG23	2.15	0.46
2:N:26:PHE:HE2	2:N:37:SER:OG	1.98	0.46
2:N:341:ALA:HB1	2:N:345:SER:OG	2.15	0.46
1:O:147:VAL:HG13	2:P:161:THR:HG22	1.98	0.46
1:A:101:LEU:HB2	1:A:103:ILE:HG13	1.97	0.46
2:D:322:VAL:O	2:D:323:LEU:C	2.53	0.46
1:A:266:TYR:O	1:E:15:GLY:HA2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:47:ILE:HD11	1:E:49:TRP:CE3	2.50	0.46
1:G:101:LEU:HB2	1:G:103:ILE:HG13	1.97	0.46
2:H:110:PHE:CE1	2:H:167:ARG:HG3	2.50	0.46
1:I:101:LEU:HB2	1:I:103:ILE:HG13	1.97	0.46
1:A:205:GLU:HB2	1:A:206:TYR:CD1	2.49	0.46
1:A:29:GLY:O	1:A:33:THR:OG1	2.33	0.46
1:A:60:LYS:HG2	1:A:60:LYS:O	2.15	0.46
3:E:1003:FLC:OG1	3:E:1003:FLC:OHB	2.30	0.46
1:A:206:TYR:CE2	1:E:72:ARG:HD3	2.51	0.46
2:F:209:LYS:HE3	2:F:209:LYS:HB3	1.36	0.46
3:G:1004:FLC:OHB	3:G:1004:FLC:OG1	2.30	0.46
1:G:19:THR:O	1:G:73:ASN:HB3	2.14	0.46
2:H:228:VAL:HG12	2:H:257:LEU:HD11	1.96	0.46
2:J:295:PRO:O	2:J:299:LEU:HB2	2.14	0.46
1:K:101:LEU:HB2	1:K:103:ILE:HG13	1.97	0.46
2:L:295:PRO:O	2:L:299:LEU:HB2	2.14	0.46
1:M:275:HIS:HB3	4:M:2007:AMP:O3P	2.14	0.46
2:P:295:PRO:O	2:P:299:LEU:HB2	2.14	0.46
2:B:110:PHE:CE1	2:B:167:ARG:HG3	2.50	0.46
1:C:119:ARG:HG2	2:D:125:THR:CG2	2.33	0.46
2:D:224:SER:O	2:D:228:VAL:HG23	2.15	0.46
1:E:29:GLY:O	1:E:33:THR:OG1	2.33	0.46
2:F:181:ARG:HH11	2:F:238:ALA:H	1.62	0.46
2:F:322:VAL:O	2:F:323:LEU:C	2.53	0.46
2:H:186:VAL:CG2	2:H:216:LEU:HD11	2.46	0.46
2:J:228:VAL:HG12	2:J:257:LEU:HD11	1.96	0.46
1:M:60:LYS:HG2	1:M:60:LYS:O	2.15	0.46
2:F:321:ALA:O	2:F:322:VAL:O	2.34	0.46
2:F:318:ILE:HG22	2:F:323:LEU:HD21	1.97	0.46
1:I:47:ILE:HD11	1:I:49:TRP:CE3	2.50	0.46
2:J:26:PHE:HE2	2:J:37:SER:OG	1.98	0.46
2:J:44:PHE:O	2:J:49:VAL:HG22	2.16	0.46
1:K:232:VAL:O	1:K:233:LEU:HD23	2.16	0.46
2:L:189:LYS:HG3	2:L:189:LYS:O	2.15	0.46
2:L:44:PHE:O	2:L:49:VAL:HG22	2.16	0.46
1:M:119:ARG:HD2	2:N:125:THR:O	2.15	0.46
1:O:232:VAL:O	1:O:233:LEU:HD23	2.16	0.46
2:P:209:LYS:HE3	2:P:209:LYS:HB3	1.36	0.46
1:A:147:VAL:HG13	2:B:161:THR:HG22	1.98	0.46
2:B:224:SER:O	2:B:228:VAL:HG23	2.16	0.46
2:D:110:PHE:CE1	2:D:167:ARG:HG3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:187:MET:HE1	2:F:156:SER:HB3	1.97	0.46
2:F:110:PHE:CE1	2:F:167:ARG:HG3	2.50	0.46
2:F:224:SER:O	2:F:228:VAL:HG23	2.15	0.46
1:I:232:VAL:O	1:I:233:LEU:HD23	2.16	0.46
1:K:119:ARG:HD2	2:L:125:THR:O	2.15	0.46
1:K:12:LYS:HB2	1:K:73:ASN:HA	1.97	0.46
2:L:186:VAL:CG2	2:L:216:LEU:HD11	2.46	0.46
2:N:186:VAL:CG2	2:N:216:LEU:HD11	2.46	0.46
2:P:26:PHE:HE2	2:P:37:SER:OG	1.98	0.46
2:P:318:ILE:HG22	2:P:323:LEU:HD21	1.97	0.46
1:E:101:LEU:HB2	1:E:103:ILE:HG13	1.97	0.46
2:F:26:PHE:HE2	2:F:37:SER:OG	1.98	0.46
1:G:29:GLY:O	1:G:33:THR:OG1	2.33	0.46
1:I:233:LEU:HD12	1:I:243:LEU:HD13	1.98	0.46
2:J:273:LYS:HE3	2:J:274:ILE:HD11	1.98	0.46
1:K:47:ILE:HD11	1:K:49:TRP:CE3	2.50	0.46
2:L:322:VAL:O	2:L:323:LEU:C	2.53	0.46
3:M:1007:FLC:OG1	3:M:1007:FLC:OHB	2.30	0.46
1:M:12:LYS:HB2	1:M:73:ASN:HA	1.97	0.46
2:N:44:PHE:O	2:N:49:VAL:HG22	2.16	0.46
1:O:60:LYS:O	1:O:60:LYS:HG2	2.15	0.46
2:P:341:ALA:HB1	2:P:345:SER:OG	2.15	0.46
2:P:44:PHE:O	2:P:49:VAL:HG22	2.16	0.46
2:B:321:ALA:O	2:B:322:VAL:O	2.34	0.46
1:G:288:PRO:HG3	1:G:335:THR:HG23	1.97	0.46
1:G:47:ILE:HD11	1:G:49:TRP:CE3	2.50	0.46
2:H:273:LYS:HE3	2:H:274:ILE:HD11	1.98	0.46
2:J:306:LEU:HA	2:J:309:MET:HE2	1.98	0.46
2:L:341:ALA:HB1	2:L:345:SER:OG	2.15	0.46
2:P:224:SER:O	2:P:228:VAL:HG23	2.15	0.46
1:C:232:VAL:O	1:C:233:LEU:HD23	2.16	0.45
1:C:342:ILE:H	1:C:342:ILE:HG12	1.62	0.45
2:D:189:LYS:HG2	2:D:192:ILE:HD13	1.98	0.45
2:F:265:THR:HA	2:F:266:PRO:HD3	1.63	0.45
2:H:44:PHE:O	2:H:49:VAL:HG22	2.16	0.45
1:I:29:GLY:O	1:I:33:THR:OG1	2.33	0.45
1:K:233:LEU:HD12	1:K:243:LEU:HD13	1.98	0.45
2:L:273:LYS:HE3	2:L:274:ILE:HD11	1.98	0.45
1:M:232:VAL:O	1:M:233:LEU:HD23	2.16	0.45
2:P:321:ALA:O	2:P:322:VAL:O	2.34	0.45
2:D:44:PHE:O	2:D:49:VAL:HG22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:62:PHE:CE1	2:D:67:THR:HG22	2.52	0.45
1:G:146:GLY:O	2:H:161:THR:HA	2.16	0.45
2:H:181:ARG:HH11	2:H:238:ALA:H	1.62	0.45
1:K:146:GLY:O	2:L:161:THR:HA	2.16	0.45
2:L:209:LYS:HB3	2:L:209:LYS:HE3	1.36	0.45
2:L:326:ILE:HG21	2:L:350:VAL:HG22	1.98	0.45
1:M:101:LEU:HB2	1:M:103:ILE:HG13	1.97	0.45
1:M:83:THR:HG1	3:M:1007:FLC:CGC	2.16	0.45
2:N:273:LYS:HE3	2:N:274:ILE:HD11	1.98	0.45
1:O:179:THR:HB	1:O:233:LEU:HD22	1.98	0.45
2:B:189:LYS:HE2	2:B:192:ILE:CD1	2.47	0.45
2:B:189:LYS:HG2	2:B:192:ILE:HD13	1.98	0.45
2:D:181:ARG:HH11	2:D:238:ALA:H	1.62	0.45
1:G:251:ILE:HD11	1:G:257:VAL:HG22	1.99	0.45
2:L:24:VAL:HG11	2:L:53:TRP:HZ3	1.82	0.45
2:L:287:ILE:O	2:L:287:ILE:HG23	2.17	0.45
1:M:179:THR:HB	1:M:233:LEU:HD22	1.98	0.45
2:N:189:LYS:O	2:N:189:LYS:HG3	2.15	0.45
2:P:265:THR:O	2:P:280:VAL:HG22	2.17	0.45
2:P:59:SER:HA	2:P:60:PRO:HD3	1.86	0.45
2:B:318:ILE:HG22	2:B:323:LEU:HD21	1.97	0.45
1:C:120:ILE:HA	1:C:121:PRO:HD3	1.76	0.45
2:D:273:LYS:HE3	2:D:274:ILE:HD11	1.98	0.45
1:E:115:GLY:CA	1:E:320:ALA:HA	2.47	0.45
1:E:232:VAL:O	1:E:233:LEU:HD23	2.16	0.45
2:F:189:LYS:HE2	2:F:192:ILE:CD1	2.47	0.45
2:H:326:ILE:HG21	2:H:350:VAL:HG22	1.98	0.45
1:K:120:ILE:HG13	2:L:125:THR:HG21	1.97	0.45
1:K:249:ALA:CB	2:L:230:THR:HG23	2.47	0.45
1:M:323:LYS:CE	1:M:323:LYS:H	2.23	0.45
2:N:189:LYS:HE2	2:N:192:ILE:CD1	2.47	0.45
2:P:189:LYS:HE2	2:P:192:ILE:CD1	2.47	0.45
1:A:233:LEU:HD12	1:A:243:LEU:HD13	1.98	0.45
1:A:32:ILE:HG13	1:A:288:PRO:HA	1.99	0.45
1:C:340:ASN:O	1:C:343:ILE:HG13	2.17	0.45
2:D:189:LYS:HE2	2:D:192:ILE:CD1	2.47	0.45
1:E:288:PRO:HG3	1:E:335:THR:HG23	1.98	0.45
2:F:155:GLN:OE1	2:H:155:GLN:NE2	2.46	0.45
2:F:265:THR:O	2:F:280:VAL:HG22	2.17	0.45
2:F:44:PHE:O	2:F:49:VAL:HG22	2.16	0.45
1:I:245:ASN:ND2	2:J:222:ASP:HA	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:288:PRO:HG3	1:I:335:THR:HG23	1.98	0.45
2:J:43:ILE:HD12	2:J:299:LEU:HD21	1.99	0.45
1:K:179:THR:HB	1:K:233:LEU:HD22	1.98	0.45
2:N:321:ALA:O	2:N:322:VAL:O	2.34	0.45
1:O:233:LEU:HD12	1:O:243:LEU:HD13	1.98	0.45
1:A:340:ASN:O	1:A:343:ILE:HG13	2.17	0.45
2:B:265:THR:O	2:B:280:VAL:HG22	2.17	0.45
2:B:44:PHE:O	2:B:49:VAL:HG22	2.16	0.45
1:C:12:LYS:HB2	1:C:73:ASN:HA	1.97	0.45
1:C:120:ILE:HG13	2:D:125:THR:HG21	1.99	0.45
2:D:146:GLU:HB3	2:D:156:SER:HA	1.99	0.45
2:D:321:ALA:O	2:D:322:VAL:O	2.34	0.45
1:E:224:VAL:HG21	2:F:253:LEU:HD21	1.99	0.45
2:F:186:VAL:CG2	2:F:216:LEU:HD11	2.46	0.45
2:H:265:THR:HA	2:H:266:PRO:HD3	1.63	0.45
1:I:151:LEU:HD13	2:J:155:GLN:NE2	2.31	0.45
2:L:321:ALA:O	2:L:322:VAL:O	2.34	0.45
1:M:340:ASN:O	1:M:343:ILE:HG13	2.17	0.45
2:N:189:LYS:HG2	2:N:192:ILE:HD13	1.98	0.45
2:N:287:ILE:O	2:N:287:ILE:HG23	2.17	0.45
3:A:1001:FLC:OG1	3:A:1001:FLC:OHB	2.30	0.45
1:A:232:VAL:O	1:A:233:LEU:HD23	2.16	0.45
1:A:136:PHE:CD1	1:A:237:SER:HB2	2.52	0.45
2:B:62:PHE:CE1	2:B:67:THR:HG22	2.52	0.45
1:C:32:ILE:HG13	1:C:288:PRO:HA	1.99	0.45
2:D:26:PHE:HE2	2:D:37:SER:OG	1.98	0.45
2:D:318:ILE:HG22	2:D:323:LEU:HD21	1.97	0.45
1:E:179:THR:HB	1:E:233:LEU:HD22	1.98	0.45
2:F:43:ILE:HD12	2:F:299:LEU:HD21	1.99	0.45
1:G:249:ALA:HB1	2:H:230:THR:HG23	1.98	0.45
2:H:321:ALA:O	2:H:322:VAL:O	2.34	0.45
2:J:321:ALA:O	2:J:322:VAL:O	2.34	0.45
1:K:136:PHE:CD1	1:K:237:SER:HB2	2.52	0.45
1:K:115:GLY:CA	1:K:320:ALA:HA	2.47	0.45
2:L:30:ASP:OD2	2:L:88:LEU:HA	2.17	0.45
1:M:29:GLY:O	1:M:33:THR:OG1	2.33	0.45
2:N:326:ILE:HG21	2:N:350:VAL:HG22	1.98	0.45
2:P:186:VAL:CG2	2:P:216:LEU:HD11	2.46	0.45
2:P:43:ILE:HD12	2:P:299:LEU:HD21	1.99	0.45
1:C:179:THR:HB	1:C:233:LEU:HD22	1.98	0.45
1:C:251:ILE:HD11	1:C:257:VAL:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:288:PRO:HG3	1:C:335:THR:HG23	1.97	0.45
1:C:187:MET:CE	2:D:156:SER:HB3	2.46	0.45
2:D:326:ILE:HG21	2:D:350:VAL:HG22	1.99	0.45
2:F:189:LYS:HG2	2:F:192:ILE:HD13	1.98	0.45
1:G:340:ASN:O	1:G:343:ILE:HG13	2.17	0.45
2:H:62:PHE:CE1	2:H:67:THR:HG22	2.52	0.45
3:I:1005:FLC:OG1	3:I:1005:FLC:OHB	2.30	0.45
1:I:136:PHE:CD1	1:I:237:SER:HB2	2.52	0.45
1:I:340:ASN:O	1:I:343:ILE:HG13	2.17	0.45
1:K:288:PRO:HG3	1:K:335:THR:HG23	1.97	0.45
1:K:340:ASN:O	1:K:343:ILE:HG13	2.17	0.45
2:L:146:GLU:HB3	2:L:156:SER:HA	1.99	0.45
2:L:189:LYS:HG2	2:L:192:ILE:HD13	1.98	0.45
2:L:62:PHE:CE1	2:L:67:THR:HG22	2.51	0.45
2:P:24:VAL:HG11	2:P:53:TRP:HZ3	1.82	0.45
2:P:62:PHE:CE1	2:P:67:THR:HG22	2.51	0.45
2:B:294:ASN:HA	2:B:295:PRO:HD2	1.74	0.45
2:F:287:ILE:HG23	2:F:287:ILE:O	2.17	0.45
1:G:232:VAL:O	1:G:233:LEU:HD23	2.16	0.45
1:G:283:GLN:CB	1:G:285:VAL:HG13	2.47	0.45
2:J:318:ILE:HG22	2:J:323:LEU:HD21	1.97	0.45
2:J:62:PHE:CE1	2:J:67:THR:HG22	2.52	0.45
1:M:283:GLN:CB	1:M:285:VAL:HG13	2.47	0.45
1:O:251:ILE:HD11	1:O:257:VAL:HG22	1.99	0.45
1:O:283:GLN:CB	1:O:285:VAL:HG13	2.47	0.45
1:O:32:ILE:HG13	1:O:288:PRO:HA	1.99	0.45
2:P:265:THR:HA	2:P:266:PRO:HD3	1.63	0.45
2:P:30:ASP:OD2	2:P:88:LEU:HA	2.17	0.45
1:A:115:GLY:CA	1:A:320:ALA:HA	2.47	0.45
2:B:146:GLU:HB3	2:B:156:SER:HA	1.99	0.45
2:B:149:VAL:O	2:B:150:CYS:HB3	2.17	0.45
2:B:30:ASP:OD2	2:B:88:LEU:HA	2.17	0.45
2:D:30:ASP:OD2	2:D:88:LEU:HA	2.17	0.45
2:D:97:ARG:HG3	2:D:102:THR:CG2	2.44	0.45
1:E:233:LEU:HD12	1:E:243:LEU:HD13	1.98	0.45
1:G:115:GLY:CA	1:G:320:ALA:HA	2.47	0.45
1:I:283:GLN:CB	1:I:285:VAL:HG13	2.47	0.45
1:I:115:GLY:CA	1:I:320:ALA:HA	2.47	0.45
2:J:189:LYS:HG2	2:J:192:ILE:HD13	1.98	0.45
1:M:32:ILE:HG13	1:M:288:PRO:HA	1.99	0.45
1:O:29:GLY:O	1:O:33:THR:OG1	2.33	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:273:LYS:HE3	2:P:274:ILE:HD11	1.98	0.45
2:B:12:THR:HB	2:B:81:LEU:CD1	2.47	0.44
1:C:283:GLN:CB	1:C:285:VAL:HG13	2.47	0.44
1:C:83:THR:HA	1:C:84:PRO:HD3	1.80	0.44
2:F:24:VAL:HG11	2:F:53:TRP:HZ3	1.82	0.44
2:F:62:PHE:CE1	2:F:67:THR:HG22	2.52	0.44
1:G:233:LEU:HD12	1:G:243:LEU:HD13	1.98	0.44
2:H:224:SER:O	2:H:228:VAL:HG23	2.15	0.44
2:H:265:THR:O	2:H:280:VAL:HG22	2.17	0.44
1:I:160:GLU:CD	1:M:8:ARG:HH21	2.20	0.44
2:J:8:ILE:HG21	2:J:171:TYR:HB2	2.00	0.44
2:J:265:THR:O	2:J:280:VAL:HG22	2.17	0.44
1:K:245:ASN:ND2	2:L:222:ASP:HA	2.31	0.44
1:M:251:ILE:HD11	1:M:257:VAL:HG22	1.99	0.44
2:N:62:PHE:CE1	2:N:67:THR:HG22	2.52	0.44
1:A:179:THR:HB	1:A:233:LEU:HD22	1.98	0.44
1:A:287:ASN:HA	1:A:288:PRO:HD3	1.85	0.44
1:C:136:PHE:CD1	1:C:237:SER:HB2	2.52	0.44
1:E:340:ASN:O	1:E:343:ILE:HG13	2.17	0.44
2:F:30:ASP:OD2	2:F:88:LEU:HA	2.17	0.44
2:H:189:LYS:HG2	2:H:192:ILE:HD13	1.98	0.44
2:J:146:GLU:HB3	2:J:156:SER:HA	1.99	0.44
2:J:30:ASP:OD2	2:J:88:LEU:HA	2.17	0.44
1:K:120:ILE:HA	1:K:121:PRO:HD3	1.76	0.44
1:K:251:ILE:HD11	1:K:257:VAL:HG22	1.99	0.44
1:K:283:GLN:CB	1:K:285:VAL:HG13	2.47	0.44
2:L:8:ILE:HG21	2:L:171:TYR:HB2	1.99	0.44
2:L:265:THR:O	2:L:280:VAL:HG22	2.17	0.44
2:N:43:ILE:HD12	2:N:299:LEU:HD21	1.99	0.44
2:D:285:PRO:HB2	2:P:286:ASP:OD2	2.03	0.44
2:B:24:VAL:HG11	2:B:53:TRP:HZ3	1.82	0.44
2:B:326:ILE:HG21	2:B:350:VAL:HG22	1.98	0.44
2:D:287:ILE:HG23	2:D:287:ILE:O	2.16	0.44
2:F:273:LYS:HE3	2:F:274:ILE:HD11	1.98	0.44
2:F:326:ILE:HG21	2:F:350:VAL:HG22	1.99	0.44
2:H:12:THR:HB	2:H:81:LEU:CD1	2.47	0.44
2:H:189:LYS:HE2	2:H:192:ILE:CD1	2.47	0.44
1:I:32:ILE:HG13	1:I:288:PRO:HA	1.99	0.44
2:J:149:VAL:O	2:J:150:CYS:HB3	2.18	0.44
1:K:158:LYS:HG2	1:K:161:ARG:NH2	2.33	0.44
1:K:32:ILE:HG13	1:K:288:PRO:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:136:PHE:CD1	1:M:237:SER:HB2	2.52	0.44
1:M:115:GLY:CA	1:M:320:ALA:HA	2.47	0.44
1:M:186:ILE:HD13	2:N:142:TYR:CD2	2.52	0.44
2:B:181:ARG:HD3	2:B:238:ALA:H	1.83	0.44
2:D:149:VAL:O	2:D:150:CYS:HB3	2.17	0.44
1:G:179:THR:HB	1:G:233:LEU:HD22	1.98	0.44
2:H:146:GLU:HB3	2:H:156:SER:HA	1.99	0.44
2:H:181:ARG:HD3	2:H:238:ALA:H	1.83	0.44
2:H:43:ILE:HD12	2:H:299:LEU:HD21	1.99	0.44
1:I:92:SER:CB	3:I:1005:FLC:OG2	2.65	0.44
2:L:189:LYS:HE2	2:L:192:ILE:CD1	2.47	0.44
2:N:30:ASP:OD2	2:N:88:LEU:HA	2.17	0.44
1:O:120:ILE:HA	1:O:121:PRO:HD3	1.76	0.44
1:O:136:PHE:CD1	1:O:237:SER:HB2	2.52	0.44
2:P:181:ARG:HD3	2:P:238:ALA:H	1.83	0.44
1:C:60:LYS:O	1:C:60:LYS:HG2	2.15	0.44
2:D:183:ARG:O	2:D:238:ALA:O	2.36	0.44
2:D:265:THR:O	2:D:280:VAL:HG22	2.17	0.44
2:J:183:ARG:O	2:J:238:ALA:O	2.36	0.44
2:L:149:VAL:O	2:L:150:CYS:HB3	2.18	0.44
1:M:14:TYR:O	1:M:15:GLY:C	2.56	0.44
1:M:245:ASN:ND2	2:N:222:ASP:HA	2.32	0.44
1:M:43:GLU:OE1	1:M:310:ARG:NH1	2.51	0.44
2:N:149:VAL:O	2:N:150:CYS:HB3	2.17	0.44
2:P:183:ARG:O	2:P:238:ALA:O	2.36	0.44
2:P:294:ASN:HA	2:P:295:PRO:HD2	1.73	0.44
2:B:183:ARG:NH1	2:B:237:ASP:OD2	2.51	0.44
2:B:273:LYS:HE3	2:B:274:ILE:HD11	1.98	0.44
2:B:25:SER:HB3	2:B:56:CYS:SG	2.58	0.44
2:D:8:ILE:HG21	2:D:171:TYR:HB2	2.00	0.44
2:D:24:VAL:HG11	2:D:53:TRP:HZ3	1.82	0.44
2:D:25:SER:HB3	2:D:56:CYS:SG	2.58	0.44
1:E:136:PHE:CD1	1:E:237:SER:HB2	2.52	0.44
1:E:283:GLN:CB	1:E:285:VAL:HG13	2.47	0.44
2:F:146:GLU:HB3	2:F:156:SER:HA	1.99	0.44
2:H:287:ILE:O	2:H:287:ILE:HG23	2.17	0.44
2:H:8:ILE:HG21	2:H:171:TYR:HB2	1.99	0.44
1:I:171:LYS:NZ	1:M:72:ARG:HH22	2.16	0.44
2:N:322:VAL:C	2:N:326:ILE:HG23	2.38	0.44
1:A:274:ARG:HG2	3:A:1001:FLC:OB1	2.18	0.44
1:A:251:ILE:HD11	1:A:257:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:8:ILE:HG21	2:B:171:TYR:HB2	2.00	0.44
2:B:186:VAL:CG2	2:B:216:LEU:HD11	2.46	0.44
1:C:233:LEU:HD12	1:C:243:LEU:HD13	1.98	0.44
1:E:251:ILE:HD11	1:E:257:VAL:HG22	1.99	0.44
2:F:183:ARG:O	2:F:238:ALA:O	2.36	0.44
