



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 11:36 AM UTC

PDB ID : 6X6S / pdb_00006x6s
EMDB ID : EMD-22081
Title : Cryo-EM Structure of the Helicobacter pylori OMC
Authors : Sheedlo, M.J.; Chung, J.M.; Sawhney, N.; Durie, C.L.; Cover, T.L.; Ohi, M.D.;
Lacy, D.B.
Deposited on : 2020-05-29
Resolution : 3.40 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

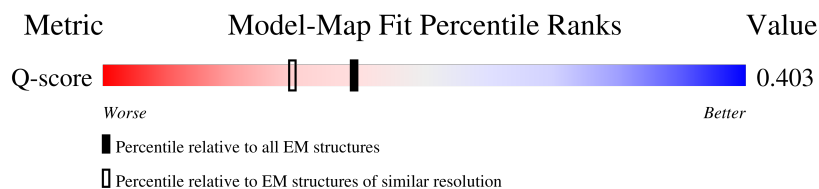
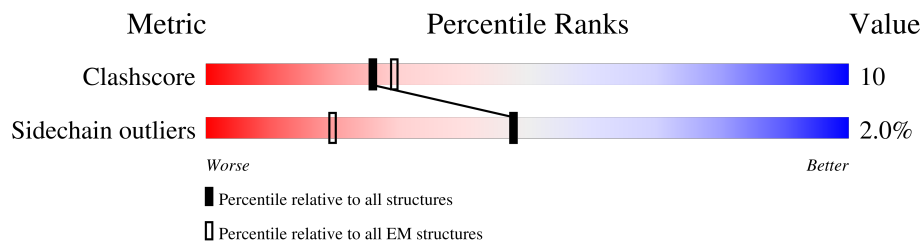
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	481	11% 36% 14% • 48%
1	AB	481	12% 6% 81%
1	AC	481	12% 7% 81%
1	AD	481	7% 12% 7% 80%
1	AE	481	10% 12% 9% 78%

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Mol	Chain	Length	Quality of chain
1	BA	481	
1	BB	481	
1	BC	481	
1	BD	481	
1	BE	481	
1	CA	481	
1	CB	481	
1	CC	481	
1	CD	481	
1	CE	481	
1	DA	481	
1	DB	481	
1	DC	481	
1	DD	481	
1	DE	481	
1	EA	481	
1	EB	481	
1	EC	481	
1	ED	481	
1	EE	481	
1	FA	481	
1	FB	481	
1	FC	481	
1	FD	481	
1	FE	481	

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Mol	Chain	Length	Quality of chain
1	GA	481	
1	GB	481	
1	GC	481	
1	GD	481	
1	GE	481	
1	HA	481	
1	HB	481	
1	HC	481	
1	HD	481	
1	HE	481	
1	IA	481	
1	IB	481	
1	IC	481	
1	ID	481	
1	IE	481	
1	JA	481	
1	JB	481	
1	JC	481	
1	JD	481	
1	JE	481	
1	KA	481	
1	KB	481	
1	KC	481	
1	KD	481	
1	KE	481	

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Mol	Chain	Length	Quality of chain
1	LA	481	
1	LB	481	
1	LC	481	
1	LD	481	
1	LE	481	
1	MA	481	
1	MB	481	
1	MC	481	
1	MD	481	
1	ME	481	
1	NA	481	
1	NB	481	
1	NC	481	
1	ND	481	
1	NE	481	
2	AM	376	
2	Am	376	
2	BM	376	
2	Bm	376	
2	CM	376	
2	Cm	376	
2	DM	376	
2	Dm	376	
2	EM	376	
2	Em	376	

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Mol	Chain	Length	Quality of chain
2	FM	376	
2	Fm	376	
2	GM	376	
2	Gm	376	
2	HM	376	
2	Hm	376	
2	IM	376	
2	Im	376	
2	JM	376	
2	Jm	376	
2	KM	376	
2	Km	376	
2	LM	376	
2	Lm	376	
2	MM	376	
2	Mm	376	
2	NM	376	
2	Nm	376	
3	AT	280	
3	At	280	
3	BT	280	
3	Bt	280	
3	CT	280	
3	Ct	280	
3	DT	280	

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Mol	Chain	Length	Quality of chain
3	Dt	280	
3	ET	280	
3	Et	280	
3	FT	280	
3	Ft	280	
3	GT	280	
3	Gt	280	
3	HT	280	
3	Ht	280	
3	IT	280	
3	It	280	
3	JT	280	
3	Jt	280	
3	KT	280	
3	Kt	280	
3	LT	280	
3	Lt	280	
3	MT	280	
3	Mt	280	
3	NT	280	
3	Nt	280	
4	AU	160	
4	BU	160	
4	CU	160	
4	DU	160	

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Mol	Chain	Length	Quality of chain
4	EU	160	58% 99%
4	FU	160	58% 99%
4	GU	160	58% 99%
4	HU	160	59% 99%
4	IU	160	56% 99%
4	JU	160	55% 99%
4	KU	160	58% 99%
4	LU	160	58% 99%
4	MU	160	58% 99%
4	NU	160	57% 99%
5	AX	522	24% 7% 68%
5	BX	522	24% 7% 68%
5	CX	522	25% 6% 68%
5	DX	522	24% 7% 68%
5	EX	522	24% 7% 68%
5	FX	522	24% 7% 68%
5	GX	522	25% 7% 68%
5	HX	522	24% 7% 68%
5	IX	522	24% 7% 68%
5	JX	522	23% 8% 68%
5	KX	522	24% 7% 68%
5	LX	522	25% 6% 68%
5	MX	522	24% 7% 68%
5	NX	522	24% 7% 68%
6	AY	1927	8% 89%

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Mol	Chain	Length	Quality of chain
6	BY	1927	 89%
6	CY	1927	 89%
6	DY	1927	 89%
6	EY	1927	 89%
6	FY	1927	 89%
6	GY	1927	 89%
6	HY	1927	 89%
6	IY	1927	 89%
6	JY	1927	 89%
6	KY	1927	 89%
6	LY	1927	 89%
6	MY	1927	 89%
6	NY	1927	 89%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 215978 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Type IV secretion system apparatus protein Cag3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	AB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	AC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	AD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	AE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	BA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	BB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	BC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	BD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	BE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	CA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	CB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	CC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	CD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	CE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	DA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	DB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	DD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	DE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	EA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	EB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	EC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	ED	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	EE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	FA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	FB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	FC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	FD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	FE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	GA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	GB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	GC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	GD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	GE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	HA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	HB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	HC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	HD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	HE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	IA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	IB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	IC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	ID	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	IE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	JA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	JB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	JC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	JD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	JE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	KA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	KB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	KC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	KD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	KE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	LA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	LB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	LC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	LD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	LE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	MA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	MB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	MC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	MD	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	ME	104	Total	C	N	O	S	0	0
			847	549	136	159	3		
1	NA	248	Total	C	N	O	S	0	0
			1986	1254	329	395	8		
1	NB	90	Total	C	N	O	S	0	0
			728	468	122	135	3		
1	NC	92	Total	C	N	O	S	0	0
			741	476	125	137	3		
1	ND	95	Total	C	N	O	S	0	0
			778	508	124	143	3		
1	NE	104	Total	C	N	O	S	0	0
			847	549	136	159	3		

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
AB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
AC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
AD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
AE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
BA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
BB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
BC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
BD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
BE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
CA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
CB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
CC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
CD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
CE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
DA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
DB	275	ALA	GLN	conflict	UNP A0A2J9KJK3

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Chain	Residue	Modelled	Actual	Comment	Reference
DC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
DD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
DE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
EA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
EB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
EC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
ED	275	ALA	GLN	conflict	UNP A0A2J9KJK3
EE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
FA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
FB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
FC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
FD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
FE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
GA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
GB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
GC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
GD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
GE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
HA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
HB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
HC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
HD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
HE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
IA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
IB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
IC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
ID	275	ALA	GLN	conflict	UNP A0A2J9KJK3
IE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
JA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
JB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
JC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
JD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
JE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
KA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
KB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
KC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
KD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
KE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
LA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
LB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
LC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
LD	275	ALA	GLN	conflict	UNP A0A2J9KJK3

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Chain	Residue	Modelled	Actual	Comment	Reference
LE	275	ALA	GLN	conflict	UNP A0A2J9KJK3
MA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
MB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
MC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
MD	275	ALA	GLN	conflict	UNP A0A2J9KJK3
ME	275	ALA	GLN	conflict	UNP A0A2J9KJK3
NA	275	ALA	GLN	conflict	UNP A0A2J9KJK3
NB	275	ALA	GLN	conflict	UNP A0A2J9KJK3
NC	275	ALA	GLN	conflict	UNP A0A2J9KJK3
ND	275	ALA	GLN	conflict	UNP A0A2J9KJK3
NE	275	ALA	GLN	conflict	UNP A0A2J9KJK3

- Molecule 2 is a protein called Type IV secretion system apparatus protein CagM.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Am	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	BM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Bm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	CM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Cm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	DM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Dm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	EM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Em	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	FM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Fm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	GM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Gm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	HM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Hm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	IM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Im	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	JM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Jm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	KM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Km	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	LM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Lm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	MM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Mm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		
2	NM	180	Total	C	N	O	S	0	0
			1485	945	250	285	5		
2	Nm	179	Total	C	N	O	S	0	0
			1474	939	246	284	5		

- Molecule 3 is a protein called Type IV secretion system apparatus protein CagT.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AT	253	Total	C	N	O	S	0	0
			2083	1308	368	402	5		
3	At	192	Total	C	N	O	S	0	0
			1615	1021	283	308	3		
3	BT	253	Total	C	N	O	S	0	0
			2083	1308	368	402	5		
3	Bt	192	Total	C	N	O	S	0	0
			1615	1021	283	308	3		
3	CT	253	Total	C	N	O	S	0	0
			2083	1308	368	402	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ct	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	DT	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	Dt	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	ET	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	Et	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	FT	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	Ft	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	GT	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	Gt	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	HT	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	Ht	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	IT	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	It	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	JT	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	Jt	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	KT	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	Kt	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	LT	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	Lt	192	Total 1615	C 1021	N 283	O 308	S 3	0	0
3	MT	253	Total 2083	C 1308	N 368	O 402	S 5	0	0
3	Mt	192	Total 1615	C 1021	N 283	O 308	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	NT	253	Total	C	N	O	S	0	0
			2083	1308	368	402	5		
3	Nt	192	Total	C	N	O	S	0	0
			1615	1021	283	308	3		

- Molecule 4 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AU	160	Total	C	N	O		0	0
			800	480	160	160			
4	BU	160	Total	C	N	O		0	0
			800	480	160	160			
4	CU	160	Total	C	N	O		0	0
			800	480	160	160			
4	DU	160	Total	C	N	O		0	0
			800	480	160	160			
4	EU	160	Total	C	N	O		0	0
			800	480	160	160			
4	FU	160	Total	C	N	O		0	0
			800	480	160	160			
4	GU	160	Total	C	N	O		0	0
			800	480	160	160			
4	HU	160	Total	C	N	O		0	0
			800	480	160	160			
4	IU	160	Total	C	N	O		0	0
			800	480	160	160			
4	JU	160	Total	C	N	O		0	0
			800	480	160	160			
4	KU	160	Total	C	N	O		0	0
			800	480	160	160			
4	LU	160	Total	C	N	O		0	0
			800	480	160	160			
4	MU	160	Total	C	N	O		0	0
			800	480	160	160			
4	NU	160	Total	C	N	O		0	0
			800	480	160	160			

- Molecule 5 is a protein called Type IV secretion system apparatus protein CagX.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	BX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	CX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	DX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	EX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	FX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	GX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	HX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	IX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	JX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	KX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	LX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	MX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		
5	NX	166	Total	C	N	O	S	0	0
			1361	871	237	248	5		

- Molecule 6 is a protein called Cag pathogenicity island protein (Cag7).

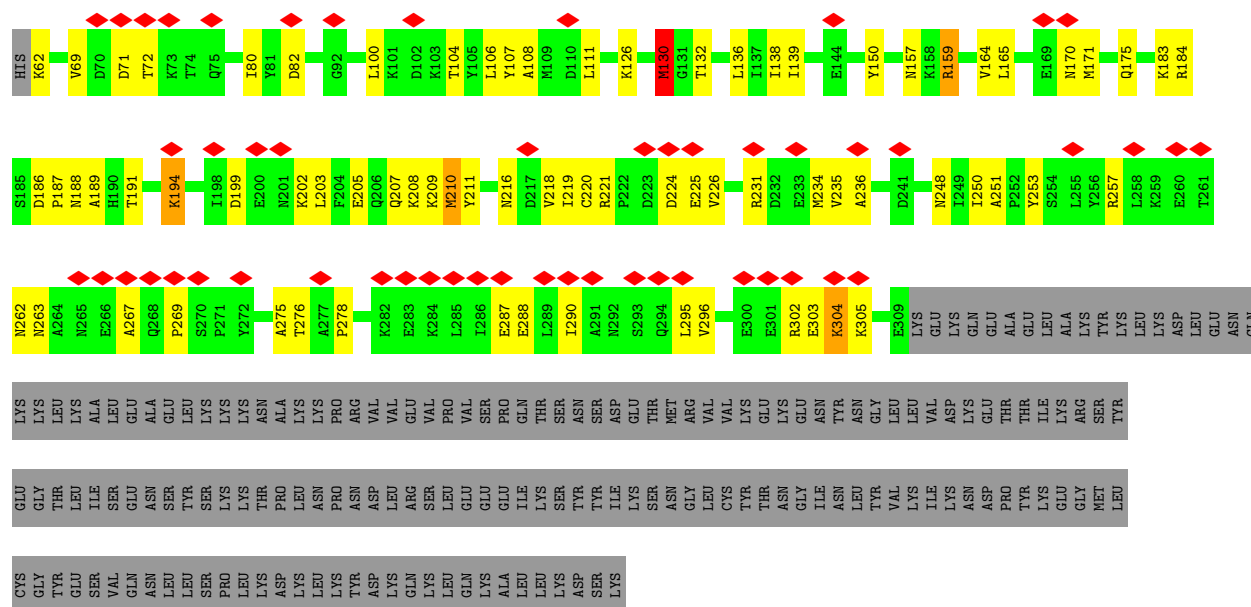
Mol	Chain	Residues	Atoms					AltConf	Trace
6	AY	203	Total	C	N	O	S	0	0
			1529	982	246	292	9		
6	BY	203	Total	C	N	O	S	0	0
			1529	982	246	292	9		
6	CY	203	Total	C	N	O	S	0	0
			1529	982	246	292	9		
6	DY	203	Total	C	N	O	S	0	0
			1529	982	246	292	9		
6	EY	203	Total	C	N	O	S	0	0
			1529	982	246	292	9		
6	FY	203	Total	C	N	O	S	0	0
			1529	982	246	292	9		

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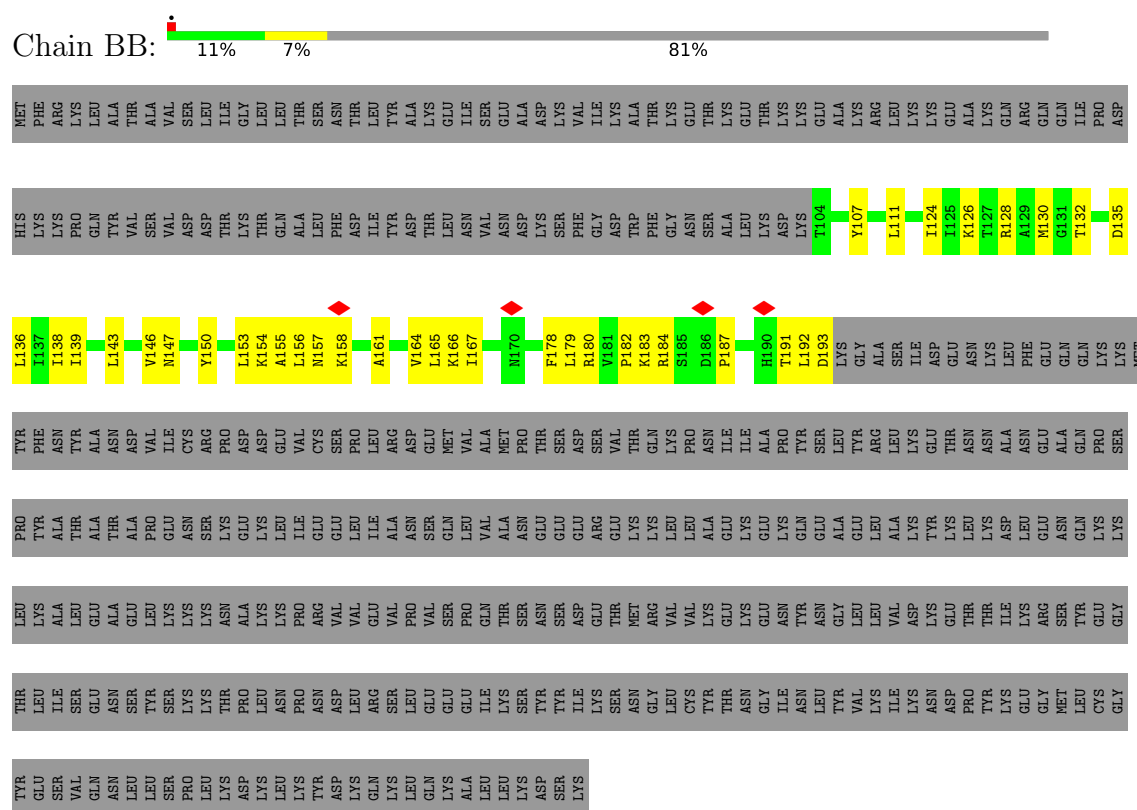
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Mol	Chain	Residues	Atoms					AltConf	Trace
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6	HY	203	Total 1529	C 982	N 246	O 292	S 9	0	0
6	IY	203	Total 1529	C 982	N 246	O 292	S 9	0	0
6	JY	203	Total 1529	C 982	N 246	O 292	S 9	0	0
6	KY	203	Total 1529	C 982	N 246	O 292	S 9	0	0
6	LY	203	Total 1529	C 982	N 246	O 292	S 9	0	0
6	MY	203	Total 1529	C 982	N 246	O 292	S 9	0	0
6	NY	203	Total 1529	C 982	N 246	O 292	S 9	0	0

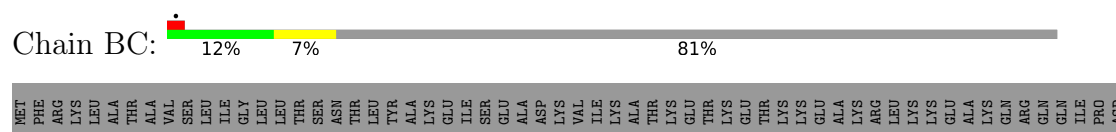


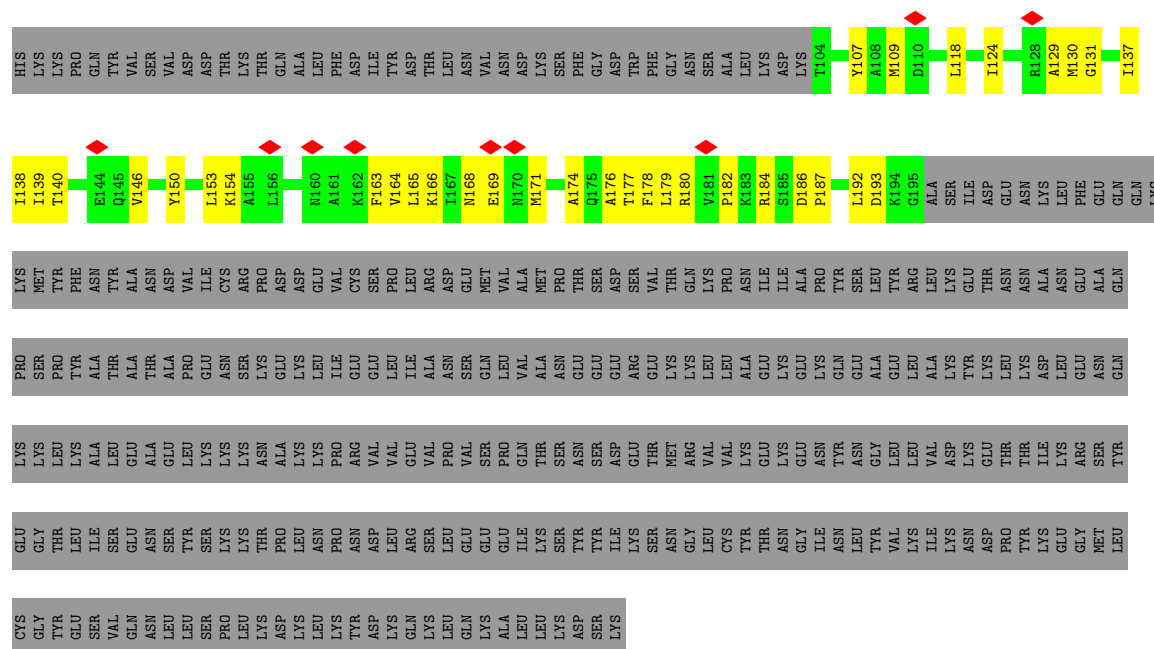


- Molecule 1: Type IV secretion system apparatus protein Cag3

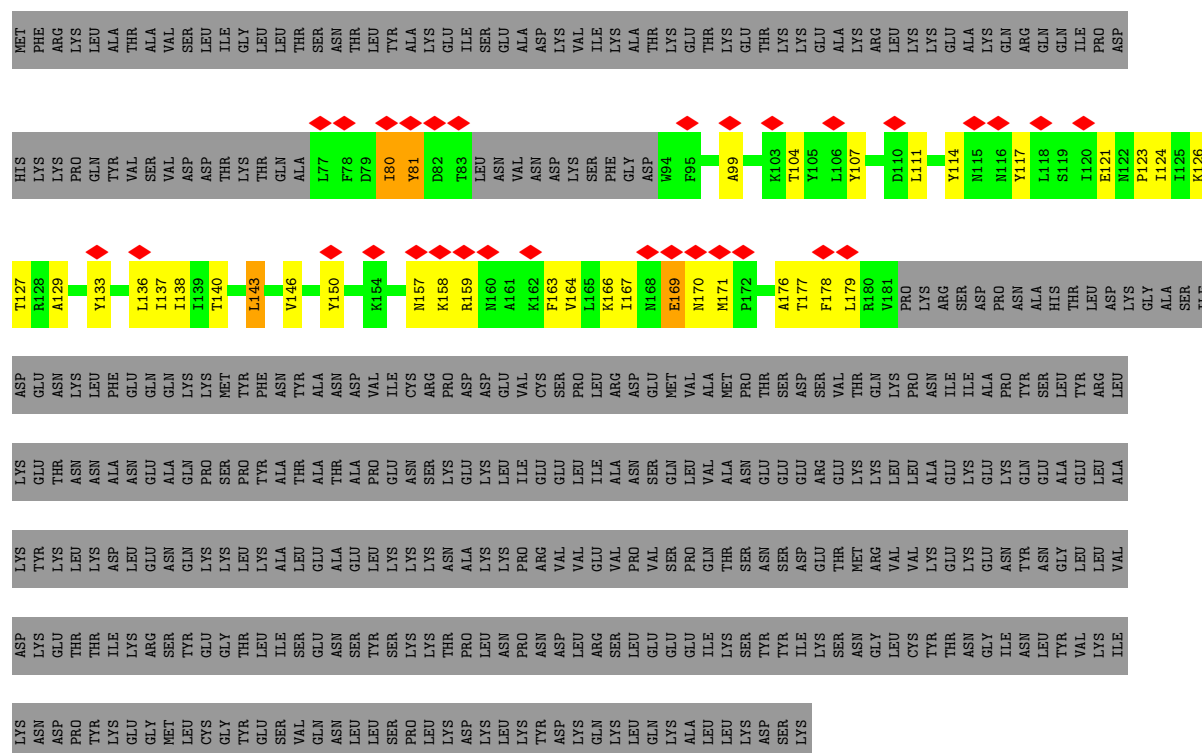


- Molecule 1: Type IV secretion system apparatus protein Cag3



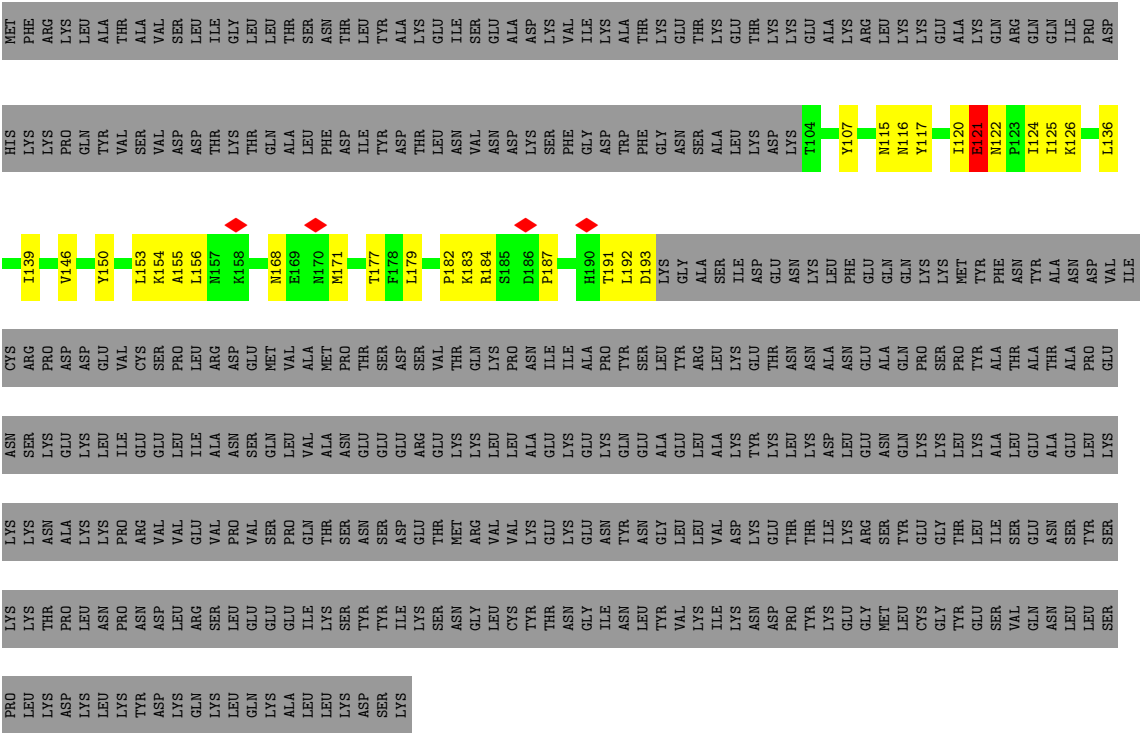


• Molecule 1: Type IV secretion system apparatus protein Cag3

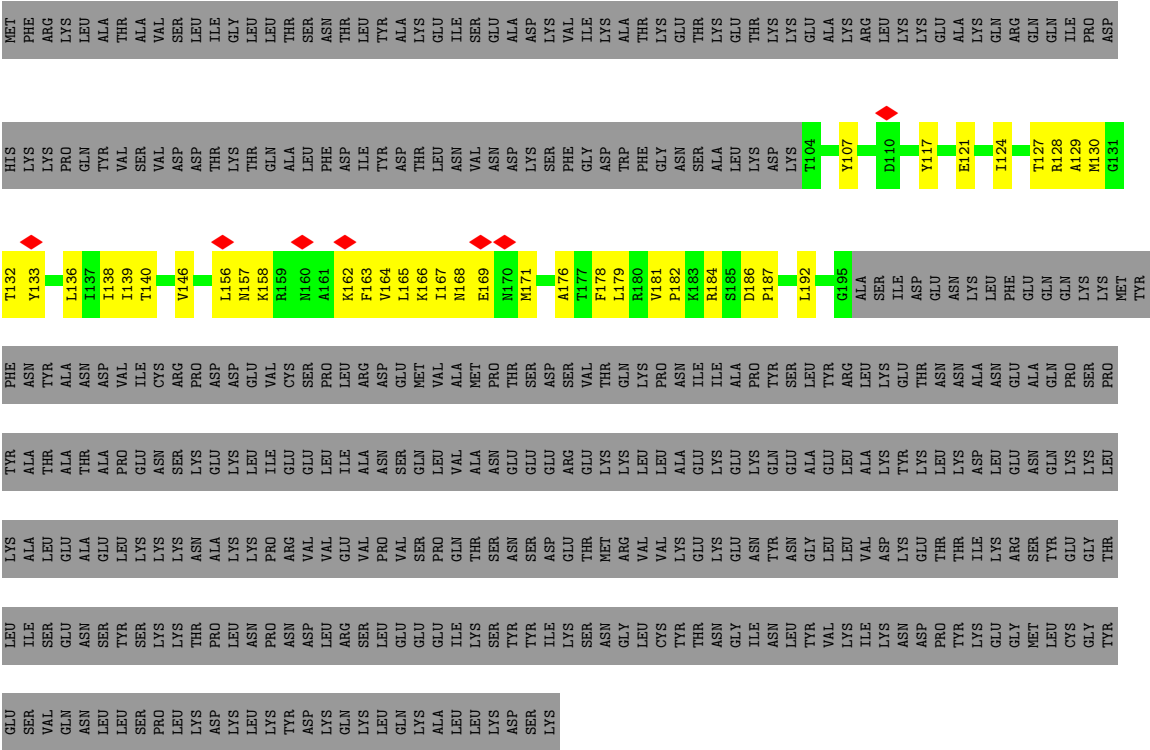


• Molecule 1: Type IV secretion system apparatus protein Cag3



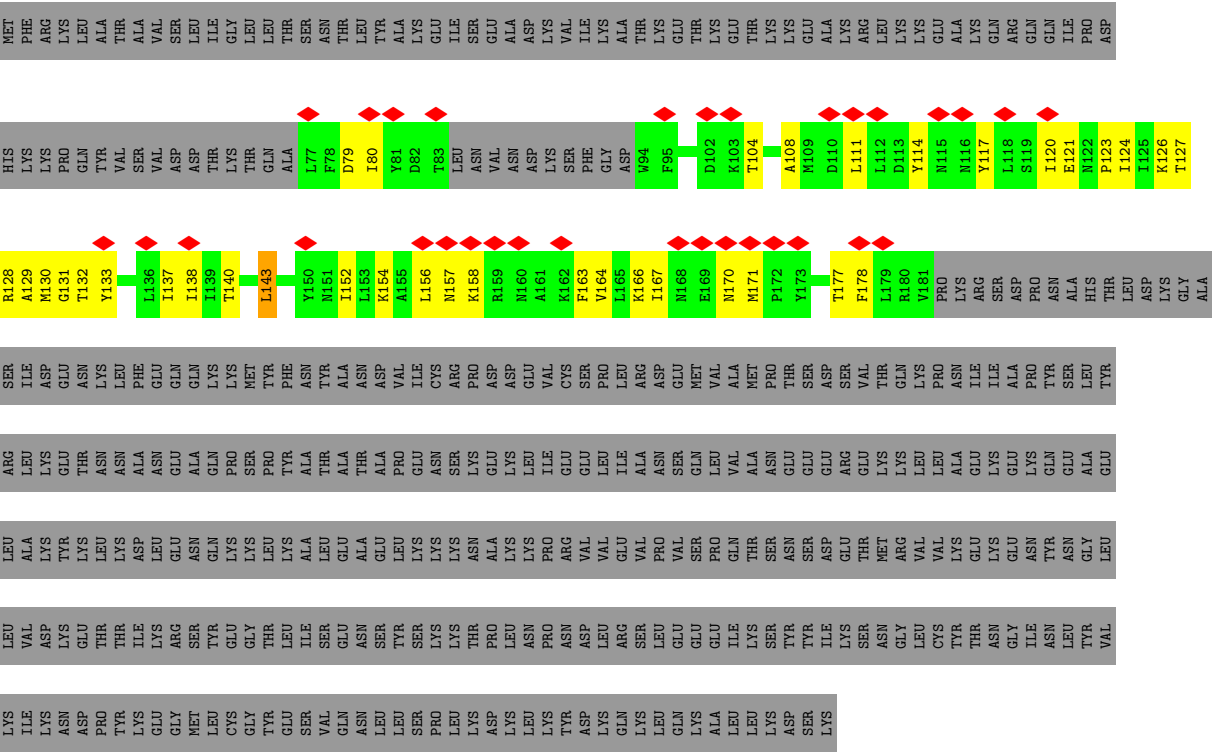


● Molecule 1: Type IV secretion system apparatus protein Cag3

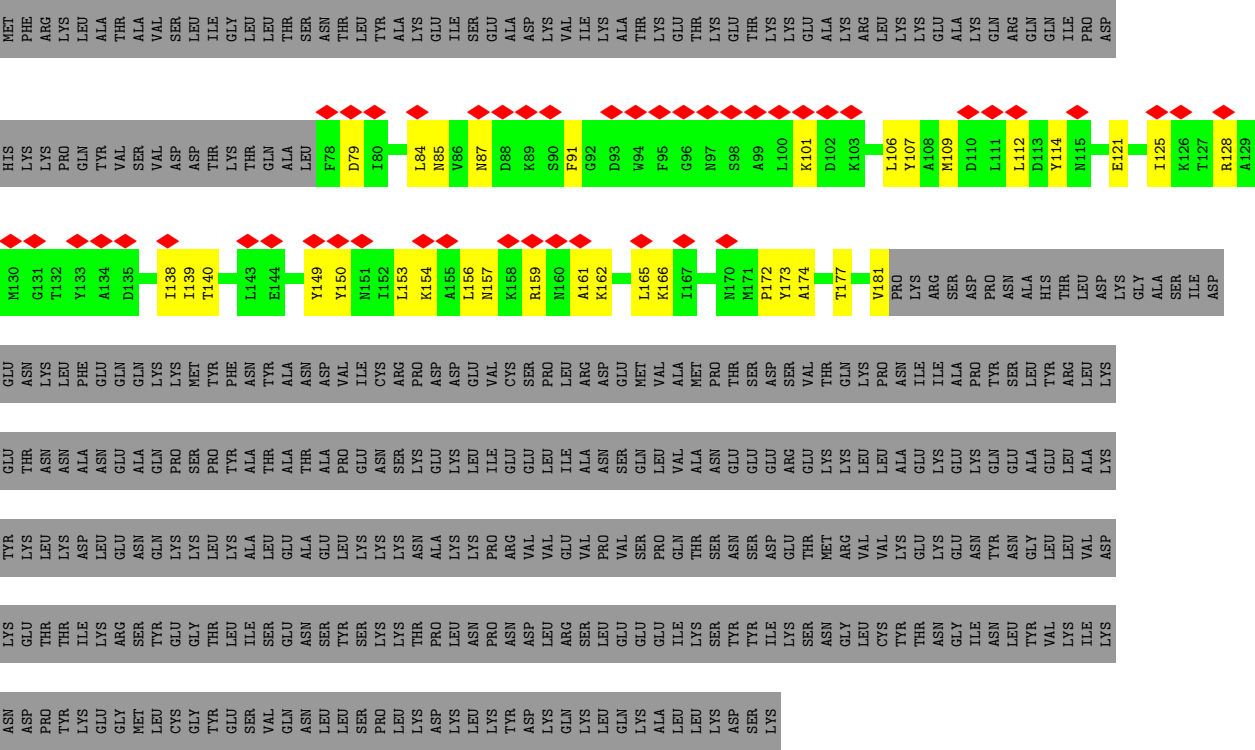


● Molecule 1: Type IV secretion system apparatus protein Cag3

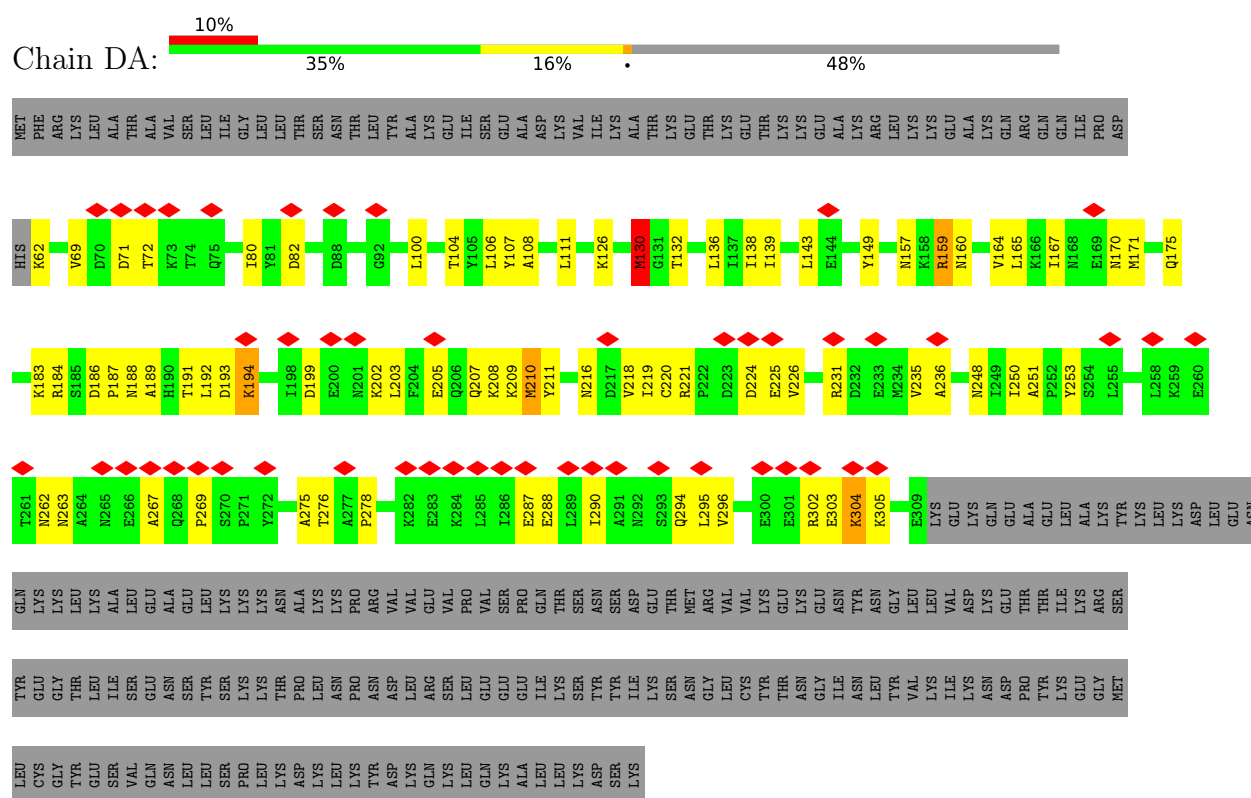




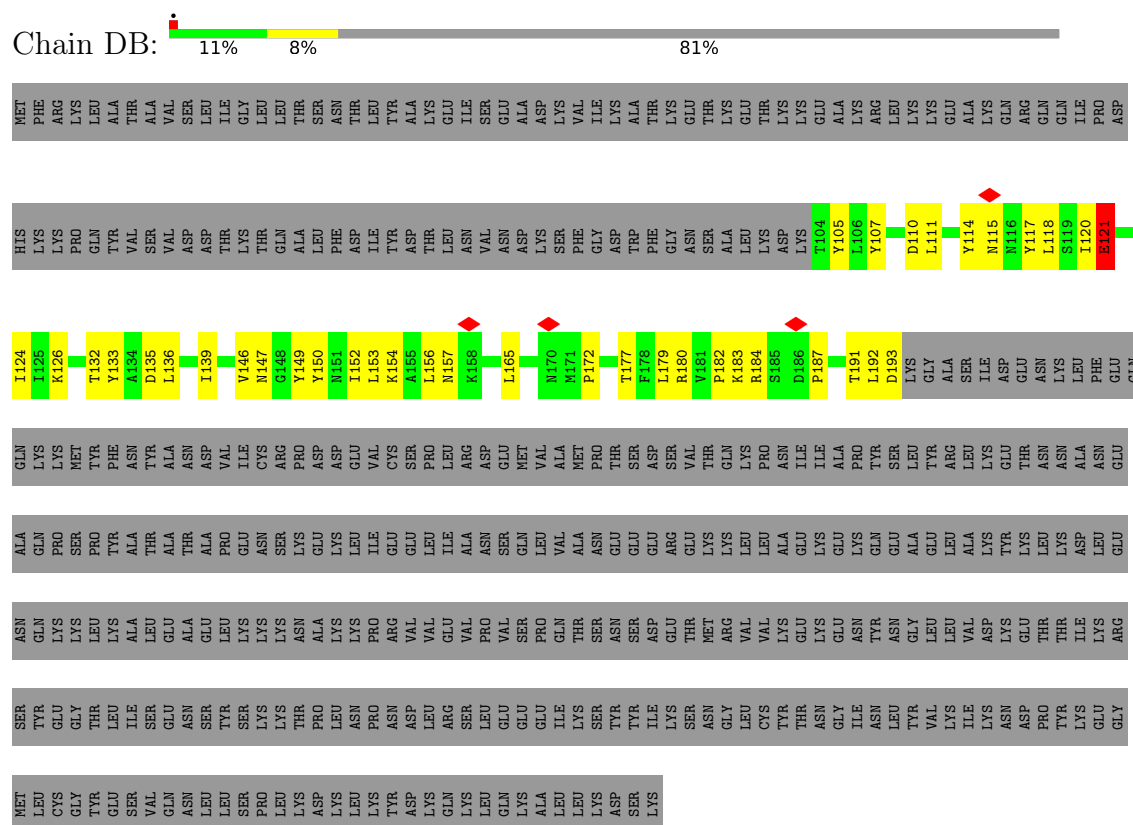
• Molecule 1: Type IV secretion system apparatus protein Cag3