3:G:1004:FLC:OA1	3:G:1004:FLC:OB1	2.36	0.44
1:G:101:LEU:HD12	1:G:103:ILE:HD11	1.99	0.44
1:G:158:LYS:HG2	1:G:161:ARG:NH2	2.33	0.44
1:G:136:PHE:CD1	1:G:237:SER:HB2	2.52	0.44
2:H:30:ASP:OD2	2:H:88:LEU:HA	2.17	0.44
2:J:183:ARG:NH1	2:J:237:ASP:OD2	2.50	0.44
2:J:24:VAL:HG11	2:J:53:TRP:HZ3	1.82	0.44
1:K:336:THR:HG22	1:K:337:ASP:N	2.33	0.44
1:K:43:GLU:OE1	1:K:310:ARG:NH1	2.51	0.44
2:N:265:THR:O	2:N:280:VAL:HG22	2.17	0.44
1:O:101:LEU:HD12	1:O:103:ILE:HD11	1.99	0.44
1:O:340:ASN:O	1:O:343:ILE:HG13	2.17	0.44
2:P:189:LYS:HG2	2:P:192:ILE:HD13	1.98	0.44
2:P:287:ILE:O	2:P:287:ILE:HG23	2.17	0.44
2:P:8:ILE:HG21	2:P:171:TYR:HB2	2.00	0.44
1:A:283:GLN:CB	1:A:285:VAL:HG13	2.47	0.44
2:B:287:ILE:HG23	2:B:287:ILE:O	2.17	0.44
2:D:64:ASN:O	2:D:66:LEU:N	2.48	0.44
2:F:348:GLU:HG2	2:F:348:GLU:H	1.62	0.44
1:I:241:THR:OG1	3:I:1005:FLC:OA2	2.31	0.44
3:M:1007:FLC:OB1	3:M:1007:FLC:OA1	2.36	0.44
3:O:1008:FLC:OB1	3:O:1008:FLC:OA1	2.36	0.44
1:A:158:LYS:HG2	1:A:161:ARG:NH2	2.33	0.44
2:B:142:TYR:N	2:B:142:TYR:CD1	2.86	0.44
2:D:142:TYR:N	2:D:142:TYR:CD1	2.86	0.44
1:E:101:LEU:HD12	1:E:103:ILE:HD11	1.99	0.44
2:F:149:VAL:O	2:F:150:CYS:HB3	2.18	0.44
2:F:8:ILE:HG21	2:F:171:TYR:HB2	2.00	0.44
2:F:183:ARG:NH1	2:F:237:ASP:OD2	2.51	0.44
2:F:25:SER:HB3	2:F:56:CYS:SG	2.58	0.44
1:G:43:GLU:OE1	1:G:310:ARG:NH1	2.51	0.44
2:H:149:VAL:O	2:H:150:CYS:HB3	2.17	0.44
2:H:24:VAL:HG11	2:H:53:TRP:HZ3	1.82	0.44
2:H:64:ASN:O	2:H:66:LEU:N	2.48	0.44
1:I:43:GLU:OE1	1:I:310:ARG:NH1	2.51	0.44
2:J:149:VAL:O	1:K:153:VAL:HG21	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:189:LYS:HE2	2:J:192:ILE:CD1	2.47	0.44
1:M:233:LEU:HD12	1:M:243:LEU:HD13	1.98	0.44
1:O:83:THR:HA	1:O:84:PRO:HD3	1.80	0.44
2:P:149:VAL:O	2:P:150:CYS:HB3	2.18	0.44
2:P:25:SER:HB3	2:P:56:CYS:SG	2.58	0.44
1:A:266:TYR:O	1:E:15:GLY:CA	2.66	0.43
1:A:342:ILE:HG12	1:A:342:ILE:H	1.62	0.43
1:A:43:GLU:OE1	1:A:310:ARG:NH1	2.51	0.43
2:D:306:LEU:HA	2:D:309:MET:HE2	1.99	0.43
1:E:32:ILE:HG13	1:E:288:PRO:HA	1.99	0.43
2:H:322:VAL:C	2:H:326:ILE:HG23	2.39	0.43
2:J:103:LEU:HA	2:J:103:LEU:HD12	1.69	0.43
2:J:186:VAL:CG2	2:J:216:LEU:HD11	2.46	0.43
2:J:322:VAL:C	2:J:326:ILE:HG23	2.39	0.43
2:J:25:SER:HB3	2:J:56:CYS:SG	2.58	0.43
2:L:306:LEU:HA	2:L:309:MET:HE2	1.99	0.43
2:L:322:VAL:C	2:L:326:ILE:HG23	2.39	0.43
2:N:146:GLU:HB3	2:N:156:SER:HA	1.99	0.43
1:C:158:LYS:HG2	1:C:161:ARG:NH2	2.33	0.43
1:I:195:ARG:O	1:I:199:THR:HG23	2.19	0.43
1:I:147:VAL:HG13	2:J:159:LEU:HD11	1.99	0.43
2:L:25:SER:HB3	2:L:56:CYS:SG	2.58	0.43
2:L:43:ILE:HD12	2:L:299:LEU:HD21	1.99	0.43
1:M:101:LEU:HD12	1:M:103:ILE:HD11	1.99	0.43
2:N:24:VAL:HG11	2:N:53:TRP:HZ3	1.82	0.43
2:P:322:VAL:C	2:P:326:ILE:HG23	2.39	0.43
1:A:101:LEU:HD12	1:A:103:ILE:HD11	1.99	0.43
2:D:43:ILE:HD12	2:D:299:LEU:HD21	1.99	0.43
2:H:221:ILE:HD12	2:H:221:ILE:N	2.34	0.43
2:H:299:LEU:HD12	2:H:299:LEU:HA	1.86	0.43
1:I:179:THR:HB	1:I:233:LEU:HD22	1.98	0.43
2:J:287:ILE:HG23	2:J:287:ILE:O	2.17	0.43
2:J:326:ILE:HD12	2:J:332:ASN:HB3	2.01	0.43
2:J:47:ALA:HB2	2:J:354:LEU:HD11	2.01	0.43
2:L:103:LEU:HD12	2:L:103:LEU:HA	1.68	0.43
2:L:274:ILE:CG2	2:L:275:SER:H	2.31	0.43
2:N:274:ILE:CG2	2:N:275:SER:H	2.31	0.43
2:B:209:LYS:HE3	2:B:209:LYS:HB3	1.36	0.43
2:B:348:GLU:H	2:B:348:GLU:HG2	1.62	0.43
3:C:1002:FLC:OB1	3:C:1002:FLC:OA1	2.36	0.43
1:E:277:GLY:HA3	4:E:2003:AMP:C8	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:221:ILE:N	2:F:221:ILE:HD12	2.33	0.43
2:F:322:VAL:C	2:F:326:ILE:HG23	2.38	0.43
2:H:142:TYR:CD1	2:H:142:TYR:N	2.86	0.43
2:H:25:SER:HB3	2:H:56:CYS:SG	2.58	0.43
2:H:306:LEU:HA	2:H:309:MET:HE2	2.00	0.43
2:H:326:ILE:HD12	2:H:332:ASN:HB3	2.01	0.43
1:I:251:ILE:HD11	1:I:257:VAL:HG22	1.99	0.43
2:J:326:ILE:HG21	2:J:350:VAL:HG22	1.98	0.43
1:K:277:GLY:N	4:K:2006:AMP:C8	2.87	0.43
1:M:120:ILE:HA	1:M:121:PRO:HD3	1.76	0.43
2:N:265:THR:HA	2:N:266:PRO:HD3	1.64	0.43
1:K:8:ARG:HH21	1:O:164:ARG:HH22	1.66	0.43
1:O:195:ARG:O	1:O:199:THR:HG23	2.19	0.43
2:P:146:GLU:HB3	2:P:156:SER:HA	1.99	0.43
2:B:183:ARG:O	2:B:238:ALA:O	2.36	0.43
1:C:101:LEU:HD12	1:C:103:ILE:HD11	1.99	0.43
1:C:195:ARG:O	1:C:199:THR:HG23	2.18	0.43
2:D:186:VAL:CG2	2:D:216:LEU:HD11	2.46	0.43
2:F:326:ILE:HD12	2:F:332:ASN:HB3	2.01	0.43
2:H:77:ILE:O	2:H:80:ASN:O	2.37	0.43
2:J:348:GLU:HG2	2:J:348:GLU:H	1.63	0.43
2:L:142:TYR:N	2:L:142:TYR:CD1	2.86	0.43
2:L:183:ARG:O	2:L:238:ALA:O	2.36	0.43
2:L:326:ILE:HD12	2:L:332:ASN:HB3	2.01	0.43
1:M:336:THR:HG22	1:M:337:ASP:N	2.33	0.43
2:N:64:ASN:O	2:N:66:LEU:N	2.48	0.43
2:P:183:ARG:NH1	2:P:237:ASP:OD2	2.50	0.43
1:C:115:GLY:CA	1:C:320:ALA:HA	2.47	0.43
1:G:32:ILE:HG13	1:G:288:PRO:HA	1.99	0.43
1:G:336:THR:HG22	1:G:337:ASP:N	2.33	0.43
1:I:336:THR:HG22	1:I:337:ASP:N	2.33	0.43
3:K:1006:FLC:OA1	3:K:1006:FLC:OB1	2.36	0.43
1:M:158:LYS:HG2	1:M:161:ARG:NH2	2.33	0.43
1:O:115:GLY:CA	1:O:320:ALA:HA	2.47	0.43
2:P:142:TYR:CD1	2:P:142:TYR:N	2.86	0.43
2:P:326:ILE:HG21	2:P:350:VAL:HG22	1.99	0.43
2:D:322:VAL:C	2:D:326:ILE:HG23	2.38	0.43
2:D:46:ALA:CB	2:D:351:ILE:HD13	2.49	0.43
3:E:1003:FLC:OB1	3:E:1003:FLC:OA1	2.36	0.43
1:E:336:THR:HG22	1:E:337:ASP:N	2.33	0.43
1:E:33:THR:HG23	1:E:291:MET:HE2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:47:ALA:HB2	2:H:354:LEU:HD11	2.01	0.43
2:L:77:ILE:O	2:L:80:ASN:O	2.37	0.43
1:O:43:GLU:OE1	1:O:310:ARG:NH1	2.51	0.43
1:A:195:ARG:O	1:A:199:THR:HG23	2.19	0.43
1:C:14:TYR:O	1:C:15:GLY:C	2.56	0.43
2:D:236:THR:HG22	2:D:236:THR:O	2.19	0.43
1:E:43:GLU:OE1	1:E:310:ARG:NH1	2.51	0.43
2:F:46:ALA:CB	2:F:351:ILE:HD13	2.49	0.43
1:G:83:THR:HB	2:H:191:THR:HG23	2.01	0.43
1:I:158:LYS:HG2	1:I:161:ARG:NH2	2.33	0.43
1:I:323:LYS:O	1:I:324:HIS:CB	2.67	0.43
1:K:101:LEU:HD12	1:K:103:ILE:HD11	1.99	0.43
1:K:8:ARG:HH21	1:O:160:GLU:CD	2.22	0.43
2:N:46:ALA:HB3	2:N:354:LEU:CD2	2.49	0.43
1:O:181:VAL:HG21	1:O:243:LEU:CD1	2.49	0.43
2:P:326:ILE:HD12	2:P:332:ASN:HB3	2.01	0.43
3:A:1001:FLC:OA1	3:A:1001:FLC:OB1	2.36	0.43
1:A:336:THR:HG22	1:A:337:ASP:N	2.33	0.43
2:D:326:ILE:HD12	2:D:332:ASN:HB3	2.01	0.43
1:E:158:LYS:HG2	1:E:161:ARG:NH2	2.33	0.43
2:F:47:ALA:HB2	2:F:354:LEU:HD11	2.01	0.43
2:F:97:ARG:HG3	2:F:102:THR:CG2	2.44	0.43
2:H:176:ALA:HA	2:H:239:VAL:HG21	2.01	0.43
1:I:101:LEU:HD12	1:I:103:ILE:HD11	1.99	0.43
1:I:119:ARG:HD2	2:J:125:THR:O	2.19	0.43
2:J:221:ILE:N	2:J:221:ILE:HD12	2.33	0.43
1:K:14:TYR:O	1:K:15:GLY:C	2.56	0.43
2:J:149:VAL:O	1:K:153:VAL:HG11	2.18	0.43
2:L:183:ARG:NH1	2:L:237:ASP:OD2	2.51	0.43
2:L:265:THR:HA	2:L:266:PRO:HD3	1.63	0.43
1:M:195:ARG:O	1:M:199:THR:HG23	2.18	0.43
2:N:25:SER:HB3	2:N:56:CYS:SG	2.58	0.43
2:P:12:THR:HB	2:P:81:LEU:CD1	2.47	0.43
2:P:221:ILE:N	2:P:221:ILE:HD12	2.34	0.43
2:P:46:ALA:HB3	2:P:354:LEU:CD2	2.49	0.43
2:P:77:ILE:O	2:P:80:ASN:O	2.37	0.43
2:B:194:ARG:O	2:B:198:GLY:HA3	2.19	0.43
1:C:181:VAL:HG21	1:C:243:LEU:CD1	2.49	0.43
1:G:181:VAL:HG21	1:G:243:LEU:CD1	2.49	0.43
1:G:195:ARG:O	1:G:199:THR:HG23	2.19	0.43
2:J:299:LEU:HD12	2:J:299:LEU:HA	1.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:46:ALA:CB	2:L:351:ILE:HD13	2.49	0.43
2:N:183:ARG:O	2:N:238:ALA:O	2.36	0.43
1:O:336:THR:HG22	1:O:337:ASP:N	2.33	0.43
2:B:274:ILE:CG2	2:B:275:SER:H	2.31	0.42
2:D:183:ARG:NH1	2:D:237:ASP:OD2	2.50	0.42
1:G:254:PRO:HG3	2:H:226:LEU:HD11	2.00	0.42
2:H:183:ARG:O	2:H:238:ALA:O	2.36	0.42
2:H:294:ASN:HA	2:H:295:PRO:HD2	1.74	0.42
2:J:181:ARG:HD3	2:J:238:ALA:H	1.83	0.42
2:J:46:ALA:HB3	2:J:354:LEU:CD2	2.49	0.42
2:L:181:ARG:HD3	2:L:238:ALA:H	1.83	0.42
2:L:299:LEU:HA	2:L:299:LEU:HD12	1.86	0.42
2:L:24:VAL:CG1	2:L:53:TRP:HZ3	2.32	0.42
1:M:284:ASN:O	1:M:334:SER:HB2	2.19	0.42
2:P:47:ALA:HB2	2:P:354:LEU:HD11	2.01	0.42
1:A:299:LEU:HA	1:A:302:LEU:CD1	2.49	0.42
2:B:221:ILE:N	2:B:221:ILE:HD12	2.33	0.42
2:B:43:ILE:HD12	2:B:299:LEU:HD21	1.99	0.42
2:B:322:VAL:C	2:B:326:ILE:HG23	2.39	0.42
2:B:46:ALA:CB	2:B:351:ILE:HD13	2.49	0.42
2:D:221:ILE:N	2:D:221:ILE:HD12	2.34	0.42
1:E:299:LEU:HA	1:E:302:LEU:CD1	2.49	0.42
2:F:236:THR:O	2:F:236:THR:HG22	2.19	0.42
2:F:294:ASN:HA	2:F:295:PRO:HD2	1.74	0.42
1:G:47:ILE:C	1:G:47:ILE:HD13	2.40	0.42
2:H:24:VAL:CG1	2:H:53:TRP:HZ3	2.33	0.42
3:I:1005:FLC:OB1	3:I:1005:FLC:OA1	2.36	0.42
2:J:274:ILE:CG2	2:J:275:SER:H	2.31	0.42
1:K:299:LEU:HA	1:K:302:LEU:CD1	2.50	0.42
1:K:151:LEU:CD2	2:L:157:ILE:HG12	2.43	0.42
2:L:294:ASN:HA	2:L:295:PRO:HD2	1.74	0.42
2:L:46:ALA:HB3	2:L:354:LEU:CD2	2.49	0.42
2:N:176:ALA:HA	2:N:239:VAL:HG21	2.01	0.42
1:O:158:LYS:HG2	1:O:161:ARG:NH2	2.33	0.42
2:P:236:THR:HG22	2:P:236:THR:O	2.19	0.42
2:P:176:ALA:HA	2:P:239:VAL:HG21	2.01	0.42
1:C:201:ILE:HG13	1:C:201:ILE:O	2.19	0.42
1:E:195:ARG:O	1:E:199:THR:HG23	2.19	0.42
2:F:142:TYR:CD1	2:F:142:TYR:N	2.86	0.42
2:F:77:ILE:O	2:F:80:ASN:O	2.37	0.42
1:G:201:ILE:HG13	1:G:201:ILE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:236:THR:O	2:H:236:THR:HG22	2.19	0.42
2:J:176:ALA:HA	2:J:239:VAL:HG21	2.01	0.42
2:N:236:THR:O	2:N:236:THR:HG22	2.19	0.42
2:P:24:VAL:CG1	2:P:53:TRP:HZ3	2.32	0.42
1:A:277:GLY:HA2	4:A:2001:AMP:H5'2	2.01	0.42
1:A:201:ILE:HG13	1:A:201:ILE:O	2.20	0.42
1:A:284:ASN:O	1:A:334:SER:HB2	2.19	0.42
2:B:326:ILE:HD12	2:B:332:ASN:HB3	2.01	0.42
1:C:187:MET:HE1	2:D:156:SER:HB3	2.01	0.42
2:D:77:ILE:O	2:D:80:ASN:O	2.37	0.42
1:E:293:LEU:HD23	1:E:293:LEU:HA	1.62	0.42
1:G:278:LEU:HD23	1:G:278:LEU:HA	1.90	0.42
1:I:47:ILE:HD11	1:I:49:TRP:CD2	2.55	0.42
2:J:142:TYR:CD1	2:J:142:TYR:N	2.86	0.42
2:J:46:ALA:CB	2:J:351:ILE:HD13	2.49	0.42
2:L:221:ILE:N	2:L:221:ILE:HD12	2.34	0.42
1:M:201:ILE:O	1:M:201:ILE:HG13	2.19	0.42
1:M:47:ILE:HD11	1:M:49:TRP:CD2	2.55	0.42
2:D:181:ARG:HD3	2:D:238:ALA:H	1.82	0.42
2:D:12:THR:HB	2:D:81:LEU:CD1	2.47	0.42
1:E:40:PHE:CD1	1:E:45:ILE:HD12	2.55	0.42
2:F:306:LEU:HA	2:F:309:MET:HE2	2.01	0.42
2:H:46:ALA:CB	2:H:351:ILE:HD13	2.49	0.42
1:I:120:ILE:HA	1:I:121:PRO:HD3	1.76	0.42
1:K:284:ASN:O	1:K:334:SER:HB2	2.19	0.42
1:K:47:ILE:C	1:K:47:ILE:HD13	2.40	0.42
2:N:8:ILE:HG21	2:N:171:TYR:HB2	2.00	0.42
2:N:221:ILE:HD12	2:N:221:ILE:N	2.33	0.42
1:O:33:THR:HG23	1:O:291:MET:CE	2.50	0.42
1:O:47:ILE:HD11	1:O:49:TRP:CD2	2.55	0.42
2:B:176:ALA:HA	2:B:239:VAL:HG21	2.02	0.42
2:B:46:ALA:HB3	2:B:354:LEU:CD2	2.49	0.42
2:B:59:SER:HA	2:B:60:PRO:HD3	1.86	0.42
1:C:299:LEU:HA	1:C:302:LEU:CD1	2.49	0.42
1:C:43:GLU:OE1	1:C:310:ARG:NH1	2.51	0.42
2:D:169:ILE:HG21	2:D:204:ALA:HA	2.02	0.42
1:G:40:PHE:CD1	1:G:45:ILE:HD12	2.55	0.42
1:G:47:ILE:HD11	1:G:49:TRP:CD2	2.55	0.42
2:H:194:ARG:O	2:H:198:GLY:HA3	2.19	0.42
2:J:236:THR:O	2:J:236:THR:HG22	2.19	0.42
2:J:265:THR:HA	2:J:266:PRO:HD3	1.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:181:VAL:HG21	1:K:243:LEU:CD1	2.49	0.42
2:L:176:ALA:HA	2:L:239:VAL:HG21	2.02	0.42
2:N:142:TYR:CD1	2:N:142:TYR:N	2.86	0.42
2:N:46:ALA:CB	2:N:351:ILE:HD13	2.49	0.42
1:A:40:PHE:CD1	1:A:45:ILE:HD12	2.55	0.42
1:A:47:ILE:HD13	1:A:47:ILE:C	2.40	0.42
2:B:236:THR:O	2:B:236:THR:HG22	2.19	0.42
1:C:33:THR:HG23	1:C:291:MET:CE	2.50	0.42
2:D:46:ALA:HB3	2:D:354:LEU:CD2	2.49	0.42
1:A:264:ARG:O	1:E:13:LYS:HG2	2.19	0.42
1:E:340:ASN:HA	1:E:343:ILE:HG13	2.01	0.42
2:F:46:ALA:HB3	2:F:354:LEU:CD2	2.49	0.42
2:F:64:ASN:O	2:F:66:LEU:N	2.48	0.42
1:G:299:LEU:HA	1:G:302:LEU:CD1	2.49	0.42
1:I:47:ILE:HD13	1:I:47:ILE:C	2.40	0.42
1:M:181:VAL:HG21	1:M:243:LEU:CD1	2.49	0.42
1:M:47:ILE:C	1:M:47:ILE:HD13	2.40	0.42
2:B:169:ILE:HG21	2:B:204:ALA:HA	2.02	0.42
1:E:14:TYR:O	1:E:15:GLY:C	2.56	0.42
1:E:27:GLY:C	1:E:29:GLY:N	2.73	0.42
2:F:181:ARG:HD3	2:F:238:ALA:H	1.82	0.42
2:F:176:ALA:HA	2:F:239:VAL:HG21	2.01	0.42
1:G:193:LEU:O	1:G:197:ILE:HG13	2.20	0.42
1:G:221:MET:HG3	2:H:256:GLY:HA3	2.02	0.42
1:I:201:ILE:O	1:I:201:ILE:HG13	2.20	0.42
2:J:26:PHE:O	2:J:27:ILE:CB	2.68	0.42
1:K:40:PHE:CD1	1:K:45:ILE:HD12	2.55	0.42
2:L:194:ARG:O	2:L:198:GLY:HA3	2.19	0.42
2:L:236:THR:O	2:L:236:THR:HG22	2.19	0.42
2:L:250:LEU:HA	2:L:250:LEU:HD23	1.82	0.42
2:L:347:THR:O	2:L:351:ILE:HG13	2.20	0.42
1:M:92:SER:OG	3:M:1007:FLC:HG2	2.19	0.42
1:M:13:LYS:HD2	1:M:18:PHE:CE1	2.54	0.42
1:M:299:LEU:HA	1:M:302:LEU:CD1	2.50	0.42
2:N:194:ARG:O	2:N:198:GLY:HA3	2.19	0.42
2:N:77:ILE:O	2:N:80:ASN:O	2.37	0.42
1:A:47:ILE:HD11	1:A:49:TRP:CD2	2.55	0.42
1:E:13:LYS:HD2	1:E:18:PHE:CE1	2.55	0.42
2:F:24:VAL:CG1	2:F:53:TRP:HZ3	2.33	0.42
1:G:232:VAL:C	1:G:233:LEU:HD23	2.41	0.42
1:G:284:ASN:O	1:G:334:SER:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:46:ALA:HB3	2:H:354:LEU:CD2	2.49	0.42
2:J:24:VAL:CG1	2:J:53:TRP:HZ3	2.33	0.42
1:K:13:LYS:HD2	1:K:18:PHE:CE1	2.55	0.42
1:M:232:VAL:C	1:M:233:LEU:HD23	2.40	0.42
2:P:169:ILE:HG21	2:P:204:ALA:HA	2.02	0.42
2:B:64:ASN:O	2:B:66:LEU:N	2.48	0.42
1:C:7:GLU:O	1:C:10:LEU:HD12	2.20	0.42
1:C:288:PRO:O	1:C:292:ILE:HG13	2.20	0.42
1:C:40:PHE:CD1	1:C:45:ILE:HD12	2.55	0.42
1:C:47:ILE:HD11	1:C:49:TRP:CD2	2.55	0.42
2:D:15:PRO:HG3	2:D:22:TYR:CZ	2.55	0.42
2:D:274:ILE:CG2	2:D:275:SER:H	2.31	0.42
2:D:322:VAL:HG12	2:D:350:VAL:CG1	2.37	0.42
2:D:24:VAL:CG1	2:D:53:TRP:HZ3	2.33	0.42
2:F:142:TYR:OH	2:F:245:LEU:HD12	2.20	0.42
1:G:120:ILE:HA	1:G:121:PRO:HD3	1.76	0.42
2:H:347:THR:O	2:H:351:ILE:HG13	2.20	0.42
1:I:284:ASN:O	1:I:334:SER:HB2	2.19	0.42
1:K:195:ARG:O	1:K:199:THR:HG23	2.19	0.42
2:L:47:ALA:HB2	2:L:354:LEU:HD11	2.01	0.42
2:L:59:SER:HA	2:L:60:PRO:HD3	1.86	0.42
2:L:97:ARG:HG3	2:L:102:THR:CG2	2.44	0.42
1:M:27:GLY:C	1:M:29:GLY:N	2.73	0.42
2:N:347:THR:O	2:N:351:ILE:HG13	2.20	0.42
1:O:299:LEU:HA	1:O:302:LEU:CD1	2.49	0.42
2:P:26:PHE:O	2:P:27:ILE:CB	2.68	0.42
1:A:193:LEU:O	1:A:197:ILE:HG13	2.20	0.41
2:B:142:TYR:OH	2:B:245:LEU:HD12	2.20	0.41
2:B:205:LYS:O	2:B:208:SER:HB3	2.20	0.41
1:C:232:VAL:C	1:C:233:LEU:HD23	2.41	0.41
1:C:50:GLU:OE1	1:G:171:LYS:NZ	2.41	0.41
2:D:205:LYS:O	2:D:208:SER:HB3	2.20	0.41
1:E:201:ILE:HG13	1:E:201:ILE:O	2.19	0.41
1:E:284:ASN:O	1:E:334:SER:HB2	2.19	0.41
2:F:194:ARG:O	2:F:198:GLY:HA3	2.19	0.41
2:F:26:PHE:O	2:F:27:ILE:CB	2.68	0.41
1:G:202:GLY:HA3	1:G:211:VAL:HG21	2.02	0.41
2:H:209:LYS:HE3	2:H:209:LYS:HB3	1.36	0.41
1:I:181:VAL:HG21	1:I:243:LEU:CD1	2.49	0.41
2:J:142:TYR:OH	2:J:245:LEU:HD12	2.20	0.41
2:J:194:ARG:O	2:J:198:GLY:HA3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:347:THR:O	2:J:351:ILE:HG13	2.20	0.41
1:K:193:LEU:O	1:K:197:ILE:HG13	2.20	0.41
1:M:7:GLU:O	1:M:10:LEU:HD12	2.20	0.41
1:M:193:LEU:O	1:M:197:ILE:HG13	2.20	0.41
1:M:342:ILE:HG12	1:M:342:ILE:H	1.62	0.41
2:N:326:ILE:HD12	2:N:332:ASN:HB3	2.01	0.41
2:N:343:THR:O	2:N:347:THR:OG1	2.38	0.41
1:O:232:VAL:C	1:O:233:LEU:HD23	2.41	0.41
1:O:40:PHE:CD1	1:O:45:ILE:HD12	2.55	0.41
1:A:27:GLY:C	1:A:29:GLY:N	2.73	0.41
2:B:15:PRO:HG3	2:B:22:TYR:CZ	2.55	0.41
1:C:284:ASN:O	1:C:334:SER:HB2	2.19	0.41
1:C:336:THR:HG22	1:C:337:ASP:N	2.33	0.41
1:C:340:ASN:HA	1:C:343:ILE:HG13	2.02	0.41
2:D:343:THR:O	2:D:347:THR:OG1	2.38	0.41
1:E:47:ILE:HD13	1:E:47:ILE:C	2.40	0.41
2:F:306:LEU:HD23	2:F:315:ALA:HA	2.02	0.41
2:F:322:VAL:HG13	2:F:354:LEU:HA	2.02	0.41
1:G:288:PRO:O	1:G:292:ILE:HG13	2.20	0.41
1:G:340:ASN:HA	1:G:343:ILE:HG13	2.01	0.41
2:H:343:THR:O	2:H:347:THR:OG1	2.38	0.41
2:J:77:ILE:O	2:J:80:ASN:O	2.37	0.41
1:K:201:ILE:O	1:K:201:ILE:HG13	2.19	0.41
1:K:33:THR:HG23	1:K:291:MET:CE	2.50	0.41
2:L:139:GLU:HB2	2:L:140:GLY:H	1.58	0.41
2:N:209:LYS:HE3	2:N:209:LYS:HB3	1.36	0.41
1:O:288:PRO:O	1:O:292:ILE:HG13	2.20	0.41
1:O:47:ILE:C	1:O:47:ILE:HD13	2.40	0.41
1:A:288:PRO:O	1:A:292:ILE:HG13	2.20	0.41
2:B:103:LEU:HD12	2:B:103:LEU:HA	1.69	0.41
2:D:253:LEU:CD2	2:D:253:LEU:C	2.89	0.41
2:D:336:ASP:O	2:D:337:LEU:HD23	2.21	0.41
2:D:347:THR:O	2:D:351:ILE:HG13	2.20	0.41
1:E:33:THR:HG23	1:E:291:MET:CE	2.50	0.41
1:E:288:PRO:O	1:E:292:ILE:HG13	2.20	0.41
2:F:253:LEU:C	2:F:253:LEU:CD2	2.89	0.41
1:I:299:LEU:HA	1:I:302:LEU:CD1	2.49	0.41
1:I:40:PHE:CD1	1:I:45:ILE:HD12	2.55	0.41
2:L:119:ILE:HD13	2:L:119:ILE:HA	1.88	0.41
1:K:119:ARG:CG	2:L:125:THR:HG22	2.45	0.41
2:N:12:THR:HB	2:N:81:LEU:CD1	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:183:ARG:NH1	2:N:237:ASP:OD2	2.51	0.41
2:N:348:GLU:H	2:N:348:GLU:HG2	1.63	0.41
1:O:223:ALA:O	1:O:227:PRO:HG3	2.21	0.41
1:A:181:VAL:HG21	1:A:243:LEU:CD1	2.49	0.41
2:B:47:ALA:HB2	2:B:354:LEU:HD11	2.01	0.41
2:B:77:ILE:O	2:B:80:ASN:O	2.37	0.41
1:C:275:HIS:CB	4:C:2002:AMP:O2P	2.57	0.41
1:C:47:ILE:HD13	1:C:47:ILE:C	2.40	0.41
2:D:322:VAL:HG13	2:D:354:LEU:HA	2.02	0.41
1:E:181:VAL:HG21	1:E:243:LEU:CD1	2.50	0.41
1:E:83:THR:HB	2:F:191:THR:HG23	2.02	0.41
2:F:169:ILE:HG21	2:F:204:ALA:HA	2.02	0.41
2:F:205:LYS:O	2:F:208:SER:HB3	2.21	0.41
2:F:15:PRO:HG3	2:F:22:TYR:CZ	2.55	0.41
2:F:336:ASP:O	2:F:337:LEU:HD23	2.21	0.41
2:F:343:THR:O	2:F:347:THR:OG1	2.38	0.41
2:H:336:ASP:O	2:H:337:LEU:HD23	2.20	0.41
2:J:322:VAL:HG13	2:J:354:LEU:HA	2.02	0.41
1:K:47:ILE:HD11	1:K:49:TRP:CD2	2.55	0.41
1:M:202:GLY:HA3	1:M:211:VAL:HG21	2.02	0.41
1:M:40:PHE:CD1	1:M:45:ILE:HD12	2.55	0.41
1:O:193:LEU:O	1:O:197:ILE:HG13	2.20	0.41
1:O:27:GLY:C	1:O:29:GLY:N	2.73	0.41
2:P:142:TYR:OH	2:P:245:LEU:HD12	2.20	0.41
2:P:205:LYS:O	2:P:208:SER:HB3	2.20	0.41
2:P:306:LEU:HD23	2:P:315:ALA:HA	2.02	0.41
1:A:202:GLY:HA3	1:A:211:VAL:HG21	2.03	0.41
1:E:193:LEU:O	1:E:197:ILE:HG13	2.20	0.41
1:G:156:ARG:N	1:G:157:PRO:CD	2.84	0.41
2:H:15:PRO:HG3	2:H:22:TYR:CZ	2.55	0.41
2:J:150:CYS:CB	2:J:151:PRO:CD	2.97	0.41
1:K:340:ASN:HA	1:K:343:ILE:HG13	2.01	0.41
1:K:83:THR:HA	1:K:84:PRO:HD3	1.80	0.41
2:L:336:ASP:O	2:L:337:LEU:HD23	2.21	0.41
2:L:348:GLU:H	2:L:348:GLU:HG2	1.62	0.41
1:M:288:PRO:O	1:M:292:ILE:HG13	2.20	0.41
2:N:26:PHE:O	2:N:27:ILE:CB	2.68	0.41
2:N:47:ALA:HB2	2:N:354:LEU:HD11	2.01	0.41
1:O:284:ASN:O	1:O:334:SER:HB2	2.19	0.41
2:P:46:ALA:CB	2:P:351:ILE:HD13	2.49	0.41
1:A:120:ILE:HA	1:A:121:PRO:HD3	1.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:299:LEU:HA	2:D:299:LEU:HD12	1.86	0.41
1:E:249:ALA:CB	2:F:230:THR:HG23	2.50	0.41
1:E:47:ILE:HD11	1:E:49:TRP:CD2	2.55	0.41
1:G:27:GLY:C	1:G:29:GLY:N	2.73	0.41
2:H:142:TYR:OH	2:H:245:LEU:HD12	2.20	0.41
2:H:183:ARG:NH1	2:H:237:ASP:OD2	2.51	0.41
2:H:253:LEU:CD2	2:H:253:LEU:C	2.89	0.41
1:I:193:LEU:O	1:I:197:ILE:HG13	2.20	0.41
1:I:224:VAL:HG21	2:J:253:LEU:HD21	2.03	0.41
1:I:232:VAL:C	1:I:233:LEU:HD23	2.41	0.41
1:I:275:HIS:CE1	2:J:223:ASN:ND2	2.88	0.41
2:N:142:TYR:OH	2:N:245:LEU:HD12	2.20	0.41
1:O:201:ILE:HG13	1:O:201:ILE:O	2.20	0.41
1:O:340:ASN:HA	1:O:343:ILE:HG13	2.01	0.41
2:P:194:ARG:O	2:P:198:GLY:HA3	2.19	0.41
2:P:253:LEU:CD2	2:P:253:LEU:C	2.89	0.41
2:P:274:ILE:CG2	2:P:275:SER:H	2.31	0.41
2:P:322:VAL:HG13	2:P:354:LEU:HA	2.02	0.41
2:P:347:THR:O	2:P:351:ILE:HG13	2.20	0.41
2:P:70:PRO:O	2:P:74:VAL:HG23	2.21	0.41
1:A:83:THR:HA	1:A:84:PRO:HD3	1.80	0.41
2:B:347:THR:O	2:B:351:ILE:HG13	2.20	0.41
2:B:24:VAL:CG1	2:B:53:TRP:HZ3	2.33	0.41
1:C:202:GLY:HA3	1:C:211:VAL:HG21	2.03	0.41
1:C:27:GLY:C	1:C:29:GLY:N	2.73	0.41
2:D:176:ALA:HA	2:D:239:VAL:HG21	2.01	0.41
2:D:142:TYR:OH	2:D:245:LEU:HD12	2.20	0.41
2:D:306:LEU:HD23	2:D:315:ALA:HA	2.03	0.41
2:D:334:THR:HG22	2:D:335:GLY:N	2.35	0.41
2:F:114:ARG:HA	2:F:115:PRO:HD3	1.85	0.41
1:E:187:MET:CE	2:F:156:SER:HB3	2.50	0.41
1:I:33:THR:HG23	1:I:291:MET:CE	2.49	0.41
2:J:139:GLU:HB2	2:J:140:GLY:H	1.57	0.41
2:L:306:LEU:HD23	2:L:315:ALA:HA	2.02	0.41
2:N:15:PRO:HG3	2:N:22:TYR:CZ	2.55	0.41
2:P:64:ASN:O	2:P:66:LEU:N	2.48	0.41
1:A:223:ALA:O	1:A:227:PRO:HG3	2.21	0.41
1:A:232:VAL:C	1:A:233:LEU:HD23	2.41	0.41
2:B:336:ASP:O	2:B:337:LEU:HD23	2.21	0.41
2:B:343:THR:O	2:B:347:THR:OG1	2.38	0.41
2:D:194:ARG:O	2:D:198:GLY:HA3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:26:PHE:CE1	2:D:84:LEU:HD23	2.56	0.41
2:D:47:ALA:HB2	2:D:354:LEU:HD11	2.01	0.41
1:E:92:SER:C	1:E:94:ASN:H	2.24	0.41
2:F:12:THR:HB	2:F:81:LEU:CD1	2.47	0.41
2:F:26:PHE:CE1	2:F:84:LEU:HD23	2.56	0.41
1:G:293:LEU:HA	1:G:293:LEU:HD23	1.62	0.41
2:H:59:SER:HA	2:H:60:PRO:HD3	1.86	0.41
1:I:288:PRO:O	1:I:292:ILE:HG13	2.20	0.41
2:J:15:PRO:HG3	2:J:22:TYR:CZ	2.55	0.41
1:K:156:ARG:N	1:K:157:PRO:CD	2.84	0.41
1:K:27:GLY:C	1:K:29:GLY:N	2.73	0.41
2:L:64:ASN:O	2:L:66:LEU:N	2.48	0.41
2:L:12:THR:HB	2:L:81:LEU:CD1	2.47	0.41
1:M:33:THR:HG23	1:M:291:MET:CE	2.50	0.41
1:M:340:ASN:HA	1:M:343:ILE:HG13	2.01	0.41
1:M:95:VAL:HG23	1:M:96:ALA:N	2.36	0.41
2:N:150:CYS:CB	2:N:151:PRO:CD	2.97	0.41
1:O:156:ARG:N	1:O:157:PRO:CD	2.84	0.41
2:P:15:PRO:HG3	2:P:22:TYR:CZ	2.55	0.41
2:P:44:PHE:HD2	2:P:49:VAL:HG21	1.85	0.41
1:A:278:LEU:HA	1:A:278:LEU:HD23	1.91	0.41
1:A:340:ASN:HA	1:A:343:ILE:HG13	2.02	0.41
1:C:156:ARG:N	1:C:157:PRO:CD	2.84	0.41
1:C:13:LYS:HD2	1:C:18:PHE:CE1	2.54	0.41
1:C:8:ARG:HH21	1:G:160:GLU:CD	2.24	0.41
1:G:33:THR:HG23	1:G:291:MET:CE	2.50	0.41
2:F:149:VAL:CG2	2:H:153:VAL:HG11	2.51	0.41
1:I:101:LEU:HB2	1:I:103:ILE:CG1	2.51	0.41
2:J:334:THR:HG22	2:J:335:GLY:N	2.35	0.41
2:L:343:THR:O	2:L:347:THR:OG1	2.38	0.41
2:L:26:PHE:CE1	2:L:84:LEU:HD23	2.56	0.41
2:N:24:VAL:CG1	2:N:53:TRP:HZ3	2.33	0.41
2:N:336:ASP:O	2:N:337:LEU:HD23	2.21	0.41
1:K:15:GLY:HA2	1:O:266:TYR:O	2.20	0.41
1:A:101:LEU:HB2	1:A:103:ILE:CG1	2.51	0.41
1:A:33:THR:HG23	1:A:291:MET:CE	2.50	0.41
2:B:299:LEU:HD12	2:B:299:LEU:HA	1.86	0.41
1:C:186:ILE:HD13	2:D:142:TYR:CD2	2.56	0.41
1:C:223:ALA:O	1:C:227:PRO:HG3	2.21	0.41
1:C:278:LEU:HD23	1:C:278:LEU:HA	1.90	0.41
1:E:223:ALA:O	1:E:227:PRO:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:323:LYS:O	1:G:324:HIS:CB	2.67	0.41
2:H:205:LYS:O	2:H:208:SER:HB3	2.20	0.41
2:H:274:ILE:CG2	2:H:275:SER:H	2.31	0.41
2:H:322:VAL:HG13	2:H:354:LEU:HA	2.02	0.41
2:J:12:THR:HB	2:J:81:LEU:CD1	2.47	0.41
2:J:169:ILE:HG21	2:J:204:ALA:HA	2.02	0.41
2:J:336:ASP:O	2:J:337:LEU:HD23	2.20	0.41
2:J:97:ARG:HG3	2:J:102:THR:CG2	2.44	0.41
2:L:220:LEU:O	2:L:221:ILE:C	2.60	0.41
2:L:15:PRO:HG3	2:L:22:TYR:CZ	2.55	0.41
2:L:253:LEU:CD2	2:L:253:LEU:C	2.89	0.41
1:M:323:LYS:O	1:M:324:HIS:CB	2.67	0.41
2:N:205:LYS:O	2:N:208:SER:HB3	2.20	0.41
2:N:253:LEU:CD2	2:N:253:LEU:C	2.89	0.41
2:N:26:PHE:CE1	2:N:84:LEU:HD23	2.56	0.41
1:O:95:VAL:HG23	1:O:96:ALA:N	2.36	0.41
2:P:63:VAL:HG12	2:P:64:ASN:ND2	2.36	0.41
1:A:18:PHE:HZ	1:E:44:ASN:HD22	1.69	0.41
2:B:26:PHE:O	2:B:27:ILE:CB	2.68	0.41
1:E:156:ARG:N	1:E:157:PRO:CD	2.84	0.41
1:E:202:GLY:HA3	1:E:211:VAL:HG21	2.03	0.41
1:E:340:ASN:HA	1:E:343:ILE:CG1	2.51	0.41
2:F:147:HIS:CD2	1:G:151:LEU:HD12	2.54	0.41
2:F:274:ILE:CG2	2:F:275:SER:H	2.31	0.41
1:G:92:SER:C	1:G:94:ASN:H	2.25	0.41
2:H:26:PHE:CE1	2:H:84:LEU:HD23	2.56	0.41
1:I:223:ALA:O	1:I:227:PRO:HG3	2.21	0.41
2:J:153:VAL:HG11	2:L:149:VAL:HG21	2.02	0.41
1:K:95:VAL:HG23	1:K:96:ALA:N	2.36	0.41
1:O:195:ARG:NH1	1:O:195:ARG:CG	2.63	0.41
1:A:156:ARG:N	1:A:157:PRO:CD	2.84	0.40
2:B:70:PRO:O	2:B:74:VAL:HG23	2.21	0.40
1:C:193:LEU:O	1:C:197:ILE:HG13	2.20	0.40
2:D:63:VAL:HG12	2:D:64:ASN:ND2	2.36	0.40
2:F:70:PRO:O	2:F:74:VAL:HG23	2.21	0.40
2:H:306:LEU:HD23	2:H:315:ALA:HA	2.03	0.40
1:I:278:LEU:HD23	1:I:278:LEU:HA	1.90	0.40
1:I:83:THR:HB	2:J:191:THR:HG23	2.04	0.40
2:J:253:LEU:CD2	2:J:253:LEU:C	2.89	0.40
1:M:92:SER:C	1:M:94:ASN:H	2.25	0.40
1:O:101:LEU:HB2	1:O:103:ILE:CG1	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:250:LEU:HD23	2:P:250:LEU:HA	1.82	0.40
1:E:232:VAL:C	1:E:233:LEU:HD23	2.41	0.40
1:E:311:ILE:O	1:E:315:VAL:HG12	2.22	0.40
1:E:323:LYS:O	1:E:324:HIS:CB	2.67	0.40
1:A:18:PHE:HZ	1:E:44:ASN:ND2	2.19	0.40
2:F:63:VAL:HG12	2:F:64:ASN:ND2	2.36	0.40
2:H:139:GLU:HB2	2:H:140:GLY:H	1.57	0.40
1:I:156:ARG:N	1:I:157:PRO:CD	2.84	0.40
1:I:165:PHE:HD1	1:M:14:TYR:CE2	2.39	0.40
1:I:27:GLY:C	1:I:29:GLY:N	2.73	0.40
1:I:340:ASN:HA	1:I:343:ILE:HG13	2.01	0.40
1:K:232:VAL:C	1:K:233:LEU:HD23	2.41	0.40
1:K:288:PRO:O	1:K:292:ILE:HG13	2.20	0.40
2:L:142:TYR:OH	2:L:245:LEU:HD12	2.20	0.40
2:L:63:VAL:HG12	2:L:64:ASN:ND2	2.36	0.40
2:L:70:PRO:O	2:L:74:VAL:HG23	2.21	0.40
1:M:223:ALA:O	1:M:227:PRO:HG3	2.21	0.40
2:N:306:LEU:HD23	2:N:315:ALA:HA	2.02	0.40
1:A:189:LEU:HB3	2:B:154:VAL:HG11	2.04	0.40
2:B:253:LEU:CD2	2:B:253:LEU:C	2.89	0.40
2:B:322:VAL:HG13	2:B:354:LEU:HA	2.02	0.40
2:B:63:VAL:HG12	2:B:64:ASN:ND2	2.36	0.40
1:C:287:ASN:HA	1:C:288:PRO:HD3	1.85	0.40
2:D:97:ARG:NE	2:D:97:ARG:HA	2.33	0.40
2:H:63:VAL:HG12	2:H:64:ASN:ND2	2.36	0.40
2:J:59:SER:HA	2:J:60:PRO:HD3	1.86	0.40
1:K:275:HIS:NE2	2:L:226:LEU:HD12	2.37	0.40
2:L:150:CYS:CB	2:L:151:PRO:CD	2.97	0.40
2:L:270:ILE:HA	2:L:275:SER:OG	2.22	0.40
1:M:101:LEU:HB2	1:M:103:ILE:CG1	2.51	0.40
1:M:156:ARG:N	1:M:157:PRO:CD	2.84	0.40
2:N:270:ILE:HA	2:N:275:SER:OG	2.22	0.40
2:P:150:CYS:CB	2:P:151:PRO:CD	2.97	0.40
1:A:92:SER:OG	3:A:1001:FLC:OG2	2.27	0.40
2:B:39:SER:OG	2:B:347:THR:HG23	2.22	0.40
2:B:26:PHE:CE1	2:B:84:LEU:HD23	2.56	0.40
1:C:340:ASN:HA	1:C:343:ILE:CG1	2.52	0.40
1:E:101:LEU:HB2	1:E:103:ILE:CG1	2.51	0.40
1:E:287:ASN:HA	1:E:288:PRO:HD3	1.86	0.40
2:F:147:HIS:CD2	1:G:151:LEU:HD11	2.56	0.40
2:F:347:THR:O	2:F:351:ILE:HG13	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:321:GLU:O	1:G:322:GLY:C	2.60	0.40
2:H:169:ILE:HG21	2:H:204:ALA:HA	2.02	0.40
1:I:92:SER:C	1:I:94:ASN:H	2.25	0.40
2:J:70:PRO:O	2:J:74:VAL:HG23	2.21	0.40
1:K:101:LEU:HB2	1:K:103:ILE:CG1	2.52	0.40
1:K:202:GLY:HA3	1:K:211:VAL:HG21	2.03	0.40
1:K:223:ALA:O	1:K:227:PRO:HG3	2.21	0.40
1:K:311:ILE:O	1:K:315:VAL:HG12	2.22	0.40
1:M:254:PRO:HG3	2:N:226:LEU:HD11	2.02	0.40
2:N:142:TYR:HD1	2:N:142:TYR:N	2.20	0.40
2:N:181:ARG:HD3	2:N:238:ALA:H	1.83	0.40
2:P:270:ILE:HA	2:P:275:SER:OG	2.22	0.40
2:P:336:ASP:O	2:P:337:LEU:HD23	2.21	0.40
2:P:97:ARG:HG3	2:P:102:THR:CG2	2.44	0.40
2:B:182:PRO:HD2	2:B:237:ASP:HB2	2.04	0.40
2:B:306:LEU:HD23	2:B:315:ALA:HA	2.03	0.40
1:C:311:ILE:O	1:C:315:VAL:HG12	2.22	0.40
2:D:175:TYR:CE1	2:D:179:ILE:HD13	2.57	0.40
1:E:7:GLU:O	1:E:10:LEU:HD12	2.20	0.40
3:G:1004:FLC:OA1	3:G:1004:FLC:CBC	2.70	0.40
1:G:223:ALA:O	1:G:227:PRO:HG3	2.21	0.40
2:H:270:ILE:HA	2:H:275:SER:OG	2.22	0.40
2:H:39:SER:OG	2:H:347:THR:HG23	2.22	0.40
1:I:293:LEU:HA	1:I:293:LEU:HD23	1.62	0.40
2:J:294:ASN:HA	2:J:295:PRO:HD2	1.73	0.40
2:J:306:LEU:HD23	2:J:315:ALA:HA	2.03	0.40
2:L:205:LYS:O	2:L:208:SER:HB3	2.21	0.40
2:L:322:VAL:HG13	2:L:354:LEU:HA	2.02	0.40
1:M:311:ILE:O	1:M:315:VAL:HG12	2.22	0.40
1:M:340:ASN:HA	1:M:343:ILE:CG1	2.52	0.40
2:N:63:VAL:HG12	2:N:64:ASN:ND2	2.36	0.40
2:P:182:PRO:HD2	2:P:237:ASP:HB2	2.04	0.40
2:P:220:LEU:O	2:P:221:ILE:C	2.60	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:286:ASP:OD2	2:N:285:PRO:CG[1_565]	1.88	0.32
2:B:286:ASP:OD2	2:N:285:PRO:CB[1_565]	1.90	0.30
1:G:122:ASP:OD2	2:P:213:ASP:CB[1_565]	2.15	0.05