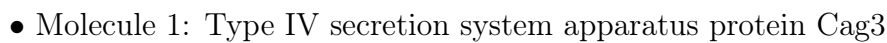
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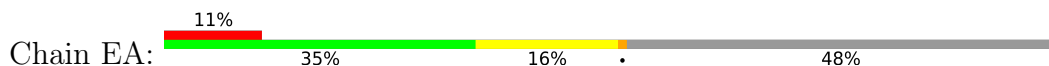
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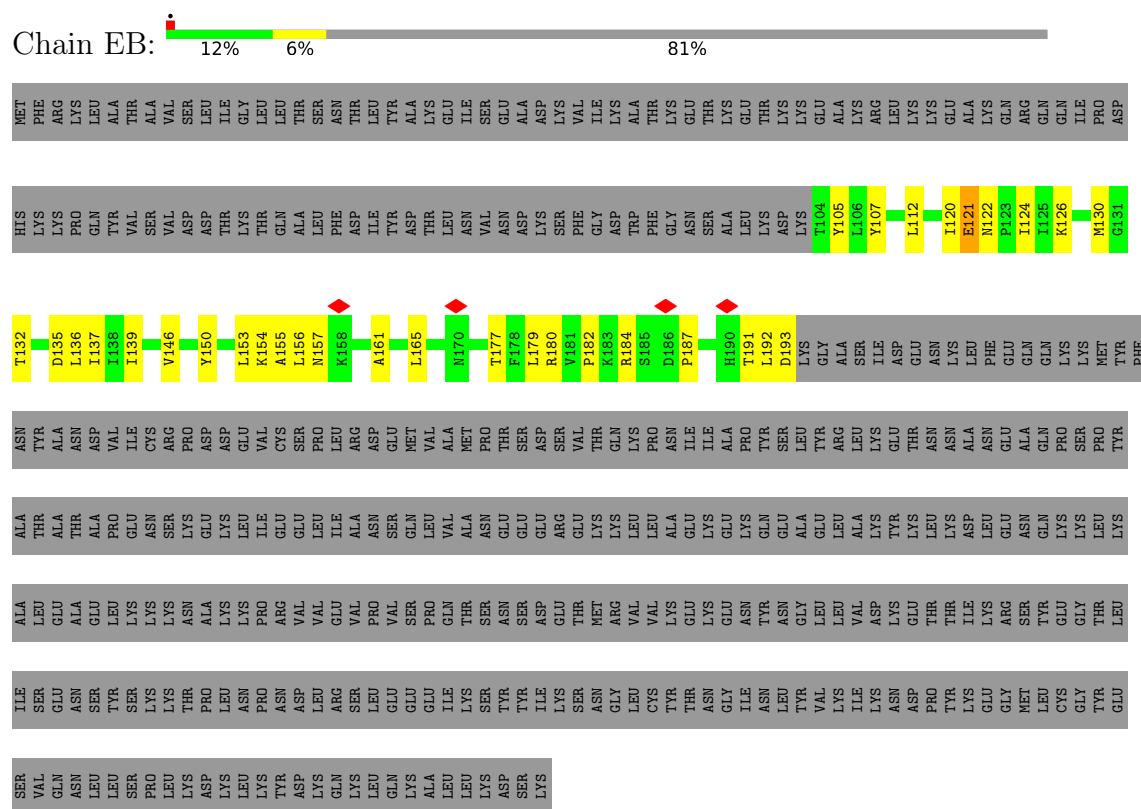
• Molecule 1: Type IV secretion system apparatus protein Cag3



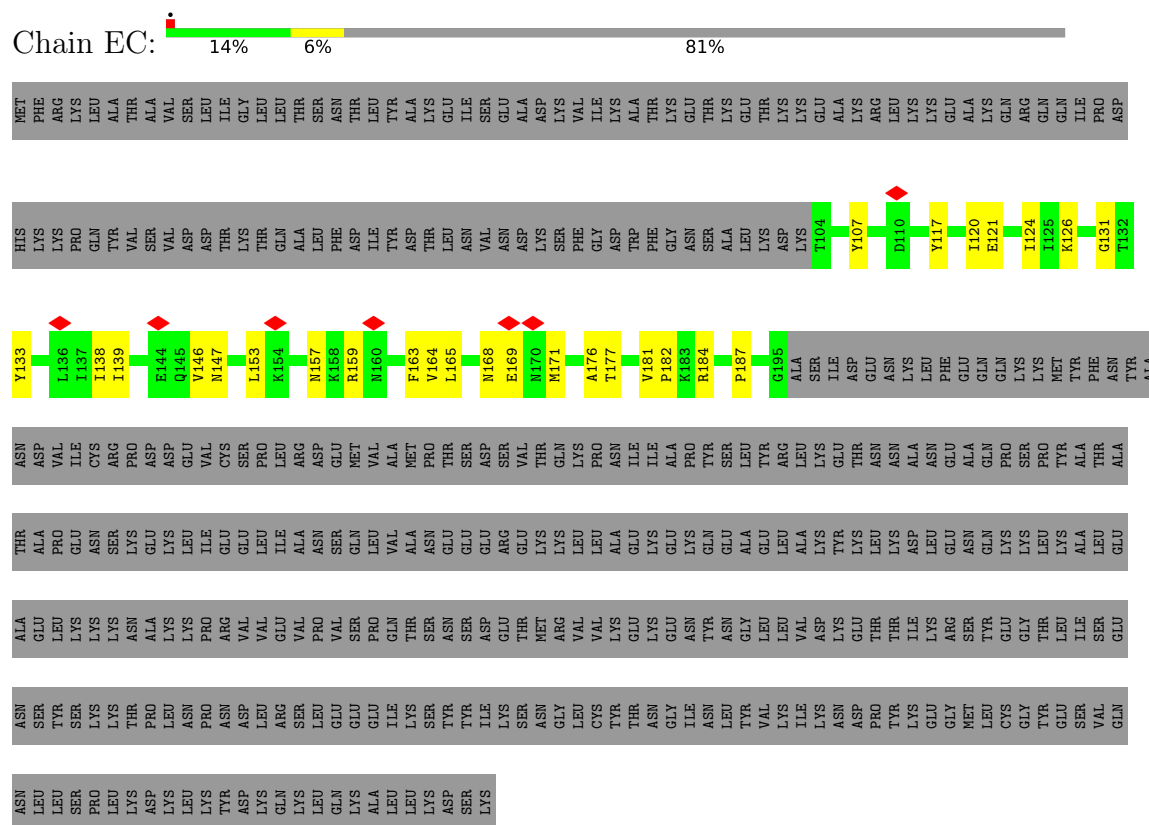
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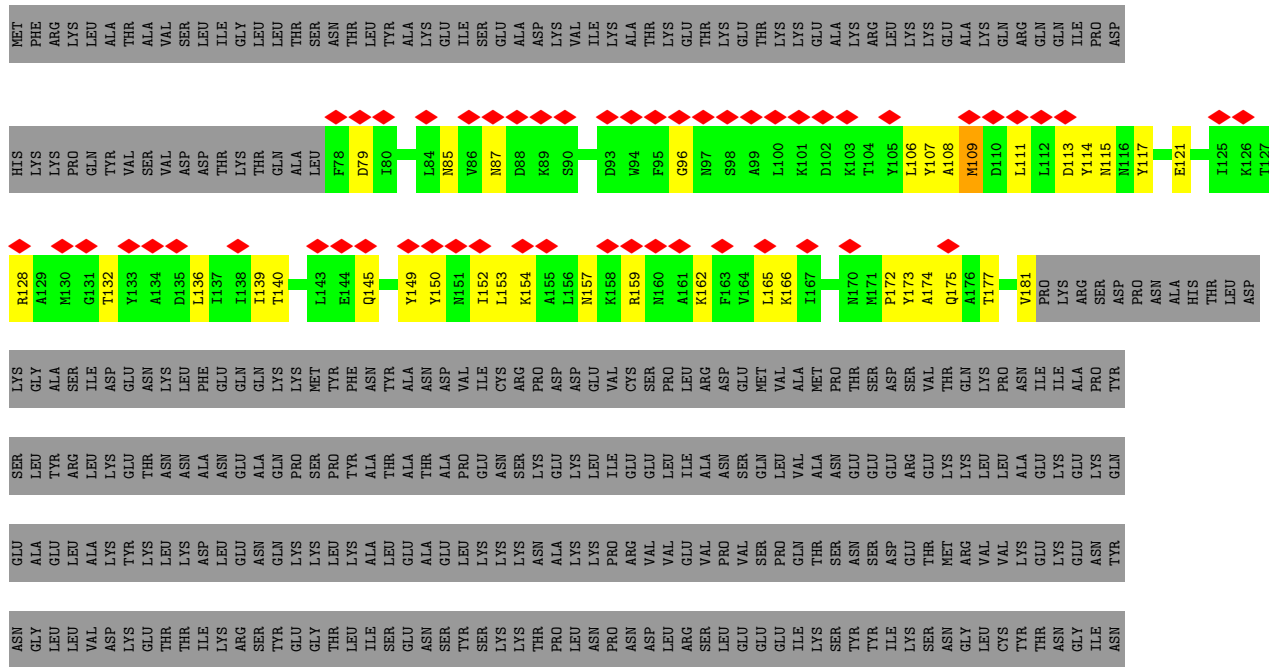
• Molecule 1: Type IV secretion system apparatus protein Cag3



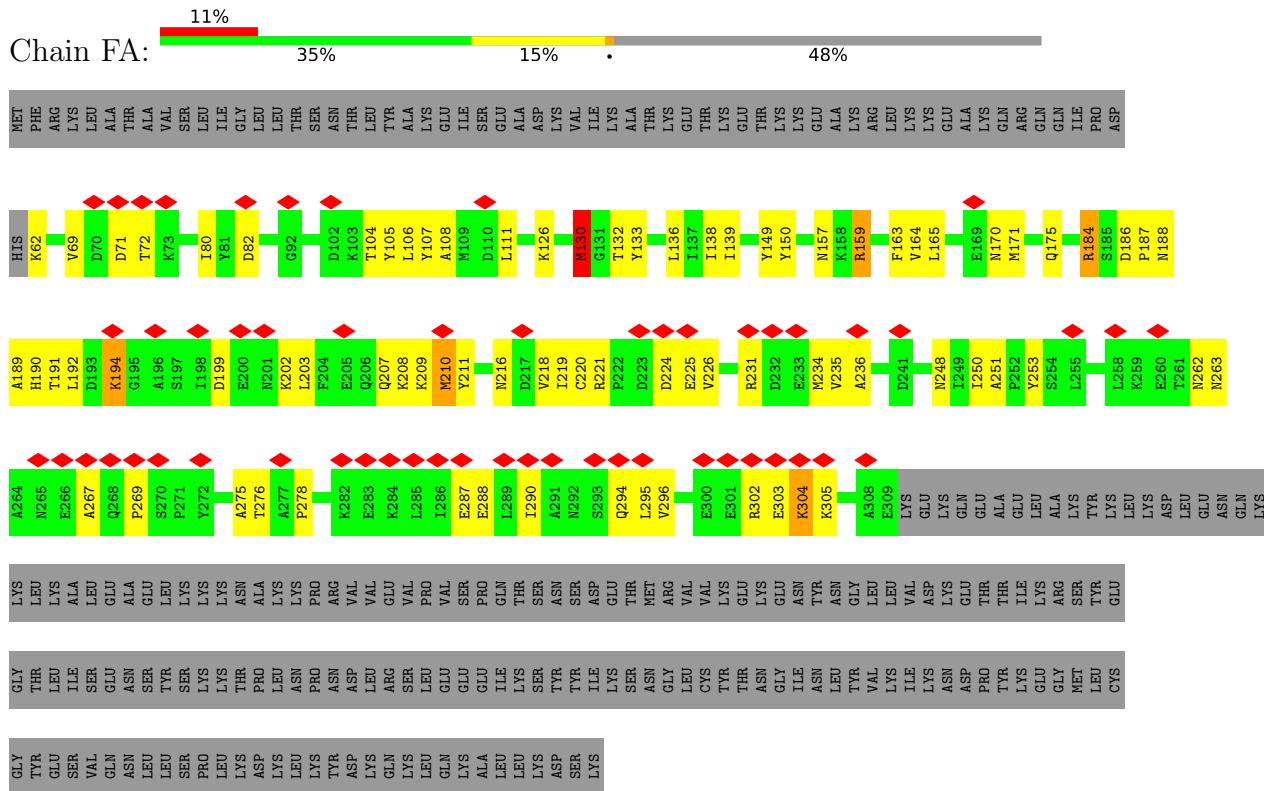
• Molecule 1: Type IV secretion system apparatus protein Cag3



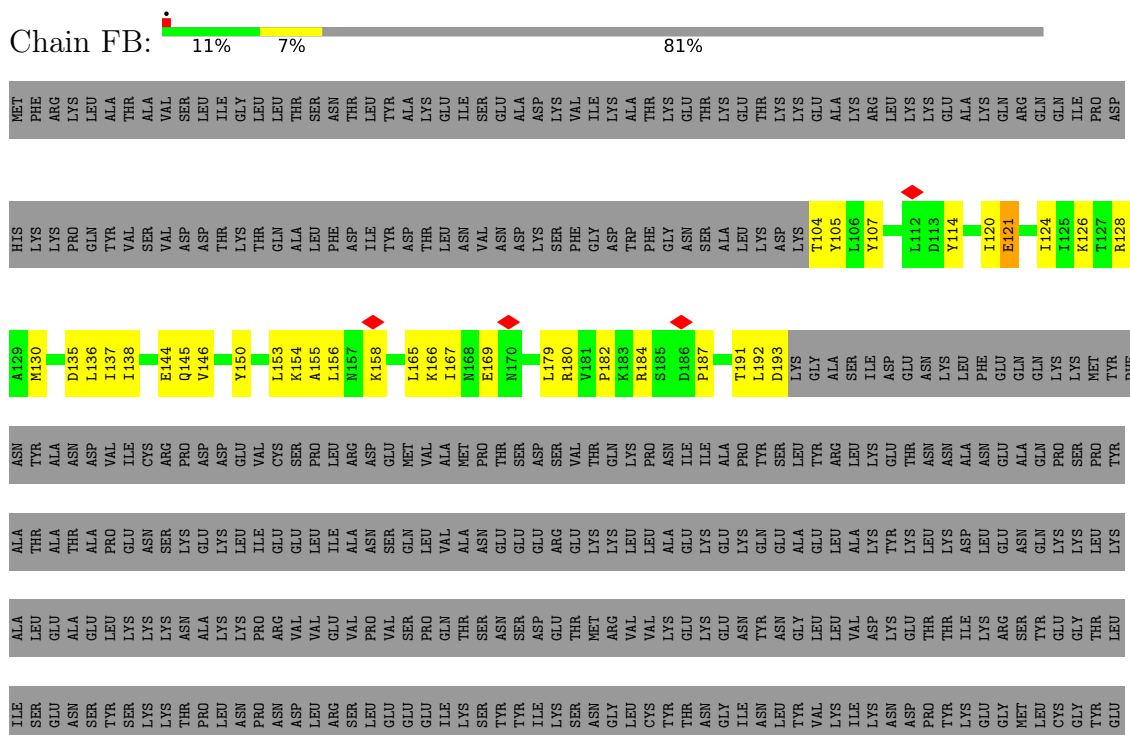
Chain ED:



- Molecule 1: Type IV secretion system apparatus protein Cag3



- Molecule 1: Type IV secretion system apparatus protein Cag3



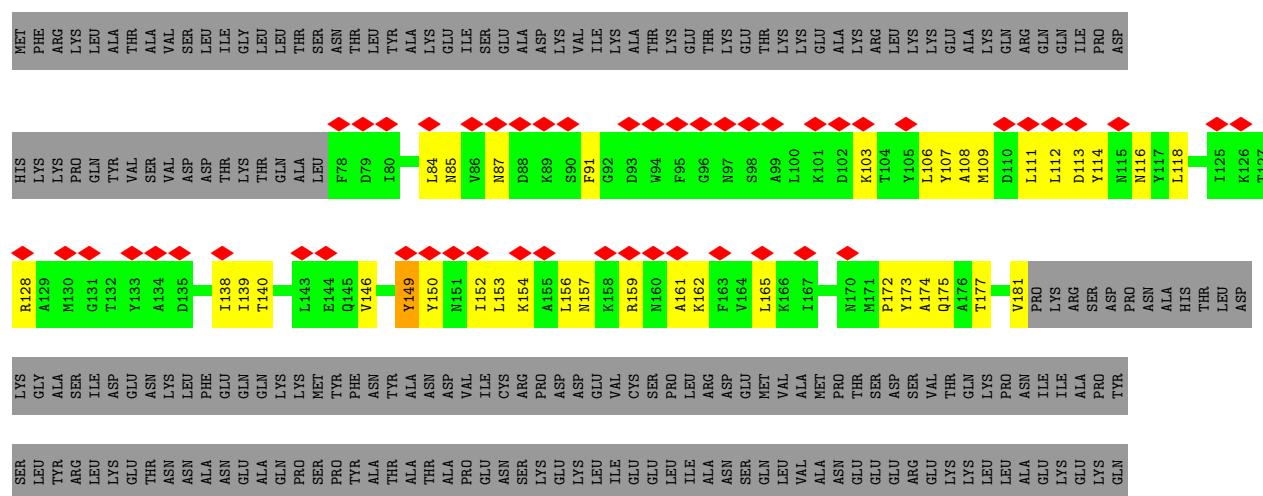


- Molecule 1: Type IV secretion system apparatus protein Cag3

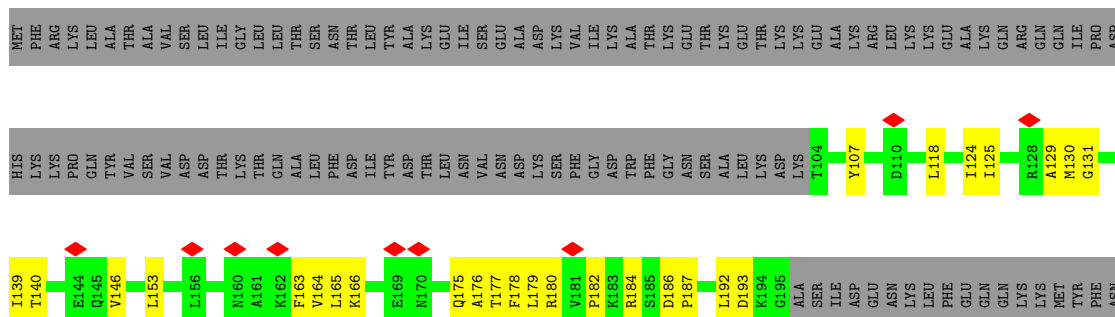
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- Molecule 1: Type IV secretion system apparatus protein Cag3

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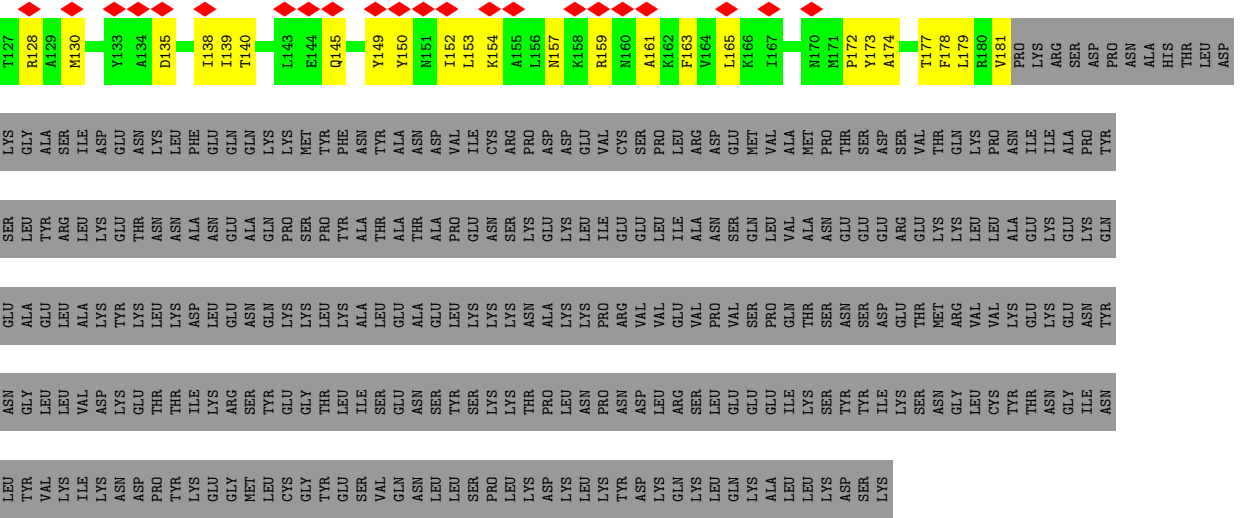
- Molecule 1: Type IV secretion system apparatus protein Cag3

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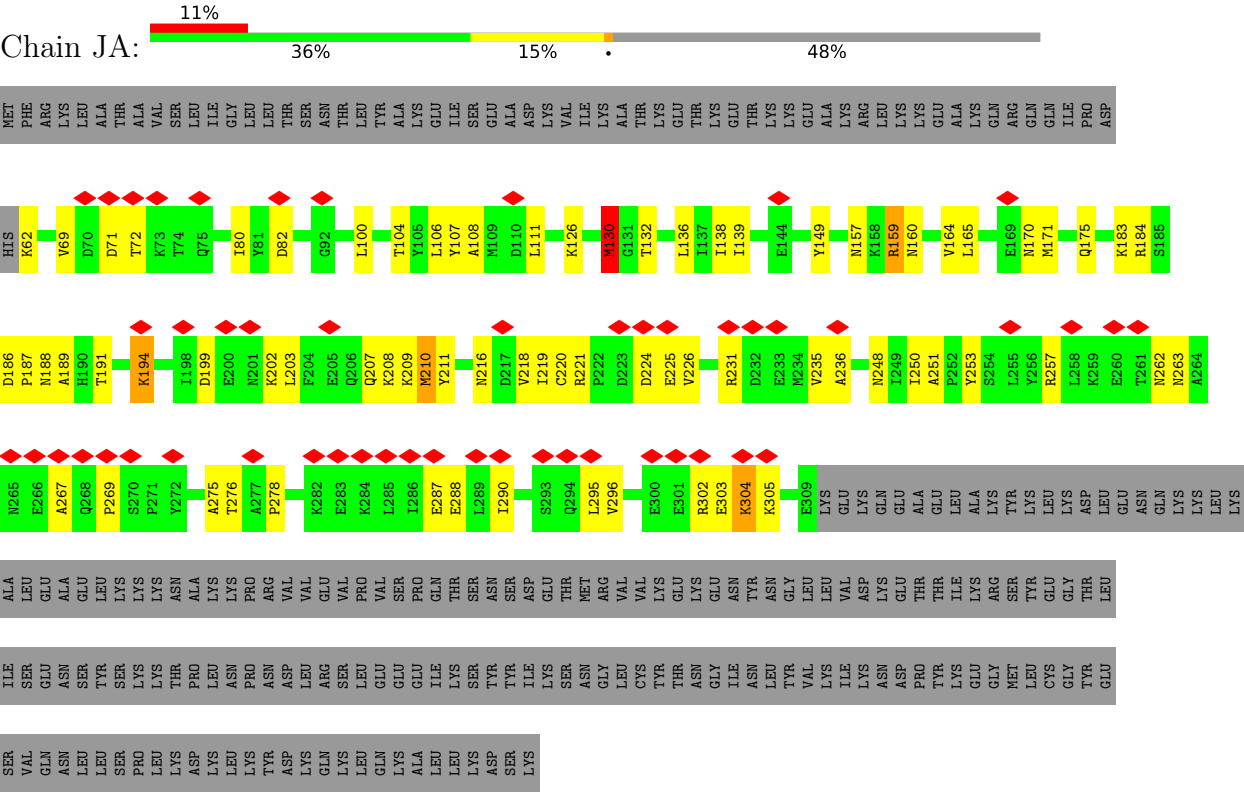
- Molecule 1: Type IV secretion system apparatus protein Cag3



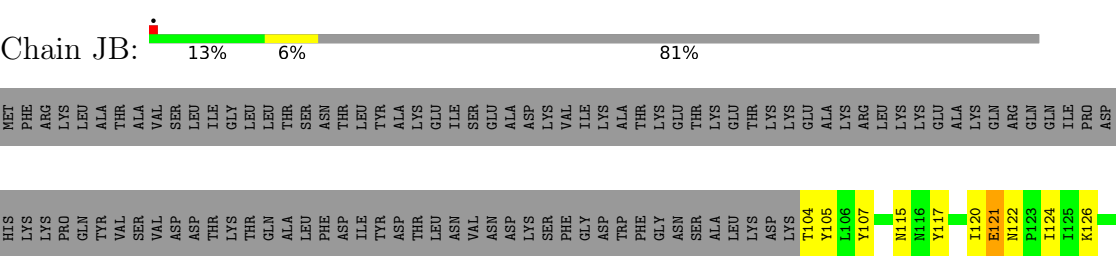
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NET	PHE	ARG	LYS	LEU	ALA	THR	ALA	VAL	SER	ILE	GLY	LEU	THR	SER	ASN	THR	LEU	TYR	ALA	LYS	GLU	ILE	GLY	ALA	ASP	LYS	VAL	ILE	LYS	ALA	THR	LYS	GLU	GLY	LYS	LYS	GLU	GLY	ALA	LYS	ARG	LYS	LYS	LYS	GLN	ARG	GLN	ILE	PRO	ASP							



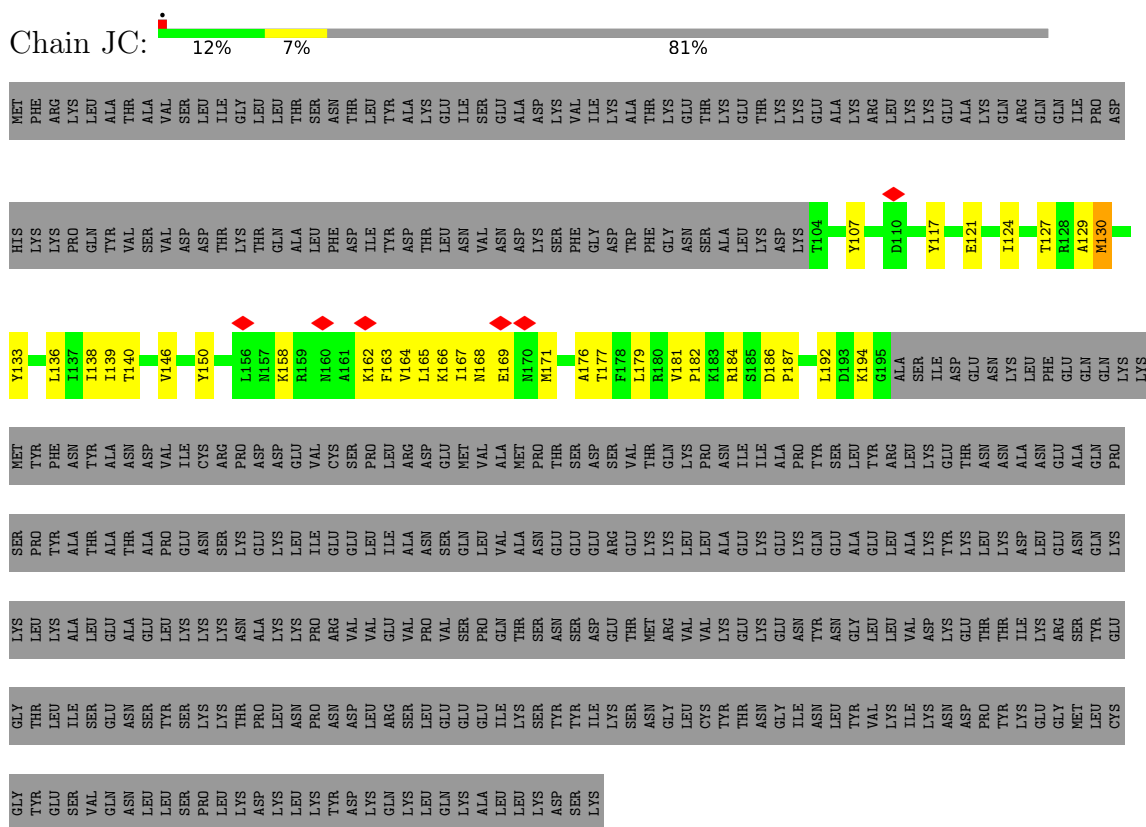
• Molecule 1: Type IV secretion system apparatus protein Cag3



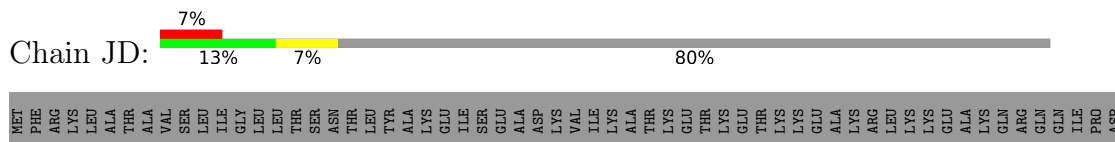
• Molecule 1: Type IV secretion system apparatus protein Cag3