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	325/349 (93%)	295 (91%)	27 (8%)	3 (1%)	17	56
1	C	334/349 (96%)	300 (90%)	31 (9%)	3 (1%)	17	56
1	E	334/349 (96%)	300 (90%)	31 (9%)	3 (1%)	17	56
1	G	325/349 (93%)	295 (91%)	27 (8%)	3 (1%)	17	56
1	I	325/349 (93%)	295 (91%)	27 (8%)	3 (1%)	17	56
1	K	333/349 (95%)	300 (90%)	30 (9%)	3 (1%)	17	56
1	M	335/349 (96%)	301 (90%)	31 (9%)	3 (1%)	17	56
1	O	326/349 (93%)	296 (91%)	27 (8%)	3 (1%)	17	56
2	B	343/354 (97%)	289 (84%)	42 (12%)	12 (4%)	3	29
2	D	343/354 (97%)	289 (84%)	41 (12%)	13 (4%)	3	27
2	F	343/354 (97%)	289 (84%)	41 (12%)	13 (4%)	3	27
2	H	342/354 (97%)	288 (84%)	41 (12%)	13 (4%)	3	27
2	J	343/354 (97%)	289 (84%)	41 (12%)	13 (4%)	3	27
2	L	342/354 (97%)	288 (84%)	41 (12%)	13 (4%)	3	27
2	N	343/354 (97%)	290 (84%)	40 (12%)	13 (4%)	3	27
2	P	343/354 (97%)	289 (84%)	41 (12%)	13 (4%)	3	27
All	All	5379/5624 (96%)	4693 (87%)	559 (10%)	127 (2%)	6	36

All (127) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	304	LEU
2	B	97	ARG
2	B	151	PRO
2	B	322	VAL
2	B	323	LEU
1	C	304	LEU

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Mol	Chain	Res	Type
2	D	97	ARG
2	D	151	PRO
2	D	322	VAL
2	D	323	LEU
1	E	304	LEU
2	F	97	ARG
2	F	151	PRO
2	F	322	VAL
2	F	323	LEU
1	G	304	LEU
2	H	97	ARG
2	H	151	PRO
2	H	322	VAL
2	H	323	LEU
1	I	304	LEU
2	J	97	ARG
2	J	151	PRO
2	J	322	VAL
2	J	323	LEU
1	K	304	LEU
2	L	97	ARG
2	L	151	PRO
2	L	322	VAL
2	L	323	LEU
1	M	304	LEU
2	N	97	ARG
2	N	151	PRO
2	N	322	VAL
2	N	323	LEU
1	O	304	LEU
2	P	97	ARG
2	P	151	PRO
2	P	322	VAL
2	P	323	LEU
1	A	322	GLY
2	B	13	GLY
2	B	98	SER
1	C	322	GLY
2	D	13	GLY
2	D	98	SER
1	E	322	GLY
2	F	13	GLY

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Mol	Chain	Res	Type
2	F	98	SER
1	G	322	GLY
2	H	13	GLY
2	H	98	SER
1	I	322	GLY
2	J	13	GLY
2	J	98	SER
1	K	322	GLY
2	L	13	GLY
2	L	98	SER
1	M	322	GLY
2	N	13	GLY
2	N	98	SER
1	O	322	GLY
2	P	13	GLY
2	P	98	SER
1	A	310	ARG
2	B	79	LYS
2	B	332	ASN
1	C	310	ARG
2	D	79	LYS
2	D	332	ASN
1	E	310	ARG
2	F	79	LYS
2	F	332	ASN
1	G	310	ARG
2	H	79	LYS
2	H	332	ASN
1	I	310	ARG
2	J	79	LYS
2	J	332	ASN
1	K	310	ARG
2	L	79	LYS
2	L	332	ASN
1	M	310	ARG
2	N	79	LYS
2	N	332	ASN
1	O	310	ARG
2	P	79	LYS
2	P	332	ASN
2	B	239	VAL
2	D	239	VAL

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Mol	Chain	Res	Type
2	F	239	VAL
2	H	239	VAL
2	J	239	VAL
2	L	239	VAL
2	N	239	VAL
2	P	239	VAL
2	B	65	GLY
2	D	65	GLY
2	F	27	ILE
2	F	65	GLY
2	H	27	ILE
2	H	65	GLY
2	J	65	GLY
2	L	27	ILE
2	L	65	GLY
2	N	65	GLY
2	P	27	ILE
2	P	65	GLY
2	B	27	ILE
2	B	50	PRO
2	D	27	ILE
2	D	50	PRO
2	F	50	PRO
2	H	50	PRO
2	J	27	ILE
2	J	50	PRO
2	L	50	PRO
2	N	27	ILE
2	N	50	PRO
2	P	50	PRO
2	D	14	LYS
2	F	14	LYS
2	H	14	LYS
2	J	14	LYS
2	L	14	LYS
2	N	14	LYS
2	P	14	LYS

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	274/289 (95%)	245 (89%)	29 (11%)	6	27
1	C	282/289 (98%)	253 (90%)	29 (10%)	7	27
1	E	282/289 (98%)	251 (89%)	31 (11%)	6	25
1	G	274/289 (95%)	247 (90%)	27 (10%)	8	29
1	I	274/289 (95%)	247 (90%)	27 (10%)	8	29
1	K	281/289 (97%)	251 (89%)	30 (11%)	6	27
1	M	282/289 (98%)	254 (90%)	28 (10%)	8	29
1	O	274/289 (95%)	245 (89%)	29 (11%)	6	27
2	B	293/297 (99%)	244 (83%)	49 (17%)	2	14
2	D	293/297 (99%)	244 (83%)	49 (17%)	2	14
2	F	293/297 (99%)	244 (83%)	49 (17%)	2	14
2	H	292/297 (98%)	244 (84%)	48 (16%)	2	14
2	J	293/297 (99%)	244 (83%)	49 (17%)	2	14
2	L	292/297 (98%)	244 (84%)	48 (16%)	2	14
2	N	293/297 (99%)	245 (84%)	48 (16%)	2	14
2	P	293/297 (99%)	244 (83%)	49 (17%)	2	14
All	All	4565/4688 (97%)	3946 (86%)	619 (14%)	3	20

All (619) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	THR
1	A	47	ILE
1	A	51	THR
1	A	52	ILE
1	A	77	LEU
1	A	78	LYS
1	A	88	THR
1	A	93	LEU
1	A	103	ILE
1	A	119	ARG
1	A	120	ILE
1	A	135	GLU

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Mol	Chain	Res	Type
1	A	195	ARG
1	A	201	ILE
1	A	215	ILE
1	A	264	ARG
1	A	274	ARG
1	A	285	VAL
1	A	291	MET
1	A	295	SER
1	A	302	LEU
1	A	311	ILE
1	A	315	VAL
1	A	319	ILE
1	A	323	LYS
1	A	324	HIS
1	A	326	THR
1	A	336	THR
1	A	342	ILE
2	B	4	LYS
2	B	5	GLN
2	B	8	ILE
2	B	19	THR
2	B	23	THR
2	B	30	ASP
2	B	35	GLU
2	B	36	ILE
2	B	38	LYS
2	B	44	PHE
2	B	45	SER
2	B	58	VAL
2	B	66	LEU
2	B	67	THR
2	B	69	ILE
2	B	71	ASP
2	B	78	THR
2	B	80	ASN
2	B	88	LEU
2	B	97	ARG
2	B	102	THR
2	B	114	ARG
2	B	129	VAL
2	B	149	VAL
2	B	162	ARG

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Mol	Chain	Res	Type
2	B	184	VAL
2	B	185	ILE
2	B	192	ILE
2	B	193	GLN
2	B	209	LYS
2	B	221	ILE
2	B	222	ASP
2	B	225	VAL
2	B	226	LEU
2	B	241	VAL
2	B	252	ASP
2	B	262	LEU
2	B	283	SER
2	B	299	LEU
2	B	306	LEU
2	B	322	VAL
2	B	323	LEU
2	B	324	SER
2	B	326	ILE
2	B	333	ARG
2	B	342	THR
2	B	347	THR
2	B	348	GLU
2	B	353	ARG
1	C	8	ARG
1	C	33	THR
1	C	47	ILE
1	C	51	THR
1	C	52	ILE
1	C	77	LEU
1	C	78	LYS
1	C	88	THR
1	C	93	LEU
1	C	103	ILE
1	C	119	ARG
1	C	120	ILE
1	C	123	ILE
1	C	135	GLU
1	C	195	ARG
1	C	201	ILE
1	C	215	ILE
1	C	274	ARG

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Mol	Chain	Res	Type
1	C	291	MET
1	C	295	SER
1	C	302	LEU
1	C	311	ILE
1	C	315	VAL
1	C	319	ILE
1	C	323	LYS
1	C	324	HIS
1	C	326	THR
1	C	336	THR
1	C	342	ILE
2	D	4	LYS
2	D	5	GLN
2	D	8	ILE
2	D	19	THR
2	D	23	THR
2	D	30	ASP
2	D	35	GLU
2	D	36	ILE
2	D	38	LYS
2	D	44	PHE
2	D	45	SER
2	D	58	VAL
2	D	66	LEU
2	D	67	THR
2	D	69	ILE
2	D	71	ASP
2	D	78	THR
2	D	80	ASN
2	D	88	LEU
2	D	97	ARG
2	D	102	THR
2	D	114	ARG
2	D	129	VAL
2	D	149	VAL
2	D	162	ARG
2	D	184	VAL
2	D	185	ILE
2	D	192	ILE
2	D	193	GLN
2	D	209	LYS
2	D	221	ILE

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Mol	Chain	Res	Type
2	D	222	ASP
2	D	225	VAL
2	D	226	LEU
2	D	241	VAL
2	D	252	ASP
2	D	262	LEU
2	D	283	SER
2	D	299	LEU
2	D	306	LEU
2	D	322	VAL
2	D	323	LEU
2	D	324	SER
2	D	326	ILE
2	D	333	ARG
2	D	342	THR
2	D	347	THR
2	D	348	GLU
2	D	353	ARG
1	E	8	ARG
1	E	33	THR
1	E	47	ILE
1	E	51	THR
1	E	52	ILE
1	E	77	LEU
1	E	78	LYS
1	E	88	THR
1	E	93	LEU
1	E	103	ILE
1	E	119	ARG
1	E	120	ILE
1	E	123	ILE
1	E	135	GLU
1	E	195	ARG
1	E	201	ILE
1	E	215	ILE
1	E	264	ARG
1	E	274	ARG
1	E	285	VAL
1	E	291	MET
1	E	295	SER
1	E	302	LEU
1	E	311	ILE

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Mol	Chain	Res	Type
1	E	315	VAL
1	E	319	ILE
1	E	323	LYS
1	E	324	HIS
1	E	326	THR
1	E	336	THR
1	E	342	ILE
2	F	4	LYS
2	F	5	GLN
2	F	8	ILE
2	F	19	THR
2	F	23	THR
2	F	30	ASP
2	F	35	GLU
2	F	36	ILE
2	F	38	LYS
2	F	44	PHE
2	F	45	SER
2	F	58	VAL
2	F	66	LEU
2	F	67	THR
2	F	69	ILE
2	F	71	ASP
2	F	78	THR
2	F	80	ASN
2	F	88	LEU
2	F	97	ARG
2	F	102	THR
2	F	114	ARG
2	F	129	VAL
2	F	149	VAL
2	F	162	ARG
2	F	184	VAL
2	F	185	ILE
2	F	192	ILE
2	F	193	GLN
2	F	209	LYS
2	F	221	ILE
2	F	222	ASP
2	F	225	VAL
2	F	226	LEU
2	F	241	VAL

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Mol	Chain	Res	Type
2	F	252	ASP
2	F	262	LEU
2	F	283	SER
2	F	299	LEU
2	F	306	LEU
2	F	322	VAL
2	F	323	LEU
2	F	324	SER
2	F	326	ILE
2	F	333	ARG
2	F	342	THR
2	F	347	THR
2	F	348	GLU
2	F	353	ARG
1	G	33	THR
1	G	47	ILE
1	G	51	THR
1	G	52	ILE
1	G	77	LEU
1	G	78	LYS
1	G	88	THR
1	G	93	LEU
1	G	103	ILE
1	G	119	ARG
1	G	120	ILE
1	G	135	GLU
1	G	195	ARG
1	G	201	ILE
1	G	215	ILE
1	G	274	ARG
1	G	291	MET
1	G	295	SER
1	G	302	LEU
1	G	311	ILE
1	G	315	VAL
1	G	319	ILE
1	G	323	LYS
1	G	324	HIS
1	G	326	THR
1	G	336	THR
1	G	342	ILE
2	H	5	GLN

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Mol	Chain	Res	Type
2	H	8	ILE
2	H	19	THR
2	H	23	THR
2	H	30	ASP
2	H	35	GLU
2	H	36	ILE
2	H	38	LYS
2	H	44	PHE
2	H	45	SER
2	H	58	VAL
2	H	66	LEU
2	H	67	THR
2	H	69	ILE
2	H	71	ASP
2	H	78	THR
2	H	80	ASN
2	H	88	LEU
2	H	97	ARG
2	H	102	THR
2	H	114	ARG
2	H	129	VAL
2	H	149	VAL
2	H	162	ARG
2	H	184	VAL
2	H	185	ILE
2	H	192	ILE
2	H	193	GLN
2	H	209	LYS
2	H	221	ILE
2	H	222	ASP
2	H	225	VAL
2	H	226	LEU
2	H	241	VAL
2	H	252	ASP
2	H	262	LEU
2	H	283	SER
2	H	299	LEU
2	H	306	LEU
2	H	322	VAL
2	H	323	LEU
2	H	324	SER
2	H	326	ILE

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Mol	Chain	Res	Type
2	H	333	ARG
2	H	342	THR
2	H	347	THR
2	H	348	GLU
2	H	353	ARG
1	I	33	THR
1	I	47	ILE
1	I	51	THR
1	I	52	ILE
1	I	77	LEU
1	I	78	LYS
1	I	88	THR
1	I	93	LEU
1	I	103	ILE
1	I	119	ARG
1	I	120	ILE
1	I	135	GLU
1	I	195	ARG
1	I	201	ILE
1	I	215	ILE
1	I	274	ARG
1	I	291	MET
1	I	295	SER
1	I	302	LEU
1	I	311	ILE
1	I	315	VAL
1	I	319	ILE
1	I	323	LYS
1	I	324	HIS
1	I	326	THR
1	I	336	THR
1	I	342	ILE
2	J	4	LYS
2	J	5	GLN
2	J	8	ILE
2	J	19	THR
2	J	23	THR
2	J	30	ASP
2	J	35	GLU
2	J	36	ILE
2	J	38	LYS
2	J	44	PHE

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Mol	Chain	Res	Type
2	J	45	SER
2	J	58	VAL
2	J	66	LEU
2	J	67	THR
2	J	69	ILE
2	J	71	ASP
2	J	78	THR
2	J	80	ASN
2	J	88	LEU
2	J	97	ARG
2	J	102	THR
2	J	114	ARG
2	J	129	VAL
2	J	149	VAL
2	J	162	ARG
2	J	184	VAL
2	J	185	ILE
2	J	192	ILE
2	J	193	GLN
2	J	209	LYS
2	J	221	ILE
2	J	222	ASP
2	J	225	VAL
2	J	226	LEU
2	J	241	VAL
2	J	252	ASP
2	J	262	LEU
2	J	283	SER
2	J	299	LEU
2	J	306	LEU
2	J	322	VAL
2	J	323	LEU
2	J	324	SER
2	J	326	ILE
2	J	333	ARG
2	J	342	THR
2	J	347	THR
2	J	348	GLU
2	J	353	ARG
1	K	8	ARG
1	K	33	THR
1	K	47	ILE

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Mol	Chain	Res	Type
1	K	51	THR
1	K	52	ILE
1	K	77	LEU
1	K	78	LYS
1	K	88	THR
1	K	93	LEU
1	K	103	ILE
1	K	119	ARG
1	K	120	ILE
1	K	123	ILE
1	K	135	GLU
1	K	195	ARG
1	K	201	ILE
1	K	215	ILE
1	K	274	ARG
1	K	285	VAL
1	K	291	MET
1	K	295	SER
1	K	302	LEU
1	K	311	ILE
1	K	315	VAL
1	K	319	ILE
1	K	323	LYS
1	K	324	HIS
1	K	326	THR
1	K	336	THR
1	K	342	ILE
2	L	5	GLN
2	L	8	ILE
2	L	19	THR
2	L	23	THR
2	L	30	ASP
2	L	35	GLU
2	L	36	ILE
2	L	38	LYS
2	L	44	PHE
2	L	45	SER
2	L	58	VAL
2	L	66	LEU
2	L	67	THR
2	L	69	ILE
2	L	71	ASP

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Mol	Chain	Res	Type
2	L	78	THR
2	L	80	ASN
2	L	88	LEU
2	L	97	ARG
2	L	102	THR
2	L	114	ARG
2	L	129	VAL
2	L	149	VAL
2	L	162	ARG
2	L	184	VAL
2	L	185	ILE
2	L	192	ILE
2	L	193	GLN
2	L	209	LYS
2	L	221	ILE
2	L	222	ASP
2	L	225	VAL
2	L	226	LEU
2	L	241	VAL
2	L	252	ASP
2	L	262	LEU
2	L	283	SER
2	L	299	LEU
2	L	306	LEU
2	L	322	VAL
2	L	323	LEU
2	L	324	SER
2	L	326	ILE
2	L	333	ARG
2	L	342	THR
2	L	347	THR
2	L	348	GLU
2	L	353	ARG
1	M	8	ARG
1	M	33	THR
1	M	47	ILE
1	M	51	THR
1	M	52	ILE
1	M	77	LEU
1	M	78	LYS
1	M	88	THR
1	M	93	LEU