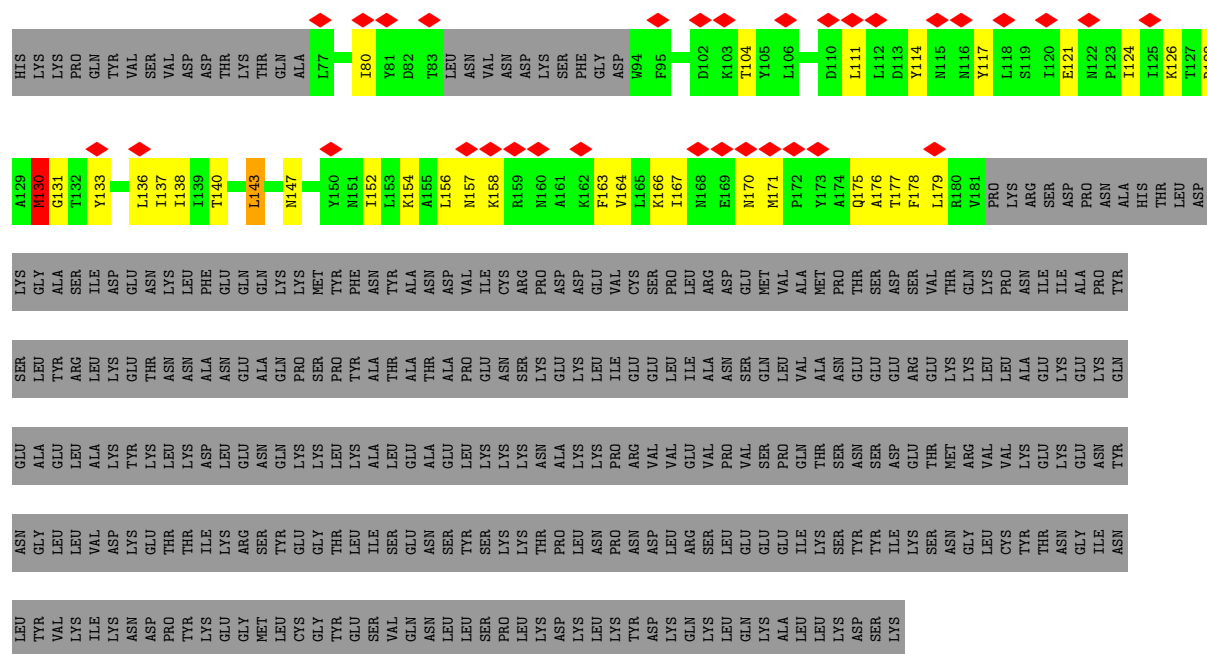


- Molecule 1: Type IV secretion system apparatus protein Cag3

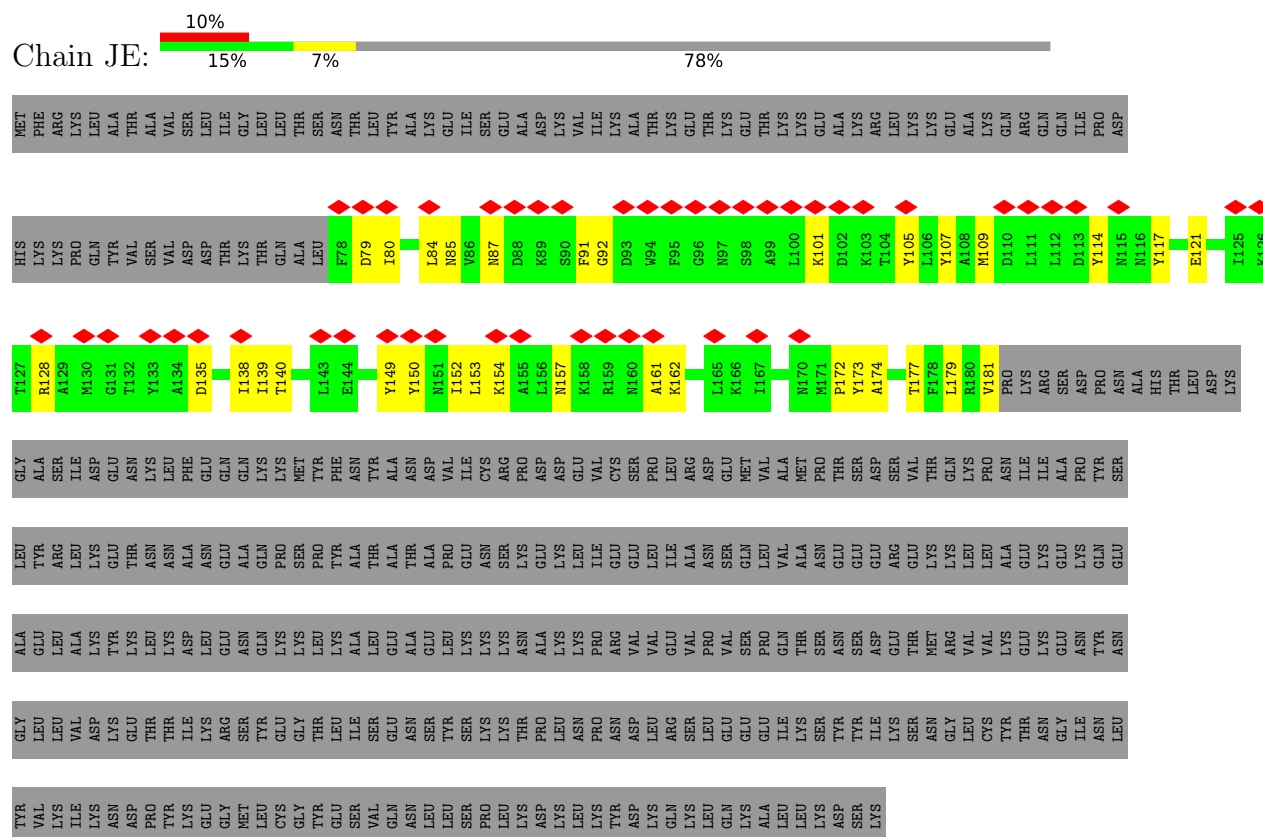


- Molecule 1: Type IV secretion system apparatus protein Cag3

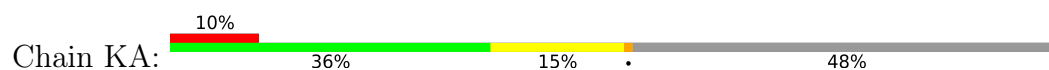


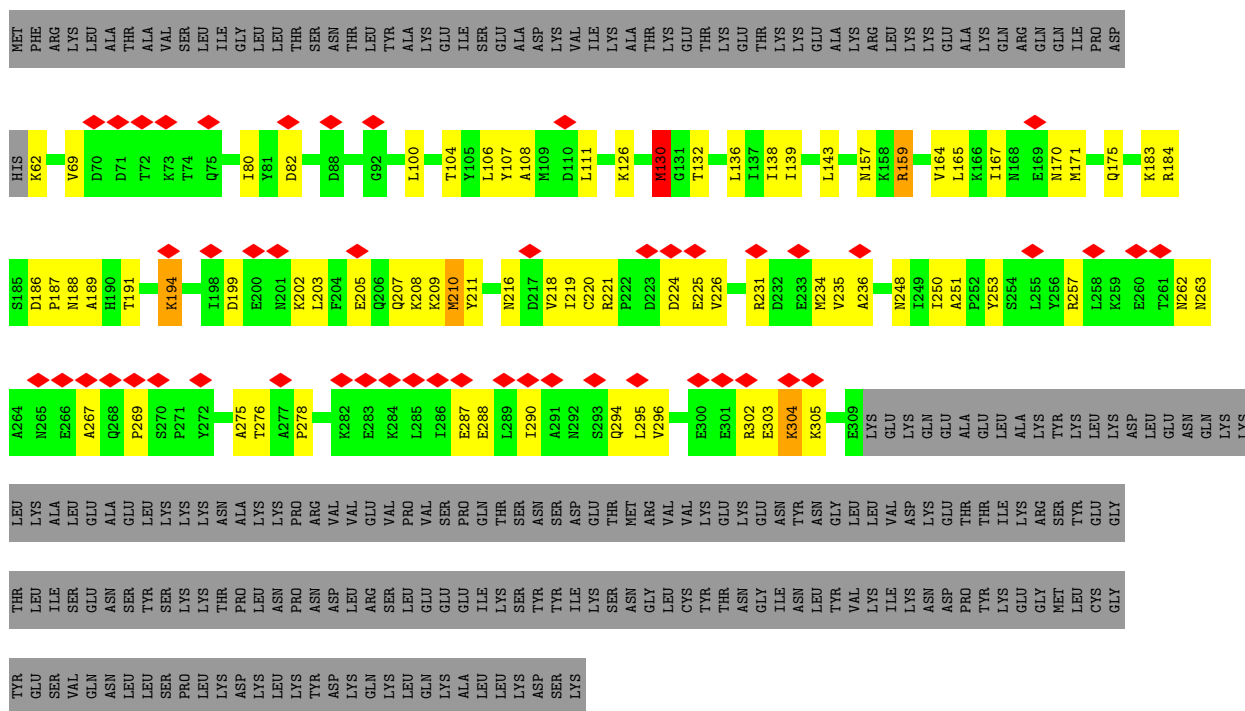


• Molecule 1: Type IV secretion system apparatus protein Cag3

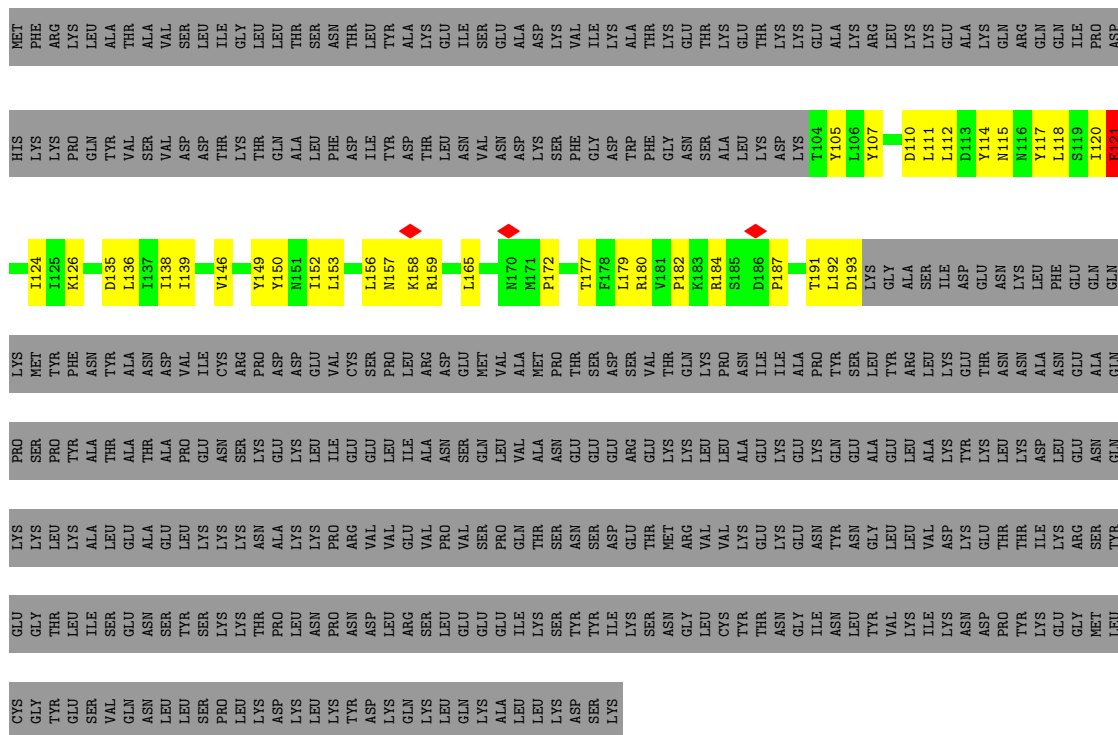


• Molecule 1: Type IV secretion system apparatus protein Cag3



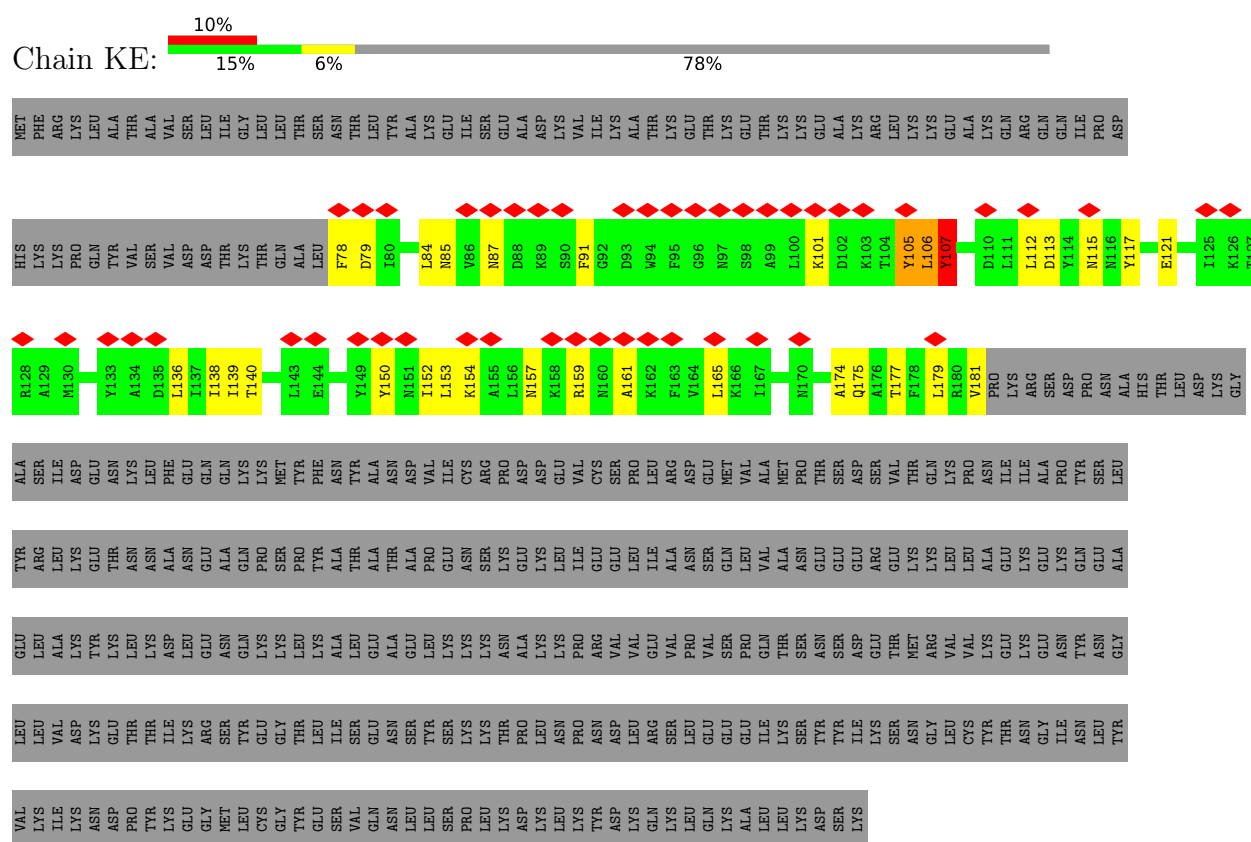


- Molecule 1: Type IV secretion system apparatus protein Cag3

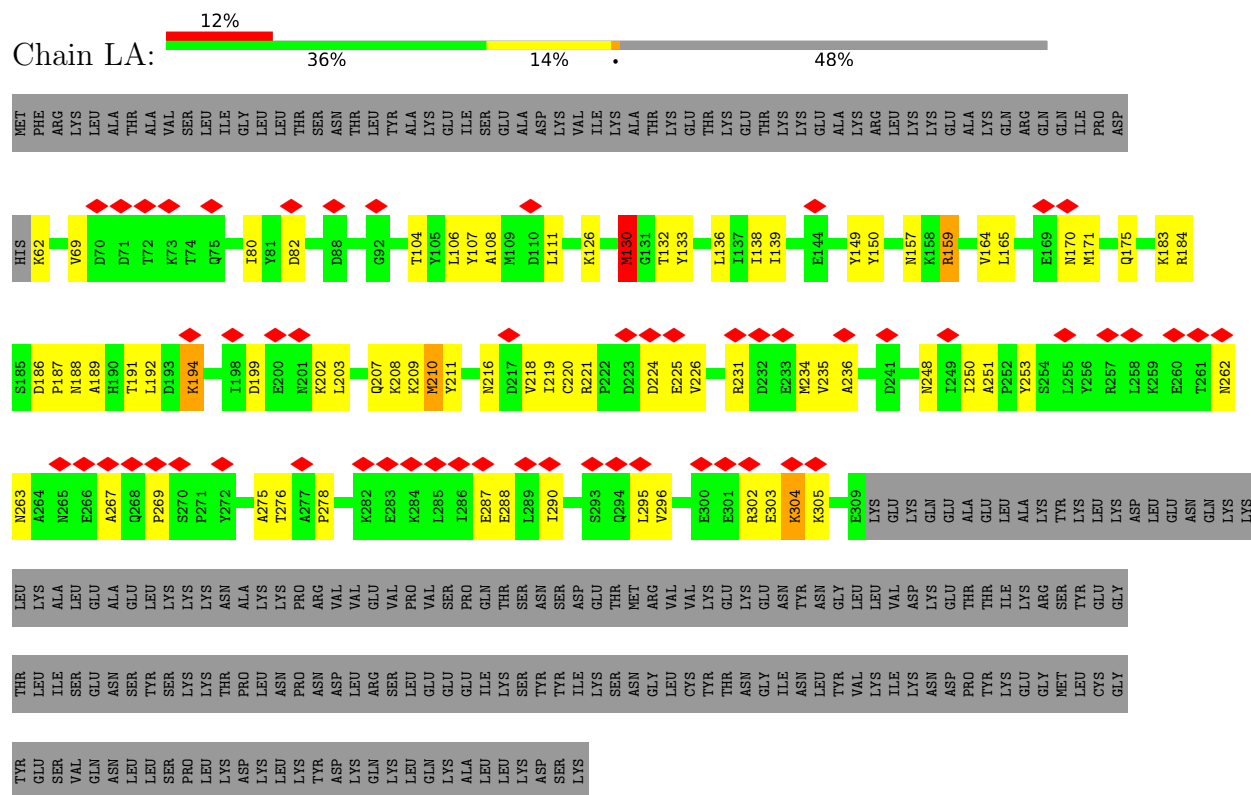


- Molecule 1: Type IV secretion system apparatus protein Cag3

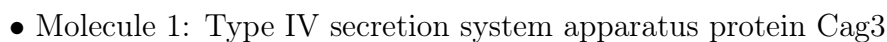
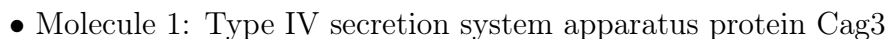


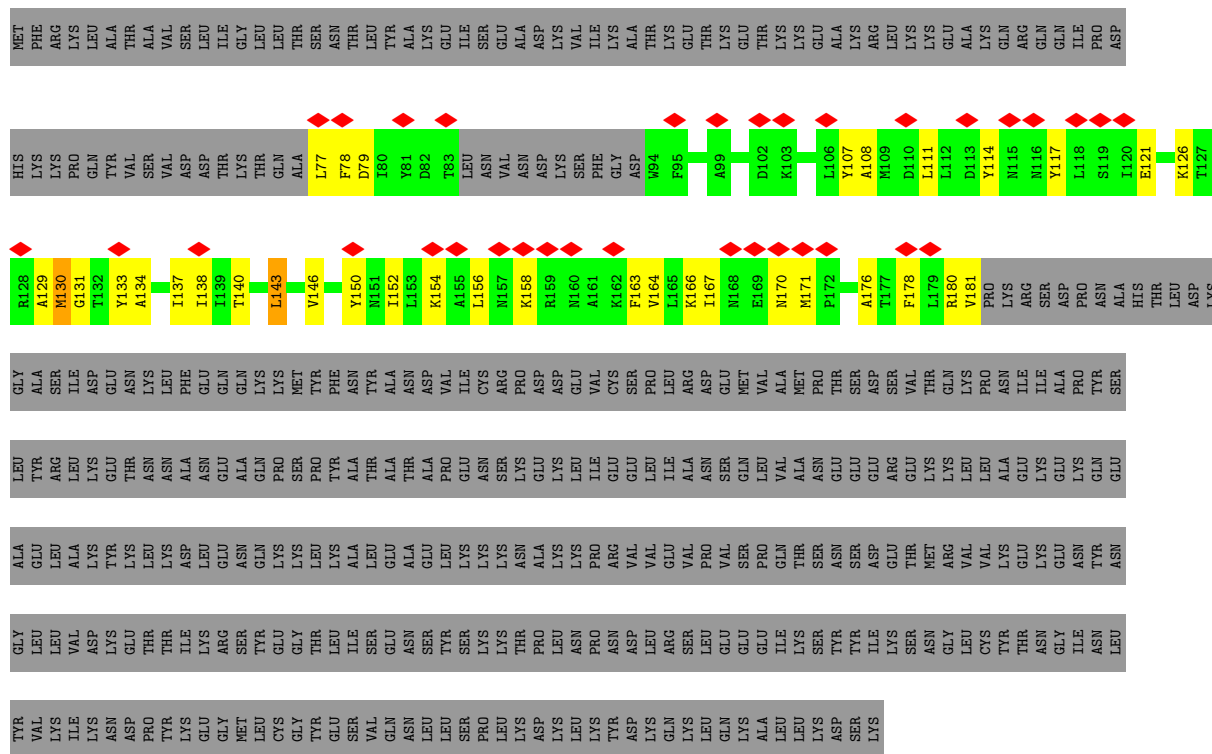


• Molecule 1: Type IV secretion system apparatus protein Cag3

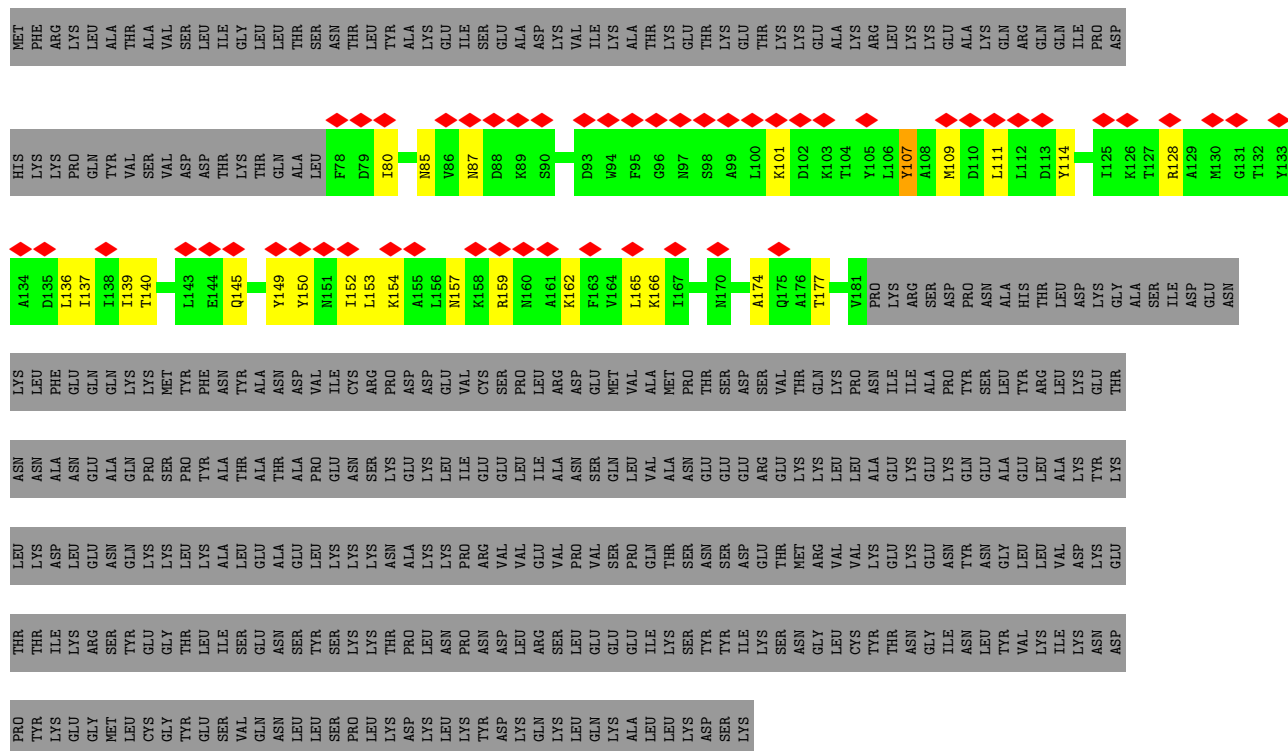


• Molecule 1: Type IV secretion system apparatus protein Cag3



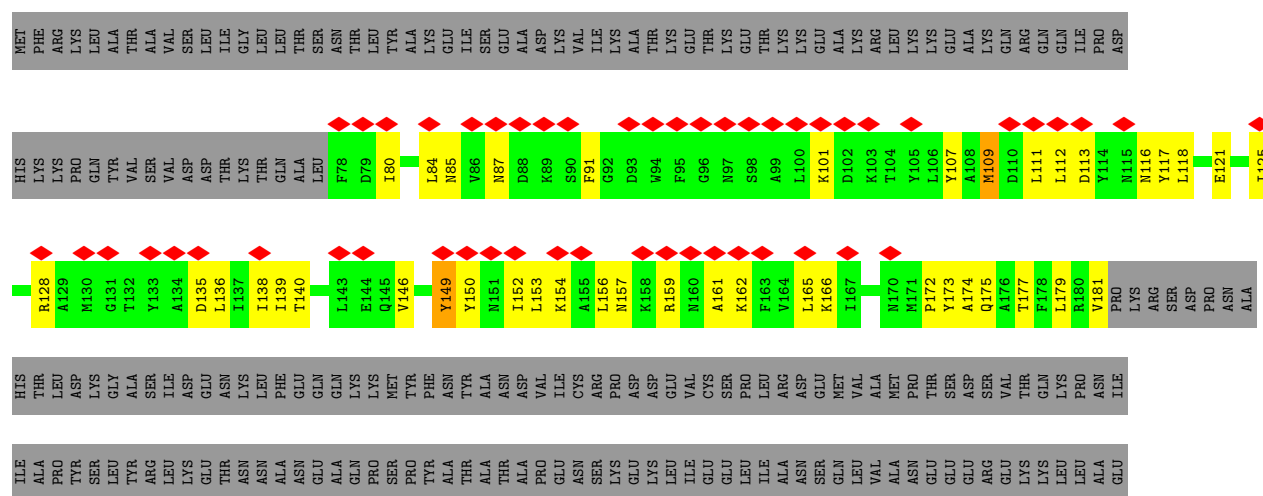


• Molecule 1: Type IV secretion system apparatus protein Cag3

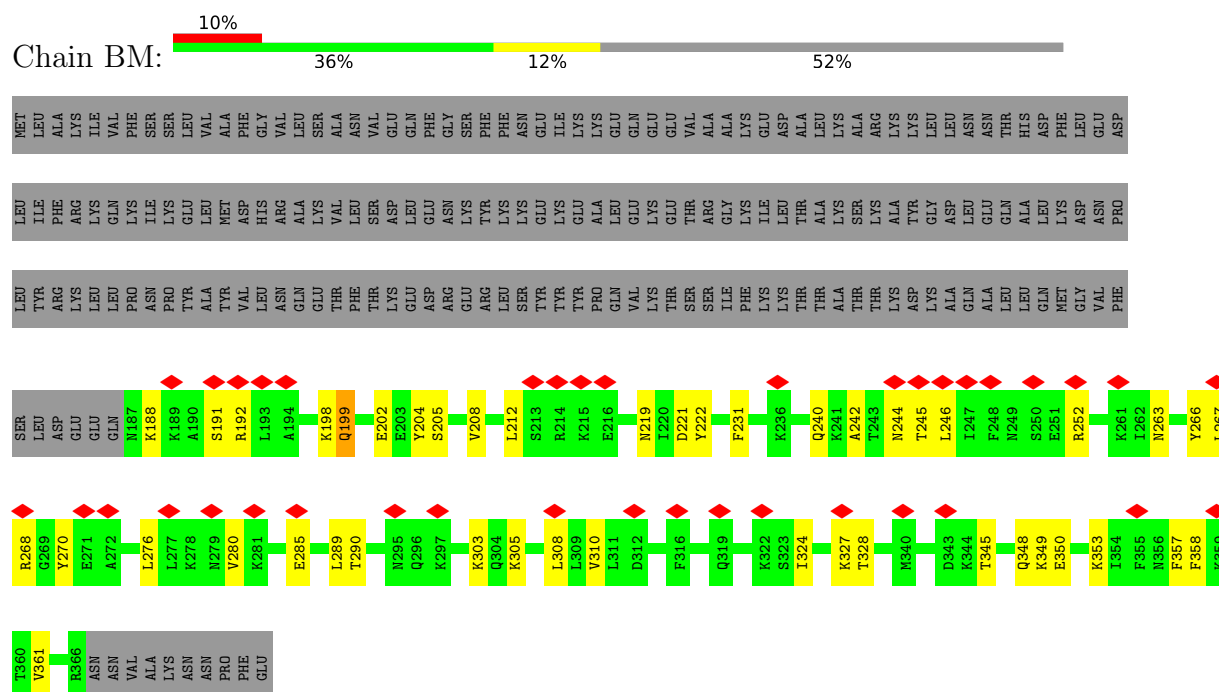


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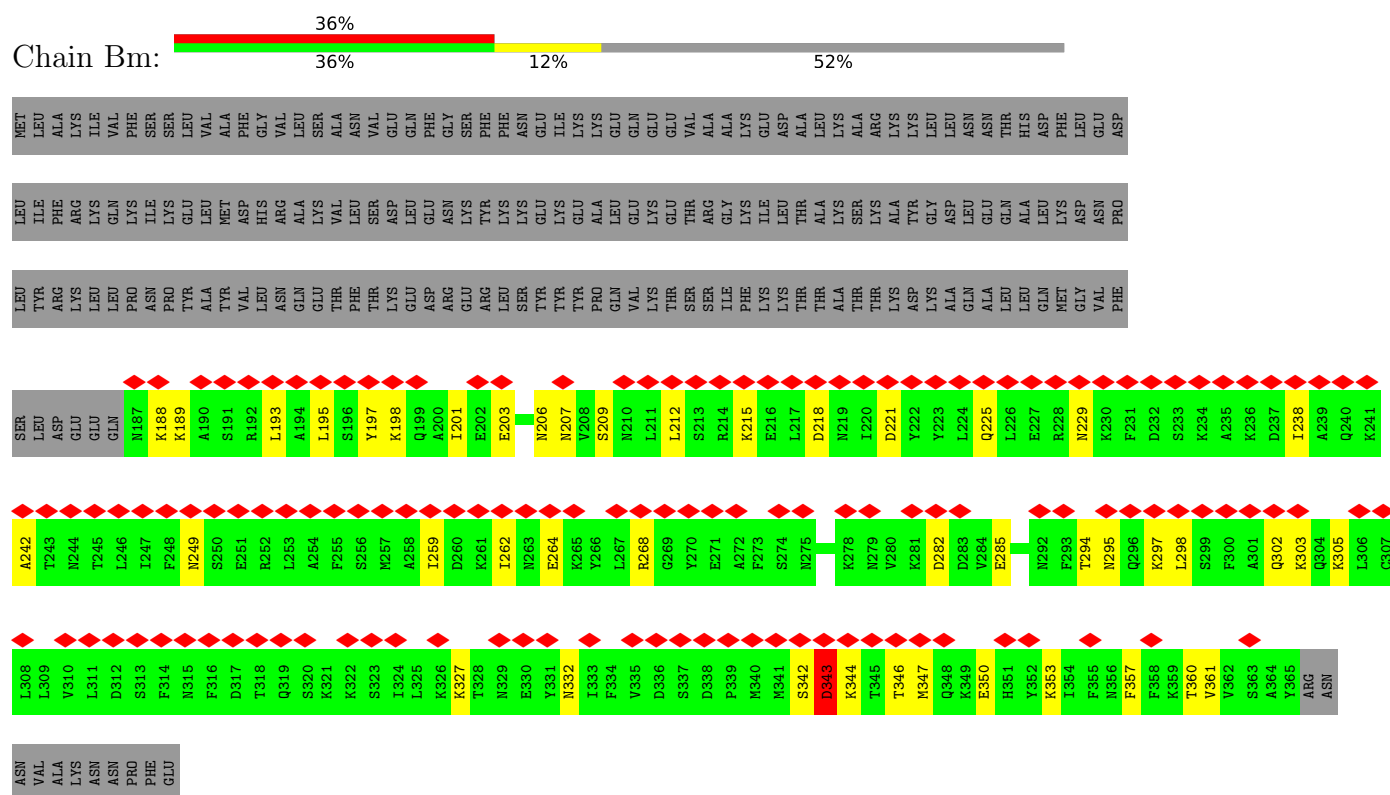




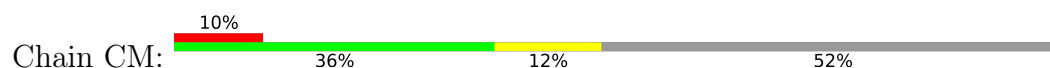
● Molecule 2: Type IV secretion system apparatus protein CagM



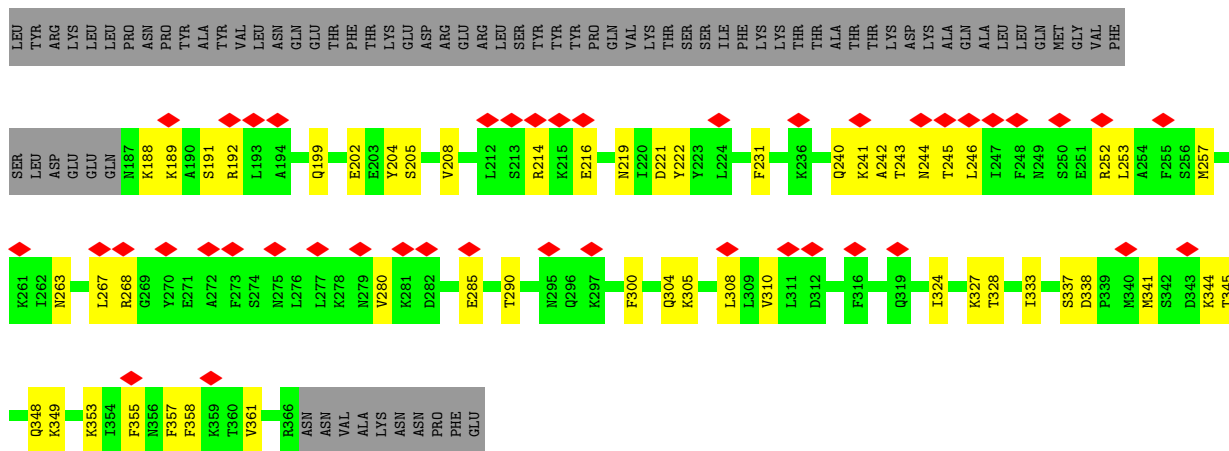
● Molecule 2: Type IV secretion system apparatus protein CagM



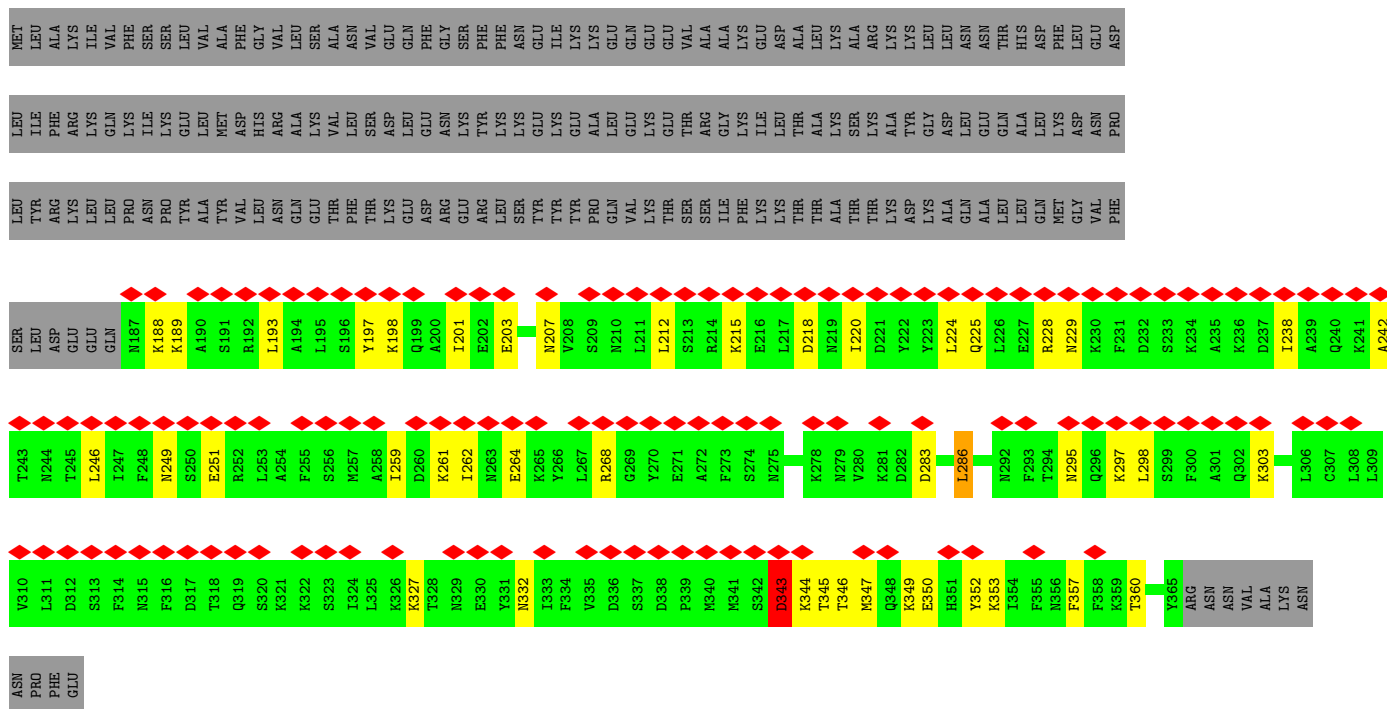
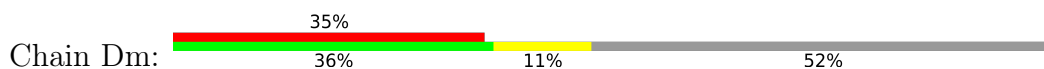
● Molecule 2: Type IV secretion system apparatus protein CagM



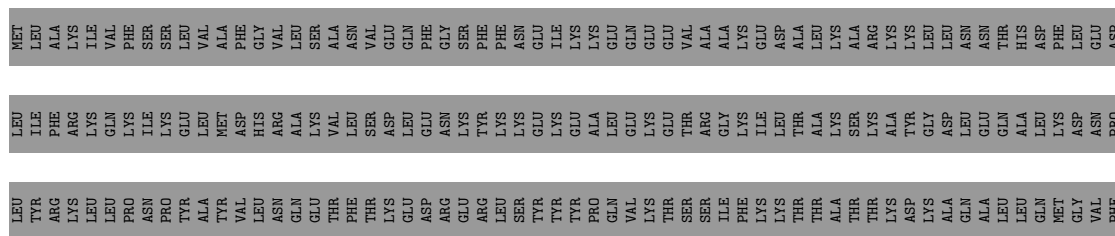
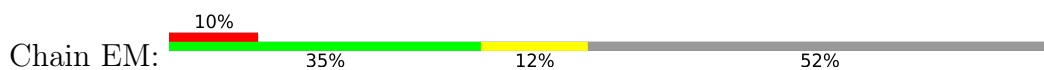


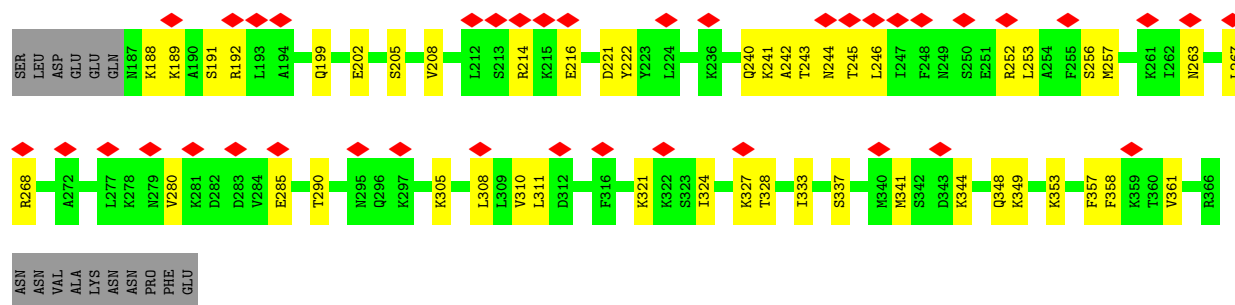


- Molecule 2: Type IV secretion system apparatus protein CagM

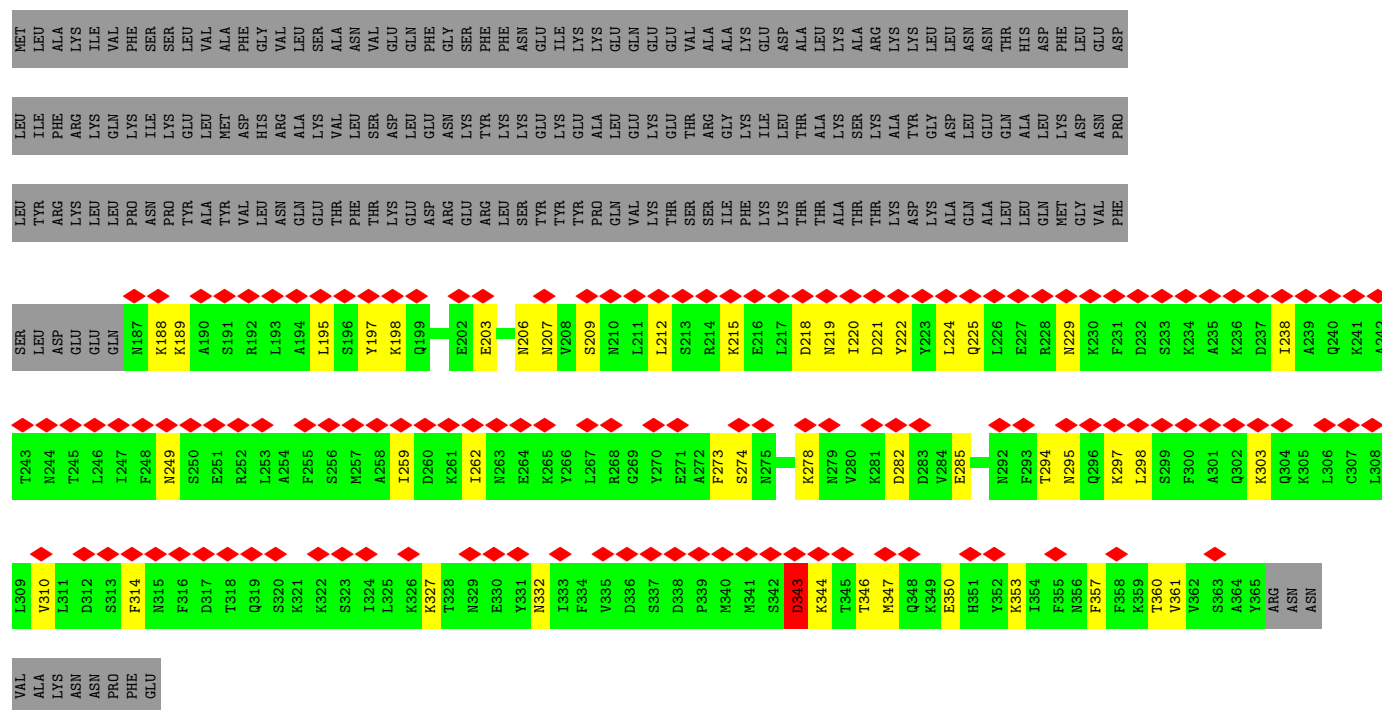
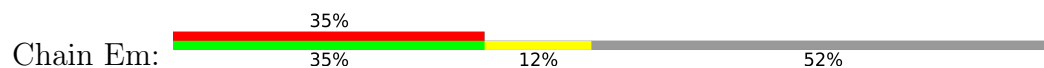


- Molecule 2: Type IV secretion system apparatus protein CagM

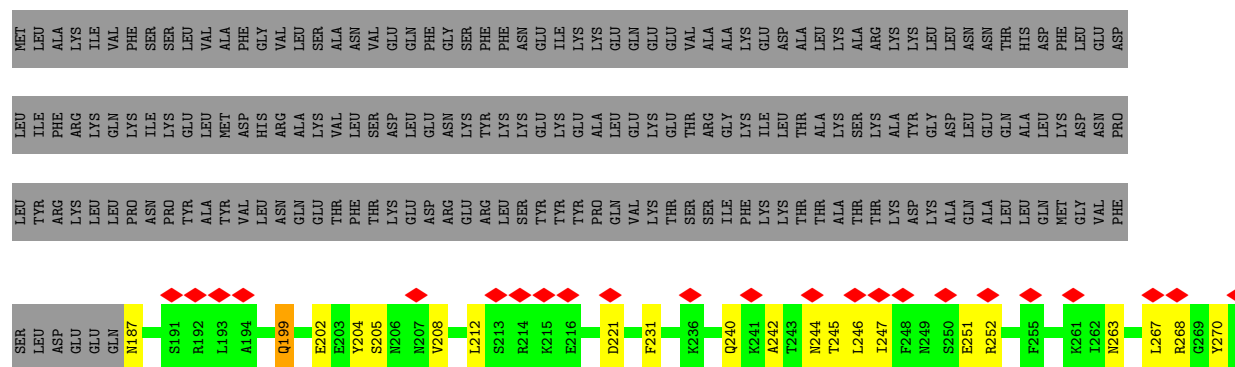
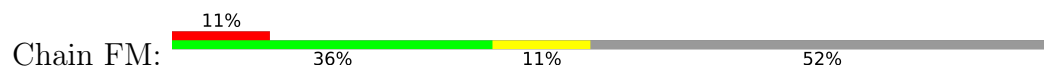


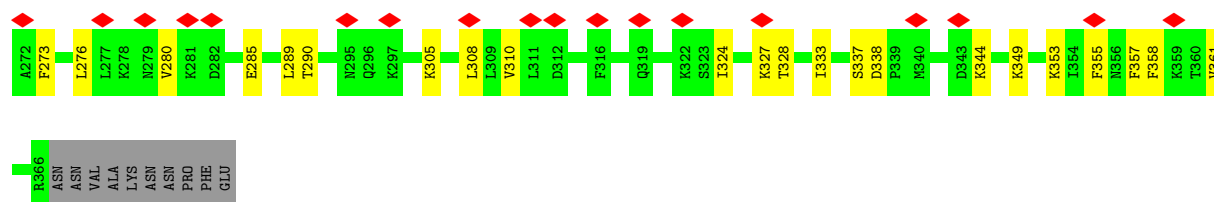


• Molecule 2: Type IV secretion system apparatus protein CagM

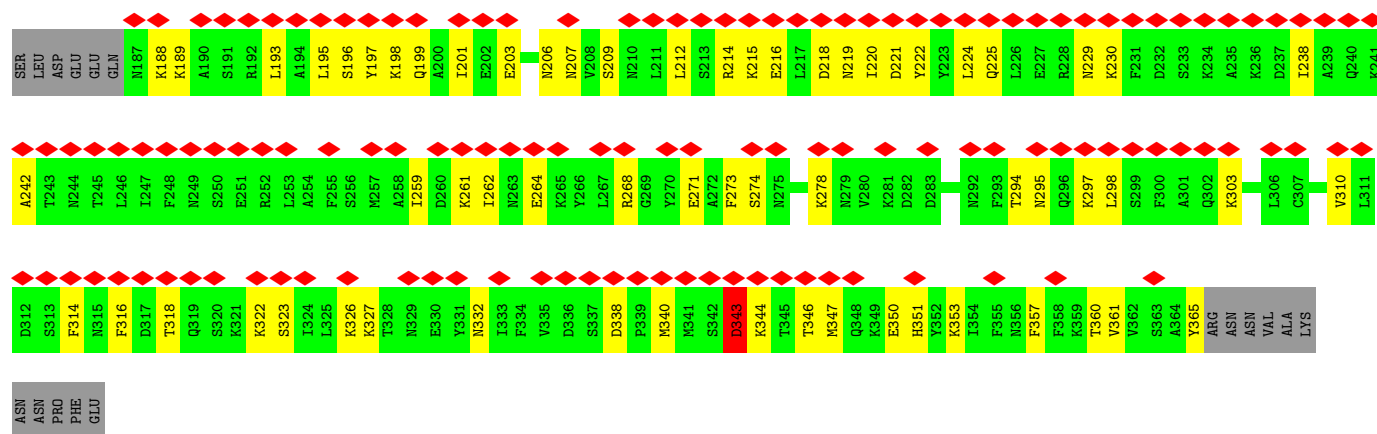
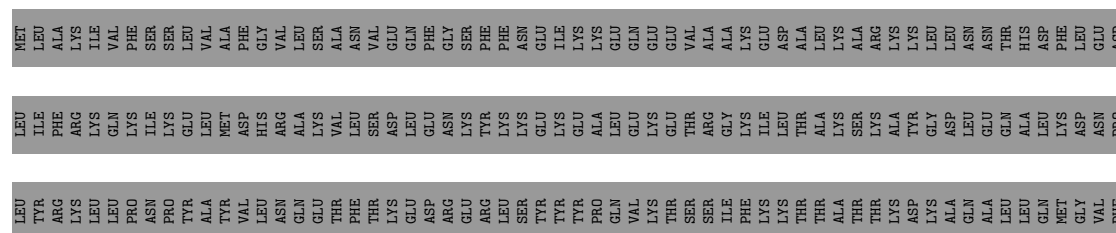
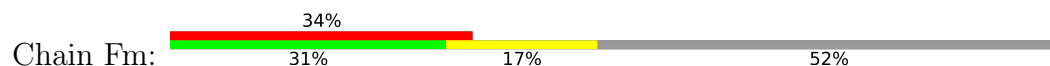


• Molecule 2: Type IV secretion system apparatus protein CagM

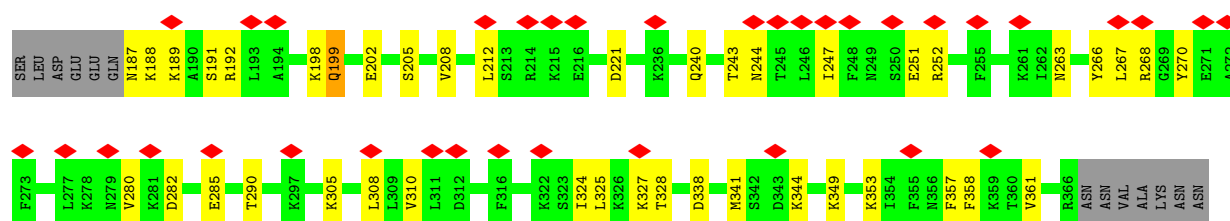
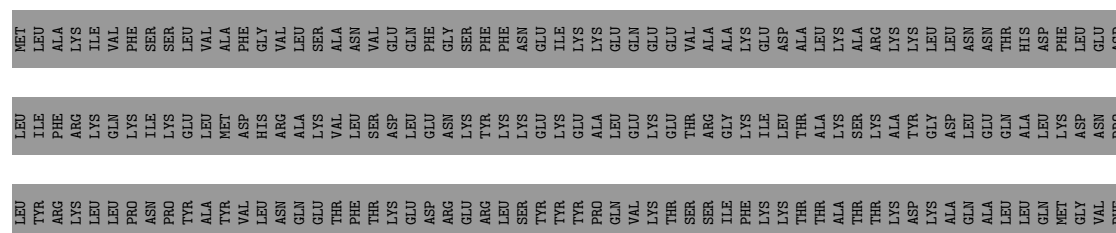


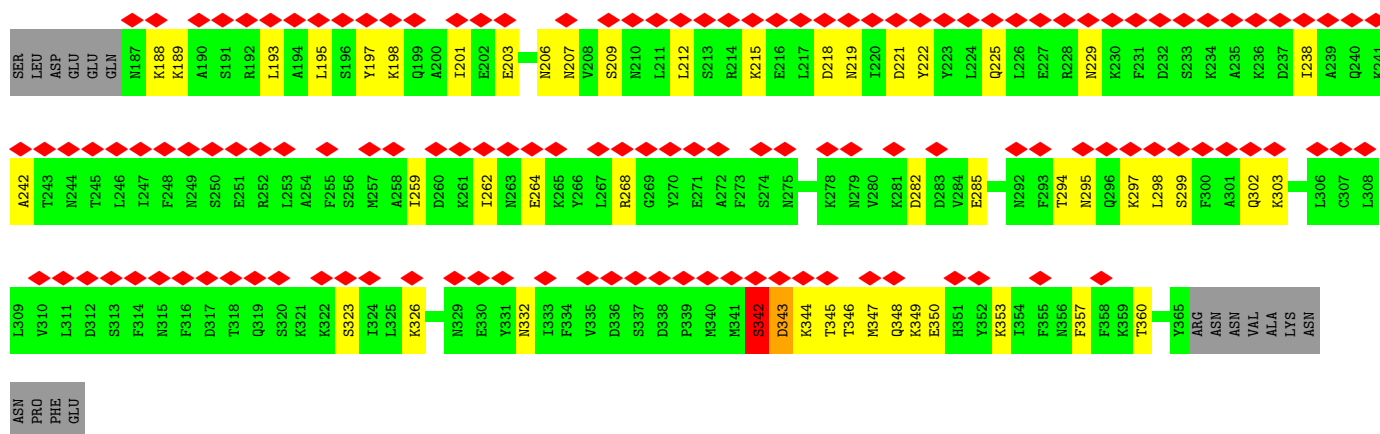


• Molecule 2: Type IV secretion system apparatus protein CagM

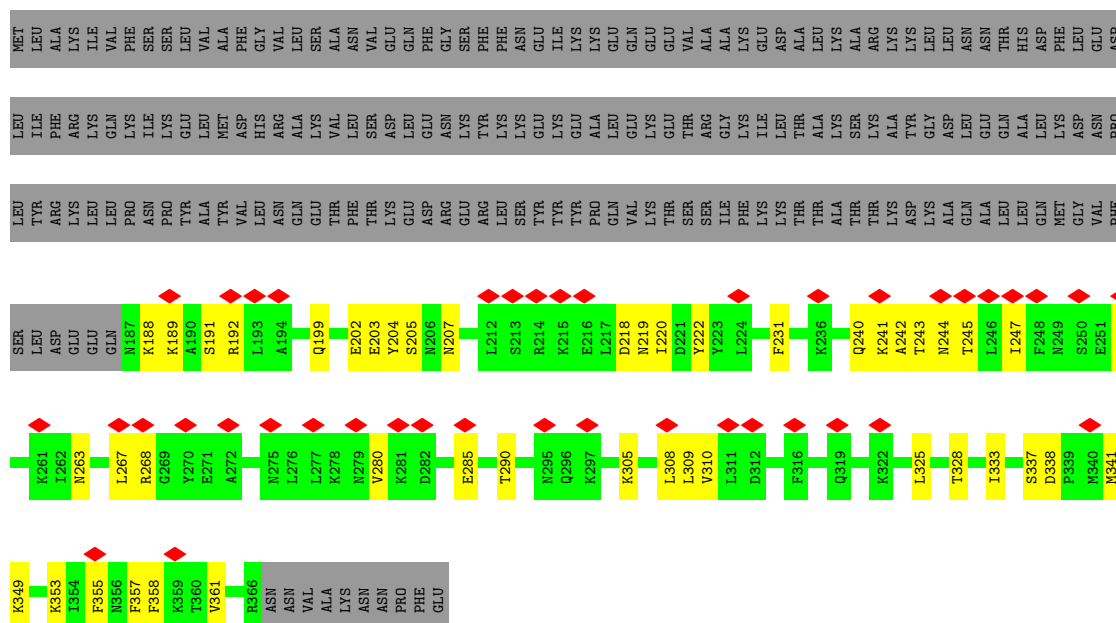
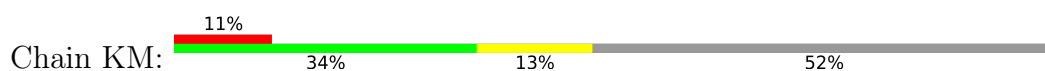


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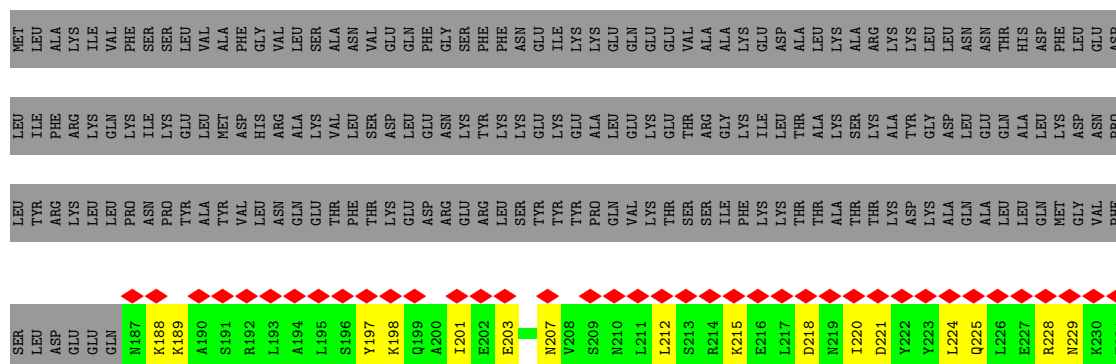
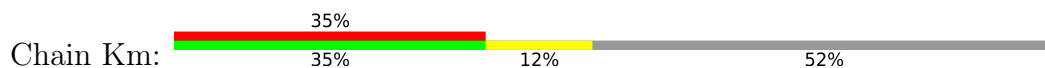


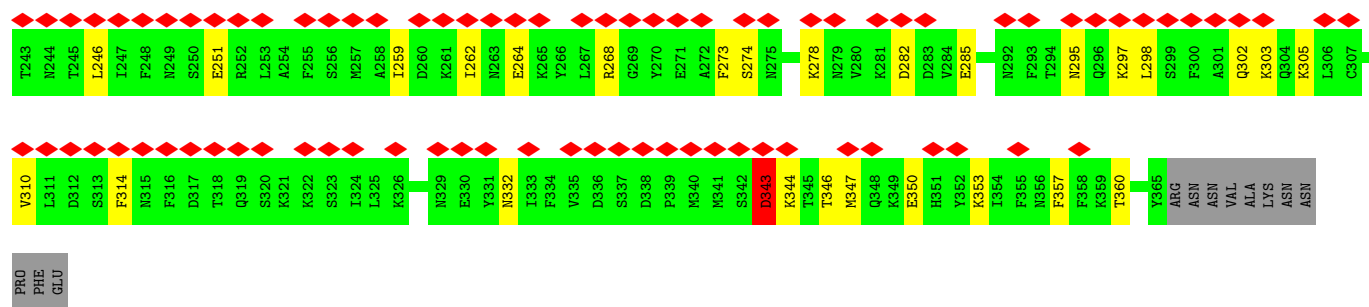


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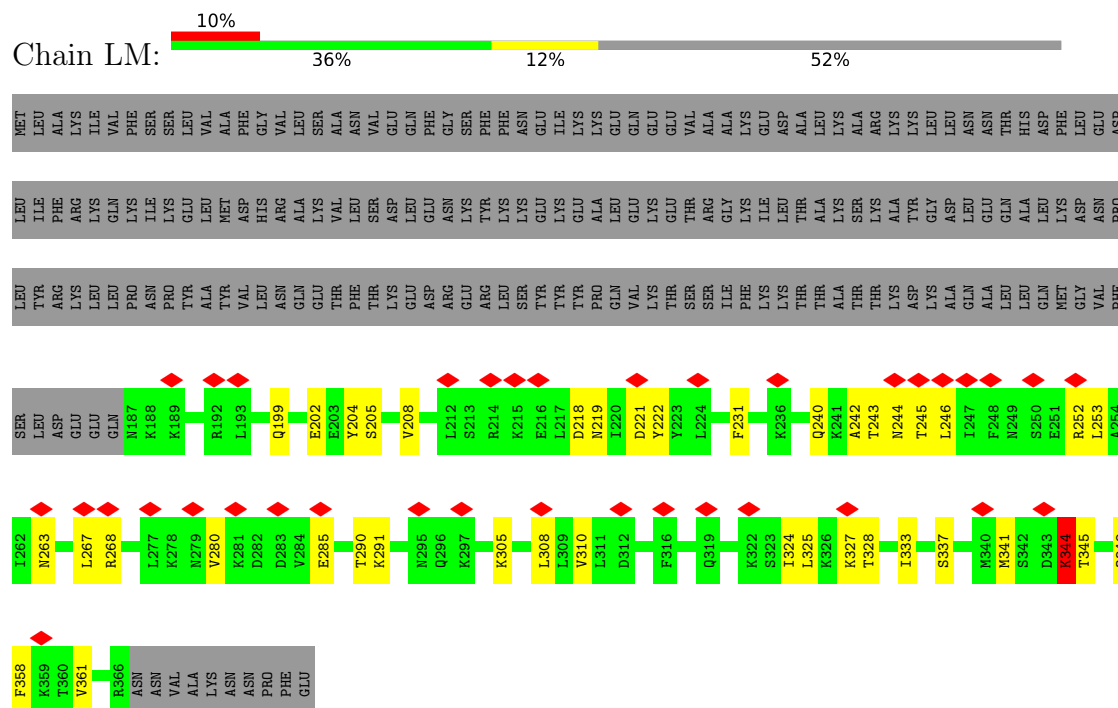


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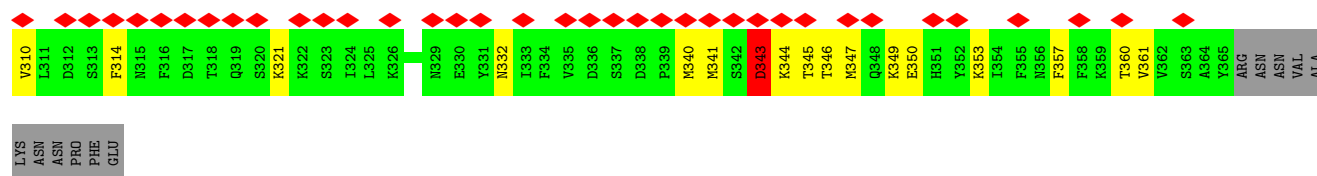


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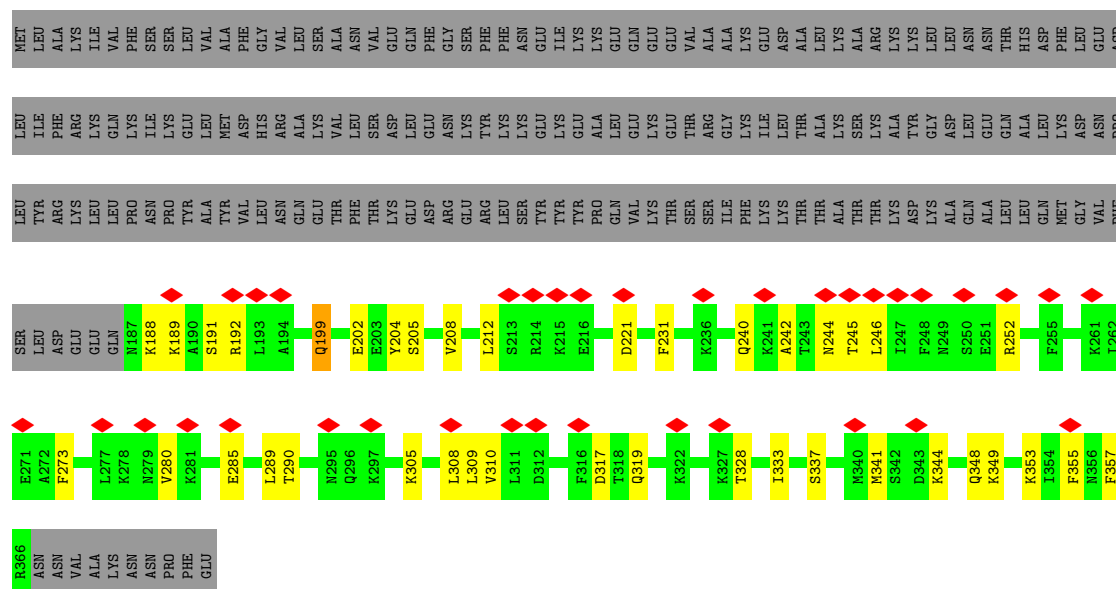


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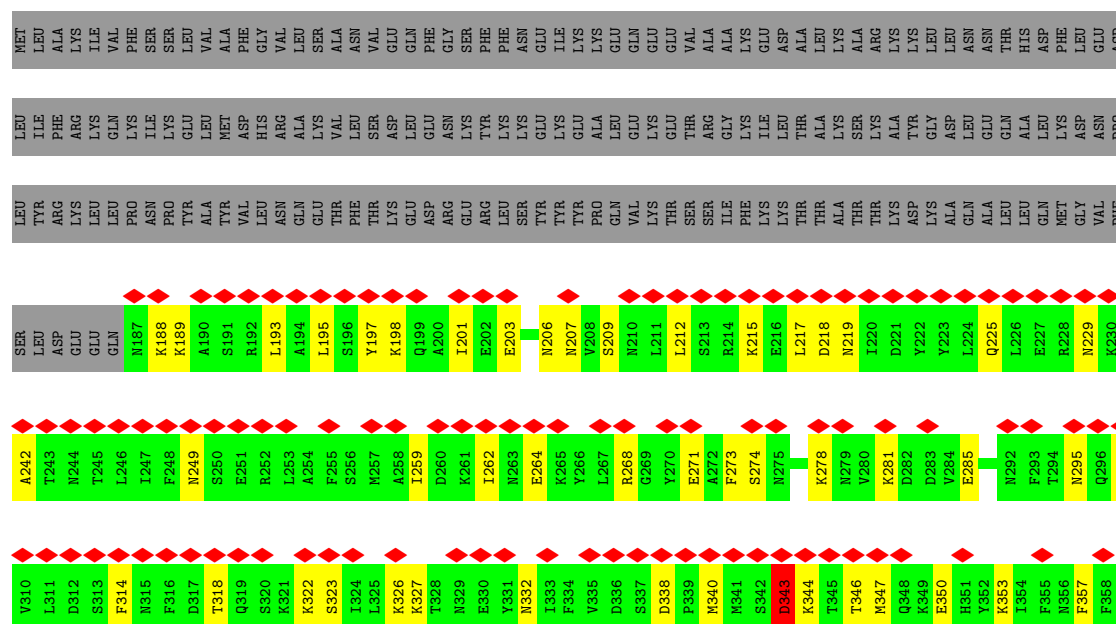
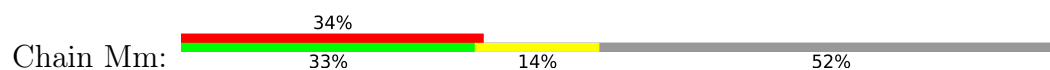




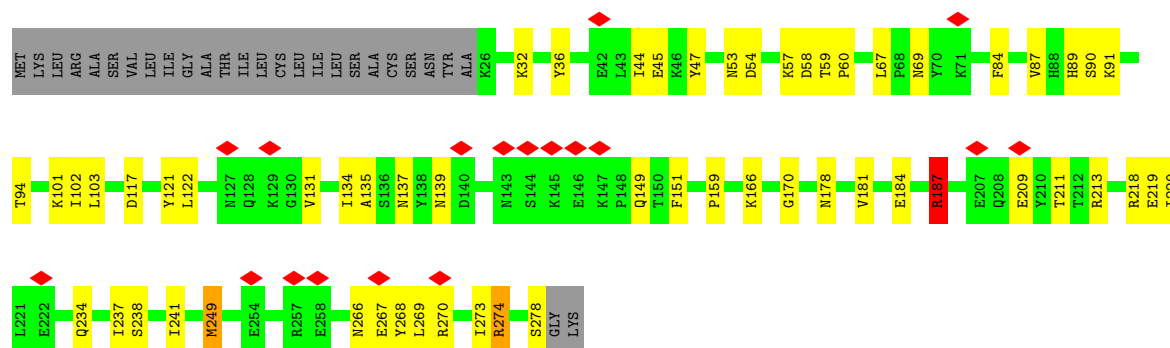
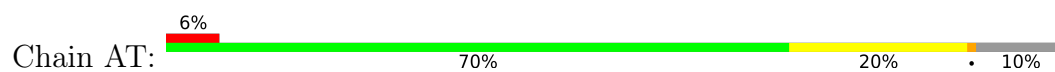
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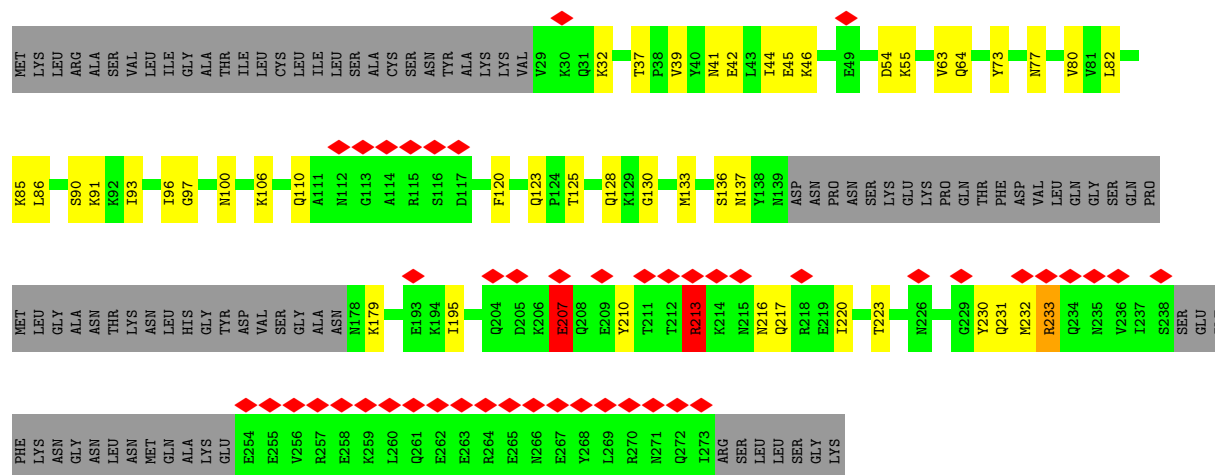
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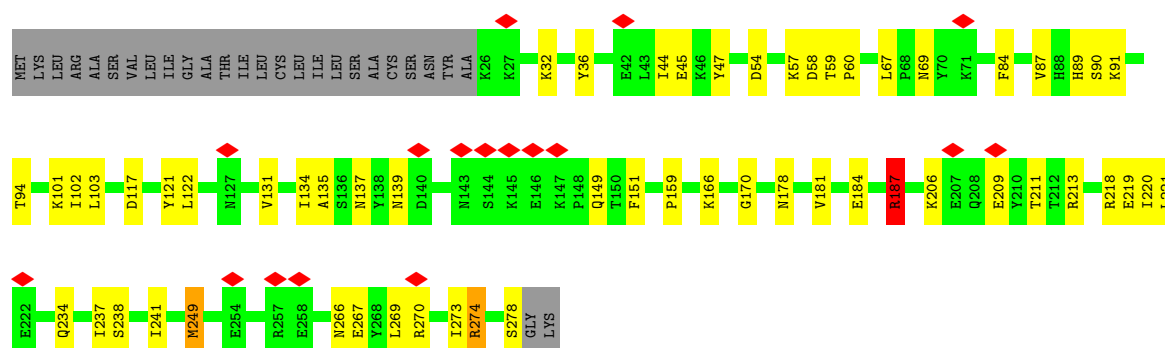




• Molecule 3: Type IV secretion system apparatus protein CagT

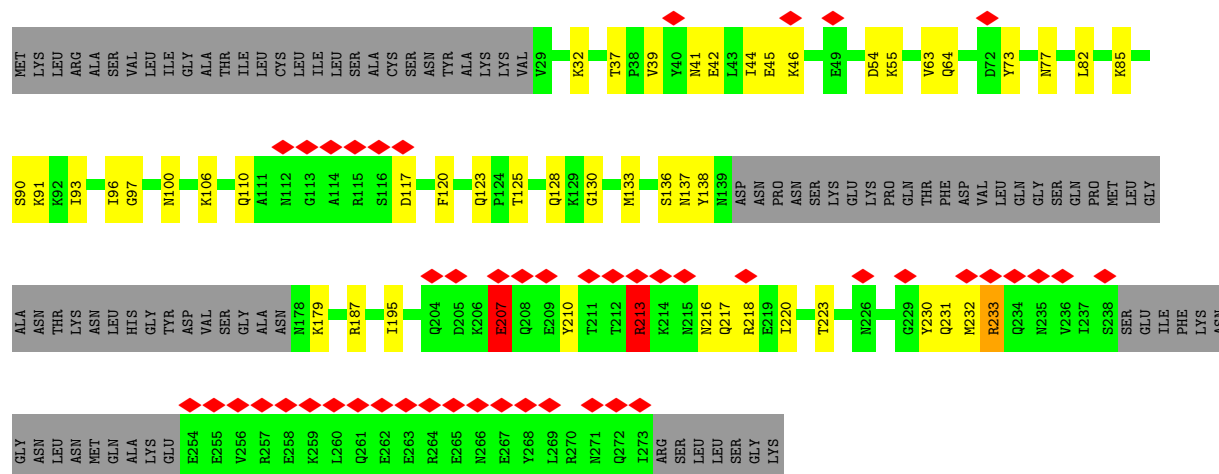


• Molecule 3: Type IV secretion system apparatus protein CagT



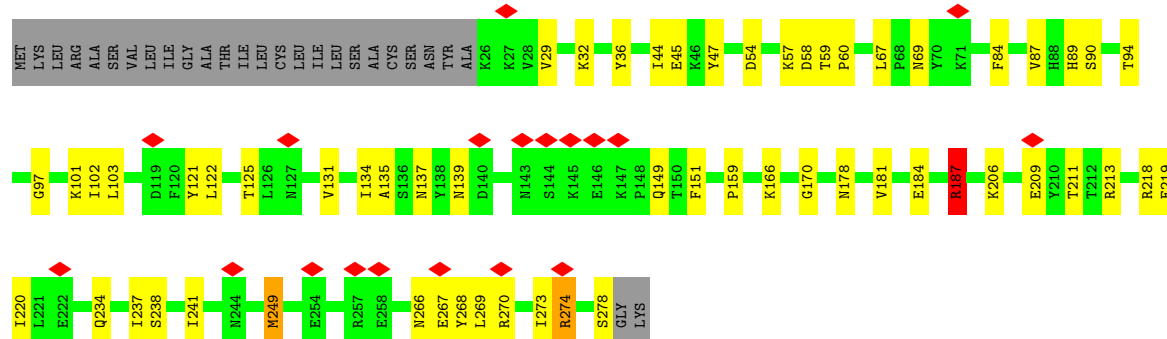
• Molecule 3: Type IV secretion system apparatus protein CagT





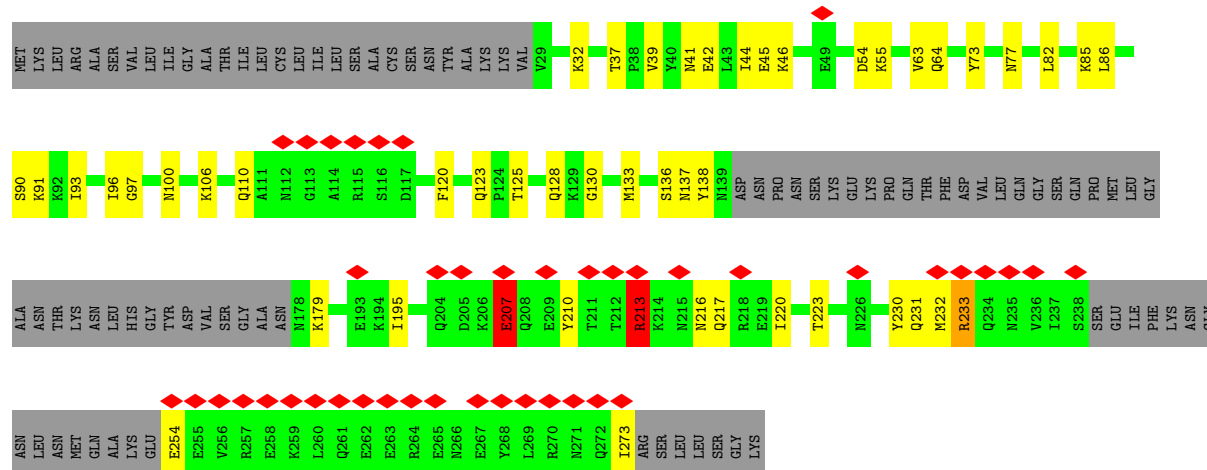
• Molecule 3: Type IV secretion system apparatus protein CagT

Chain CT: 7% 69% 20% 10%

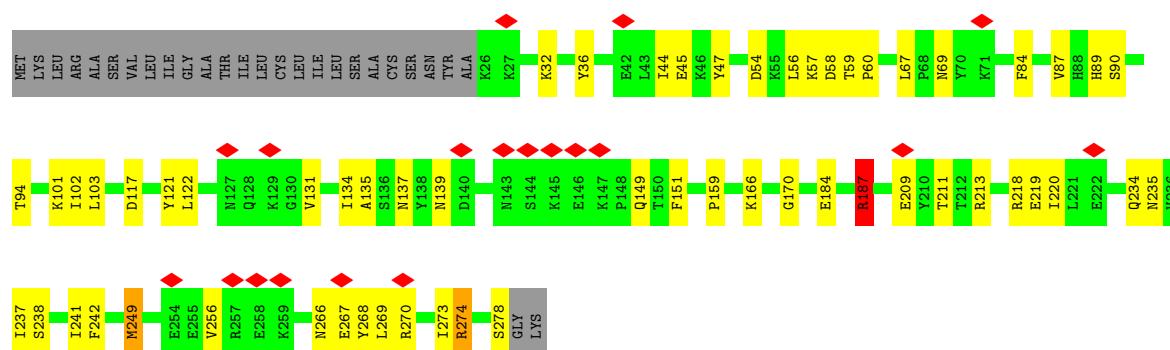
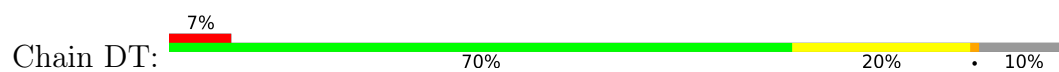


• Molecule 3: Type IV secretion system apparatus protein CagT

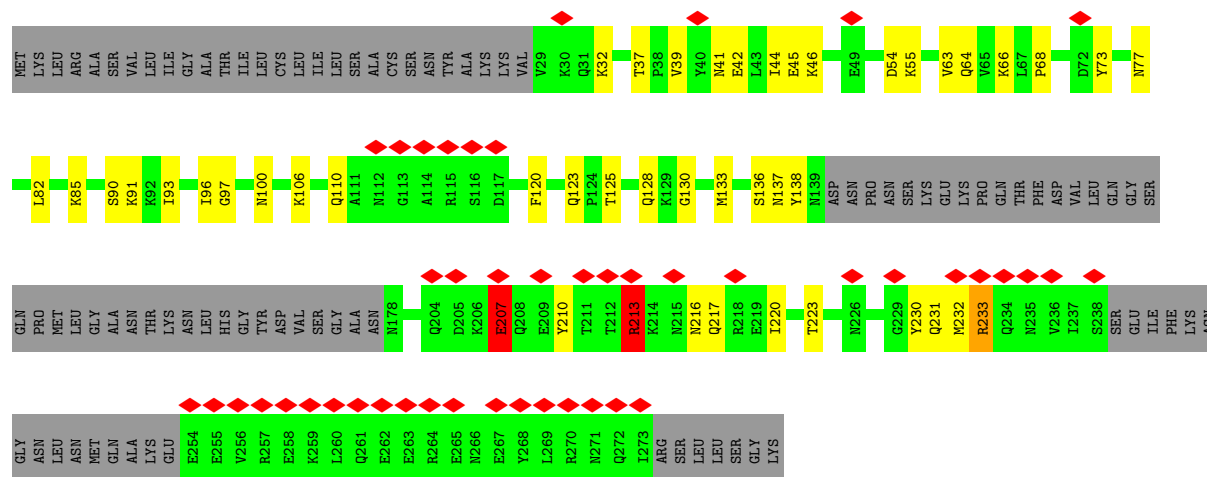
Chain Ct: 15% 51% 16% 31%



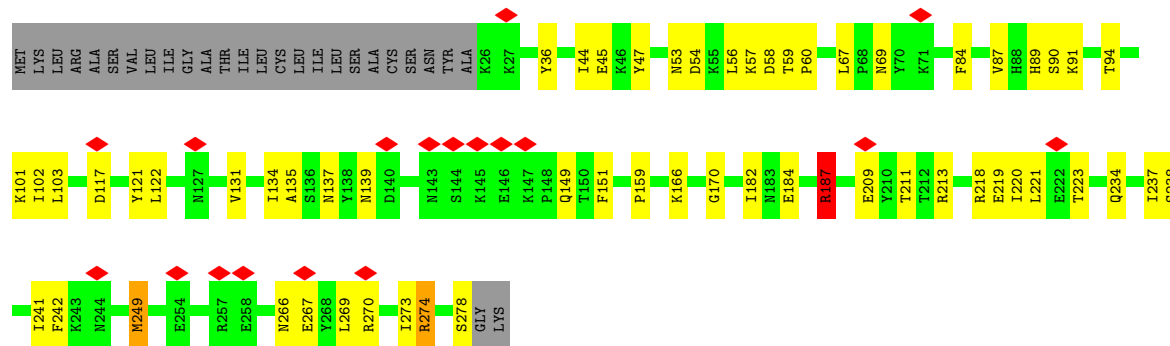
• Molecule 3: Type IV secretion system apparatus protein CagT



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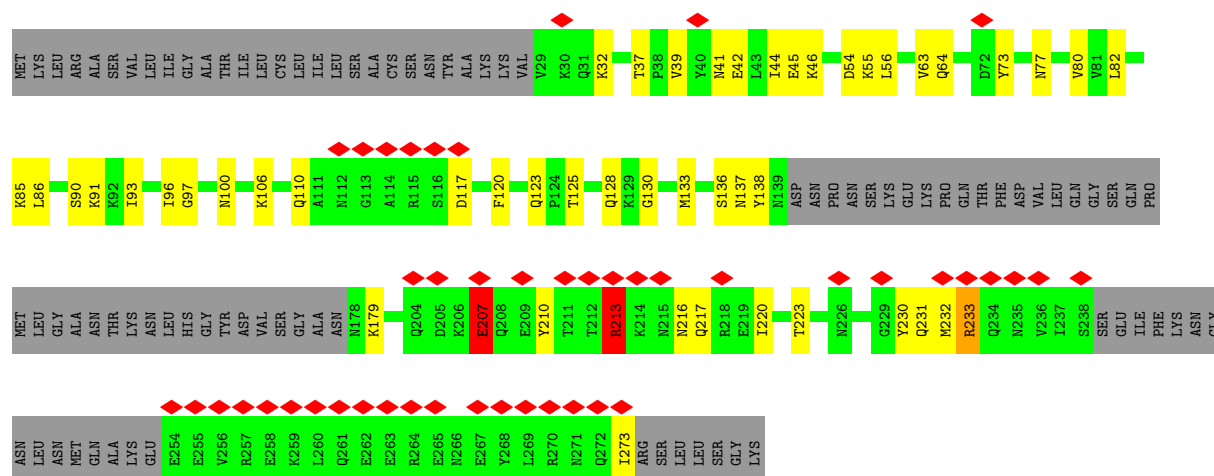