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Mol	Chain	Res	Type
1	M	103	ILE
1	M	119	ARG
1	M	120	ILE
1	M	135	GLU
1	M	195	ARG
1	M	201	ILE
1	M	215	ILE
1	M	274	ARG
1	M	291	MET
1	M	295	SER
1	M	302	LEU
1	M	311	ILE
1	M	315	VAL
1	M	319	ILE
1	M	323	LYS
1	M	324	HIS
1	M	326	THR
1	M	336	THR
1	M	342	ILE
2	N	4	LYS
2	N	5	GLN
2	N	8	ILE
2	N	19	THR
2	N	23	THR
2	N	30	ASP
2	N	35	GLU
2	N	36	ILE
2	N	38	LYS
2	N	44	PHE
2	N	45	SER
2	N	58	VAL
2	N	66	LEU
2	N	67	THR
2	N	69	ILE
2	N	71	ASP
2	N	78	THR
2	N	80	ASN
2	N	88	LEU
2	N	97	ARG
2	N	102	THR
2	N	114	ARG
2	N	129	VAL

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Mol	Chain	Res	Type
2	N	149	VAL
2	N	162	ARG
2	N	184	VAL
2	N	185	ILE
2	N	192	ILE
2	N	193	GLN
2	N	209	LYS
2	N	221	ILE
2	N	222	ASP
2	N	225	VAL
2	N	226	LEU
2	N	241	VAL
2	N	252	ASP
2	N	262	LEU
2	N	283	SER
2	N	299	LEU
2	N	306	LEU
2	N	322	VAL
2	N	323	LEU
2	N	324	SER
2	N	326	ILE
2	N	342	THR
2	N	347	THR
2	N	348	GLU
2	N	353	ARG
1	O	33	THR
1	O	47	ILE
1	O	51	THR
1	O	52	ILE
1	O	77	LEU
1	O	78	LYS
1	O	88	THR
1	O	93	LEU
1	O	103	ILE
1	O	119	ARG
1	O	120	ILE
1	O	135	GLU
1	O	195	ARG
1	O	201	ILE
1	O	215	ILE
1	O	264	ARG
1	O	274	ARG

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Mol	Chain	Res	Type
1	O	285	VAL
1	O	291	MET
1	O	295	SER
1	O	302	LEU
1	O	311	ILE
1	O	315	VAL
1	O	319	ILE
1	O	323	LYS
1	O	324	HIS
1	O	326	THR
1	O	336	THR
1	O	342	ILE
2	P	4	LYS
2	P	5	GLN
2	P	8	ILE
2	P	19	THR
2	P	23	THR
2	P	30	ASP
2	P	35	GLU
2	P	36	ILE
2	P	38	LYS
2	P	44	PHE
2	P	45	SER
2	P	58	VAL
2	P	66	LEU
2	P	67	THR
2	P	69	ILE
2	P	71	ASP
2	P	78	THR
2	P	80	ASN
2	P	88	LEU
2	P	97	ARG
2	P	102	THR
2	P	114	ARG
2	P	129	VAL
2	P	149	VAL
2	P	162	ARG
2	P	184	VAL
2	P	185	ILE
2	P	192	ILE
2	P	193	GLN
2	P	209	LYS

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Mol	Chain	Res	Type
2	P	221	ILE
2	P	222	ASP
2	P	225	VAL
2	P	226	LEU
2	P	241	VAL
2	P	252	ASP
2	P	262	LEU
2	P	283	SER
2	P	299	LEU
2	P	306	LEU
2	P	322	VAL
2	P	323	LEU
2	P	324	SER
2	P	326	ILE
2	P	333	ARG
2	P	342	THR
2	P	347	THR
2	P	348	GLU
2	P	353	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	245	ASN
2	B	64	ASN
2	B	193	GLN
2	B	223	ASN
1	C	106	ASN
1	C	245	ASN
1	C	301	HIS
2	D	64	ASN
2	D	193	GLN
2	D	223	ASN
1	E	44	ASN
1	E	106	ASN
1	E	245	ASN
1	E	301	HIS
2	F	64	ASN
2	F	193	GLN
1	G	106	ASN
1	G	245	ASN

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Mol	Chain	Res	Type
2	H	64	ASN
2	H	193	GLN
2	H	231	ASN
1	I	106	ASN
1	I	245	ASN
2	J	64	ASN
2	J	193	GLN
2	J	223	ASN
1	K	106	ASN
1	K	245	ASN
1	K	301	HIS
2	L	64	ASN
2	L	193	GLN
1	M	106	ASN
1	M	245	ASN
1	M	301	HIS
2	N	64	ASN
2	N	193	GLN
2	N	223	ASN
2	N	231	ASN
1	O	106	ASN
1	O	245	ASN
2	P	193	GLN
2	P	223	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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$
4	AMP	I	2005	-	22,25,25	0.98	1 (4%)	25,38,38	1.45	3 (12%)
4	AMP	M	2007	-	22,25,25	0.98	1 (4%)	25,38,38	1.45	3 (12%)
3	FLC	A	1001	-	3,12,12	0.92	0	3,17,17	2.78	2 (66%)
3	FLC	M	1007	-	3,12,12	0.99	0	3,17,17	2.78	2 (66%)
3	FLC	G	1004	-	3,12,12	0.92	0	3,17,17	2.76	2 (66%)
4	AMP	K	2006	-	22,25,25	0.98	1 (4%)	25,38,38	1.45	3 (12%)
4	AMP	A	2001	-	22,25,25	0.98	1 (4%)	25,38,38	1.46	3 (12%)
3	FLC	O	1008	-	3,12,12	0.96	0	3,17,17	2.75	2 (66%)
4	AMP	C	2002	-	22,25,25	0.98	1 (4%)	25,38,38	1.45	3 (12%)
3	FLC	I	1005	-	3,12,12	0.89	0	3,17,17	2.76	2 (66%)
4	AMP	O	2008	-	22,25,25	0.98	1 (4%)	25,38,38	1.45	3 (12%)
3	FLC	E	1003	-	3,12,12	0.89	0	3,17,17	2.73	2 (66%)
3	FLC	K	1006	-	3,12,12	0.96	0	3,17,17	2.76	2 (66%)
4	AMP	G	2004	-	22,25,25	0.98	1 (4%)	25,38,38	1.45	3 (12%)
4	AMP	E	2003	-	22,25,25	0.98	1 (4%)	25,38,38	1.45	3 (12%)
3	FLC	C	1002	-	3,12,12	0.88	0	3,17,17	2.74	2 (66%)

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
4	AMP	I	2005	-	-	1/6/26/26	0/3/3/3
4	AMP	M	2007	-	-	4/6/26/26	0/3/3/3
3	FLC	A	1001	-	-	6/6/16/16	-
3	FLC	M	1007	-	-	6/6/16/16	-
3	FLC	G	1004	-	-	6/6/16/16	-
4	AMP	K	2006	-	-	2/6/26/26	0/3/3/3
4	AMP	A	2001	-	-	1/6/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FLC	O	1008	-	-	6/6/16/16	-
4	AMP	C	2002	-	-	5/6/26/26	0/3/3/3
3	FLC	I	1005	-	-	6/6/16/16	-
4	AMP	O	2008	-	-	2/6/26/26	0/3/3/3
3	FLC	E	1003	-	-	6/6/16/16	-
3	FLC	K	1006	-	-	6/6/16/16	-
4	AMP	G	2004	-	-	4/6/26/26	0/3/3/3
4	AMP	E	2003	-	-	4/6/26/26	0/3/3/3
3	FLC	C	1002	-	-	6/6/16/16	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2001	AMP	C5-C4	2.54	1.47	1.40
4	G	2004	AMP	C5-C4	2.51	1.47	1.40
4	E	2003	AMP	C5-C4	2.50	1.47	1.40
4	O	2008	AMP	C5-C4	2.49	1.47	1.40
4	M	2007	AMP	C5-C4	2.48	1.47	1.40
4	K	2006	AMP	C5-C4	2.48	1.47	1.40
4	C	2002	AMP	C5-C4	2.48	1.47	1.40
4	I	2005	AMP	C5-C4	2.47	1.47	1.40

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	2005	AMP	C3'-C2'-C1'	3.53	106.29	100.98
4	K	2006	AMP	C3'-C2'-C1'	3.52	106.27	100.98
4	G	2004	AMP	C3'-C2'-C1'	3.51	106.26	100.98
4	O	2008	AMP	C3'-C2'-C1'	3.50	106.24	100.98
4	E	2003	AMP	C3'-C2'-C1'	3.49	106.23	100.98
4	C	2002	AMP	C3'-C2'-C1'	3.48	106.22	100.98
4	A	2001	AMP	C3'-C2'-C1'	3.48	106.21	100.98
4	M	2007	AMP	C3'-C2'-C1'	3.47	106.21	100.98
3	A	1001	FLC	CB-CG-CGC	-3.41	109.52	114.98
3	M	1007	FLC	CB-CA-CAC	-3.41	109.52	114.98
3	O	1008	FLC	CB-CA-CAC	-3.41	109.53	114.98
3	I	1005	FLC	CB-CA-CAC	-3.41	109.53	114.98
3	M	1007	FLC	CB-CG-CGC	-3.40	109.54	114.98
3	G	1004	FLC	CB-CA-CAC	-3.40	109.54	114.98
3	A	1001	FLC	CB-CA-CAC	-3.39	109.55	114.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	1006	FLC	CB-CG-CGC	-3.39	109.56	114.98
3	K	1006	FLC	CB-CA-CAC	-3.38	109.57	114.98
3	G	1004	FLC	CB-CG-CGC	-3.37	109.60	114.98
3	E	1003	FLC	CB-CG-CGC	-3.36	109.60	114.98
3	C	1002	FLC	CB-CA-CAC	-3.36	109.61	114.98
3	C	1002	FLC	CB-CG-CGC	-3.34	109.63	114.98
3	I	1005	FLC	CB-CG-CGC	-3.34	109.63	114.98
3	O	1008	FLC	CB-CG-CGC	-3.33	109.65	114.98
3	E	1003	FLC	CB-CA-CAC	-3.32	109.66	114.98
4	O	2008	AMP	N3-C2-N1	-3.19	123.70	128.68
4	C	2002	AMP	N3-C2-N1	-3.18	123.71	128.68
4	K	2006	AMP	N3-C2-N1	-3.18	123.71	128.68
4	A	2001	AMP	N3-C2-N1	-3.17	123.72	128.68
4	G	2004	AMP	N3-C2-N1	-3.17	123.73	128.68
4	E	2003	AMP	N3-C2-N1	-3.16	123.73	128.68
4	M	2007	AMP	N3-C2-N1	-3.15	123.76	128.68
4	I	2005	AMP	N3-C2-N1	-3.12	123.80	128.68
4	A	2001	AMP	C4-C5-N7	-2.71	106.57	109.40
4	I	2005	AMP	C4-C5-N7	-2.70	106.59	109.40
4	O	2008	AMP	C4-C5-N7	-2.69	106.59	109.40
4	G	2004	AMP	C4-C5-N7	-2.69	106.60	109.40
4	K	2006	AMP	C4-C5-N7	-2.67	106.61	109.40
4	M	2007	AMP	C4-C5-N7	-2.66	106.62	109.40
4	C	2002	AMP	C4-C5-N7	-2.66	106.62	109.40
4	E	2003	AMP	C4-C5-N7	-2.66	106.63	109.40

There are no chirality outliers.

All (71) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	I	2005	AMP	C4'-C5'-O5'-P
4	M	2007	AMP	C5'-O5'-P-O2P
4	M	2007	AMP	C5'-O5'-P-O3P
3	A	1001	FLC	CAC-CA-CB-CBC
3	A	1001	FLC	CA-CB-CG-CGC
3	A	1001	FLC	CBC-CB-CG-CGC
3	A	1001	FLC	OHB-CB-CG-CGC
3	M	1007	FLC	CAC-CA-CB-CBC
3	M	1007	FLC	CA-CB-CG-CGC
3	M	1007	FLC	CBC-CB-CG-CGC
3	M	1007	FLC	OHB-CB-CG-CGC
3	G	1004	FLC	CAC-CA-CB-CBC

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Mol	Chain	Res	Type	Atoms
3	G	1004	FLC	CA-CB-CG-CGC
3	G	1004	FLC	CBC-CB-CG-CGC
3	G	1004	FLC	OHB-CB-CG-CGC
4	K	2006	AMP	C3'-C4'-C5'-O5'
3	O	1008	FLC	CAC-CA-CB-CBC
3	O	1008	FLC	CA-CB-CG-CGC
3	O	1008	FLC	CBC-CB-CG-CGC
3	O	1008	FLC	OHB-CB-CG-CGC
4	C	2002	AMP	C5'-O5'-P-O1P
4	C	2002	AMP	C5'-O5'-P-O2P
4	C	2002	AMP	C5'-O5'-P-O3P
4	C	2002	AMP	C3'-C4'-C5'-O5'
3	I	1005	FLC	CAC-CA-CB-CBC
3	I	1005	FLC	CA-CB-CG-CGC
3	I	1005	FLC	CBC-CB-CG-CGC
3	I	1005	FLC	OHB-CB-CG-CGC
3	E	1003	FLC	CAC-CA-CB-CBC
3	E	1003	FLC	CA-CB-CG-CGC
3	E	1003	FLC	CBC-CB-CG-CGC
3	E	1003	FLC	OHB-CB-CG-CGC
3	K	1006	FLC	CAC-CA-CB-CBC
3	K	1006	FLC	CA-CB-CG-CGC
3	K	1006	FLC	CBC-CB-CG-CGC
3	K	1006	FLC	OHB-CB-CG-CGC
4	G	2004	AMP	C3'-C4'-C5'-O5'
4	E	2003	AMP	C5'-O5'-P-O3P
3	C	1002	FLC	CAC-CA-CB-CBC
3	C	1002	FLC	CA-CB-CG-CGC
3	C	1002	FLC	CBC-CB-CG-CGC
3	C	1002	FLC	OHB-CB-CG-CGC
4	M	2007	AMP	C3'-C4'-C5'-O5'
4	C	2002	AMP	O4'-C4'-C5'-O5'
4	O	2008	AMP	O4'-C4'-C5'-O5'
4	M	2007	AMP	O4'-C4'-C5'-O5'
4	G	2004	AMP	O4'-C4'-C5'-O5'
4	K	2006	AMP	O4'-C4'-C5'-O5'
3	I	1005	FLC	CAC-CA-CB-OHB
4	G	2004	AMP	C5'-O5'-P-O1P
4	E	2003	AMP	C5'-O5'-P-O1P
3	C	1002	FLC	CAC-CA-CB-OHB
4	O	2008	AMP	C3'-C4'-C5'-O5'
4	E	2003	AMP	C5'-O5'-P-O2P

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Mol	Chain	Res	Type	Atoms
3	A	1001	FLC	CAC-CA-CB-OHB
3	M	1007	FLC	CAC-CA-CB-OHB
3	G	1004	FLC	CAC-CA-CB-OHB
3	O	1008	FLC	CAC-CA-CB-OHB
3	E	1003	FLC	CAC-CA-CB-OHB
3	K	1006	FLC	CAC-CA-CB-OHB
4	E	2003	AMP	C3'-C4'-C5'-O5'
4	A	2001	AMP	C4'-C5'-O5'-P
4	G	2004	AMP	C5'-O5'-P-O3P
3	A	1001	FLC	CAC-CA-CB-CG
3	M	1007	FLC	CAC-CA-CB-CG
3	G	1004	FLC	CAC-CA-CB-CG
3	O	1008	FLC	CAC-CA-CB-CG
3	I	1005	FLC	CAC-CA-CB-CG
3	E	1003	FLC	CAC-CA-CB-CG
3	K	1006	FLC	CAC-CA-CB-CG
3	C	1002	FLC	CAC-CA-CB-CG

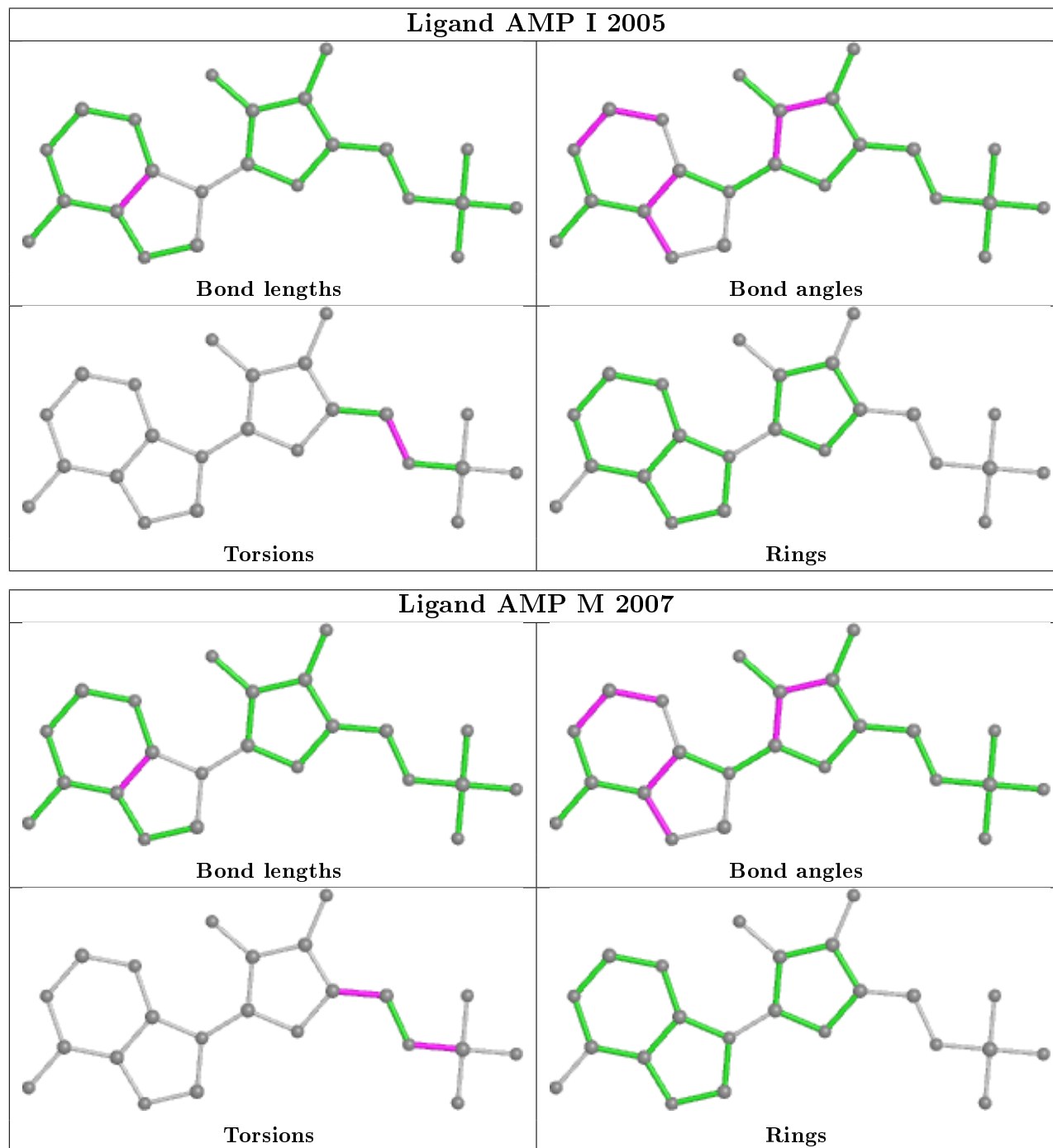
There are no ring outliers.