• Molecule 3: Type IV secretion system apparatus protein CagT

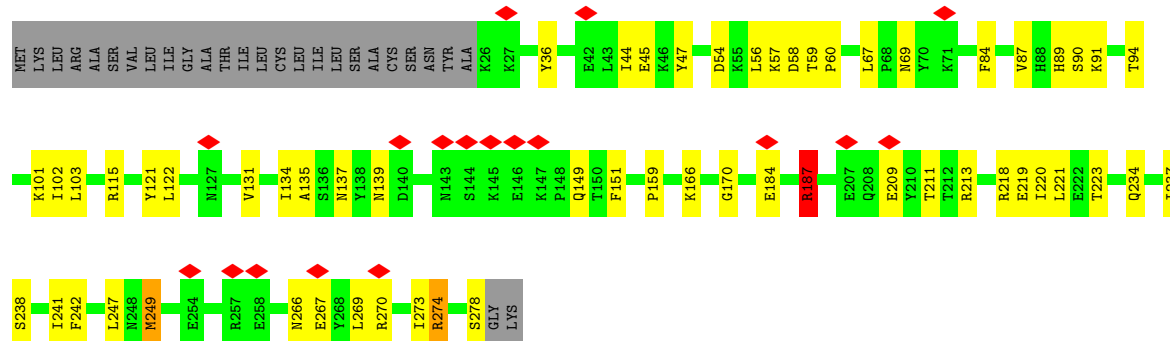


• Molecule 3: Type IV secretion system apparatus protein CagT

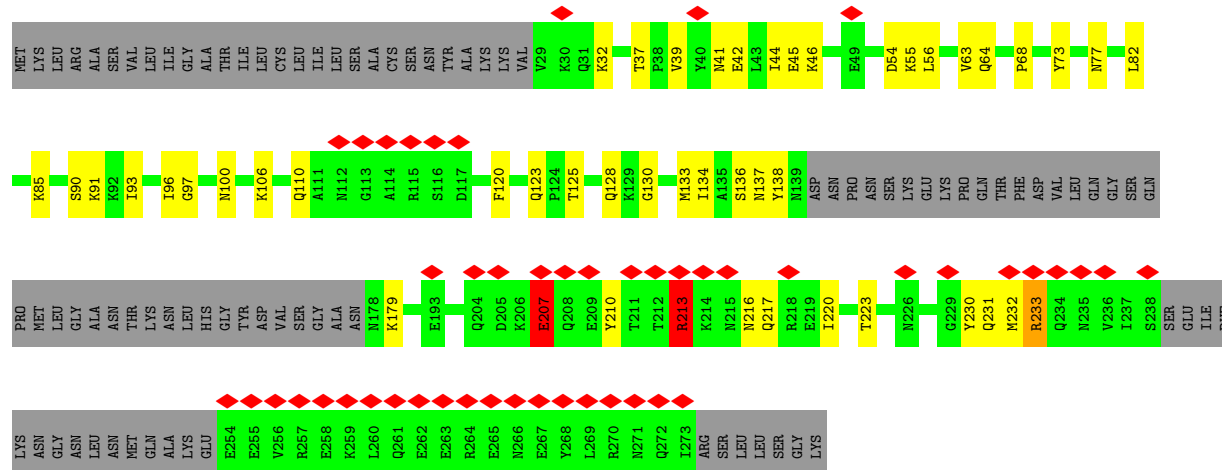




- Molecule 3: Type IV secretion system apparatus protein CagT

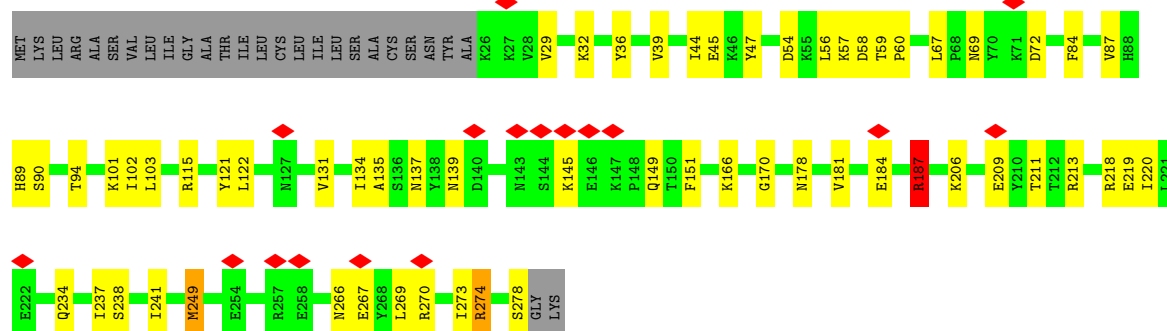


- Molecule 3: Type IV secretion system apparatus protein CagT



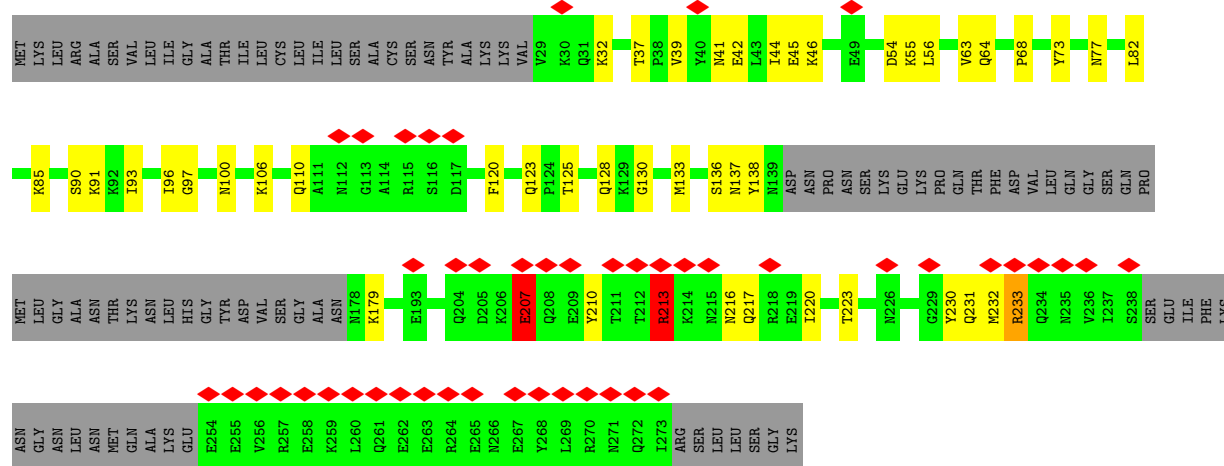
- Molecule 3: Type IV secretion system apparatus protein CagT

Chain GT: 



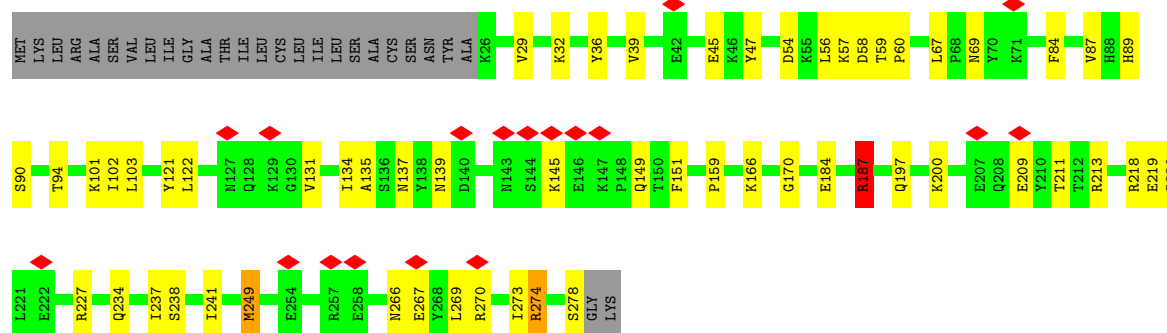
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Chain Gt: 



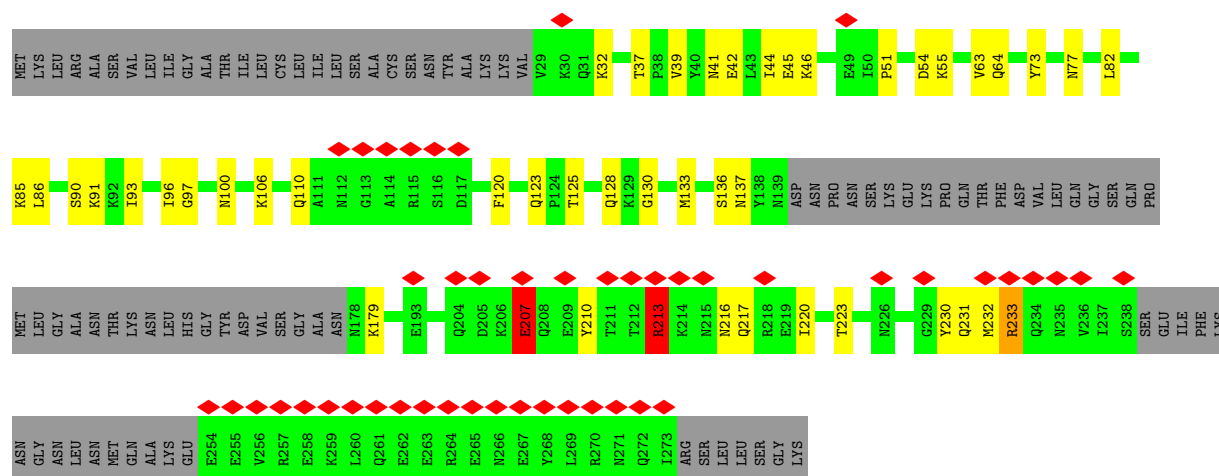
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Chain HT: 



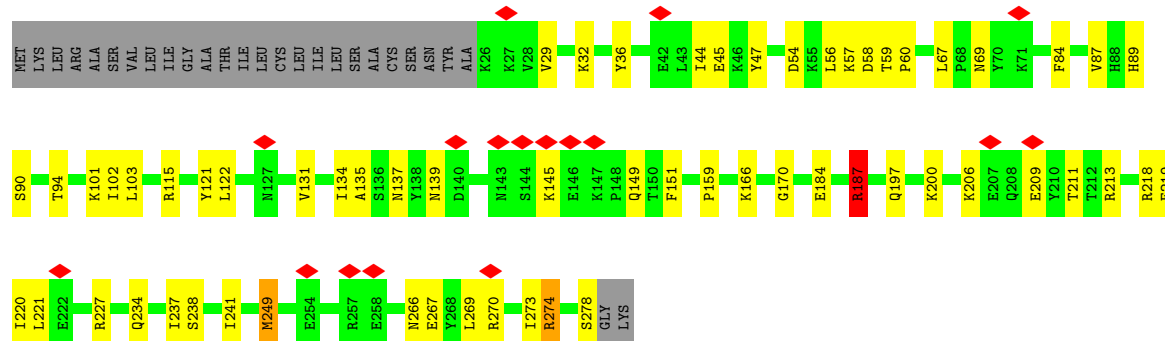
• Molecule 3: Type IV secretion system apparatus protein CagT

Chain Ht: 



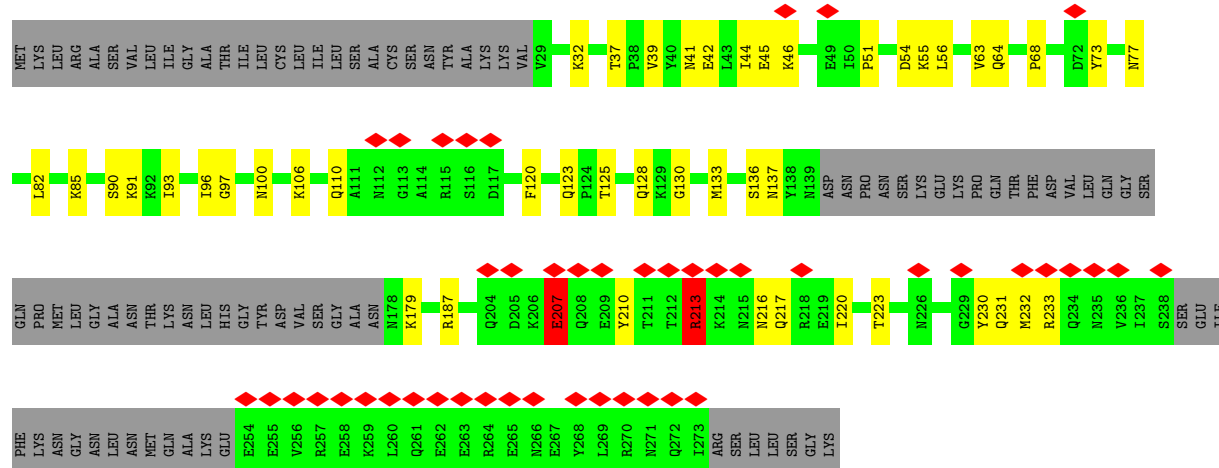
- Molecule 3: Type IV secretion system apparatus protein CagT

Chain IT: 6% 69% 21% 10%

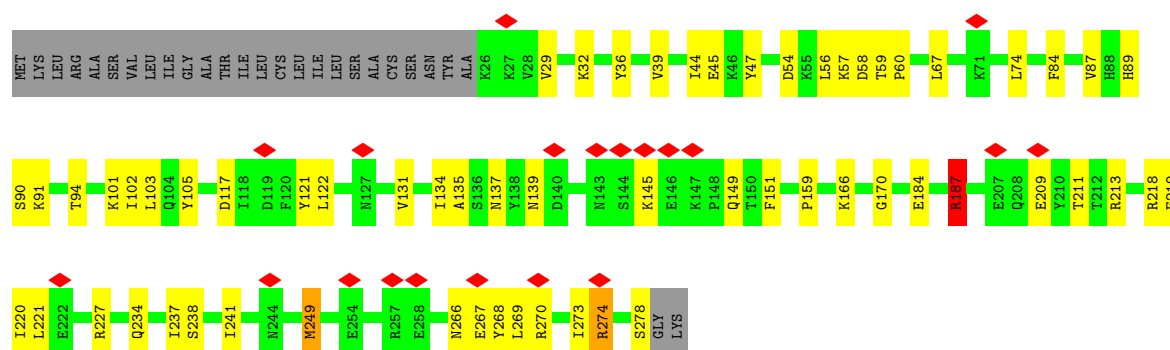


- Molecule 3: Type IV secretion system apparatus protein CagT

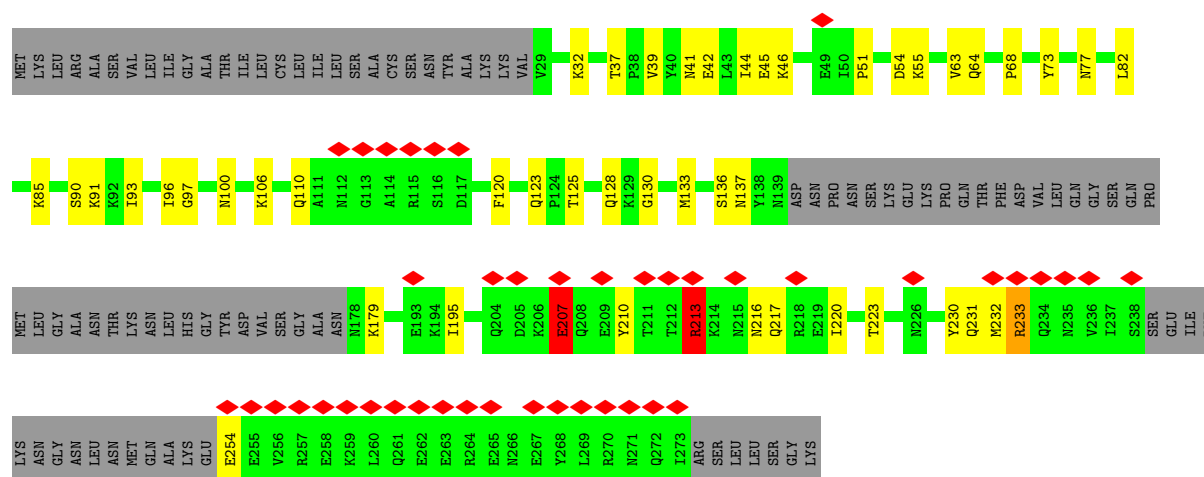
Chain It: 16% 51% 16% 31%



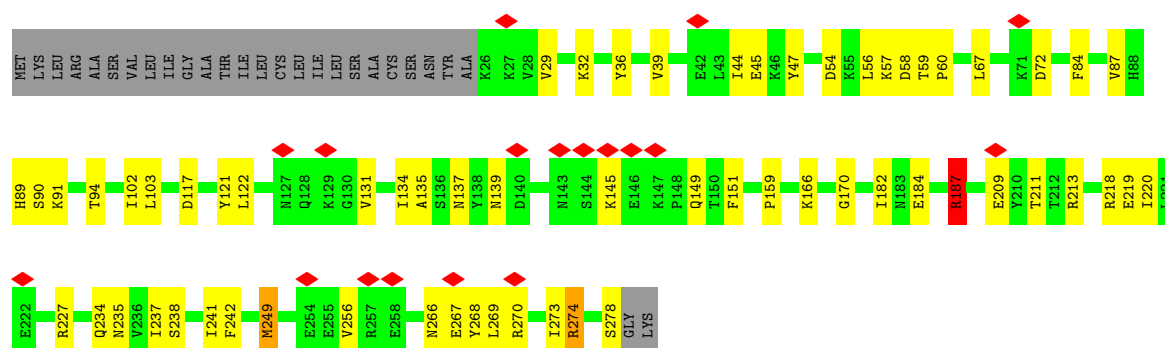
- Molecule 3: Type IV secretion system apparatus protein CagT



• Molecule 3: Type IV secretion system apparatus protein CagT

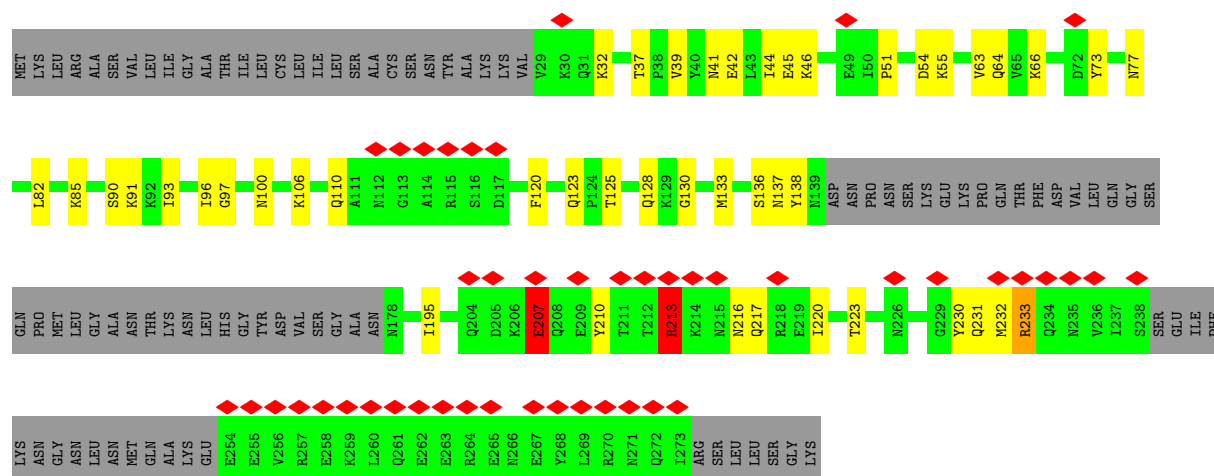


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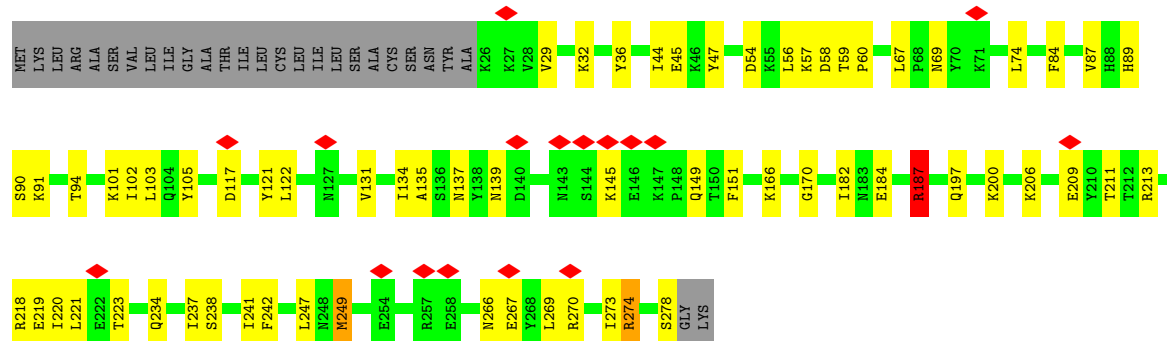


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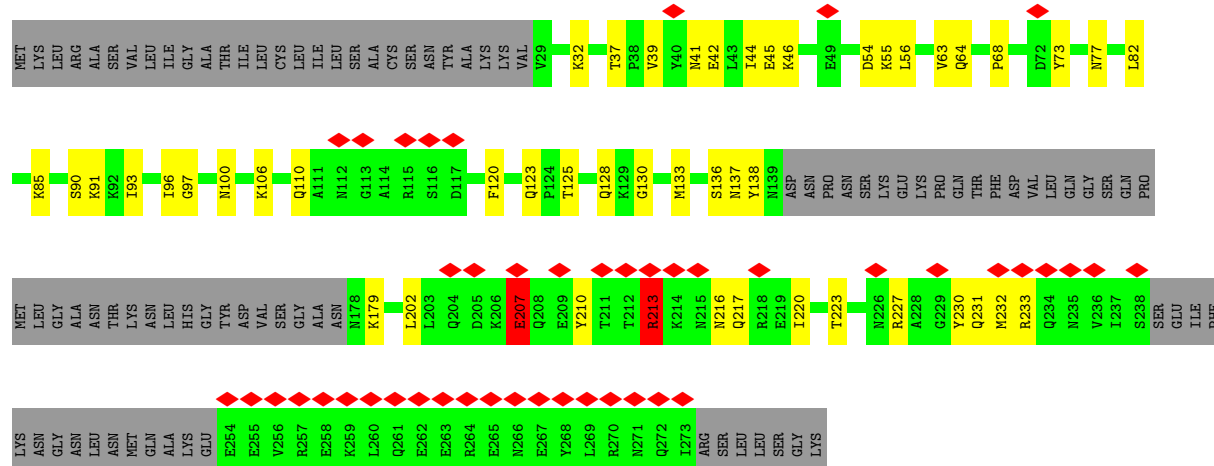




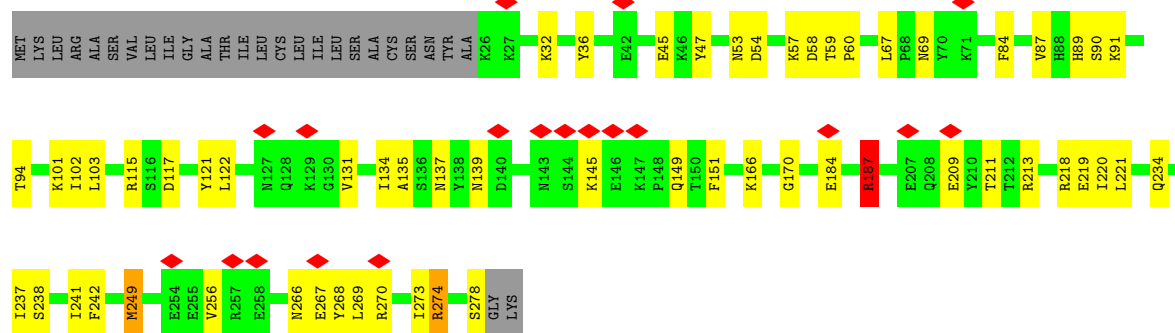
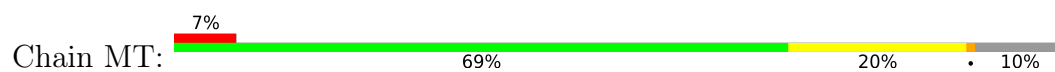
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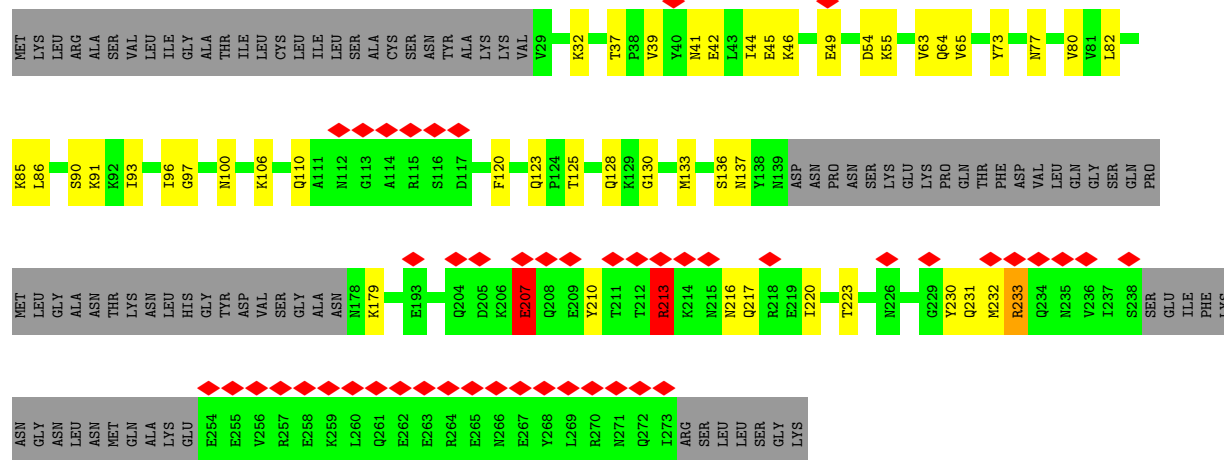
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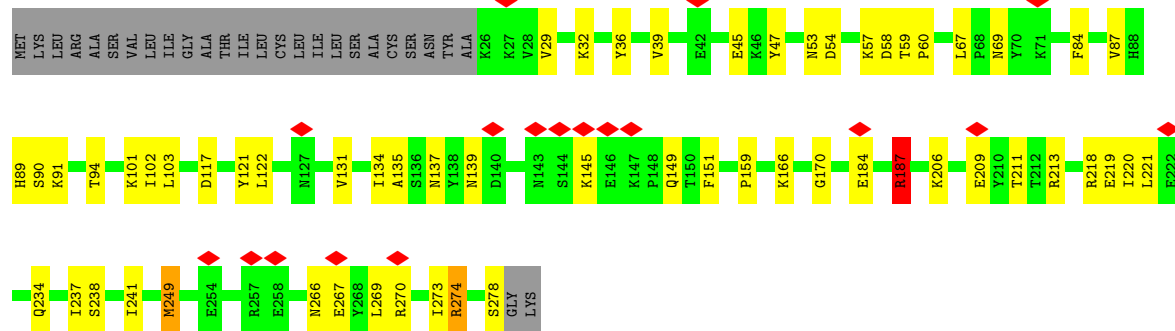
• Molecule 3: Type IV secretion system apparatus protein CagT



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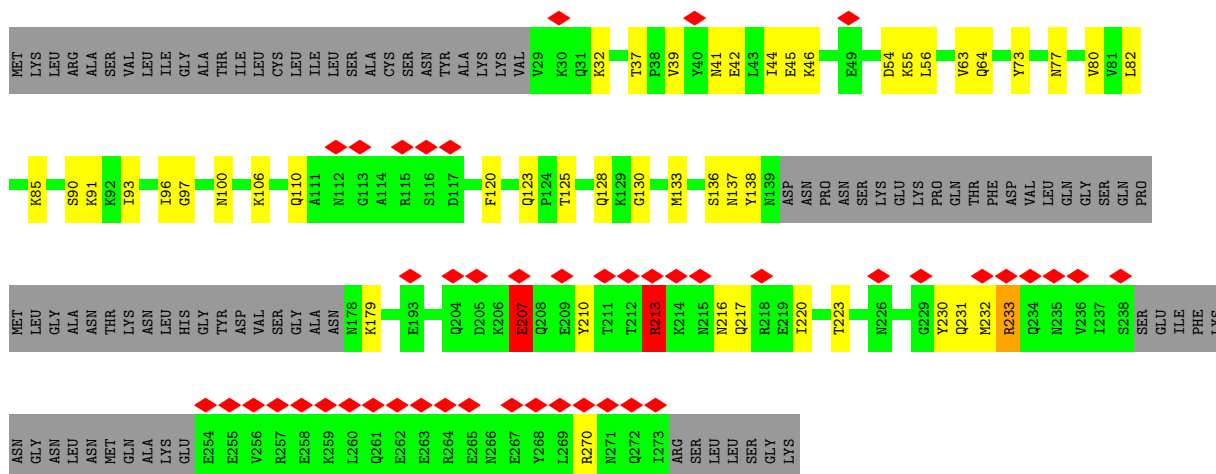


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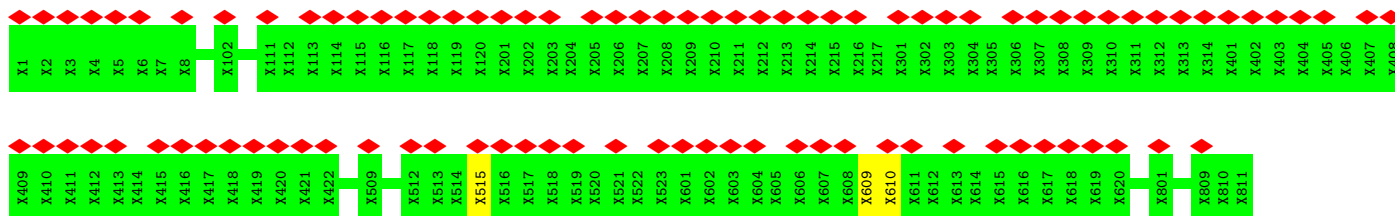


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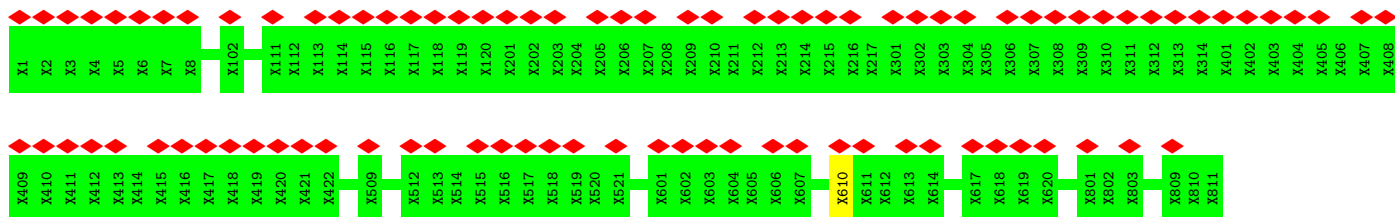




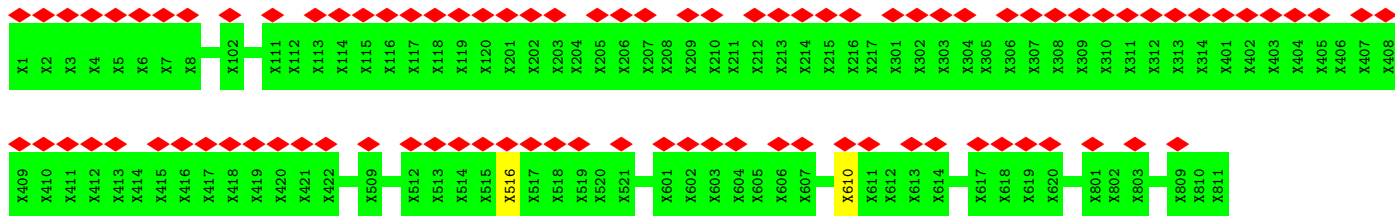
- Molecule 4: Unknown protein fragment



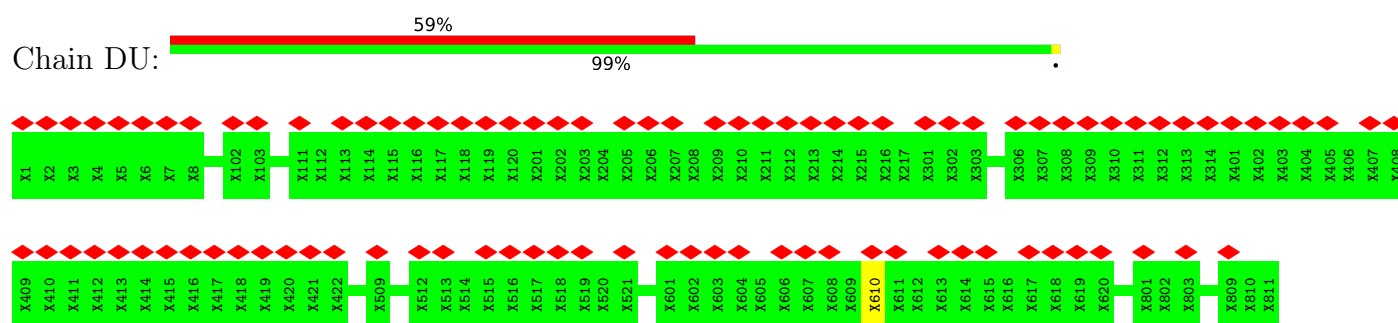
- Molecule 4: Unknown protein fragment



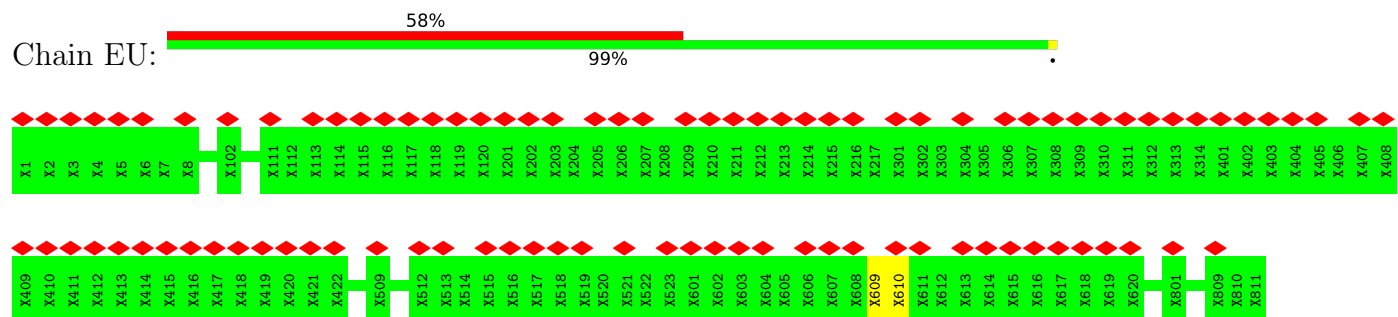
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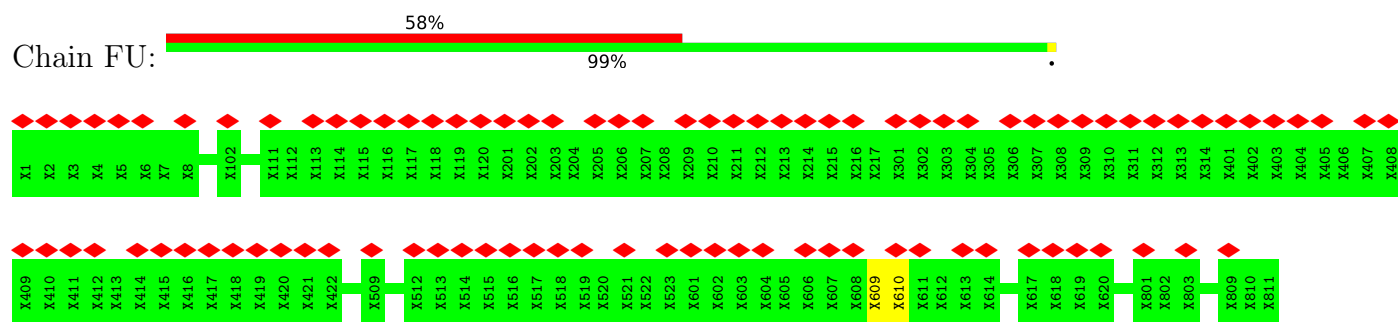
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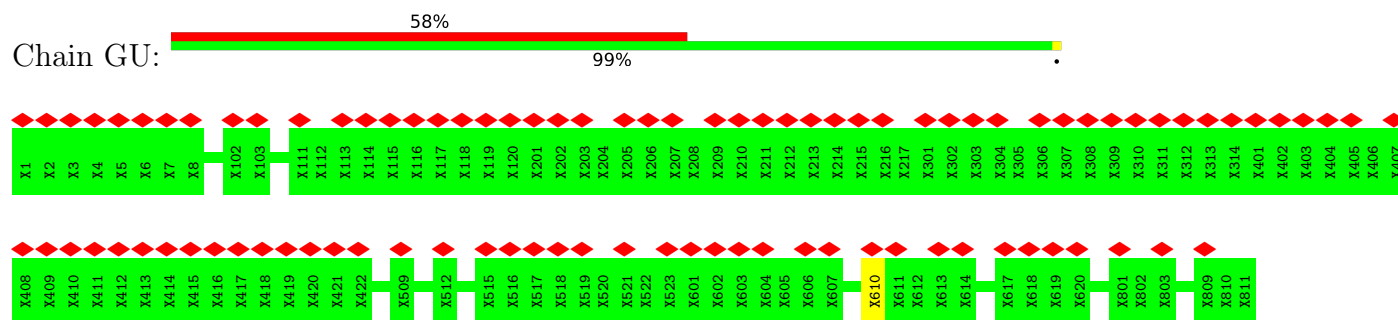
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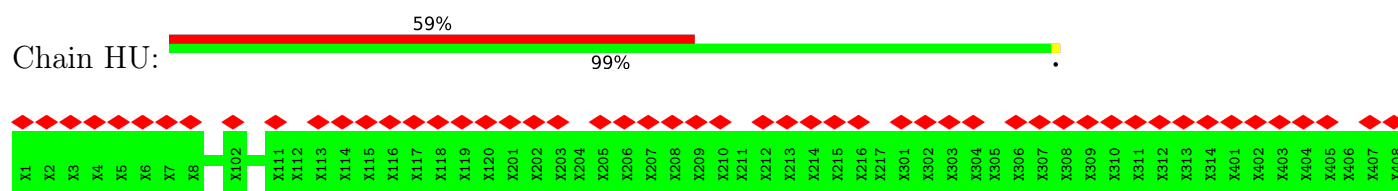
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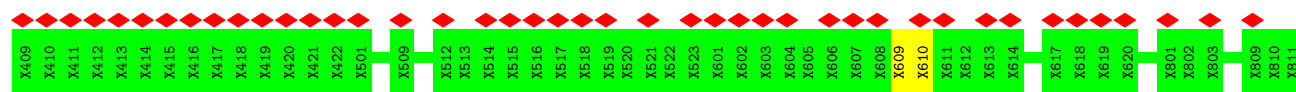


- Molecule 4: Unknown protein fragment



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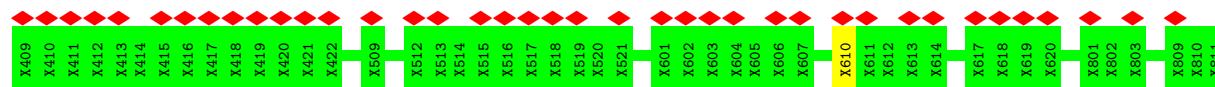
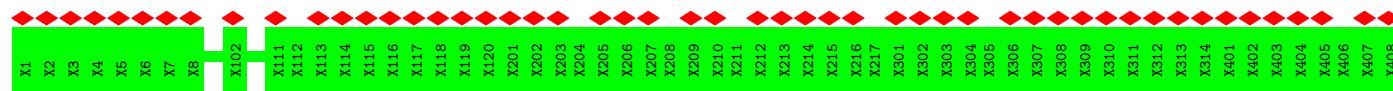




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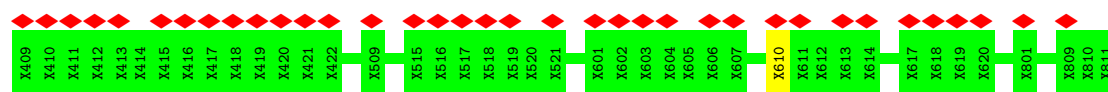
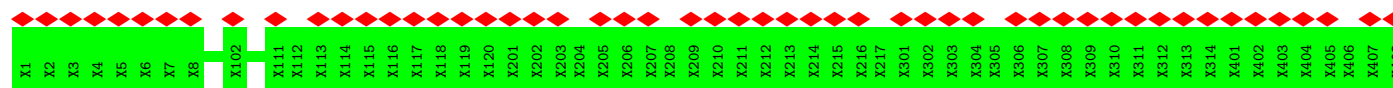
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- Molecule 4: Unknown protein fragment



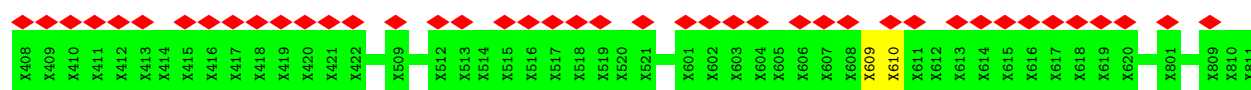
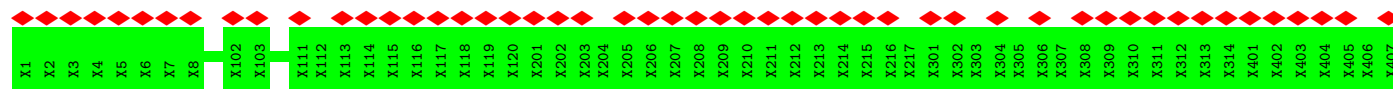
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- Molecule 4: Unknown protein fragment



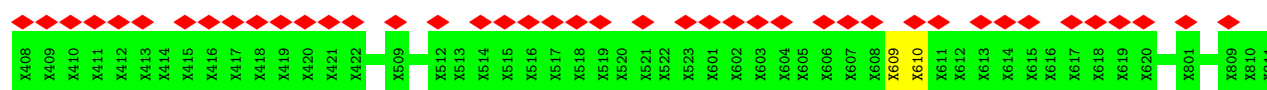
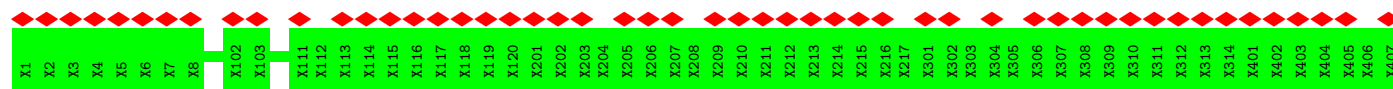
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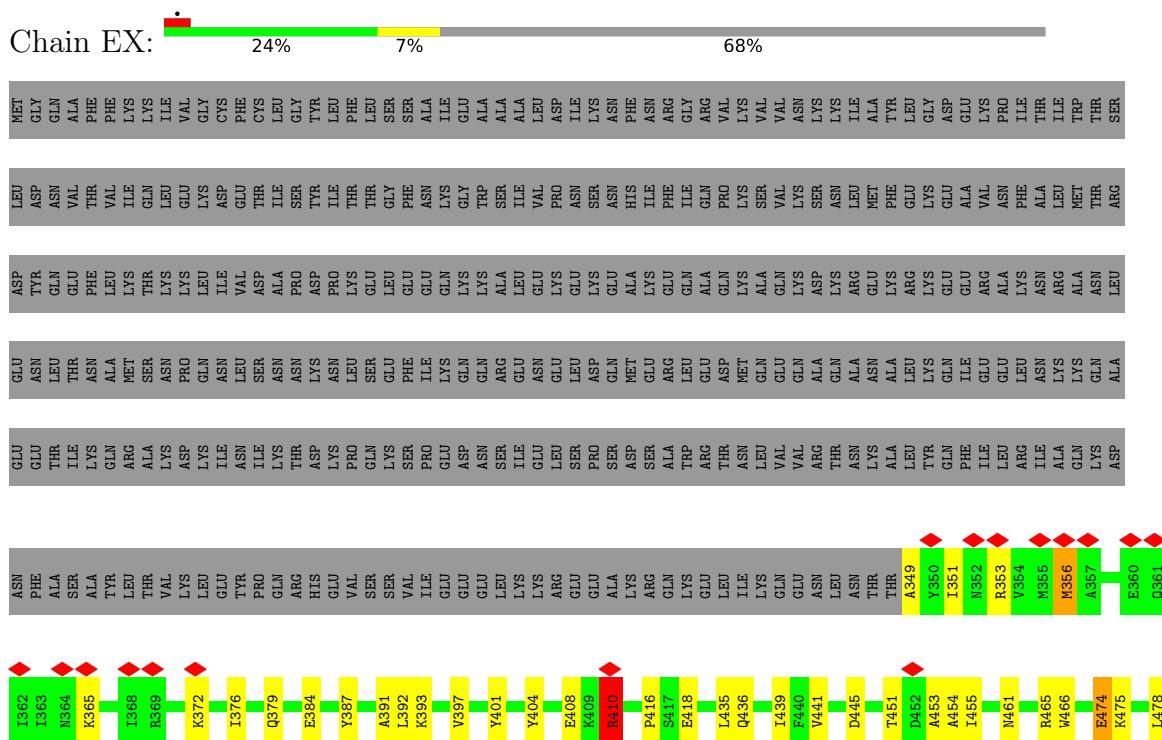
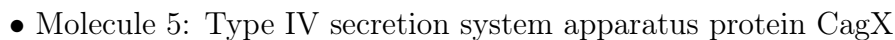
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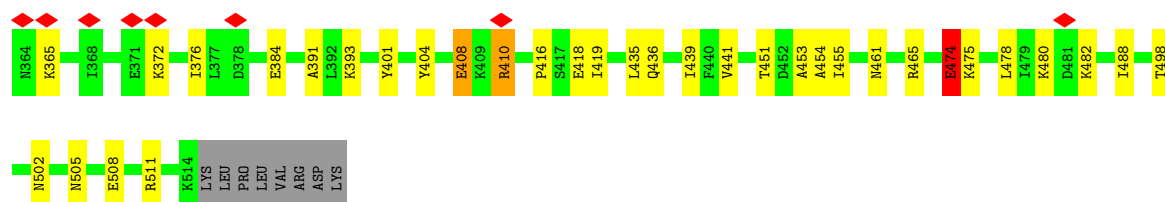


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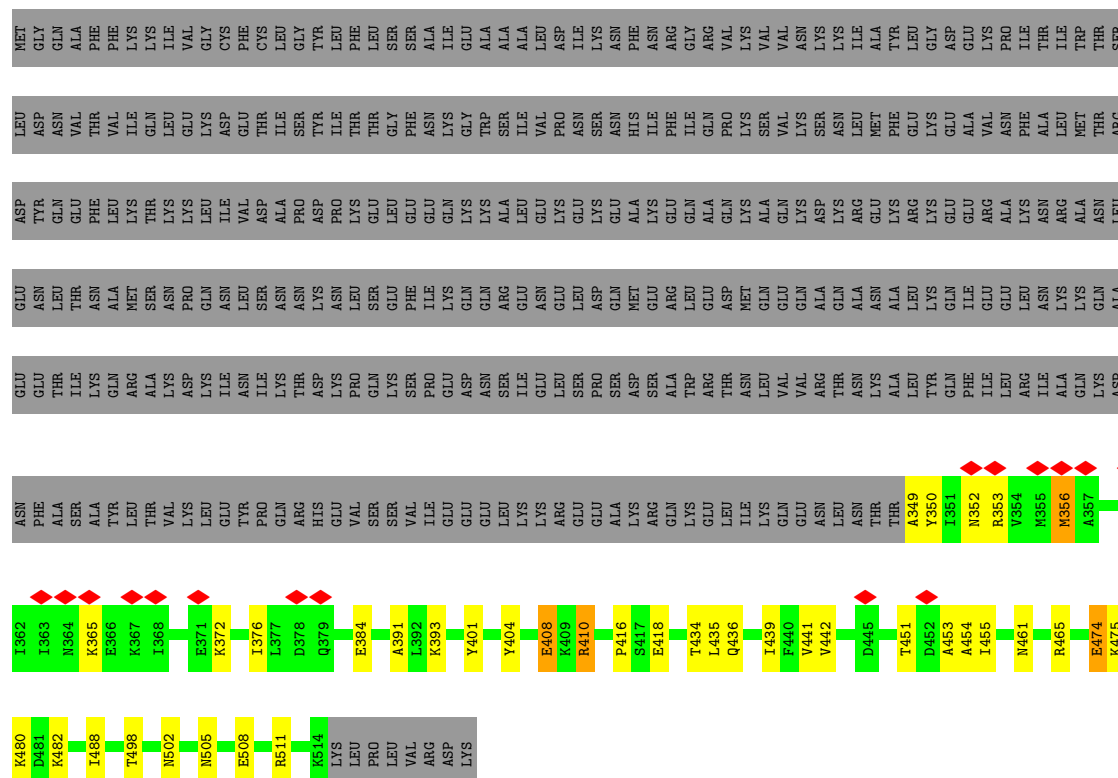


- Molecule 4: Unknown protein fragment



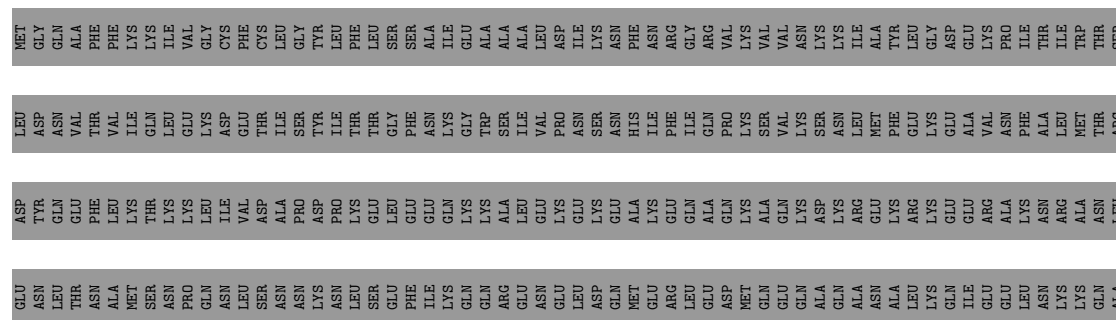


• Molecule 5: Type IV secretion system apparatus protein CagX

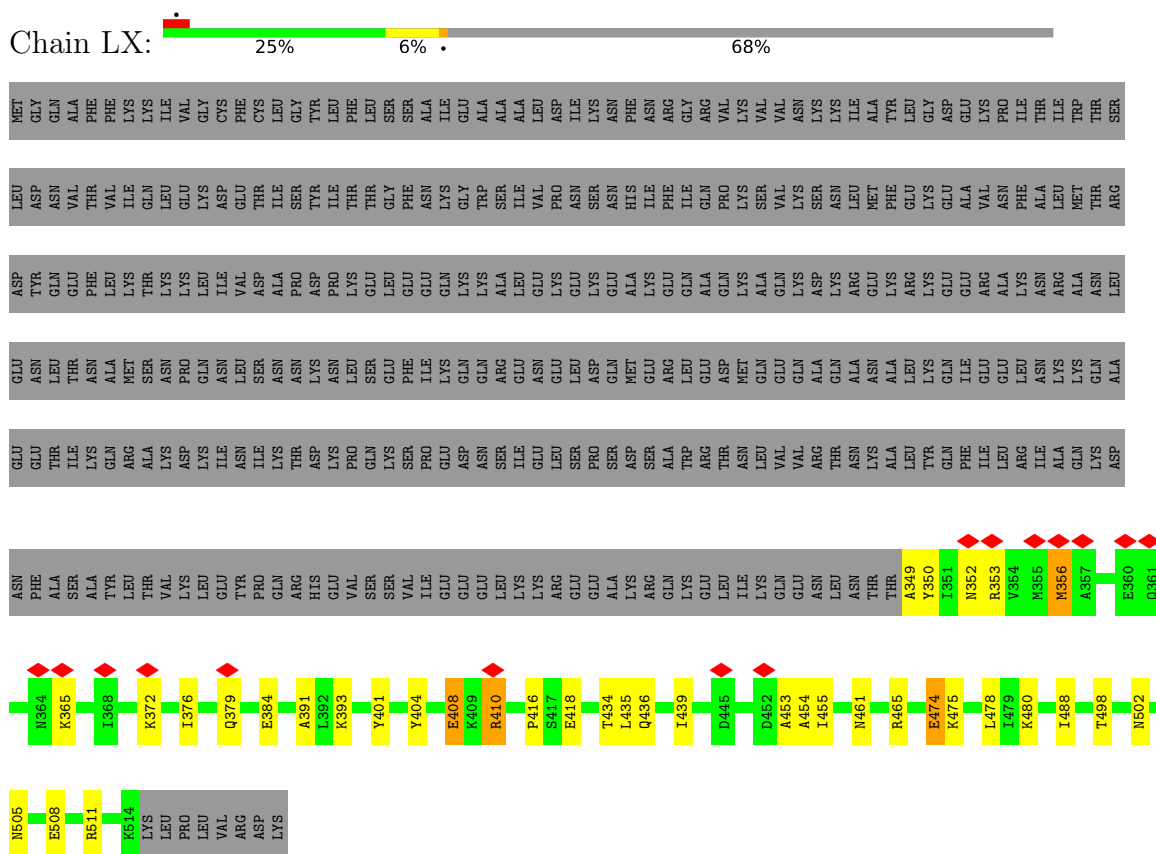


• Molecule 5: Type IV secretion system apparatus protein CagX

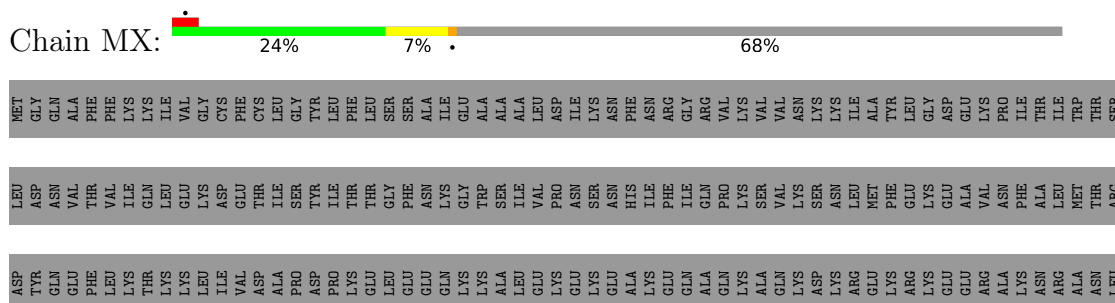


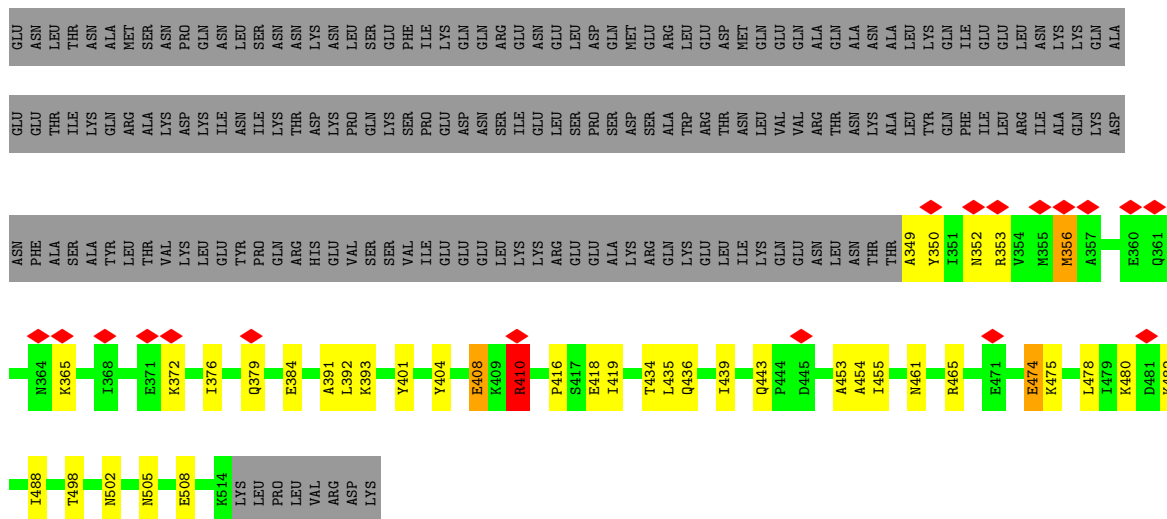


- Molecule 5: Type IV secretion system apparatus protein CagX

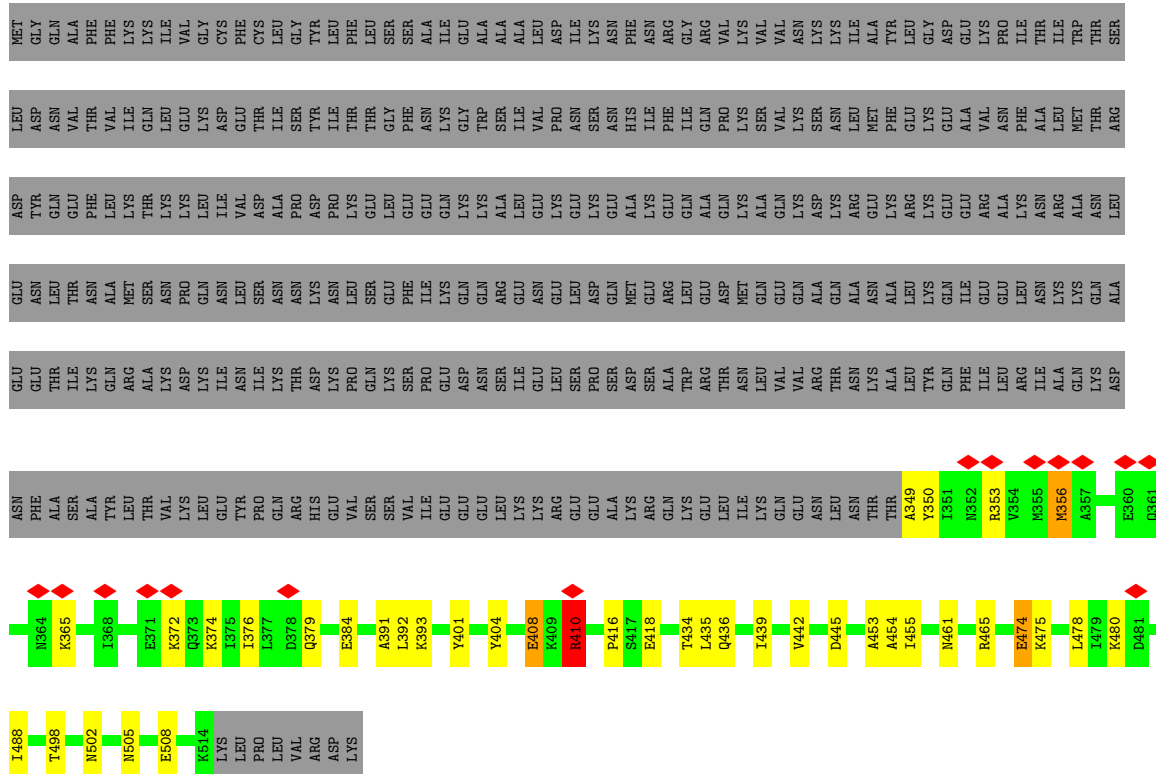


- Molecule 5: Type IV secretion system apparatus protein CagX

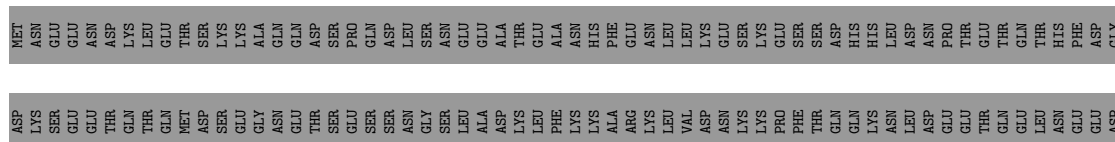




- Molecule 5: Type IV secretion system apparatus protein CagX



- Molecule 6: Cag pathogenicity island protein (Cag7)

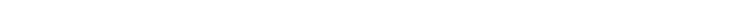








- Molecule 6: Cag pathogenicity island protein (Cag7)

Chain DY:  8% 1% 89%

MET	ASN	GLU	GLU	ASN	ASP	LYS	LEU	GLU	THR	SER	SER	LYS	LYS	ALA	GLN	GLN	ASP	SER	PRO	GLN	ASP	LEU	SER	ASN	GLU	GLU	ALA	ALA	HIS	PHE	GLU	GLU	ASN	LEU	LEU	LYS	GLU	SER	SER	ASP	HIS	HIS	LEU	ASP	ASN	PRO	THR	GLU	THR	GLN	THR	HIS	PHE	ASP	GLY
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----









- Molecule 6: Cag pathogenicity island protein (Cag7)





- Molecule 6: Cag pathogenicity island protein (Cag7)





Chain JY: 8% 1% 89%

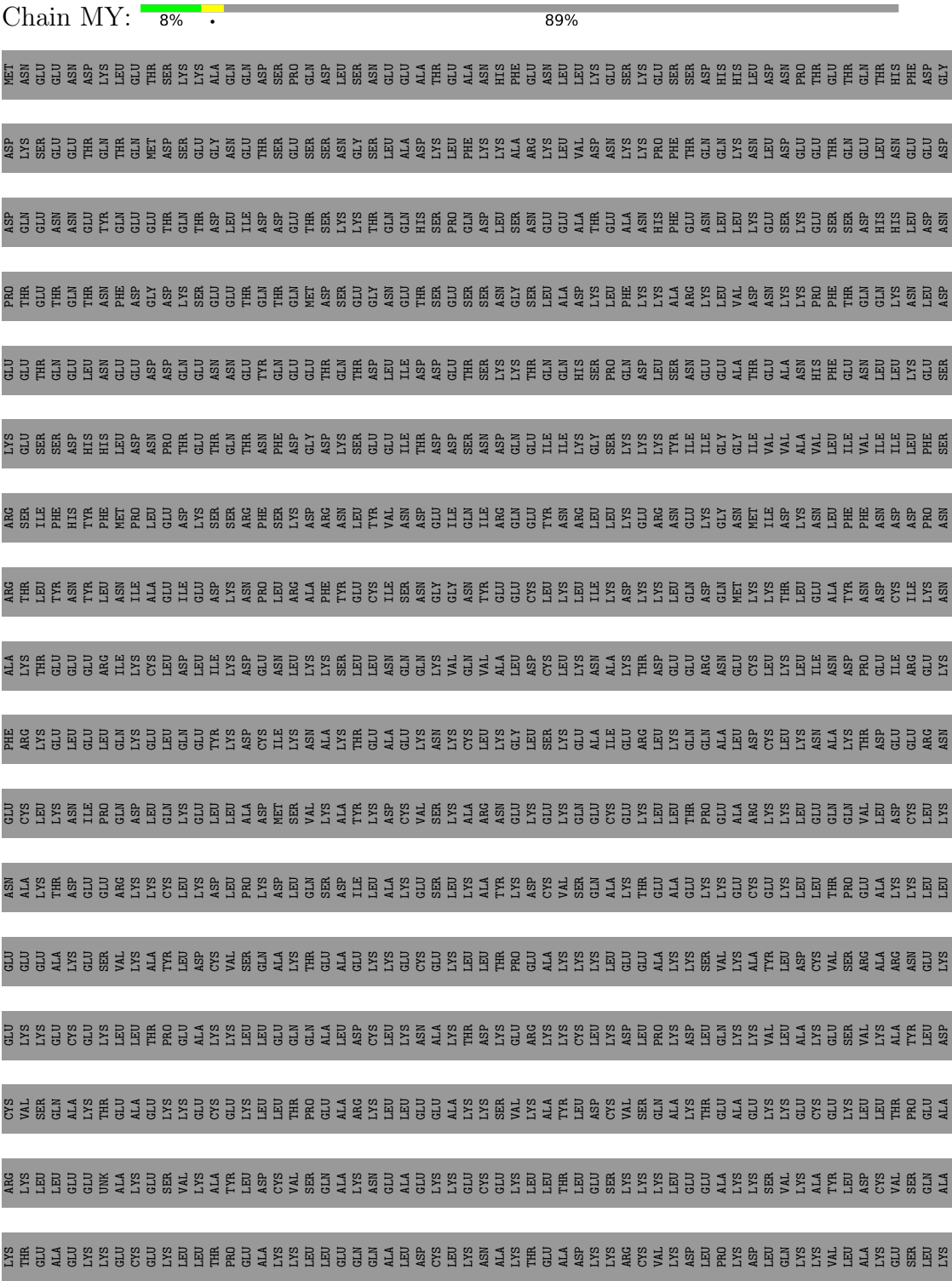






T1896	ASP
N1897	ASP
T1905	ASP
K1906	ASN
Q1907	ASN
S1908	LYS
T1909	LYS
THR	THR
LEU	LEU
SER	SER
LYS	LYS
ARG	ARG
GLU	GLU
HIS	HIS
GLN	GLN
GLU	GLU
GLU	GLU
ILE	ILE
SER	SER
THR	THR
THR	THR
SER	SER
PRO	PRO
LYS	LYS
GLY	GLY
GLY	GLY
ASN	ASN

● Molecule 6: Cag pathogenicity island protein (Cag7)







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C14	Depositor
Number of particles used	47440	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59.2, 59.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.139	Depositor
Minimum map value	-0.056	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	836.39996, 836.39996, 836.39996	wwPDB
Map dimensions	510, 510, 510	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.64, 1.64, 1.64	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.46	0/2023	0.87	7/2742 (0.3%)
1	AB	0.53	0/742	0.90	0/1007
1	AC	0.52	0/755	0.88	0/1023
1	AD	0.54	0/793	1.02	0/1073
1	AE	0.50	0/864	0.92	2/1170 (0.2%)
1	BA	0.46	0/2023	0.87	7/2742 (0.3%)
1	BB	0.53	0/742	0.86	0/1007
1	BC	0.51	0/755	0.86	0/1023
1	BD	0.58	0/793	1.05	5/1073 (0.5%)
1	BE	0.42	0/864	0.82	2/1170 (0.2%)
1	CA	0.46	0/2023	0.87	7/2742 (0.3%)
1	CB	0.60	1/742 (0.1%)	0.97	4/1007 (0.4%)
1	CC	0.55	0/755	0.94	0/1023
1	CD	0.50	0/793	0.93	2/1073 (0.2%)
1	CE	0.39	0/864	0.86	0/1170
1	DA	0.46	0/2023	0.87	7/2742 (0.3%)
1	DB	0.68	2/742 (0.3%)	1.07	3/1007 (0.3%)
1	DC	0.57	0/755	0.94	1/1023 (0.1%)
1	DD	0.55	0/793	0.98	1/1073 (0.1%)
1	DE	0.40	0/864	0.93	3/1170 (0.3%)
1	EA	0.46	0/2023	0.87	7/2742 (0.3%)
1	EB	0.62	1/742 (0.1%)	1.01	2/1007 (0.2%)
1	EC	0.53	0/755	0.93	0/1023
1	ED	0.58	0/793	1.08	3/1073 (0.3%)
1	EE	0.42	0/864	0.87	1/1170 (0.1%)
1	FA	0.46	0/2023	0.87	7/2742 (0.3%)
1	FB	0.62	1/742 (0.1%)	0.97	6/1007 (0.6%)
1	FC	0.60	0/755	1.05	3/1023 (0.3%)
1	FD	0.58	0/793	1.05	5/1073 (0.5%)
1	FE	0.40	0/864	0.86	3/1170 (0.3%)
1	GA	0.46	0/2023	0.87	7/2742 (0.3%)
1	GB	0.55	1/742 (0.1%)	0.87	0/1007
1	GC	0.60	0/755	0.93	1/1023 (0.1%)
1	GD	0.52	0/793	1.02	0/1073

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GE	0.47	0/864	0.88	0/1170
1	HA	0.46	0/2023	0.87	7/2742 (0.3%)
1	HB	0.61	2/742 (0.3%)	0.91	3/1007 (0.3%)
1	HC	0.55	0/755	0.88	0/1023
1	HD	0.51	0/793	1.04	5/1073 (0.5%)
1	HE	0.45	0/864	0.89	4/1170 (0.3%)
1	IA	0.46	0/2023	0.87	7/2742 (0.3%)
1	IB	0.51	0/742	0.81	0/1007
1	IC	0.47	0/755	0.83	0/1023
1	ID	0.58	0/793	1.06	9/1073 (0.8%)
1	IE	0.43	0/864	0.83	2/1170 (0.2%)
1	JA	0.46	0/2023	0.87	7/2742 (0.3%)
1	JB	0.62	1/742 (0.1%)	0.96	4/1007 (0.4%)
1	JC	0.53	0/755	0.95	1/1023 (0.1%)
1	JD	0.62	0/793	1.07	6/1073 (0.6%)
1	JE	0.43	0/864	0.87	3/1170 (0.3%)
1	KA	0.46	0/2023	0.87	7/2742 (0.3%)
1	KB	0.64	2/742 (0.3%)	0.98	3/1007 (0.3%)
1	KC	0.54	0/755	0.90	0/1023
1	KD	1.08	6/793 (0.8%)	1.22	6/1073 (0.6%)
1	KE	0.75	5/864 (0.6%)	1.12	7/1170 (0.6%)
1	LA	0.46	0/2023	0.87	7/2742 (0.3%)
1	LB	0.61	1/742 (0.1%)	0.96	4/1007 (0.4%)
1	LC	0.55	0/755	0.90	1/1023 (0.1%)
1	LD	0.56	0/793	1.06	2/1073 (0.2%)
1	LE	0.40	0/864	0.89	2/1170 (0.2%)
1	MA	0.46	0/2023	0.87	7/2742 (0.3%)
1	MB	0.64	2/742 (0.3%)	1.00	5/1007 (0.5%)
1	MC	0.56	0/755	0.98	1/1023 (0.1%)
1	MD	0.61	0/793	1.13	7/1073 (0.7%)
1	ME	0.45	0/864	0.85	3/1170 (0.3%)
1	NA	0.46	0/2023	0.87	7/2742 (0.3%)
1	NB	0.58	0/742	0.92	2/1007 (0.2%)
1	NC	0.54	0/755	0.90	1/1023 (0.1%)
1	ND	0.64	2/793 (0.3%)	1.07	2/1073 (0.2%)
1	NE	0.46	0/864	0.86	1/1170 (0.1%)
2	AM	0.37	0/1507	0.72	1/2019 (0.0%)
2	Am	0.40	0/1496	0.83	4/2005 (0.2%)
2	BM	0.34	0/1507	0.70	1/2019 (0.0%)
2	Bm	0.32	0/1496	0.79	2/2005 (0.1%)
2	CM	0.35	0/1507	0.72	2/2019 (0.1%)
2	Cm	0.30	0/1496	0.78	2/2005 (0.1%)
2	DM	0.39	0/1507	0.77	0/2019

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	Dm	0.37	0/1496	0.82	3/2005 (0.1%)
2	EM	0.38	0/1507	0.76	2/2019 (0.1%)
2	Em	0.35	0/1496	0.81	2/2005 (0.1%)
2	FM	0.39	0/1507	0.80	1/2019 (0.0%)
2	Fm	0.37	0/1496	0.81	2/2005 (0.1%)
2	GM	0.35	0/1507	0.70	1/2019 (0.0%)
2	Gm	0.35	0/1496	0.85	4/2005 (0.2%)
2	HM	0.36	0/1507	0.72	0/2019
2	Hm	0.39	0/1496	0.84	4/2005 (0.2%)
2	IM	0.35	0/1507	0.70	1/2019 (0.0%)
2	Im	0.36	0/1496	0.83	4/2005 (0.2%)
2	JM	0.35	0/1507	0.73	2/2019 (0.1%)
2	Jm	0.35	0/1496	0.86	4/2005 (0.2%)
2	KM	0.35	0/1507	0.74	3/2019 (0.1%)
2	Km	0.36	0/1496	0.80	2/2005 (0.1%)
2	LM	0.49	2/1507 (0.1%)	0.79	3/2019 (0.1%)
2	Lm	0.36	0/1496	0.82	2/2005 (0.1%)
2	MM	0.41	0/1507	0.78	1/2019 (0.0%)
2	Mm	0.36	0/1496	0.80	2/2005 (0.1%)
2	NM	0.38	0/1507	0.71	1/2019 (0.0%)
2	Nm	0.34	0/1496	0.77	2/2005 (0.1%)
3	AT	0.53	0/2115	0.78	3/2847 (0.1%)
3	At	0.44	0/1638	0.79	3/2203 (0.1%)
3	BT	0.52	0/2115	0.78	3/2847 (0.1%)
3	Bt	0.45	0/1638	0.80	3/2203 (0.1%)
3	CT	0.53	0/2115	0.78	3/2847 (0.1%)
3	Ct	0.44	0/1638	0.79	3/2203 (0.1%)
3	DT	0.53	0/2115	0.78	3/2847 (0.1%)
3	Dt	0.44	0/1638	0.79	3/2203 (0.1%)
3	ET	0.52	0/2115	0.78	3/2847 (0.1%)
3	Et	0.45	0/1638	0.79	3/2203 (0.1%)
3	FT	0.52	0/2115	0.78	3/2847 (0.1%)
3	Ft	0.44	0/1638	0.80	3/2203 (0.1%)
3	GT	0.52	0/2115	0.78	3/2847 (0.1%)
3	Gt	0.45	0/1638	0.79	3/2203 (0.1%)
3	HT	0.52	0/2115	0.78	3/2847 (0.1%)
3	Ht	0.44	0/1638	0.80	3/2203 (0.1%)
3	IT	0.52	0/2115	0.78	3/2847 (0.1%)
3	It	0.45	0/1638	0.79	3/2203 (0.1%)
3	JT	0.52	0/2115	0.78	3/2847 (0.1%)
3	Jt	0.45	0/1638	0.79	3/2203 (0.1%)
3	KT	0.52	0/2115	0.78	3/2847 (0.1%)
3	Kt	0.45	0/1638	0.80	3/2203 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	LT	0.52	0/2115	0.78	3/2847 (0.1%)
3	Lt	0.44	0/1638	0.79	3/2203 (0.1%)
3	MT	0.53	0/2115	0.78	3/2847 (0.1%)
3	Mt	0.45	0/1638	0.79	3/2203 (0.1%)
3	NT	0.53	0/2115	0.78	3/2847 (0.1%)
3	Nt	0.44	0/1638	0.79	3/2203 (0.1%)
5	AX	0.59	0/1388	0.87	6/1870 (0.3%)
5	BX	0.59	0/1388	0.87	6/1870 (0.3%)
5	CX	0.59	0/1388	0.87	6/1870 (0.3%)
5	DX	0.59	0/1388	0.87	6/1870 (0.3%)
5	EX	0.59	0/1388	0.87	6/1870 (0.3%)
5	FX	0.59	0/1388	0.88	6/1870 (0.3%)
5	GX	0.59	0/1388	0.87	6/1870 (0.3%)
5	HX	0.59	0/1388	0.87	6/1870 (0.3%)
5	IX	0.59	0/1388	0.87	6/1870 (0.3%)
5	JX	0.59	0/1388	0.87	6/1870 (0.3%)
5	KX	0.59	0/1388	0.87	6/1870 (0.3%)
5	LX	0.59	0/1388	0.88	6/1870 (0.3%)
5	MX	0.59	0/1388	0.87	6/1870 (0.3%)
5	NX	0.59	0/1388	0.87	6/1870 (0.3%)
6	AY	0.62	0/1553	0.74	3/2106 (0.1%)
6	BY	0.62	0/1553	0.74	3/2106 (0.1%)
6	CY	0.62	0/1553	0.74	3/2106 (0.1%)
6	DY	0.62	0/1553	0.74	3/2106 (0.1%)
6	EY	0.62	0/1553	0.74	3/2106 (0.1%)
6	FY	0.62	0/1553	0.74	3/2106 (0.1%)
6	GY	0.62	0/1553	0.74	3/2106 (0.1%)
6	HY	0.62	0/1553	0.74	3/2106 (0.1%)
6	IY	0.62	0/1553	0.74	3/2106 (0.1%)
6	JY	0.62	0/1553	0.74	3/2106 (0.1%)
6	KY	0.62	0/1553	0.74	3/2106 (0.1%)
6	LY	0.62	0/1553	0.74	3/2106 (0.1%)
6	MY	0.62	0/1553	0.74	3/2106 (0.1%)
6	NY	0.62	0/1553	0.74	3/2106 (0.1%)
All	All	0.51	29/208236 (0.0%)	0.84	497/280910 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	AD	0	2
1	AE	0	1
1	BA	0	3
1	BD	0	2
1	CA	0	3
1	CB	0	1
1	CD	0	1
1	DA	0	3
1	DB	0	1
1	EA	0	3
1	ED	0	1
1	EE	0	1
1	FA	0	3
1	FB	0	1
1	FE	0	1
1	GA	0	3
1	GC	0	1
1	GD	0	2
1	GE	0	1
1	HA	0	3
1	HB	0	1
1	HD	0	2
1	IA	0	3
1	JA	0	3
1	JB	0	1
1	JD	0	2
1	KA	0	3
1	KB	0	1
1	KD	0	2
1	KE	0	2
1	LA	0	3
1	LB	0	1
1	LD	0	1
1	MA	0	3
1	MB	0	1
1	MD	0	1
1	ME	0	1
1	NA	0	3
1	NC	0	1
1	ND	0	1
1	NE	0	1
2	Am	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	Bm	0	2
2	Cm	0	1
2	Dm	0	1
2	Em	0	1
2	Fm	0	1
2	Gm	0	1
2	Hm	0	1
2	Im	0	1
2	Jm	0	1
2	Km	0	1
2	LM	0	1
2	Lm	0	1
2	Mm	0	1
2	Nm	0	1
5	AX	0	1
5	BX	0	1
5	CX	0	1
5	DX	0	1
5	EX	0	1
5	FX	0	1
5	GX	0	1
5	HX	0	1
5	IX	0	1
5	JX	0	1
5	KX	0	1
5	LX	0	1
5	MX	0	1
5	NX	0	1
All	All	0	107