15 monomers are involved in 64 short contacts:

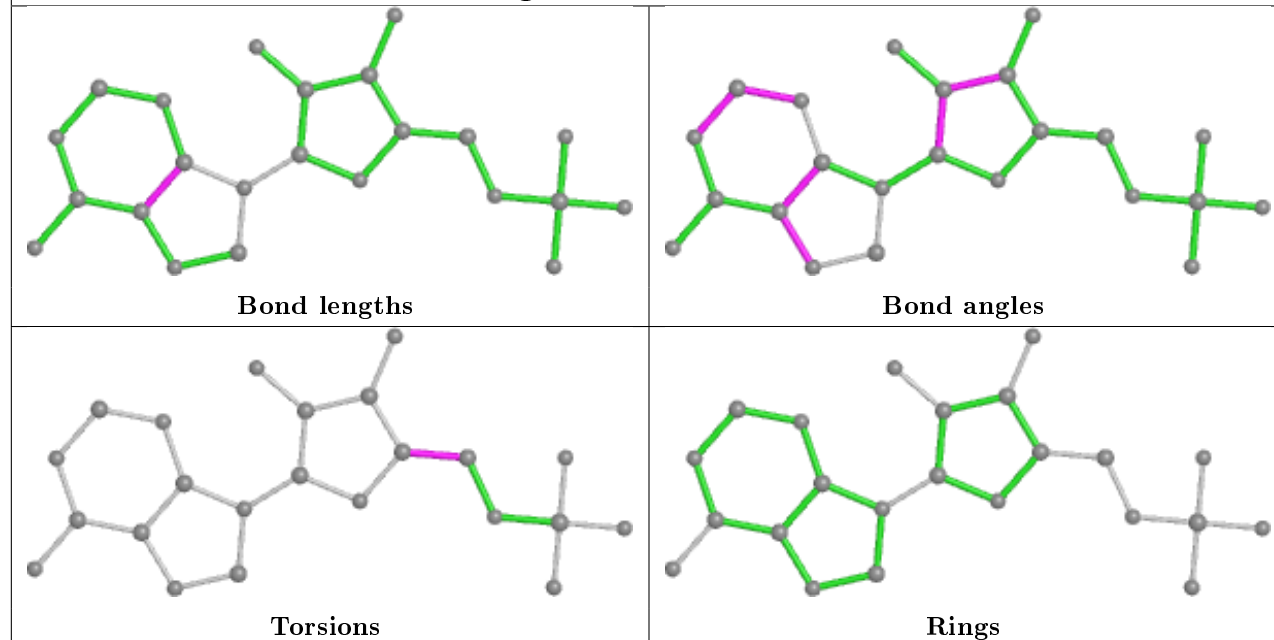
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	2005	AMP	3	0
4	M	2007	AMP	3	0
3	A	1001	FLC	5	0
3	M	1007	FLC	6	0
3	G	1004	FLC	5	0
4	K	2006	AMP	9	0
4	A	2001	AMP	2	0
3	O	1008	FLC	5	0
4	C	2002	AMP	2	0
3	I	1005	FLC	5	0
3	E	1003	FLC	4	0
3	K	1006	FLC	4	0
4	G	2004	AMP	1	0
4	E	2003	AMP	6	0
3	C	1002	FLC	4	0

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 than 5% of the Mogul distribution of torsion angles is

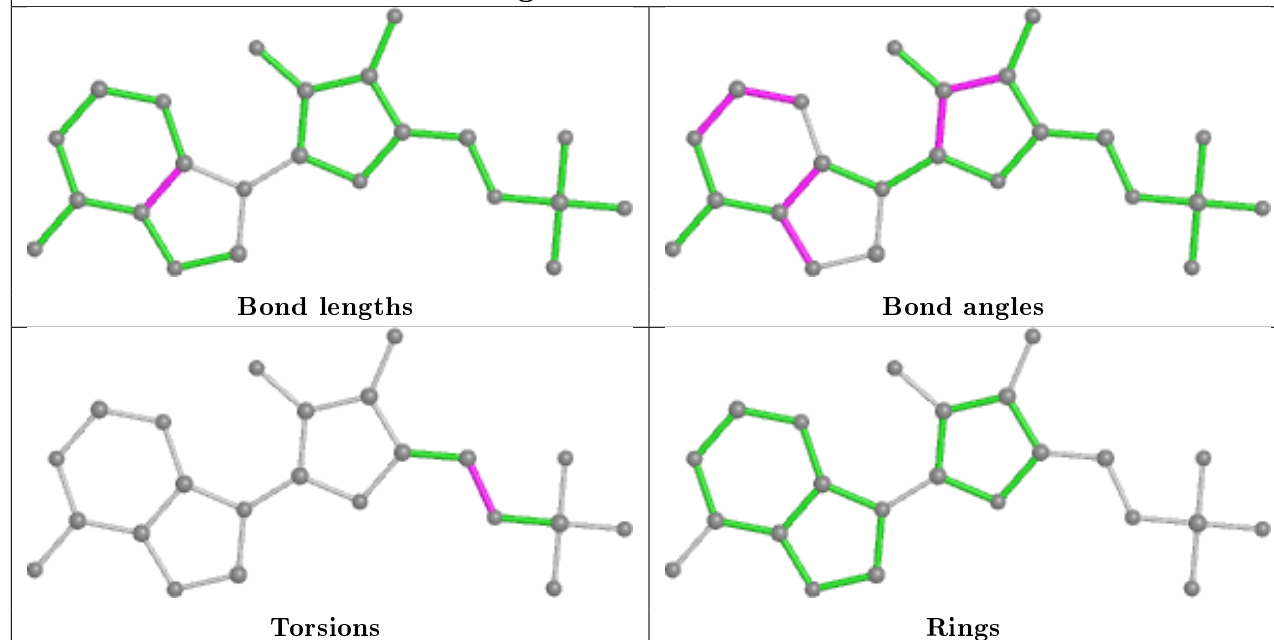
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.



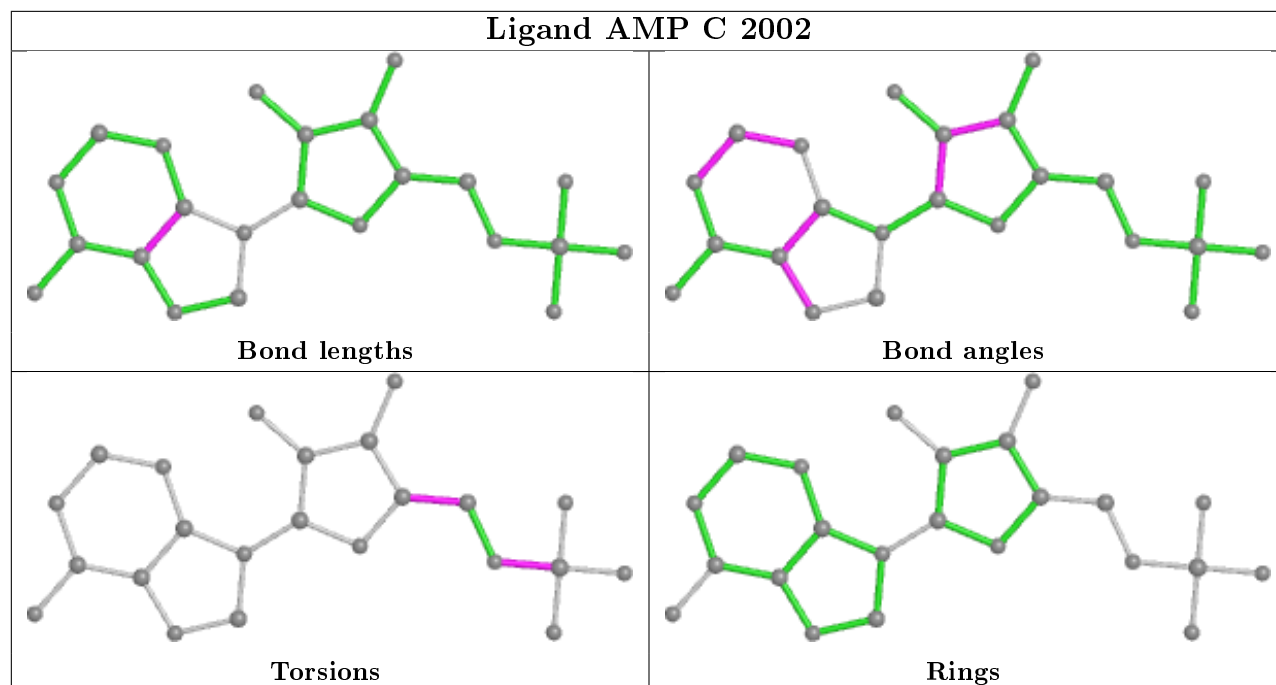
Ligand AMP K 2006



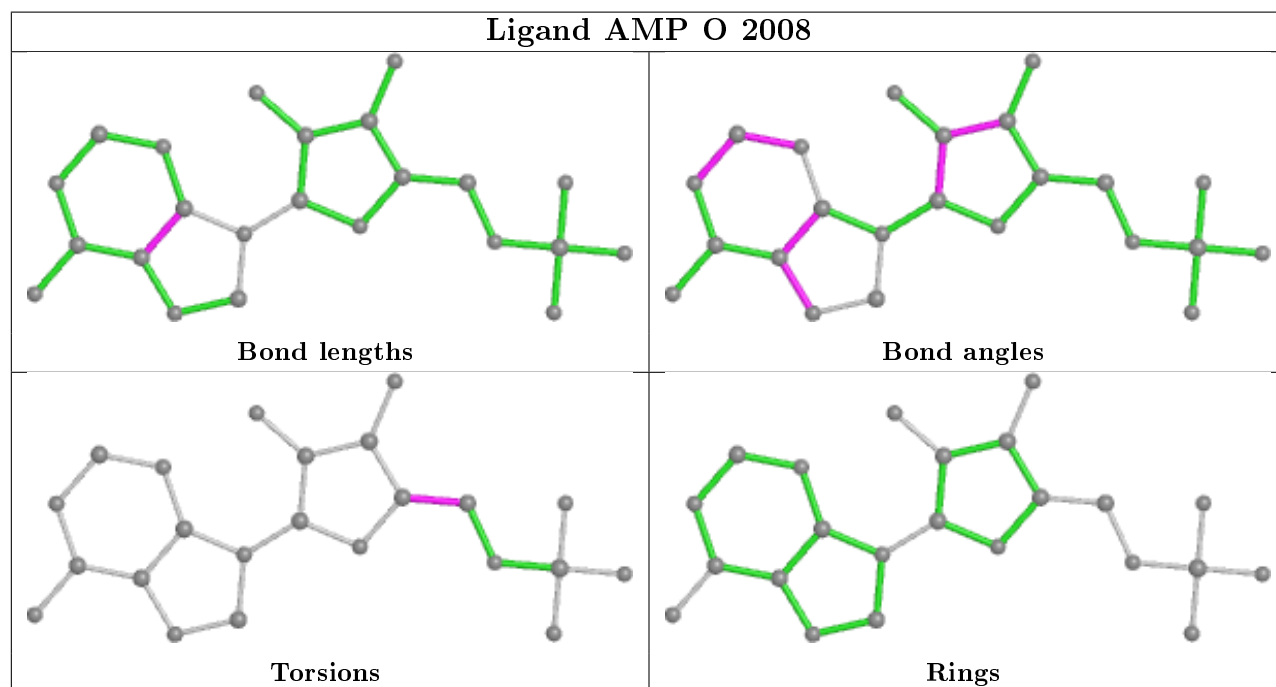
Ligand AMP A 2001

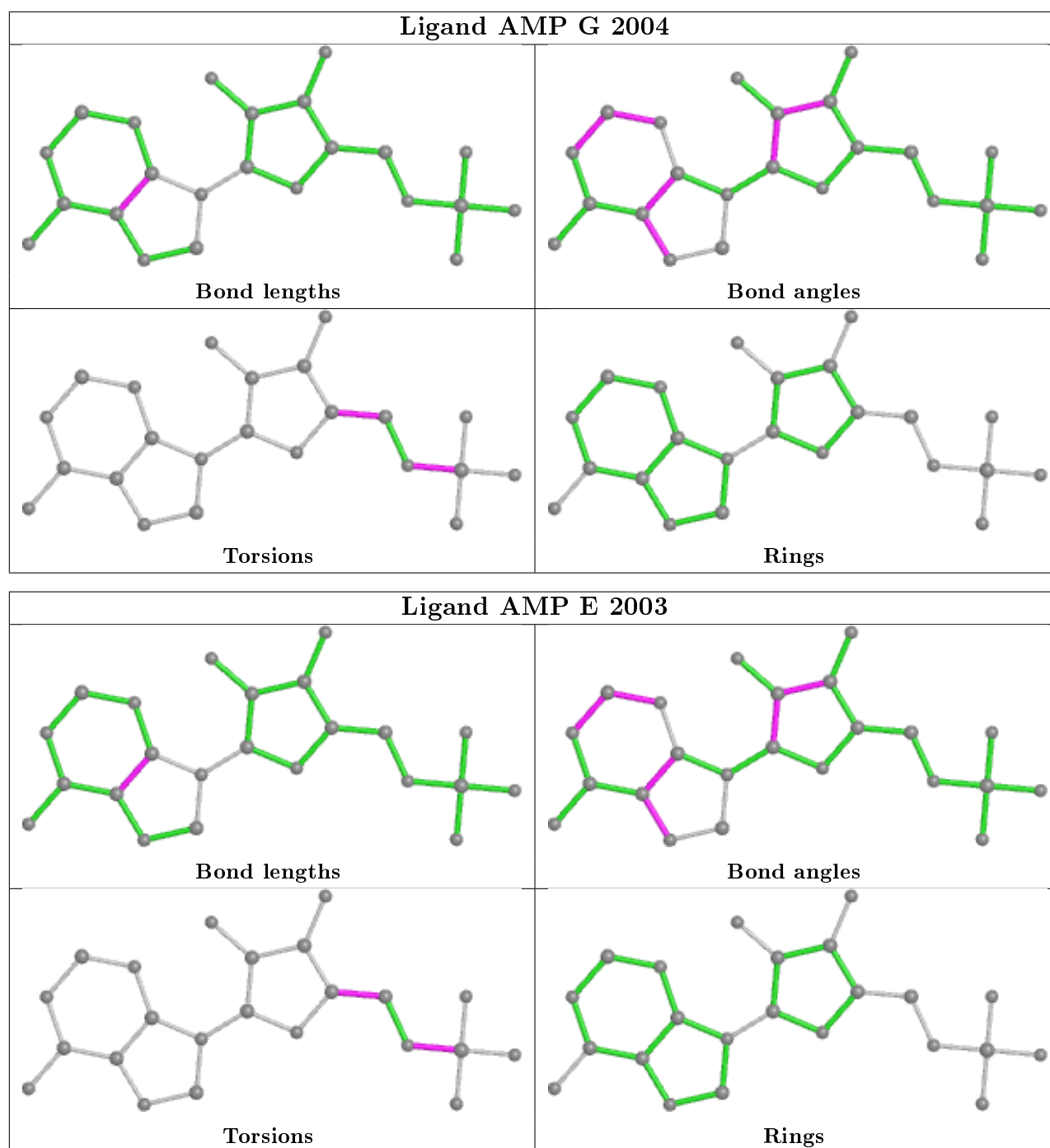


Ligand AMP C 2002



Ligand AMP O 2008





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	329/349 (94%)	-0.07	3 (0%) 84 77	120, 159, 225, 290	0
1	C	338/349 (96%)	-0.17	0 100 100	120, 151, 227, 309	0
1	E	338/349 (96%)	-0.03	4 (1%) 79 70	121, 194, 255, 288	0
1	G	329/349 (94%)	-0.16	1 (0%) 94 90	122, 185, 247, 313	0
1	I	329/349 (94%)	-0.18	1 (0%) 94 90	120, 176, 240, 331	0
1	K	337/349 (96%)	-0.01	10 (2%) 50 39	121, 195, 256, 286	0
1	M	339/349 (97%)	-0.14	0 100 100	120, 151, 210, 264	0
1	O	330/349 (94%)	-0.10	2 (0%) 89 84	120, 159, 234, 295	0
2	B	347/354 (98%)	-0.01	8 (2%) 60 51	120, 162, 233, 325	0
2	D	347/354 (98%)	-0.02	3 (0%) 84 77	121, 185, 269, 309	0
2	F	347/354 (98%)	0.15	12 (3%) 44 35	129, 234, 299, 325	0
2	H	346/354 (97%)	0.45	35 (10%) 7 7	123, 237, 317, 353	0
2	J	347/354 (98%)	0.31	18 (5%) 27 24	124, 229, 302, 357	0
2	L	346/354 (97%)	0.30	14 (4%) 38 30	137, 230, 289, 322	0
2	N	347/354 (98%)	0.10	9 (2%) 56 46	120, 186, 270, 304	0
2	P	347/354 (98%)	0.01	7 (2%) 65 56	120, 162, 234, 316	0
All	All	5443/5624 (96%)	0.03	127 (2%) 60 51	120, 185, 276, 357	0

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	82	VAL	6.4
2	J	65	GLY	4.7
2	N	28	GLU	4.5
2	H	59	SER	4.4
2	H	67	THR	4.3