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	KD	81	TYR	CE2-CZ	11.68	1.66	1.38
1	KD	81	TYR	CG-CD2	11.37	1.63	1.39
1	KE	107	TYR	CB-CG	11.18	1.76	1.51
1	KD	81	TYR	CD2-CE2	10.83	1.71	1.38
2	LM	341	MET	CA-CB	9.46	1.65	1.53
1	KD	81	TYR	CG-CD1	-8.95	1.20	1.39
1	HB	121	GLU	CB-CG	-7.27	1.30	1.52
1	JB	121	GLU	CB-CG	-7.25	1.30	1.52
1	MB	121	GLU	CB-CG	-7.20	1.30	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CB	121	GLU	CB-CG	-7.10	1.31	1.52
1	EB	121	GLU	CB-CG	-6.80	1.32	1.52
1	KE	107	TYR	CE1-CZ	-6.78	1.22	1.38
1	KB	121	GLU	CB-CG	-6.53	1.32	1.52
1	DB	121	GLU	CB-CG	-6.48	1.33	1.52
1	LB	121	GLU	CB-CG	-6.46	1.33	1.52
1	KE	107	TYR	N-CA	6.33	1.53	1.45
1	KD	81	TYR	CZ-OH	6.18	1.51	1.38
1	FB	121	GLU	CB-CG	-6.11	1.34	1.52
1	KD	81	TYR	CE1-CZ	-6.08	1.23	1.38
2	LM	344	LYS	CD-CE	-5.67	1.35	1.52
1	ND	126	LYS	CD-CE	-5.67	1.35	1.52
1	ND	126	LYS	CE-NZ	-5.67	1.32	1.49
1	MB	121	GLU	CG-CD	-5.58	1.38	1.52
1	HB	121	GLU	CG-CD	-5.45	1.38	1.52
1	KE	107	TYR	CG-CD2	5.17	1.50	1.39
1	KB	121	GLU	CG-CD	-5.16	1.39	1.52
1	KE	106	LEU	C-N	5.09	1.40	1.33
1	GB	125	ILE	CG1-CD1	-5.07	1.31	1.51
1	DB	121	GLU	CG-CD	-5.04	1.39	1.52

All (497) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	KE	107	TYR	CA-CB-CG	14.62	140.22	113.90
1	KD	81	TYR	CA-CB-CG	13.65	138.47	113.90
2	LM	344	LYS	CD-CE-NZ	-11.40	75.43	111.90
2	Jm	343	ASP	CA-C-N	9.84	139.41	121.70
2	Jm	343	ASP	C-N-CA	9.84	139.41	121.70
1	MD	81	TYR	CA-CB-CG	9.68	131.33	113.90
1	HA	210	MET	CB-CG-SD	9.21	140.34	112.70
1	CA	210	MET	CB-CG-SD	9.21	140.33	112.70
1	JA	210	MET	CB-CG-SD	9.21	140.33	112.70
1	AA	210	MET	CB-CG-SD	9.21	140.32	112.70
1	FA	210	MET	CB-CG-SD	9.21	140.32	112.70
1	KA	210	MET	CB-CG-SD	9.21	140.32	112.70
1	IA	210	MET	CB-CG-SD	9.21	140.31	112.70
1	GA	210	MET	CB-CG-SD	9.20	140.31	112.70
1	LA	210	MET	CB-CG-SD	9.20	140.31	112.70
1	NA	210	MET	CB-CG-SD	9.20	140.30	112.70
1	BA	210	MET	CB-CG-SD	9.20	140.29	112.70
1	EA	210	MET	CB-CG-SD	9.20	140.29	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	MA	210	MET	CB-CG-SD	9.20	140.29	112.70
1	DA	210	MET	CB-CG-SD	9.19	140.27	112.70
2	Bm	343	ASP	CA-C-N	9.09	138.06	121.70
2	Bm	343	ASP	C-N-CA	9.09	138.06	121.70
1	HD	81	TYR	CB-CA-C	9.08	128.35	109.38
1	HD	81	TYR	CA-CB-CG	9.06	130.20	113.90
2	Hm	343	ASP	CA-C-N	8.91	137.74	121.70
2	Hm	343	ASP	C-N-CA	8.91	137.74	121.70
2	Am	343	ASP	CA-C-N	8.80	137.55	121.70
2	Am	343	ASP	C-N-CA	8.80	137.55	121.70
2	Dm	343	ASP	CA-C-N	8.78	137.49	121.70
2	Dm	343	ASP	C-N-CA	8.78	137.49	121.70
2	Km	343	ASP	CA-C-N	8.69	137.34	121.70
2	Km	343	ASP	C-N-CA	8.69	137.34	121.70
1	MD	81	TYR	CB-CA-C	8.67	127.46	110.30
2	Lm	343	ASP	CA-C-N	8.60	137.18	121.70
2	Lm	343	ASP	C-N-CA	8.60	137.18	121.70
2	Mm	343	ASP	CA-C-N	8.59	137.17	121.70
2	Mm	343	ASP	C-N-CA	8.59	137.17	121.70
2	Em	343	ASP	CA-C-N	8.56	137.12	121.70
2	Em	343	ASP	C-N-CA	8.56	137.12	121.70
2	Gm	343	ASP	CA-C-N	8.49	136.97	121.70
2	Gm	343	ASP	C-N-CA	8.49	136.97	121.70
2	Cm	343	ASP	CA-C-N	8.45	136.90	121.70
2	Cm	343	ASP	C-N-CA	8.45	136.90	121.70
1	DA	210	MET	CA-CB-CG	8.37	130.84	114.10
2	Fm	343	ASP	CA-C-N	8.37	136.76	121.70
2	Fm	343	ASP	C-N-CA	8.37	136.76	121.70
1	LA	210	MET	CA-CB-CG	8.36	130.83	114.10
2	Im	343	ASP	CA-C-N	8.36	136.75	121.70
2	Im	343	ASP	C-N-CA	8.36	136.75	121.70
1	BA	210	MET	CA-CB-CG	8.36	130.82	114.10
1	EA	210	MET	CA-CB-CG	8.36	130.81	114.10
1	KA	210	MET	CA-CB-CG	8.36	130.81	114.10
1	AA	210	MET	CA-CB-CG	8.35	130.81	114.10
1	GA	210	MET	CA-CB-CG	8.35	130.81	114.10
1	IA	210	MET	CA-CB-CG	8.35	130.81	114.10
1	FA	210	MET	CA-CB-CG	8.35	130.80	114.10
1	MA	210	MET	CA-CB-CG	8.34	130.78	114.10
1	HA	210	MET	CA-CB-CG	8.34	130.78	114.10
1	CA	210	MET	CA-CB-CG	8.34	130.77	114.10
1	JA	210	MET	CA-CB-CG	8.34	130.77	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	NA	210	MET	CA-CB-CG	8.33	130.76	114.10
1	KE	107	TYR	CD1-CG-CD2	-8.27	105.70	118.10
2	Nm	343	ASP	CA-C-N	8.22	136.50	121.70
2	Nm	343	ASP	C-N-CA	8.22	136.50	121.70
1	ND	143	LEU	CB-CG-CD1	-7.92	86.94	110.70
3	Bt	207	GLU	CA-CB-CG	7.83	129.76	114.10
3	Dt	207	GLU	CA-CB-CG	7.82	129.74	114.10
1	KE	107	TYR	CB-CG-CD1	7.81	132.52	120.80
3	Mt	207	GLU	CA-CB-CG	7.81	129.72	114.10
3	Gt	207	GLU	CA-CB-CG	7.81	129.71	114.10
3	At	207	GLU	CA-CB-CG	7.81	129.71	114.10
3	Jt	207	GLU	CA-CB-CG	7.81	129.71	114.10
3	Et	207	GLU	CA-CB-CG	7.80	129.71	114.10
3	Ft	207	GLU	CA-CB-CG	7.80	129.71	114.10
3	It	207	GLU	CA-CB-CG	7.80	129.71	114.10
3	Kt	207	GLU	CA-CB-CG	7.80	129.71	114.10
3	Ht	207	GLU	CA-CB-CG	7.80	129.71	114.10
3	Nt	207	GLU	CA-CB-CG	7.80	129.70	114.10
3	FT	187	ARG	CB-CG-CD	7.79	129.21	111.30
3	AT	187	ARG	CB-CG-CD	7.79	129.21	111.30
3	Lt	207	GLU	CA-CB-CG	7.78	129.67	114.10
3	KT	187	ARG	CB-CG-CD	7.78	129.20	111.30
3	NT	187	ARG	CB-CG-CD	7.78	129.20	111.30
3	Ct	207	GLU	CA-CB-CG	7.78	129.66	114.10
3	DT	187	ARG	CB-CG-CD	7.78	129.19	111.30
3	BT	187	ARG	CB-CG-CD	7.77	129.17	111.30
3	IT	187	ARG	CB-CG-CD	7.77	129.17	111.30
3	CT	187	ARG	CB-CG-CD	7.77	129.16	111.30
3	ET	187	ARG	CB-CG-CD	7.77	129.16	111.30
3	HT	187	ARG	CB-CG-CD	7.76	129.15	111.30
3	GT	187	ARG	CB-CG-CD	7.76	129.15	111.30
3	JT	187	ARG	CB-CG-CD	7.76	129.15	111.30
3	LT	187	ARG	CB-CG-CD	7.76	129.14	111.30
3	MT	187	ARG	CB-CG-CD	7.75	129.14	111.30
1	KE	107	TYR	N-CA-CB	7.68	125.82	111.53
1	FD	81	TYR	CB-CA-C	7.66	125.46	110.30
1	HE	130	MET	CG-SD-CE	-7.58	84.23	100.90
5	HX	356	MET	CB-CG-SD	7.55	135.34	112.70
5	KX	356	MET	CB-CG-SD	7.54	135.33	112.70
5	NX	356	MET	CB-CG-SD	7.54	135.32	112.70
5	GX	356	MET	CB-CG-SD	7.54	135.32	112.70
5	IX	356	MET	CB-CG-SD	7.54	135.32	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	MX	356	MET	CB-CG-SD	7.54	135.32	112.70
5	CX	356	MET	CB-CG-SD	7.54	135.32	112.70
5	FX	356	MET	CB-CG-SD	7.54	135.31	112.70
5	DX	356	MET	CB-CG-SD	7.54	135.31	112.70
5	AX	356	MET	CB-CG-SD	7.53	135.30	112.70
5	JX	356	MET	CB-CG-SD	7.53	135.30	112.70
5	LX	356	MET	CB-CG-SD	7.53	135.30	112.70
5	BX	356	MET	CB-CG-SD	7.53	135.29	112.70
5	EX	356	MET	CB-CG-SD	7.53	135.29	112.70
1	JB	121	GLU	CB-CA-C	-7.50	98.35	110.79
1	KD	81	TYR	CB-CA-C	7.41	124.88	109.38
3	KT	249	MET	CB-CG-SD	7.41	134.94	112.70
3	DT	249	MET	CB-CG-SD	7.41	134.92	112.70
3	HT	249	MET	CB-CG-SD	7.41	134.92	112.70
3	JT	249	MET	CB-CG-SD	7.41	134.91	112.70
3	BT	249	MET	CB-CG-SD	7.40	134.91	112.70
3	IT	249	MET	CB-CG-SD	7.40	134.90	112.70
3	ET	249	MET	CB-CG-SD	7.40	134.90	112.70
3	AT	249	MET	CB-CG-SD	7.40	134.89	112.70
3	CT	249	MET	CB-CG-SD	7.40	134.89	112.70
3	LT	249	MET	CB-CG-SD	7.39	134.88	112.70
3	MT	249	MET	CB-CG-SD	7.39	134.88	112.70
3	NT	249	MET	CB-CG-SD	7.39	134.87	112.70
3	GT	249	MET	CB-CG-SD	7.39	134.87	112.70
3	FT	249	MET	CB-CG-SD	7.39	134.86	112.70
1	CB	121	GLU	CB-CA-C	-7.33	98.61	110.79
1	FE	105	TYR	CA-CB-CG	7.33	127.08	113.90
1	DE	81	TYR	CA-C-N	7.31	135.50	121.54
1	DE	81	TYR	C-N-CA	7.31	135.50	121.54
1	DA	130	MET	CB-CG-SD	7.23	134.38	112.70
1	EA	130	MET	CB-CG-SD	7.23	134.38	112.70
1	GA	130	MET	CB-CG-SD	7.23	134.38	112.70
1	KA	130	MET	CB-CG-SD	7.22	134.37	112.70
1	LA	130	MET	CB-CG-SD	7.22	134.37	112.70
1	NA	130	MET	CB-CG-SD	7.22	134.36	112.70
1	EB	121	GLU	N-CA-C	7.22	119.15	111.28
1	AA	130	MET	CB-CG-SD	7.22	134.35	112.70
1	BA	130	MET	CB-CG-SD	7.22	134.35	112.70
1	KD	81	TYR	CD1-CE1-CZ	7.22	132.59	119.60
1	HA	130	MET	CB-CG-SD	7.21	134.34	112.70
1	MA	130	MET	CB-CG-SD	7.21	134.34	112.70
1	IA	130	MET	CB-CG-SD	7.21	134.33	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	130	MET	CB-CG-SD	7.21	134.32	112.70
1	FA	130	MET	CB-CG-SD	7.21	134.32	112.70
1	JA	130	MET	CB-CG-SD	7.21	134.32	112.70
1	FB	121	GLU	CB-CA-C	-7.20	97.32	110.63
1	EE	109	MET	CB-CG-SD	7.16	134.19	112.70
1	KD	81	TYR	CZ-CE2-CD2	-7.14	106.76	119.60
1	MB	169	GLU	CA-C-N	7.13	132.57	122.08
1	MB	169	GLU	C-N-CA	7.13	132.57	122.08
5	LX	410	ARG	NE-CZ-NH2	7.13	125.62	119.20
5	HX	410	ARG	NE-CZ-NH2	7.12	125.61	119.20
5	MX	410	ARG	NE-CZ-NH2	7.12	125.61	119.20
5	NX	410	ARG	NE-CZ-NH2	7.12	125.61	119.20
5	EX	410	ARG	NE-CZ-NH2	7.11	125.59	119.20
5	JX	410	ARG	NE-CZ-NH2	7.10	125.59	119.20
1	LE	107	TYR	CA-CB-CG	7.10	126.68	113.90
5	BX	410	ARG	NE-CZ-NH2	7.10	125.59	119.20
5	IX	410	ARG	NE-CZ-NH2	7.09	125.58	119.20
5	KX	410	ARG	NE-CZ-NH2	7.07	125.56	119.20
5	DX	410	ARG	NE-CZ-NH2	7.07	125.56	119.20
5	GX	410	ARG	NE-CZ-NH2	7.06	125.56	119.20
5	CX	410	ARG	NE-CZ-NH2	7.06	125.55	119.20
5	FX	410	ARG	NE-CZ-NH2	7.05	125.55	119.20
5	AX	410	ARG	NE-CZ-NH2	7.03	125.53	119.20
2	Dm	286	LEU	CA-CB-CG	6.95	140.64	116.30
2	Im	347	MET	CA-C-N	-6.93	112.17	122.56
2	Im	347	MET	C-N-CA	-6.93	112.17	122.56
1	ID	130	MET	CG-SD-CE	-6.91	85.70	100.90
1	JD	143	LEU	CA-CB-CG	6.86	140.32	116.30
1	JB	121	GLU	N-CA-C	6.74	118.63	111.28
1	EB	121	GLU	CA-CB-CG	-6.74	100.63	114.10
1	KD	81	TYR	CB-CG-CD2	6.73	130.90	120.80
1	JC	130	MET	CG-SD-CE	-6.72	86.12	100.90
1	CB	121	GLU	N-CA-C	6.71	118.60	111.28
1	MC	151	ASN	N-CA-CB	-6.68	100.32	110.01
6	HY	1780	MET	CB-CG-SD	6.65	132.64	112.70
6	MY	1780	MET	CB-CG-SD	6.64	132.63	112.70
6	CY	1780	MET	CB-CG-SD	6.64	132.61	112.70
6	JY	1780	MET	CB-CG-SD	6.64	132.61	112.70
6	BY	1780	MET	CB-CG-SD	6.63	132.60	112.70
6	EY	1780	MET	CB-CG-SD	6.63	132.60	112.70
6	KY	1780	MET	CB-CG-SD	6.63	132.60	112.70
6	IY	1780	MET	CB-CG-SD	6.63	132.59	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	LY	1780	MET	CB-CG-SD	6.63	132.59	112.70
6	AY	1780	MET	CB-CG-SD	6.62	132.57	112.70
6	FY	1780	MET	CB-CG-SD	6.62	132.57	112.70
6	DY	1780	MET	CB-CG-SD	6.62	132.57	112.70
6	GY	1780	MET	CB-CG-SD	6.62	132.56	112.70
6	NY	1780	MET	CB-CG-SD	6.62	132.56	112.70
5	FX	474	GLU	CA-CB-CG	6.60	127.30	114.10
1	LD	143	LEU	CB-CG-CD2	-6.60	90.90	110.70
5	GX	474	GLU	CA-CB-CG	6.59	127.29	114.10
5	JX	474	GLU	CA-CB-CG	6.59	127.28	114.10
5	MX	474	GLU	CA-CB-CG	6.59	127.28	114.10
5	EX	474	GLU	CA-CB-CG	6.58	127.27	114.10
5	KX	474	GLU	CA-CB-CG	6.58	127.26	114.10
5	LX	474	GLU	CA-CB-CG	6.58	127.26	114.10
5	NX	474	GLU	CA-CB-CG	6.58	127.26	114.10
5	BX	474	GLU	CA-CB-CG	6.58	127.25	114.10
5	HX	474	GLU	CA-CB-CG	6.58	127.25	114.10
5	IX	474	GLU	CA-CB-CG	6.57	127.24	114.10
5	AX	474	GLU	CA-CB-CG	6.57	127.23	114.10
5	CX	474	GLU	CA-CB-CG	6.57	127.23	114.10
5	DX	474	GLU	CA-CB-CG	6.57	127.23	114.10
2	Gm	286	LEU	CA-CB-CG	6.55	139.22	116.30
1	FD	81	TYR	CA-CB-CG	6.54	125.67	113.90
1	BD	143	LEU	CA-CB-CG	6.53	139.14	116.30
1	ID	143	LEU	CA-CB-CG	6.52	139.11	116.30
1	JD	143	LEU	CB-CG-CD2	-6.47	91.29	110.70
2	MM	199	GLN	N-CA-CB	6.42	120.23	110.28
1	CD	143	LEU	CB-CG-CD1	-6.40	91.49	110.70
1	FB	121	GLU	N-CA-CB	6.37	120.03	110.22
1	JB	121	GLU	CG-CD-OE2	-6.25	104.03	118.40
1	MB	121	GLU	CG-CD-OE2	-6.22	104.08	118.40
1	DA	288	GLU	CA-CB-CG	6.17	126.45	114.10
1	LA	288	GLU	CA-CB-CG	6.17	126.43	114.10
1	IA	288	GLU	CA-CB-CG	6.16	126.41	114.10
1	BA	288	GLU	CA-CB-CG	6.16	126.41	114.10
2	Am	347	MET	CA-C-N	-6.15	115.12	122.44
2	Am	347	MET	C-N-CA	-6.15	115.12	122.44
1	NA	288	GLU	CA-CB-CG	6.15	126.40	114.10
1	AA	288	GLU	CA-CB-CG	6.15	126.39	114.10
1	CA	288	GLU	CA-CB-CG	6.15	126.39	114.10
1	FA	288	GLU	CA-CB-CG	6.15	126.40	114.10
1	EA	288	GLU	CA-CB-CG	6.15	126.39	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	GA	288	GLU	CA-CB-CG	6.14	126.39	114.10
1	KA	288	GLU	CA-CB-CG	6.14	126.39	114.10
1	HA	288	GLU	CA-CB-CG	6.14	126.38	114.10
2	CM	270	TYR	CB-CA-C	6.14	121.07	112.11
1	JA	288	GLU	CA-CB-CG	6.14	126.37	114.10
1	MA	288	GLU	CA-CB-CG	6.14	126.38	114.10
1	ID	143	LEU	CB-CG-CD2	-6.12	92.34	110.70
1	CB	121	GLU	N-CA-CB	6.10	119.09	110.12
1	JB	121	GLU	N-CA-CB	6.10	119.09	110.12
1	NA	194	LYS	CB-CA-C	6.10	118.99	111.43
1	KA	194	LYS	CB-CA-C	6.09	118.99	111.43
5	FX	410	ARG	CG-CD-NE	6.09	125.40	112.00
5	CX	410	ARG	CG-CD-NE	6.09	125.39	112.00
1	LB	121	GLU	CB-CA-C	-6.08	99.37	110.63
1	BA	194	LYS	CB-CA-C	6.08	118.97	111.43
1	JA	194	LYS	CB-CA-C	6.08	118.97	111.43
5	DX	410	ARG	CG-CD-NE	6.08	125.38	112.00
1	AA	194	LYS	CB-CA-C	6.08	118.97	111.43
5	AX	410	ARG	CG-CD-NE	6.08	125.37	112.00
1	FA	194	LYS	CB-CA-C	6.08	118.97	111.43
5	GX	410	ARG	CG-CD-NE	6.08	125.37	112.00
5	MX	410	ARG	CG-CD-NE	6.08	125.37	112.00
5	IX	410	ARG	CG-CD-NE	6.08	125.37	112.00
5	EX	410	ARG	CG-CD-NE	6.08	125.37	112.00
5	LX	410	ARG	CG-CD-NE	6.08	125.36	112.00
1	FD	80	ILE	CA-C-N	-6.07	112.62	122.82
1	FD	80	ILE	C-N-CA	-6.07	112.62	122.82
2	FM	199	GLN	N-CA-CB	6.07	119.69	110.28
5	HX	410	ARG	CG-CD-NE	6.07	125.36	112.00
5	NX	410	ARG	CG-CD-NE	6.07	125.35	112.00
1	DA	194	LYS	CB-CA-C	6.06	118.94	111.43
1	GA	194	LYS	CB-CA-C	6.06	118.94	111.43
5	KX	410	ARG	CG-CD-NE	6.06	125.33	112.00
1	MA	194	LYS	CB-CA-C	6.06	118.94	111.43
5	BX	410	ARG	CG-CD-NE	6.06	125.32	112.00
1	CA	194	LYS	CB-CA-C	6.05	118.94	111.43
1	LA	194	LYS	CB-CA-C	6.05	118.94	111.43
5	JX	410	ARG	CG-CD-NE	6.05	125.31	112.00
1	BD	143	LEU	CB-CG-CD2	-6.05	92.56	110.70
1	IA	194	LYS	CB-CA-C	6.04	118.92	111.43
1	ID	81	TYR	CB-CA-C	6.04	121.38	109.66
1	EA	194	LYS	CB-CA-C	6.04	118.92	111.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	HA	194	LYS	CB-CA-C	6.03	118.91	111.43
1	FB	121	GLU	CG-CD-OE2	-6.03	104.54	118.40
2	CM	199	GLN	N-CA-CB	6.01	120.36	110.39
1	CB	121	GLU	CG-CD-OE2	-5.99	104.62	118.40
2	AM	199	GLN	N-CA-CB	5.96	120.28	110.39
1	HB	121	GLU	CB-CA-C	-5.96	97.86	110.31
2	IM	199	GLN	N-CA-CB	5.95	120.27	110.39
1	HB	121	GLU	CG-CD-OE2	-5.95	104.72	118.40
1	MB	121	GLU	CB-CA-C	-5.93	98.14	109.95
1	ED	143	LEU	CB-CG-CD2	-5.93	92.92	110.70
2	Jm	342	SER	CB-CA-C	-5.89	105.97	114.87
1	ED	175	GLN	CA-CB-CG	5.88	125.86	114.10
1	KE	107	TYR	CB-CA-C	-5.87	96.53	109.56
1	LB	121	GLU	CG-CD-OE2	-5.85	104.95	118.40
1	FC	151	ASN	N-CA-CB	-5.84	101.54	110.01
1	MD	80	ILE	CA-C-N	-5.84	113.01	122.82
1	MD	80	ILE	C-N-CA	-5.84	113.01	122.82
1	DD	94	TRP	CA-CB-CG	5.80	124.63	113.60
1	BD	80	ILE	CA-C-N	-5.80	112.81	122.21
1	BD	80	ILE	C-N-CA	-5.80	112.81	122.21
1	ID	129	ALA	CA-C-N	-5.75	112.55	122.79
1	ID	129	ALA	C-N-CA	-5.75	112.55	122.79
3	LT	187	ARG	CG-CD-NE	5.75	124.65	112.00
3	JT	187	ARG	CG-CD-NE	5.74	124.63	112.00
3	MT	187	ARG	CG-CD-NE	5.74	124.63	112.00
3	FT	187	ARG	CG-CD-NE	5.74	124.62	112.00
3	IT	187	ARG	CG-CD-NE	5.74	124.62	112.00
3	KT	187	ARG	CG-CD-NE	5.74	124.62	112.00
3	CT	187	ARG	CG-CD-NE	5.73	124.61	112.00
3	ET	187	ARG	CG-CD-NE	5.73	124.61	112.00
3	NT	187	ARG	CG-CD-NE	5.73	124.61	112.00
3	HT	187	ARG	CG-CD-NE	5.73	124.61	112.00
3	DT	187	ARG	CG-CD-NE	5.73	124.60	112.00
3	AT	187	ARG	CG-CD-NE	5.72	124.59	112.00
3	BT	187	ARG	CG-CD-NE	5.72	124.60	112.00
3	GT	187	ARG	CG-CD-NE	5.72	124.58	112.00
2	KM	256	SER	CA-C-N	-5.70	111.45	122.06
2	KM	256	SER	C-N-CA	-5.70	111.45	122.06
3	Ct	207	GLU	CB-CG-CD	5.64	122.19	112.60
1	LD	130	MET	CB-CG-SD	-5.64	95.77	112.70
2	NM	199	GLN	N-CA-CB	5.64	119.76	110.39
3	Mt	207	GLU	CB-CG-CD	5.64	122.19	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	At	207	GLU	CB-CG-CD	5.63	122.17	112.60
3	It	207	GLU	CB-CG-CD	5.63	122.17	112.60
3	Nt	207	GLU	CB-CG-CD	5.63	122.17	112.60
2	GM	199	GLN	N-CA-CB	5.62	119.72	110.39
3	Kt	207	GLU	CB-CG-CD	5.62	122.15	112.60
3	Et	207	GLU	CB-CG-CD	5.62	122.15	112.60
3	Jt	207	GLU	CB-CG-CD	5.62	122.15	112.60
3	Lt	207	GLU	CB-CG-CD	5.61	122.14	112.60
3	Ft	207	GLU	CB-CG-CD	5.61	122.14	112.60
3	Dt	207	GLU	CB-CG-CD	5.61	122.13	112.60
5	MX	410	ARG	NE-CZ-NH1	-5.60	115.90	121.50
3	Gt	207	GLU	CB-CG-CD	5.60	122.12	112.60
3	Ht	207	GLU	CB-CG-CD	5.60	122.12	112.60
1	ID	120	ILE	CG1-CB-CG2	-5.60	93.90	110.70
3	Bt	207	GLU	CB-CG-CD	5.59	122.11	112.60
1	KE	105	TYR	CA-CB-CG	5.58	123.95	113.90
1	ME	107	TYR	N-CA-C	5.58	118.30	108.75
5	HX	410	ARG	NE-CZ-NH1	-5.58	115.92	121.50
5	FX	410	ARG	NE-CZ-NH1	-5.57	115.93	121.50
2	Jm	342	SER	N-CA-CB	5.57	115.19	109.51
5	LX	410	ARG	NE-CZ-NH1	-5.57	115.93	121.50
1	DB	121	GLU	CG-CD-OE2	-5.57	105.60	118.40
5	JX	410	ARG	NE-CZ-NH1	-5.56	115.94	121.50
1	MD	158	LYS	CG-CD-CE	5.56	124.08	111.30
5	IX	410	ARG	NE-CZ-NH1	-5.55	115.95	121.50
5	CX	410	ARG	NE-CZ-NH1	-5.55	115.95	121.50
1	HD	80	ILE	CA-C-N	-5.54	113.98	122.62
1	HD	80	ILE	C-N-CA	-5.54	113.98	122.62
5	EX	410	ARG	NE-CZ-NH1	-5.54	115.96	121.50
5	BX	410	ARG	NE-CZ-NH1	-5.54	115.96	121.50
5	NX	410	ARG	NE-CZ-NH1	-5.53	115.97	121.50
5	DX	410	ARG	NE-CZ-NH1	-5.53	115.97	121.50
5	GX	410	ARG	NE-CZ-NH1	-5.53	115.97	121.50
5	AX	410	ARG	NE-CZ-NH1	-5.53	115.97	121.50
1	GC	154	LYS	CB-CG-CD	-5.52	98.60	111.30
1	ME	92	GLY	CA-C-N	5.50	132.04	121.54
1	ME	92	GLY	C-N-CA	5.50	132.04	121.54
1	FE	92	GLY	CA-C-N	5.49	132.03	121.54
1	FE	92	GLY	C-N-CA	5.49	132.03	121.54
5	KX	410	ARG	NE-CZ-NH1	-5.49	116.01	121.50
1	AE	92	GLY	CA-C-N	5.47	131.99	121.54
1	AE	92	GLY	C-N-CA	5.47	131.99	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	KE	107	TYR	CE1-CZ-OH	5.47	136.31	119.90
1	HE	92	GLY	CA-C-N	5.46	131.97	121.54
1	HE	92	GLY	C-N-CA	5.46	131.97	121.54
1	KB	121	GLU	CG-CD-OE2	-5.46	105.85	118.40
1	LC	184	ARG	CA-CB-CG	5.45	125.00	114.10
1	MD	158	LYS	N-CA-C	5.44	118.31	109.06
1	JD	80	ILE	CA-C-N	-5.42	113.80	122.53
1	JD	80	ILE	C-N-CA	-5.42	113.80	122.53
1	NA	210	MET	CB-CA-C	5.41	121.41	110.38
1	LB	121	GLU	N-CA-C	5.40	117.92	111.71
1	CA	210	MET	CB-CA-C	5.39	121.37	110.38
1	GA	210	MET	CB-CA-C	5.39	121.37	110.38
1	JA	210	MET	CB-CA-C	5.39	121.37	110.38
1	FA	210	MET	CB-CA-C	5.38	121.36	110.38
1	IA	210	MET	CB-CA-C	5.38	121.36	110.38
1	MA	210	MET	CB-CA-C	5.38	121.35	110.38
1	AA	210	MET	CB-CA-C	5.37	121.34	110.38
1	EA	210	MET	CB-CA-C	5.37	121.34	110.38
1	LA	210	MET	CB-CA-C	5.37	121.34	110.38
1	KA	210	MET	CB-CA-C	5.37	121.33	110.38
1	IE	92	GLY	CA-C-N	5.37	131.79	121.54
1	IE	92	GLY	C-N-CA	5.37	131.79	121.54
1	MB	121	GLU	N-CA-CB	5.37	119.42	110.41
1	DB	121	GLU	N-CA-CB	5.36	119.42	110.41
1	HA	210	MET	CB-CA-C	5.36	121.31	110.38
1	ED	128	ARG	NE-CZ-NH1	-5.35	116.15	121.50
1	DB	121	GLU	CB-CA-C	-5.35	99.30	109.95
1	DA	210	MET	CB-CA-C	5.35	121.29	110.38
1	JD	143	LEU	CB-CA-C	-5.35	102.66	110.95
1	FB	121	GLU	N-CA-C	5.34	117.86	111.71
1	BA	210	MET	CB-CA-C	5.34	121.28	110.38
1	JE	92	GLY	CA-C-N	5.34	131.74	121.54
1	JE	92	GLY	C-N-CA	5.34	131.74	121.54
1	ID	143	LEU	CB-CA-C	-5.34	102.50	110.88
1	KB	121	GLU	CB-CA-C	-5.34	99.33	109.95
1	KB	121	GLU	N-CA-CB	5.33	119.37	110.41
2	KM	257	MET	N-CA-CB	5.33	118.83	110.46
1	HE	107	TYR	CA-CB-CG	5.33	123.49	113.90
1	BE	92	GLY	CA-C-N	5.32	131.70	121.54
1	BE	92	GLY	C-N-CA	5.32	131.70	121.54
1	FB	169	GLU	CA-C-N	5.32	129.90	122.08
1	FB	169	GLU	C-N-CA	5.32	129.90	122.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	HB	121	GLU	N-CA-CB	5.30	119.19	110.39
1	NA	194	LYS	CG-CD-CE	-5.30	99.12	111.30
1	NE	109	MET	CB-CG-SD	5.29	128.57	112.70
1	FD	143	LEU	CB-CG-CD2	-5.29	94.83	110.70
1	IA	194	LYS	CG-CD-CE	-5.29	99.14	111.30
1	EA	194	LYS	CG-CD-CE	-5.28	99.16	111.30
1	ND	143	LEU	CA-CB-CG	5.28	134.78	116.30
1	CA	194	LYS	CG-CD-CE	-5.28	99.16	111.30
1	FA	194	LYS	CG-CD-CE	-5.28	99.16	111.30
1	BA	194	LYS	CG-CD-CE	-5.27	99.17	111.30
1	BD	81	TYR	CA-CB-CG	5.27	123.39	113.90
1	MA	194	LYS	CG-CD-CE	-5.27	99.17	111.30
5	KX	410	ARG	CD-NE-CZ	5.27	131.78	124.40
1	JA	194	LYS	CG-CD-CE	-5.27	99.19	111.30
1	DA	194	LYS	CG-CD-CE	-5.26	99.19	111.30
1	KA	194	LYS	CG-CD-CE	-5.26	99.19	111.30
1	AA	194	LYS	CG-CD-CE	-5.26	99.19	111.30
1	GA	194	LYS	CG-CD-CE	-5.26	99.21	111.30
1	HA	194	LYS	CG-CD-CE	-5.26	99.21	111.30
1	LA	194	LYS	CG-CD-CE	-5.25	99.22	111.30
5	DX	410	ARG	CD-NE-CZ	5.24	131.74	124.40
5	AX	410	ARG	CD-NE-CZ	5.24	131.74	124.40
5	IX	410	ARG	CD-NE-CZ	5.24	131.74	124.40
2	JM	270	TYR	CB-CA-C	5.24	119.76	112.11
3	Ft	213	ARG	CB-CG-CD	5.24	123.34	111.30
5	GX	410	ARG	CD-NE-CZ	5.23	131.73	124.40
5	BX	410	ARG	CD-NE-CZ	5.23	131.72	124.40
3	Gt	213	ARG	CB-CG-CD	5.23	123.33	111.30
5	EX	410	ARG	CD-NE-CZ	5.23	131.72	124.40
5	CX	410	ARG	CD-NE-CZ	5.23	131.72	124.40
5	JX	410	ARG	CD-NE-CZ	5.23	131.72	124.40
5	NX	410	ARG	CD-NE-CZ	5.23	131.72	124.40
3	It	213	ARG	CB-CG-CD	5.23	123.32	111.30
1	LE	101	LYS	CA-CB-CG	5.22	124.55	114.10
3	Ht	213	ARG	CB-CG-CD	5.22	123.30	111.30
3	Et	213	ARG	CB-CG-CD	5.22	123.30	111.30
5	FX	410	ARG	CD-NE-CZ	5.22	131.70	124.40
3	Kt	213	ARG	CB-CG-CD	5.22	123.30	111.30
1	NB	169	GLU	CA-C-N	5.22	129.75	122.08
1	NB	169	GLU	C-N-CA	5.22	129.75	122.08
5	LX	410	ARG	CD-NE-CZ	5.21	131.70	124.40
3	Nt	213	ARG	CB-CG-CD	5.21	123.30	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CD	143	LEU	CA-CB-CG	5.21	134.54	116.30
3	Bt	213	ARG	CB-CG-CD	5.21	123.27	111.30
3	Dt	213	ARG	CB-CG-CD	5.21	123.27	111.30
3	Lt	213	ARG	CB-CG-CD	5.21	123.28	111.30
1	JE	105	TYR	CA-CB-CG	5.20	123.26	113.90
3	Ct	213	ARG	CB-CG-CD	5.20	123.26	111.30
3	Jt	213	ARG	CB-CG-CD	5.20	123.26	111.30
3	At	213	ARG	CB-CG-CD	5.20	123.26	111.30
5	MX	410	ARG	CD-NE-CZ	5.20	131.68	124.40
3	Mt	213	ARG	CB-CG-CD	5.20	123.26	111.30
5	HX	410	ARG	CD-NE-CZ	5.20	131.68	124.40
2	EM	256	SER	CA-C-N	-5.18	112.42	122.06
2	EM	256	SER	C-N-CA	-5.18	112.42	122.06
2	LM	256	SER	CA-C-N	-5.16	112.46	122.06
2	LM	256	SER	C-N-CA	-5.16	112.46	122.06
2	Gm	202	GLU	N-CA-CB	5.16	118.25	110.30
2	Hm	347	MET	CA-C-N	-5.16	114.42	122.42
2	Hm	347	MET	C-N-CA	-5.16	114.42	122.42
1	DE	105	TYR	CA-CB-CG	5.16	123.18	113.90
1	MD	143	LEU	CB-CG-CD2	-5.12	95.33	110.70
1	LB	121	GLU	N-CA-CB	5.12	118.11	110.22
2	BM	199	GLN	N-CA-CB	5.10	118.71	110.40
1	FC	150	TYR	CA-C-N	5.10	127.07	120.44
1	FC	150	TYR	C-N-CA	5.10	127.07	120.44
6	AY	1780	MET	CG-SD-CE	5.09	112.11	100.90
6	DY	1780	MET	CG-SD-CE	5.09	112.09	100.90
6	JY	1780	MET	CG-SD-CE	5.09	112.09	100.90
6	KY	1780	MET	CG-SD-CE	5.09	112.09	100.90
6	CY	1780	MET	CG-SD-CE	5.09	112.09	100.90
6	FY	1780	MET	CG-SD-CE	5.08	112.09	100.90
6	LY	1780	MET	CG-SD-CE	5.08	112.09	100.90
6	IY	1780	MET	CG-SD-CE	5.08	112.08	100.90
6	BY	1780	MET	CG-SD-CE	5.08	112.06	100.90
6	EY	1780	MET	CG-SD-CE	5.08	112.06	100.90
6	GY	1780	MET	CG-SD-CE	5.08	112.06	100.90
6	MY	1780	MET	CG-SD-CE	5.08	112.06	100.90
6	NY	1780	MET	CG-SD-CE	5.08	112.06	100.90
6	BY	1746	LYS	CB-CG-CD	5.07	122.97	111.30
1	ID	81	TYR	CA-CB-CG	5.07	123.03	113.90
6	IY	1746	LYS	CB-CG-CD	5.07	122.96	111.30
6	CY	1746	LYS	CB-CG-CD	5.07	122.95	111.30
6	HY	1780	MET	CG-SD-CE	5.06	112.02	100.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	KD	81	TYR	OH-CZ-CE2	5.05	135.06	119.90
6	EY	1746	LYS	CB-CG-CD	5.05	122.92	111.30
1	JD	130	MET	CA-CB-CG	-5.05	103.99	114.10
6	MY	1746	LYS	CB-CG-CD	5.05	122.92	111.30
6	KY	1746	LYS	CB-CG-CD	5.04	122.90	111.30
6	NY	1746	LYS	CB-CG-CD	5.04	122.90	111.30
6	AY	1746	LYS	CB-CG-CD	5.04	122.89	111.30
6	HY	1746	LYS	CB-CG-CD	5.04	122.89	111.30
6	JY	1746	LYS	CB-CG-CD	5.04	122.90	111.30
6	LY	1746	LYS	CB-CG-CD	5.04	122.90	111.30
1	HD	130	MET	CA-CB-CG	-5.04	104.02	114.10
6	FY	1746	LYS	CB-CG-CD	5.04	122.89	111.30
6	DY	1746	LYS	CB-CG-CD	5.04	122.88	111.30
6	GY	1746	LYS	CB-CG-CD	5.03	122.88	111.30
1	DC	130	MET	CA-CB-CG	-5.02	104.05	114.10
2	JM	214	ARG	CA-CB-CG	5.02	124.14	114.10
1	NC	130	MET	CG-SD-CE	-5.00	89.89	100.90

There are no chirality outliers.