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Mol	Chain	Res	Type	RSRZ
2	J	67	THR	4.2
2	H	333	ARG	3.9
2	J	64	ASN	3.6
2	H	81	LEU	3.6
2	L	53	TRP	3.6
2	N	14	LYS	3.5
2	H	44	PHE	3.5
2	H	80	ASN	3.5
2	H	332	ASN	3.5
2	J	66	LEU	3.5
2	J	333	ARG	3.5
2	L	87	PRO	3.5
2	H	121	GLY	3.4
2	J	97	ARG	3.4
2	B	96	HIS	3.4
2	B	353	ARG	3.3
2	J	332	ASN	3.3
2	J	18	SER	3.3
2	J	282	GLY	3.3
2	P	333	ARG	3.3
2	H	122	PHE	3.3
2	L	272	HIS	3.2
2	N	353	ARG	3.2
2	H	62	PHE	3.2
1	K	87	GLN	3.2
2	L	205	LYS	3.2
2	N	82	VAL	3.2
2	F	26	PHE	3.1
1	E	60	LYS	3.1
2	J	190	SER	3.1
2	H	352	LYS	3.1
2	H	312	THR	3.1
2	F	272	HIS	3.0
1	K	176	LYS	3.0
2	H	354	LEU	3.0
2	D	82	VAL	3.0
1	K	202	GLY	2.9
2	L	241	VAL	2.9
2	H	17	PRO	2.8
1	A	346	LEU	2.8
2	L	338	ALA	2.8
1	K	83	THR	2.8

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Mol	Chain	Res	Type	RSRZ
2	N	333	ARG	2.8
1	K	60	LYS	2.8
2	H	24	VAL	2.7
2	P	354	LEU	2.7
2	H	331	GLU	2.7
1	E	87	GLN	2.6
2	H	25	SER	2.6
2	H	320	ASN	2.6
2	B	232	PRO	2.6
2	N	83	ALA	2.6
1	K	321	GLU	2.6
2	J	96	HIS	2.6
2	H	83	ALA	2.6
2	B	310	GLY	2.6
2	H	293	ALA	2.5
2	L	177	ARG	2.5
2	J	59	SER	2.5
2	J	16	ASN	2.5
2	P	353	ARG	2.5
2	F	331	GLU	2.5
2	H	341	ALA	2.5
2	J	341	ALA	2.4
2	J	334	THR	2.4
1	G	286	ALA	2.4
2	N	334	THR	2.4
2	P	85	LYS	2.4
1	I	203	GLN	2.4
1	E	321	GLU	2.4
1	O	60	LYS	2.4
2	H	334	THR	2.4
2	H	77	ILE	2.4
2	J	340	THR	2.3
1	K	315	VAL	2.3
1	A	87	GLN	2.3
2	B	311	LEU	2.3
2	B	354	LEU	2.3
2	H	49	VAL	2.3
2	J	17	PRO	2.3
1	K	325	THR	2.3
2	H	48	ASN	2.3
2	F	53	TRP	2.3
2	H	16	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
2	H	64	ASN	2.2
1	E	253	GLY	2.2
2	B	121	GLY	2.2
2	L	340	THR	2.2
1	K	324	HIS	2.2
2	B	240	SER	2.2
2	H	328	SER	2.2
1	O	346	LEU	2.2
2	D	28	GLU	2.2
2	F	232	PRO	2.2
2	L	18	SER	2.2
2	F	343	THR	2.2
2	N	111	ALA	2.2
2	L	334	THR	2.2
2	P	183	ARG	2.2
2	L	191	THR	2.2
2	H	45	SER	2.2
2	F	87	PRO	2.1
2	D	126	TYR	2.1
2	P	120	GLU	2.1
2	L	51	ILE	2.1
2	L	341	ALA	2.1
2	F	25	SER	2.1
2	F	194	ARG	2.1
2	F	96	HIS	2.1
2	P	328	SER	2.1
2	L	206	GLU	2.1
2	H	58	VAL	2.1
2	H	40	VAL	2.1
2	N	18	SER	2.1
2	F	241	VAL	2.1
2	H	65	GLY	2.1
1	A	266	TYR	2.1
1	K	275	HIS	2.0
2	H	340	THR	2.0
2	J	216	LEU	2.0
2	F	126	TYR	2.0
2	H	351	ILE	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

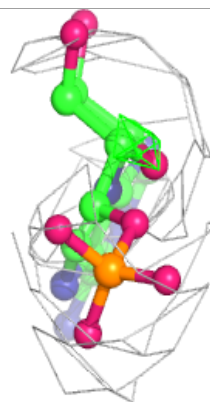
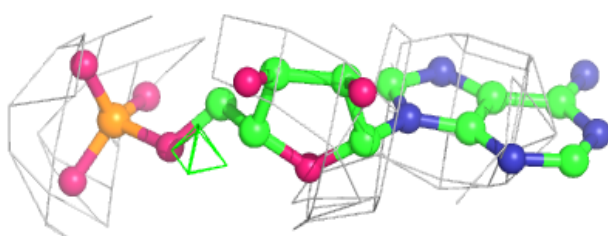
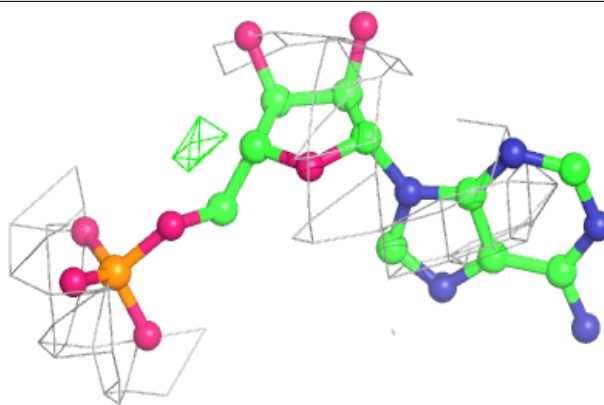
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	FLC	C	1002	13/13	0.71	0.34	179,179,179,179	0
4	AMP	K	2006	23/23	0.78	0.42	240,240,240,240	0
4	AMP	E	2003	23/23	0.79	0.36	215,215,215,215	0
4	AMP	G	2004	23/23	0.79	0.49	164,164,164,164	0
3	FLC	O	1008	13/13	0.81	0.34	148,148,148,148	0
3	FLC	I	1005	13/13	0.83	0.29	185,185,185,185	0
4	AMP	M	2007	23/23	0.83	0.29	137,137,137,137	0
4	AMP	A	2001	23/23	0.84	0.26	150,150,150,150	0
3	FLC	A	1001	13/13	0.84	0.32	121,121,121,121	0
4	AMP	I	2005	23/23	0.86	0.34	162,162,162,162	0
3	FLC	M	1007	13/13	0.86	0.31	158,158,158,158	0
3	FLC	K	1006	13/13	0.86	0.32	155,155,155,155	0
4	AMP	O	2008	23/23	0.87	0.26	135,135,135,135	0
3	FLC	G	1004	13/13	0.88	0.20	192,192,192,192	0
3	FLC	E	1003	13/13	0.88	0.31	173,173,173,173	0
4	AMP	C	2002	23/23	0.91	0.23	148,148,148,148	0

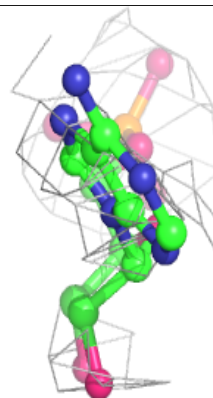
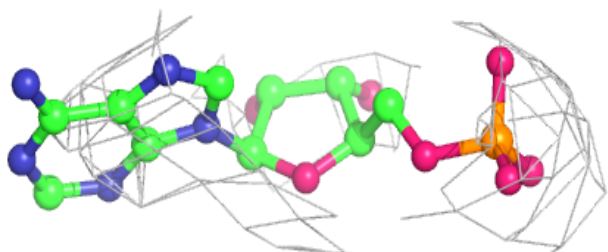
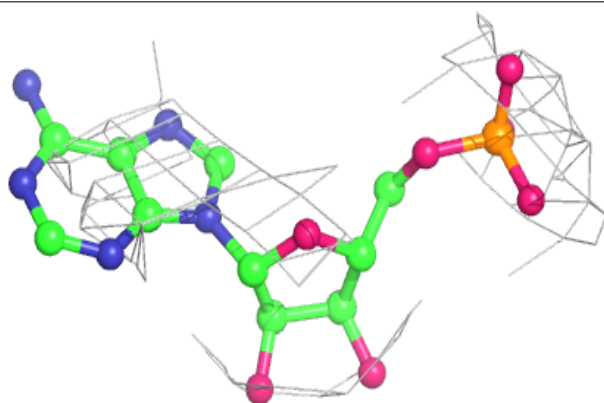
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around AMP K 2006:

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

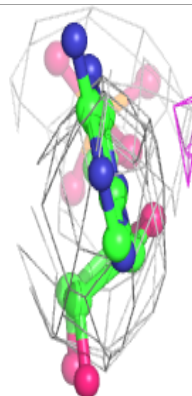
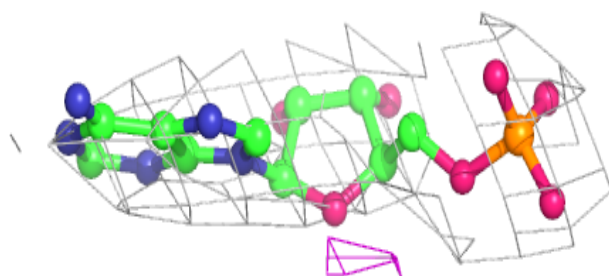
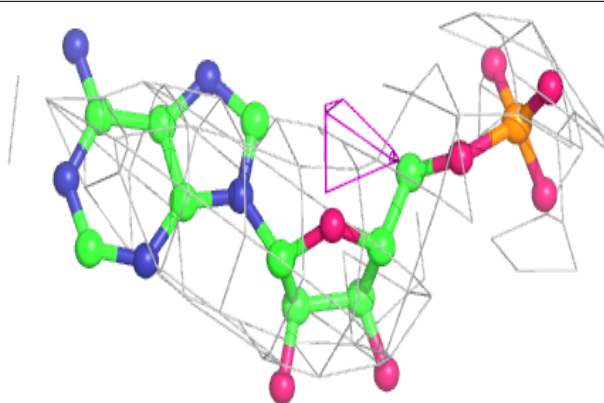
**Electron density around AMP E 2003:**

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

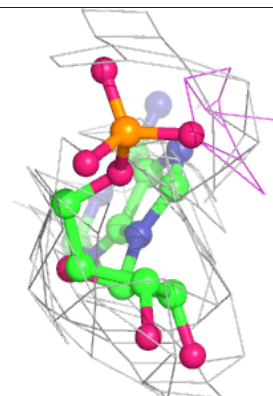
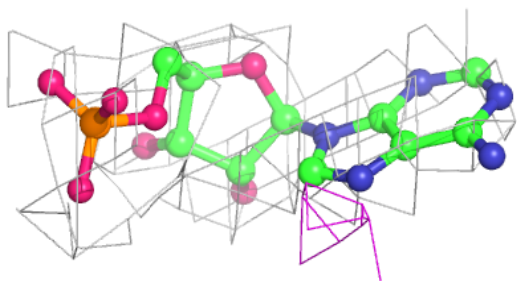
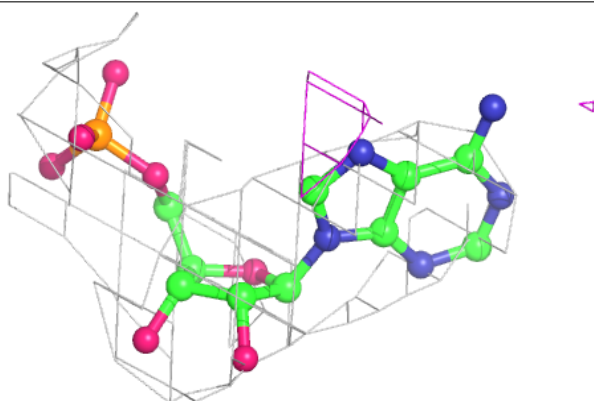


Electron density around AMP G 2004:

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

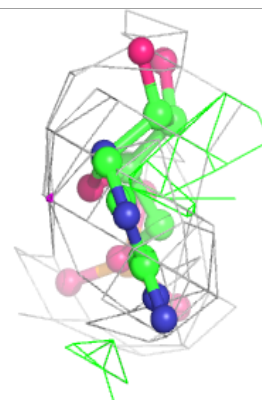
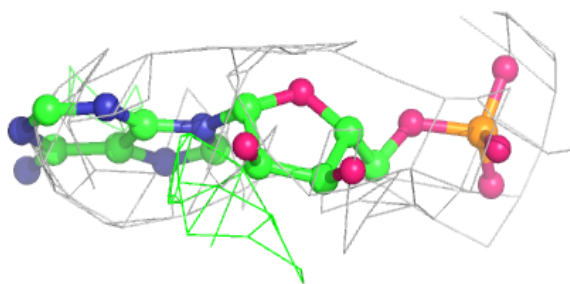
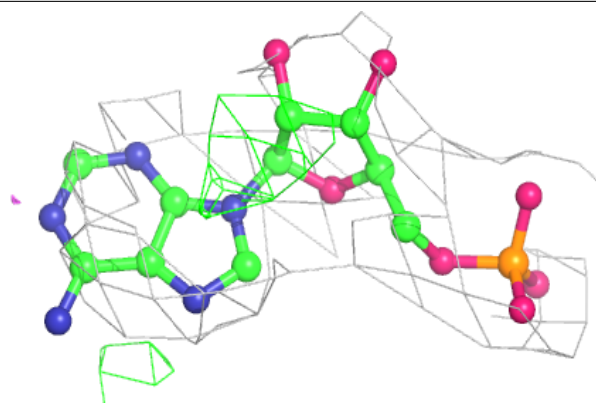
**Electron density around AMP M 2007:**

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

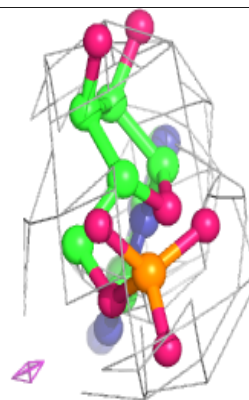
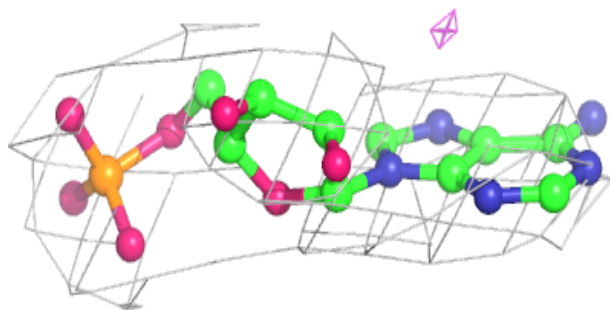
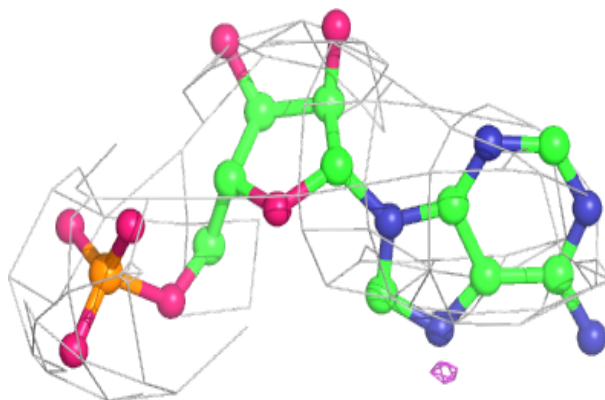


Electron density around AMP A 2001:

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

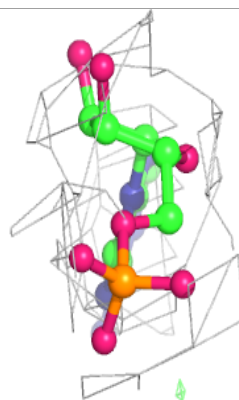
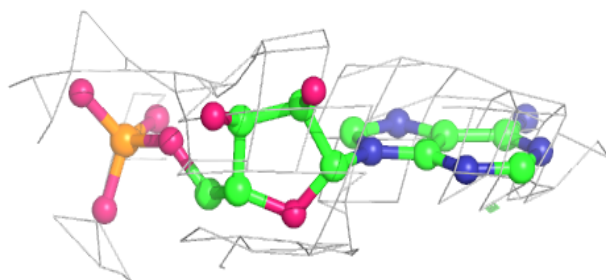
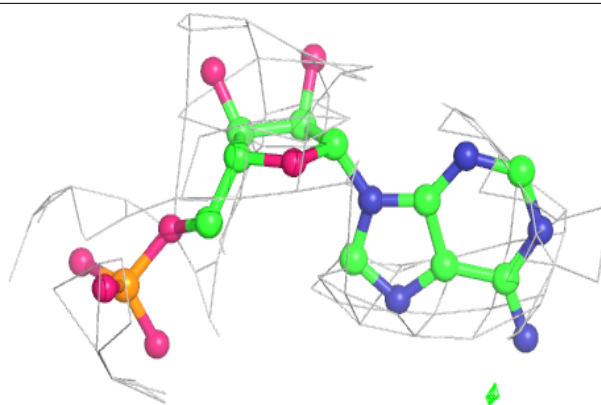
**Electron density around AMP I 2005:**

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

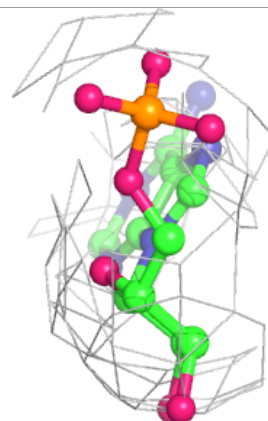
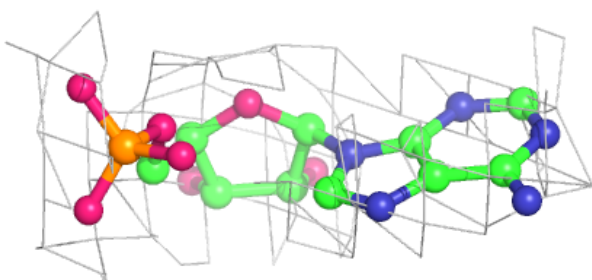
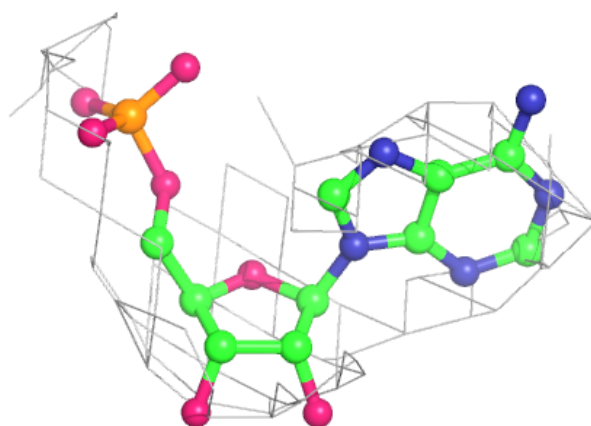


Electron density around AMP O 2008:

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

**Electron density around AMP C 2002:**

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



6.5 Other polymers

There are no such residues in this entry.