All (107) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	253	TYR	Peptide
1	AA	275	ALA	Peptide
1	AA	304	LYS	Peptide
1	AD	131	GLY	Peptide
1	AD	94	TRP	Peptide
1	AE	104	THR	Peptide
5	AX	498	THR	Peptide
2	Am	343	ASP	Peptide
1	BA	253	TYR	Peptide
1	BA	275	ALA	Peptide
1	BA	304	LYS	Peptide
1	BD	169	GLU	Sidechain
1	BD	81	TYR	Sidechain
5	BX	498	THR	Peptide
2	Bm	342	SER	Peptide
2	Bm	343	ASP	Peptide
1	CA	253	TYR	Peptide
1	CA	275	ALA	Peptide
1	CA	304	LYS	Peptide
1	CB	121	GLU	Sidechain

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Mol	Chain	Res	Type	Group
1	CD	131	GLY	Peptide
5	CX	498	THR	Peptide
2	Cm	343	ASP	Peptide
1	DA	253	TYR	Peptide
1	DA	275	ALA	Peptide
1	DA	304	LYS	Peptide
1	DB	121	GLU	Sidechain
5	DX	498	THR	Peptide
2	Dm	343	ASP	Peptide
1	EA	253	TYR	Peptide
1	EA	275	ALA	Peptide
1	EA	304	LYS	Peptide
1	ED	131	GLY	Peptide
1	EE	108	ALA	Peptide
5	EX	498	THR	Peptide
2	Em	343	ASP	Peptide
1	FA	253	TYR	Peptide
1	FA	275	ALA	Peptide
1	FA	304	LYS	Peptide
1	FB	121	GLU	Sidechain
1	FE	107	TYR	Sidechain
5	FX	498	THR	Peptide
2	Fm	343	ASP	Peptide
1	GA	253	TYR	Peptide
1	GA	275	ALA	Peptide
1	GA	304	LYS	Peptide
1	GC	179	LEU	Peptide
1	GD	131	GLY	Peptide
1	GD	94	TRP	Peptide
1	GE	149	TYR	Sidechain
5	GX	498	THR	Peptide
2	Gm	343	ASP	Peptide
1	HA	253	TYR	Peptide
1	HA	275	ALA	Peptide
1	HA	304	LYS	Peptide
1	HB	121	GLU	Sidechain
1	HD	131	GLY	Peptide
1	HD	179	LEU	Peptide
5	HX	498	THR	Peptide
2	Hm	343	ASP	Peptide
1	IA	253	TYR	Peptide
1	IA	275	ALA	Peptide

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Mol	Chain	Res	Type	Group
1	IA	304	LYS	Peptide
5	IX	498	THR	Peptide
2	Im	343	ASP	Peptide
1	JA	253	TYR	Peptide
1	JA	275	ALA	Peptide
1	JA	304	LYS	Peptide
1	JB	121	GLU	Sidechain
1	JD	130	MET	Peptide
1	JD	131	GLY	Peptide
5	JX	498	THR	Peptide
2	Jm	342	SER	Peptide
1	KA	253	TYR	Peptide
1	KA	275	ALA	Peptide
1	KA	304	LYS	Peptide
1	KB	121	GLU	Sidechain
1	KD	142	SER	Peptide
1	KD	81	TYR	Sidechain
1	KE	105	TYR	Sidechain
1	KE	107	TYR	Sidechain
5	KX	498	THR	Peptide
2	Km	343	ASP	Peptide
1	LA	253	TYR	Peptide
1	LA	275	ALA	Peptide
1	LA	304	LYS	Peptide
1	LB	121	GLU	Sidechain
1	LD	131	GLY	Peptide
2	LM	344	LYS	Peptide
5	LX	498	THR	Peptide
2	Lm	343	ASP	Peptide
1	MA	253	TYR	Peptide
1	MA	275	ALA	Peptide
1	MA	304	LYS	Peptide
1	MB	121	GLU	Sidechain
1	MD	81	TYR	Sidechain
1	ME	107	TYR	Sidechain
5	MX	498	THR	Peptide
2	Mm	343	ASP	Peptide
1	NA	253	TYR	Peptide
1	NA	275	ALA	Peptide
1	NA	304	LYS	Peptide
1	NC	179	LEU	Peptide
1	ND	131	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	NE	149	TYR	Sidechain
5	NX	498	THR	Peptide
2	Nm	343	ASP	Peptide

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	AA	1986	0	1962	51	0
1	AB	728	0	737	23	0
1	AC	741	0	753	25	0
1	AD	778	0	781	35	0
1	AE	847	0	841	42	0
1	BA	1986	0	1962	56	0
1	BB	728	0	737	31	0
1	BC	741	0	753	29	0
1	BD	778	0	781	32	0
1	BE	847	0	841	29	0
1	CA	1986	0	1962	55	0
1	CB	728	0	737	22	0
1	CC	741	0	753	32	0
1	CD	778	0	781	36	0
1	CE	847	0	841	29	0
1	DA	1986	0	1962	62	0
1	DB	728	0	737	35	0
1	DC	741	0	753	29	0
1	DD	778	0	781	34	0
1	DE	847	0	841	32	0
1	EA	1986	0	1962	61	0
1	EB	728	0	737	26	0
1	EC	741	0	753	25	0
1	ED	778	0	781	37	0
1	EE	847	0	841	33	0
1	FA	1986	0	1962	61	0
1	FB	728	0	737	25	0
1	FC	741	0	753	32	0
1	FD	778	0	781	36	0
1	FE	847	0	841	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GA	1986	0	1962	58	0
1	GB	728	0	737	25	0
1	GC	741	0	753	20	0
1	GD	778	0	781	29	0
1	GE	847	0	841	30	0
1	HA	1986	0	1962	55	0
1	HB	728	0	737	20	0
1	HC	741	0	753	31	0
1	HD	778	0	781	35	0
1	HE	847	0	841	32	0
1	IA	1986	0	1962	55	0
1	IB	728	0	737	26	0
1	IC	741	0	753	23	0
1	ID	778	0	781	40	0
1	IE	847	0	841	34	0
1	JA	1986	0	1962	56	0
1	JB	728	0	737	19	0
1	JC	741	0	753	28	0
1	JD	778	0	781	34	0
1	JE	847	0	841	27	0
1	KA	1986	0	1962	59	0
1	KB	728	0	737	30	0
1	KC	741	0	753	28	0
1	KD	778	0	781	30	0
1	KE	847	0	841	33	0
1	LA	1986	0	1962	53	0
1	LB	728	0	737	31	0
1	LC	741	0	753	35	0
1	LD	778	0	781	38	0
1	LE	847	0	841	25	0
1	MA	1986	0	1962	64	0
1	MB	728	0	737	22	0
1	MC	741	0	753	23	0
1	MD	778	0	781	29	0
1	ME	847	0	841	31	0
1	NA	1986	0	1962	56	0
1	NB	728	0	737	23	0
1	NC	741	0	753	23	0
1	ND	778	0	781	38	0
1	NE	847	0	841	37	0
2	AM	1485	0	1503	25	0
2	Am	1474	0	1490	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	BM	1485	0	1503	27	0
2	Bm	1474	0	1490	30	0
2	CM	1485	0	1503	28	0
2	Cm	1474	0	1490	33	0
2	DM	1485	0	1503	33	0
2	Dm	1474	0	1490	32	0
2	EM	1485	0	1503	30	0
2	Em	1474	0	1490	32	0
2	FM	1485	0	1503	29	0
2	Fm	1474	0	1490	44	0
2	GM	1485	0	1503	27	0
2	Gm	1474	0	1490	31	0
2	HM	1485	0	1503	25	0
2	Hm	1474	0	1490	39	0
2	IM	1485	0	1503	29	0
2	Im	1474	0	1490	31	0
2	JM	1485	0	1503	35	0
2	Jm	1474	0	1490	32	0
2	KM	1485	0	1503	33	0
2	Km	1474	0	1490	30	0
2	LM	1485	0	1501	31	0
2	Lm	1474	0	1490	36	0
2	MM	1485	0	1503	29	0
2	Mm	1474	0	1490	36	0
2	NM	1485	0	1503	29	0
2	Nm	1474	0	1490	28	0
3	AT	2083	0	2096	44	0
3	At	1615	0	1629	36	0
3	BT	2083	0	2096	41	0
3	Bt	1615	0	1629	38	0
3	CT	2083	0	2096	42	0
3	Ct	1615	0	1629	38	0
3	DT	2083	0	2096	43	0
3	Dt	1615	0	1629	35	0
3	ET	2083	0	2096	47	0
3	Et	1615	0	1629	38	0
3	FT	2083	0	2096	41	0
3	Ft	1615	0	1629	37	0
3	GT	2083	0	2096	45	0
3	Gt	1615	0	1629	35	0
3	HT	2083	0	2096	40	0
3	Ht	1615	0	1629	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	IT	2083	0	2096	45	0
3	It	1615	0	1629	36	0
3	JT	2083	0	2096	45	0
3	Jt	1615	0	1629	37	0
3	KT	2083	0	2096	49	0
3	Kt	1615	0	1629	36	0
3	LT	2083	0	2096	49	0
3	Lt	1615	0	1629	38	0
3	MT	2083	0	2096	45	0
3	Mt	1615	0	1629	39	0
3	NT	2083	0	2096	44	0
3	Nt	1615	0	1629	36	0
4	AU	800	0	181	4	0
4	BU	800	0	181	1	0
4	CU	800	0	181	2	0
4	DU	800	0	181	1	0
4	EU	800	0	181	3	0
4	FU	800	0	181	3	0
4	GU	800	0	181	1	0
4	HU	800	0	181	2	0
4	IU	800	0	181	1	0
4	JU	800	0	181	1	0
4	KU	800	0	181	3	0
4	LU	800	0	181	3	0
4	MU	800	0	181	3	0
4	NU	800	0	181	1	0
5	AX	1361	0	1389	29	0
5	BX	1361	0	1389	24	0
5	CX	1361	0	1389	22	0
5	DX	1361	0	1389	27	0
5	EX	1361	0	1389	33	0
5	FX	1361	0	1389	27	0
5	GX	1361	0	1389	24	0
5	HX	1361	0	1389	24	0
5	IX	1361	0	1389	25	0
5	JX	1361	0	1389	33	0
5	KX	1361	0	1389	25	0
5	LX	1361	0	1389	22	0
5	MX	1361	0	1389	28	0
5	NX	1361	0	1389	28	0
6	AY	1529	0	1576	35	0
6	BY	1529	0	1576	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	CY	1529	0	1576	33	0
6	DY	1529	0	1576	35	0
6	EY	1529	0	1576	34	0
6	FY	1529	0	1576	33	0
6	GY	1529	0	1576	32	0
6	HY	1529	0	1576	33	0
6	IY	1529	0	1576	38	0
6	JY	1529	0	1576	34	0
6	KY	1529	0	1576	34	0
6	LY	1529	0	1576	34	0
6	MY	1529	0	1576	33	0
6	NY	1529	0	1576	34	0
All	All	215978	0	209130	4319	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (4319) 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:KE:107:TYR:CB	1:KE:107:TYR:CG	1.76	1.68
1:BD:117:TYR:O	1:BD:121:GLU:HB2	1.62	1.00
1:FD:117:TYR:O	1:FD:121:GLU:HB2	1.60	1.00
1:CD:117:TYR:O	1:CD:121:GLU:HB2	1.62	0.99
1:MD:117:TYR:O	1:MD:121:GLU:HB2	1.60	0.99
1:ED:117:TYR:O	1:ED:121:GLU:HB2	1.63	0.98
1:FB:126:LYS:O	1:FB:130:MET:HB2	1.63	0.98
1:GD:117:TYR:O	1:GD:121:GLU:HB2	1.64	0.98
1:ND:117:TYR:O	1:ND:121:GLU:HB2	1.63	0.97
1:DD:117:TYR:O	1:DD:121:GLU:HB2	1.63	0.97
1:KD:117:TYR:O	1:KD:121:GLU:HB2	1.66	0.94
1:ED:129:ALA:O	1:ED:133:TYR:HB2	1.68	0.93
1:ID:129:ALA:O	1:ID:133:TYR:HB2	1.68	0.93
1:LD:117:TYR:O	1:LD:121:GLU:HB2	1.67	0.92
1:DD:129:ALA:O	1:DD:133:TYR:HB2	1.69	0.91
1:HD:117:TYR:O	1:HD:121:GLU:HB2	1.68	0.91
1:ID:117:TYR:O	1:ID:121:GLU:HB2	1.71	0.91
1:LD:129:ALA:O	1:LD:133:TYR:HB2	1.71	0.90
1:KD:129:ALA:O	1:KD:133:TYR:HB2	1.71	0.89
1:JD:117:TYR:O	1:JD:121:GLU:HB2	1.74	0.87
3:GT:60:PRO:HA	3:GT:137:ASN:O	1.75	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LT:60:PRO:HA	3:LT:137:ASN:O	1.75	0.87
3:BT:60:PRO:HA	3:BT:137:ASN:O	1.75	0.87
3:FT:60:PRO:HA	3:FT:137:ASN:O	1.75	0.87
3:MT:60:PRO:HA	3:MT:137:ASN:O	1.75	0.87
3:AT:60:PRO:HA	3:AT:137:ASN:O	1.75	0.87
3:KT:60:PRO:HA	3:KT:137:ASN:O	1.75	0.86
3:HT:60:PRO:HA	3:HT:137:ASN:O	1.75	0.86
3:CT:60:PRO:HA	3:CT:137:ASN:O	1.75	0.86
3:ET:60:PRO:HA	3:ET:137:ASN:O	1.75	0.86
3:NT:60:PRO:HA	3:NT:137:ASN:O	1.75	0.86
3:JT:60:PRO:HA	3:JT:137:ASN:O	1.75	0.85
1:GD:177:THR:HA	1:GE:107:TYR:O	1.75	0.85
3:DT:60:PRO:HA	3:DT:137:ASN:O	1.75	0.85
3:IT:60:PRO:HA	3:IT:137:ASN:O	1.75	0.85
1:FD:129:ALA:O	1:FD:133:TYR:HB2	1.78	0.83
1:MD:129:ALA:O	1:MD:133:TYR:HB2	1.77	0.83
1:KA:203:LEU:O	1:KA:207:GLN:HB2	1.79	0.83
1:CA:203:LEU:O	1:CA:207:GLN:HB2	1.79	0.83
1:IA:203:LEU:O	1:IA:207:GLN:HB2	1.79	0.83
1:AA:203:LEU:O	1:AA:207:GLN:HB2	1.79	0.82
1:FA:203:LEU:O	1:FA:207:GLN:HB2	1.79	0.82
1:NA:203:LEU:O	1:NA:207:GLN:HB2	1.79	0.82
1:ND:177:THR:HA	1:NE:107:TYR:O	1.78	0.82
1:DA:203:LEU:O	1:DA:207:GLN:HB2	1.79	0.82
1:MA:203:LEU:O	1:MA:207:GLN:HB2	1.79	0.82
1:LA:203:LEU:O	1:LA:207:GLN:HB2	1.79	0.82
1:BA:203:LEU:O	1:BA:207:GLN:HB2	1.79	0.82
1:HA:203:LEU:O	1:HA:207:GLN:HB2	1.79	0.82
1:AD:117:TYR:O	1:AD:121:GLU:HB2	1.79	0.81
1:EA:203:LEU:O	1:EA:207:GLN:HB2	1.79	0.81
1:MD:177:THR:HA	1:ME:107:TYR:O	1.79	0.81
1:FC:130:MET:HE1	1:FC:182:PRO:HB3	1.63	0.81
1:BD:129:ALA:O	1:BD:133:TYR:HB2	1.79	0.81
1:GA:203:LEU:O	1:GA:207:GLN:HB2	1.79	0.81
1:JA:203:LEU:O	1:JA:207:GLN:HB2	1.79	0.81
1:AD:129:ALA:O	1:AD:133:TYR:HB2	1.81	0.80
1:FA:104:THR:HA	3:Ft:137:ASN:O	1.83	0.79
1:BD:169:GLU:OE2	3:Bt:218:ARG:NH1	2.14	0.79
1:GA:106:LEU:HD13	3:Gt:136:SER:HB3	1.65	0.78
1:JD:177:THR:HA	1:JE:107:TYR:O	1.84	0.78
1:MA:111:LEU:HD11	3:Mt:133:MET:HB2	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:168:ASN:HB3	1:CC:171:MET:HE1	1.67	0.77
1:BC:168:ASN:HB3	1:BC:171:MET:HE1	1.67	0.76
1:MD:126:LYS:HB3	1:MD:130:MET:HE2	1.66	0.76
1:FC:168:ASN:HB3	1:FC:171:MET:HE1	1.67	0.76
1:MC:147:ASN:O	1:MC:151:ASN:HB2	1.86	0.76
1:AC:168:ASN:HB3	1:AC:171:MET:HE1	1.66	0.76
3:ET:274:ARG:O	3:ET:278:SER:HB3	1.86	0.76
1:CD:129:ALA:O	1:CD:133:TYR:HB2	1.87	0.75
1:HC:130:MET:HE1	1:HC:182:PRO:HB3	1.67	0.75
3:KT:274:ARG:O	3:KT:278:SER:HB3	1.86	0.75
3:LT:274:ARG:O	3:LT:278:SER:HB3	1.86	0.75
3:MT:274:ARG:O	3:MT:278:SER:HB3	1.86	0.75
3:FT:274:ARG:O	3:FT:278:SER:HB3	1.86	0.75
3:JT:274:ARG:O	3:JT:278:SER:HB3	1.86	0.75
3:DT:274:ARG:O	3:DT:278:SER:HB3	1.86	0.75
3:NT:274:ARG:O	3:NT:278:SER:HB3	1.86	0.75
3:IT:274:ARG:O	3:IT:278:SER:HB3	1.86	0.75
1:DC:168:ASN:HB3	1:DC:171:MET:HE1	1.69	0.74
1:GA:130:MET:HG3	3:Gt:63:VAL:HG21	1.68	0.74
1:KE:107:TYR:CG	1:KE:107:TYR:HB2	2.17	0.74
3:AT:274:ARG:O	3:AT:278:SER:HB3	1.86	0.74
1:CC:187:PRO:HD3	1:DA:191:THR:HB	1.69	0.74
3:GT:274:ARG:O	3:GT:278:SER:HB3	1.86	0.74
3:HT:274:ARG:O	3:HT:278:SER:HB3	1.86	0.74
1:GA:104:THR:HA	3:Gt:137:ASN:O	1.87	0.74
1:KD:80:ILE:HA	1:KE:106:LEU:O	1.88	0.74
1:DA:104:THR:HA	3:Dt:137:ASN:O	1.88	0.74
1:CA:104:THR:HA	3:Ct:137:ASN:O	1.88	0.74
3:CT:274:ARG:O	3:CT:278:SER:HB3	1.86	0.74
1:ND:126:LYS:NZ	1:NE:109:MET:SD	2.60	0.74
3:BT:274:ARG:O	3:BT:278:SER:HB3	1.86	0.73
1:LA:104:THR:HA	3:Lt:137:ASN:O	1.88	0.73
1:BC:187:PRO:HD3	1:CA:191:THR:HB	1.69	0.73
1:FD:177:THR:HA	1:FE:107:TYR:O	1.89	0.73
1:FA:294:GLN:O	1:FC:162:LYS:NZ	2.22	0.73
1:JC:187:PRO:HD3	1:KA:191:THR:HB	1.69	0.73
1:EA:104:THR:HA	3:Et:137:ASN:O	1.89	0.73
1:IC:187:PRO:HD3	1:JA:191:THR:HB	1.69	0.73
1:GC:187:PRO:HD3	1:HA:191:THR:HB	1.70	0.73
1:HA:104:THR:HA	3:Ht:137:ASN:O	1.88	0.73
2:Jm:345:THR:O	2:Jm:349:LYS:HB2	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KA:104:THR:HA	3:Kt:137:ASN:O	1.88	0.73
1:CA:296:VAL:HB	1:CC:164:VAL:HG12	1.71	0.72
1:NA:104:THR:HA	3:Nt:137:ASN:O	1.89	0.72
1:KA:296:VAL:HB	1:KC:164:VAL:HG12	1.70	0.72
1:EB:126:LYS:HG2	1:EB:184:ARG:HH12	1.53	0.72
1:FD:126:LYS:HB3	1:FD:130:MET:HE2	1.71	0.72
1:KE:107:TYR:CG	1:KE:107:TYR:HB3	2.17	0.72
1:AA:191:THR:HB	1:NC:187:PRO:HD3	1.71	0.72
1:KC:187:PRO:HD3	1:LA:191:THR:HB	1.70	0.72
1:BA:104:THR:HA	3:Bt:137:ASN:O	1.90	0.72
1:JA:104:THR:HA	3:Jt:137:ASN:O	1.88	0.72
1:AC:187:PRO:HD3	1:BA:191:THR:HB	1.70	0.72
1:HD:167:ILE:HB	1:IA:194:LYS:HZ2	1.54	0.72
1:JD:175:GLN:HA	1:JE:109:MET:O	1.90	0.72
1:FA:130:MET:HG3	3:Ft:63:VAL:HG21	1.72	0.72
1:CD:114:TYR:HA	1:CD:117:TYR:HB3	1.71	0.72
1:HC:187:PRO:HD3	1:IA:191:THR:HB	1.70	0.72
1:JC:168:ASN:HB3	1:JC:171:MET:HE1	1.72	0.71
1:JA:296:VAL:HB	1:JC:164:VAL:HG12	1.71	0.71
1:AD:114:TYR:HA	1:AD:117:TYR:HB3	1.72	0.71
1:EA:106:LEU:HD13	3:Et:136:SER:HB3	1.72	0.71
1:HC:168:ASN:HB3	1:HC:171:MET:HE1	1.70	0.71
1:JD:114:TYR:HA	1:JD:117:TYR:HB3	1.73	0.71
1:IA:104:THR:HA	3:It:137:ASN:O	1.91	0.70
1:KD:81:TYR:HE1	1:KE:107:TYR:HB2	1.57	0.70
1:DC:187:PRO:HD3	1:EA:191:THR:HB	1.74	0.70
1:KD:81:TYR:CE1	1:KE:107:TYR:HB2	2.26	0.70
1:HA:294:GLN:O	1:HC:162:LYS:NZ	2.24	0.70
1:NA:296:VAL:HB	1:NC:164:VAL:HG12	1.74	0.70
1:KD:114:TYR:HA	1:KD:117:TYR:HB3	1.73	0.69
1:AD:177:THR:HA	1:AE:107:TYR:O	1.93	0.69
1:EB:112:LEU:HD21	3:ET:238:SER:HB3	1.75	0.69
1:EC:168:ASN:HB3	1:EC:171:MET:HE1	1.74	0.69
1:EC:187:PRO:HD3	1:FA:191:THR:HB	1.73	0.69
1:DA:296:VAL:HB	1:DC:164:VAL:HG12	1.72	0.69
1:BD:114:TYR:HA	1:BD:117:TYR:HB3	1.73	0.69
1:FA:296:VAL:HB	1:FC:164:VAL:HG12	1.73	0.69
1:FC:187:PRO:HD3	1:GA:191:THR:HB	1.75	0.69
1:MA:296:VAL:HB	1:MC:164:VAL:HG12	1.75	0.69
1:FB:146:VAL:HB	1:FB:165:LEU:HD22	1.74	0.69
1:ED:114:TYR:HA	1:ED:117:TYR:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:143:LEU:HD23	3:BT:221:LEU:HD22	1.75	0.68
1:LD:111:LEU:HD11	1:LE:174:ALA:HB3	1.76	0.68
1:FA:106:LEU:HD13	3:Ft:136:SER:HB3	1.76	0.68
1:ID:114:TYR:HA	1:ID:117:TYR:HB3	1.74	0.68
1:NA:106:LEU:HD13	3:Nt:136:SER:HB3	1.74	0.68
1:DA:106:LEU:HD13	3:Dt:136:SER:HB3	1.76	0.68
1:CD:111:LEU:HD11	1:CE:174:ALA:HB3	1.76	0.68
2:EM:333:ILE:O	2:EM:337:SER:HB3	1.94	0.68
1:HE:150:TYR:O	1:HE:154:LYS:HB2	1.94	0.68
1:MA:106:LEU:HD13	3:Mt:136:SER:HB3	1.76	0.68
1:AD:167:ILE:HB	1:BA:194:LYS:HZ2	1.58	0.68
1:CA:106:LEU:HD13	3:Ct:136:SER:HB3	1.76	0.68
2:Jm:264:GLU:HB2	2:Jm:268:ARG:HH21	1.59	0.68
1:IA:276:THR:HG22	1:IA:278:PRO:HD2	1.76	0.67
1:JD:111:LEU:HD11	1:JE:174:ALA:HB3	1.76	0.67
2:Am:264:GLU:HB2	2:Am:268:ARG:HH21	1.60	0.67
2:Am:273:PHE:HD2	2:Am:310:VAL:HG11	1.60	0.67
1:LC:168:ASN:HB3	1:LC:171:MET:HE1	1.75	0.67
1:HA:276:THR:HG22	1:HA:278:PRO:HD2	1.76	0.67
1:AD:174:ALA:O	1:AE:111:LEU:HB3	1.94	0.67
1:IB:182:PRO:HG3	1:IC:107:TYR:HB2	1.75	0.67
1:JA:276:THR:HG22	1:JA:278:PRO:HD2	1.76	0.67
1:DC:126:LYS:HD2	1:EA:192:LEU:HD12	1.77	0.67
1:GA:276:THR:HG22	1:GA:278:PRO:HD2	1.76	0.67
1:ID:126:LYS:HB3	1:ID:130:MET:HE1	1.74	0.67
1:KA:276:THR:HG22	1:KA:278:PRO:HD2	1.76	0.67
1:GE:150:TYR:O	1:GE:154:LYS:HB2	1.94	0.67
1:HA:106:LEU:HD13	3:Ht:136:SER:HB3	1.76	0.67
1:ID:143:LEU:HD23	3:IT:221:LEU:HD22	1.76	0.67
1:ID:177:THR:HA	1:IE:107:TYR:O	1.94	0.67
2:MM:333:ILE:O	2:MM:337:SER:HB3	1.93	0.67
1:BA:234:MET:O	1:BB:166:LYS:NZ	2.27	0.67
1:FA:276:THR:HG22	1:FA:278:PRO:HD2	1.76	0.67
1:GD:114:TYR:HA	1:GD:117:TYR:HB3	1.75	0.67
2:Hm:264:GLU:HB2	2:Hm:268:ARG:HH21	1.59	0.67
1:CA:276:THR:HG22	1:CA:278:PRO:HD2	1.76	0.67
1:DA:276:THR:HG22	1:DA:278:PRO:HD2	1.76	0.67
1:EA:276:THR:HG22	1:EA:278:PRO:HD2	1.76	0.67
1:GD:167:ILE:HB	1:HA:194:LYS:HZ2	1.58	0.67
1:LC:184:ARG:HH11	1:LC:186:ASP:H	1.42	0.67
1:BA:276:THR:HG22	1:BA:278:PRO:HD2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:117:TYR:O	1:CC:121:GLU:HB2	1.93	0.67
1:LA:276:THR:HG22	1:LA:278:PRO:HD2	1.76	0.67
1:DE:150:TYR:O	1:DE:154:LYS:HB2	1.94	0.67
1:LC:187:PRO:HD3	1:MA:191:THR:HB	1.74	0.67
1:BA:106:LEU:HD13	3:Bt:136:SER:HB3	1.77	0.66
2:Dm:264:GLU:HB2	2:Dm:268:ARG:HH21	1.60	0.66
1:GA:296:VAL:HB	1:GC:164:VAL:HG12	1.77	0.66
1:ME:150:TYR:O	1:ME:154:LYS:HB2	1.94	0.66
2:Nm:264:GLU:HB2	2:Nm:268:ARG:HH21	1.60	0.66
2:Mm:344:LYS:HB3	2:Mm:347:MET:HB2	1.77	0.66
1:AA:276:THR:HG22	1:AA:278:PRO:HD2	1.76	0.66
5:DX:475:LYS:HG3	5:DX:488:ILE:HG22	1.77	0.66
1:HD:114:TYR:HA	1:HD:117:TYR:HB3	1.75	0.66
2:Jm:348:GLN:HE21	2:Jm:349:LYS:HE2	1.59	0.66
1:NA:276:THR:HG22	1:NA:278:PRO:HD2	1.76	0.66
2:Im:264:GLU:HB2	2:Im:268:ARG:HH21	1.61	0.66
1:MA:276:THR:HG22	1:MA:278:PRO:HD2	1.76	0.66
5:EX:475:LYS:HG3	5:EX:488:ILE:HG22	1.77	0.66
1:HC:131:GLY:HA3	1:HC:153:LEU:HD22	1.76	0.66
5:CX:475:LYS:HG3	5:CX:488:ILE:HG22	1.77	0.66
1:JA:106:LEU:HD13	3:Jt:136:SER:HB3	1.76	0.66
5:BX:475:LYS:HG3	5:BX:488:ILE:HG22	1.77	0.66
1:DA:304:LYS:HZ3	1:DD:79:ASP:HA	1.61	0.66
1:FE:150:TYR:O	1:FE:154:LYS:HB2	1.95	0.66
5:FX:475:LYS:HG3	5:FX:488:ILE:HG22	1.77	0.66
1:HD:111:LEU:HD11	1:HE:174:ALA:HB3	1.76	0.66
1:KA:106:LEU:HD13	3:Kt:136:SER:HB3	1.76	0.66
1:FD:111:LEU:HD11	1:FE:174:ALA:HB3	1.76	0.66
1:LA:106:LEU:HD13	3:Lt:136:SER:HB3	1.76	0.66
1:MD:111:LEU:HD11	1:ME:174:ALA:HB3	1.78	0.66
1:AE:150:TYR:O	1:AE:154:LYS:HB2	1.95	0.65
5:AX:475:LYS:HG3	5:AX:488:ILE:HG22	1.77	0.65
2:Mm:264:GLU:HB2	2:Mm:268:ARG:HH21	1.61	0.65
5:GX:475:LYS:HG3	5:GX:488:ILE:HG22	1.77	0.65
1:ND:143:LEU:HD13	3:NT:221:LEU:HD22	1.78	0.65
1:IC:131:GLY:HA3	1:IC:153:LEU:HD22	1.78	0.65
5:NX:475:LYS:HG3	5:NX:488:ILE:HG22	1.77	0.65
1:ID:111:LEU:HD11	1:IE:174:ALA:HB3	1.78	0.65
1:KD:111:LEU:HD11	1:KE:174:ALA:HB3	1.79	0.65
1:NE:150:TYR:O	1:NE:154:LYS:HB2	1.95	0.65
2:Nm:282:ASP:HB3	2:Nm:285:GLU:H	1.59	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EE:150:TYR:O	1:EE:154:LYS:HB2	1.96	0.65
5:MX:475:LYS:HG3	5:MX:488:ILE:HG22	1.77	0.65
1:CB:126:LYS:HG2	1:CB:184:ARG:HH12	1.62	0.65
1:HD:166:LYS:HD3	1:IA:194:LYS:HE3	1.79	0.65
1:LE:150:TYR:O	1:LE:154:LYS:HB2	1.96	0.65
1:DD:111:LEU:HD11	1:DE:174:ALA:HB3	1.77	0.65
5:HX:475:LYS:HG3	5:HX:488:ILE:HG22	1.77	0.65
2:Fm:264:GLU:HB2	2:Fm:268:ARG:HH21	1.61	0.65
1:GB:126:LYS:HG2	1:GB:184:ARG:HH12	1.61	0.65
2:KM:253:LEU:HG	2:KM:257:MET:HE1	1.79	0.65
5:LX:475:LYS:HG3	5:LX:488:ILE:HG22	1.77	0.65
5:JX:475:LYS:HG3	5:JX:488:ILE:HG22	1.77	0.64
1:KA:294:GLN:O	1:KC:162:LYS:NZ	2.30	0.64
1:MB:126:LYS:HG2	1:MB:184:ARG:HH12	1.63	0.64
1:IB:126:LYS:HG2	1:IB:184:ARG:HH12	1.62	0.64
2:Bm:264:GLU:HB2	2:Bm:268:ARG:HH21	1.60	0.64
1:ED:111:LEU:HD11	1:EE:174:ALA:HB3	1.76	0.64
4:FU:610:UNK:HA	2:Fm:212:LEU:HD21	1.78	0.64
5:IX:475:LYS:HG3	5:IX:488:ILE:HG22	1.77	0.64
1:LD:114:TYR:HA	1:LD:117:TYR:HB3	1.78	0.64
2:Bm:344:LYS:HB3	2:Bm:347:MET:HB2	1.78	0.64
2:Bm:346:THR:HA	2:Bm:350:GLU:HB2	1.79	0.64
3:Ft:217:GLN:HG3	3:GT:273:ILE:HD12	1.80	0.64
5:KX:475:LYS:HG3	5:KX:488:ILE:HG22	1.77	0.64
1:DE:136:LEU:HB2	1:DE:179:LEU:HB2	1.78	0.64
2:Im:298:LEU:HB2	2:Im:303:LYS:HE3	1.80	0.64
1:JB:126:LYS:HG2	1:JB:184:ARG:HH12	1.62	0.64
1:DD:114:TYR:HA	1:DD:117:TYR:HB3	1.78	0.64
1:KE:150:TYR:O	1:KE:154:LYS:HB2	1.97	0.64
1:LA:130:MET:HG3	3:Lt:63:VAL:HG21	1.79	0.64
3:LT:211:THR:O	1:MA:159:ARG:NH2	2.31	0.64
1:FC:157:ASN:ND2	1:FC:159:ARG:O	2.31	0.64
1:JD:166:LYS:HD3	1:KA:194:LYS:HE3	1.80	0.64
1:AA:194:LYS:HE3	1:ND:166:LYS:HD3	1.80	0.64
1:MB:120:ILE:HG13	3:MT:242:PHE:HE1	1.62	0.64
4:MU:610:UNK:HA	2:Mm:212:LEU:HD21	1.80	0.64
1:AD:111:LEU:HD11	1:AE:174:ALA:HB3	1.80	0.64
2:Cm:215:LYS:NZ	2:Cm:295:ASN:O	2.31	0.64
1:FA:234:MET:O	1:FB:166:LYS:NZ	2.31	0.64
4:DU:610:UNK:HA	2:Dm:212:LEU:HD21	1.80	0.63
1:GB:126:LYS:HE2	1:GB:184:ARG:HH22	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GB:182:PRO:HG3	1:GC:107:TYR:HB2	1.81	0.63
1:IE:150:TYR:O	1:IE:154:LYS:HB2	1.98	0.63
1:BD:146:VAL:O	1:BD:150:TYR:HB2	1.97	0.63
1:EB:120:ILE:HG13	3:ET:242:PHE:HE1	1.63	0.63
1:BB:136:LEU:HB3	1:BB:179:LEU:HB2	1.81	0.63
1:ID:146:VAL:O	1:ID:150:TYR:HB2	1.99	0.63
6:IY:1693:ALA:HB2	6:IY:1725:MET:HG2	1.80	0.63
1:MA:107:TYR:CG	3:Mt:44:ILE:HD11	2.33	0.63
1:AD:166:LYS:HD3	1:BA:194:LYS:HE3	1.80	0.63
1:NC:168:ASN:HB3	1:NC:171:MET:HE1	1.80	0.63
1:BD:111:LEU:HD11	1:BE:174:ALA:HB3	1.80	0.63
6:GY:1693:ALA:HB2	6:GY:1725:MET:HG2	1.80	0.63
6:HY:1693:ALA:HB2	6:HY:1725:MET:HG2	1.80	0.63
2:AM:263:ASN:O	2:AM:267:LEU:HB2	1.98	0.63
6:AY:1693:ALA:HB2	6:AY:1725:MET:HG2	1.80	0.63
6:JY:1693:ALA:HB2	6:JY:1725:MET:HG2	1.80	0.63
1:KE:107:TYR:CB	1:KE:107:TYR:CD2	2.76	0.63
2:Km:264:GLU:HB2	2:Km:268:ARG:HH21	1.63	0.63
6:BY:1693:ALA:HB2	6:BY:1725:MET:HG2	1.80	0.63
6:CY:1693:ALA:HB2	6:CY:1725:MET:HG2	1.80	0.63
2:Cm:264:GLU:HB2	2:Cm:268:ARG:HH21	1.62	0.63
1:ND:129:ALA:O	1:ND:133:TYR:HB2	1.98	0.63
1:JC:146:VAL:HB	1:JC:165:LEU:HD12	1.80	0.62
6:KY:1693:ALA:HB2	6:KY:1725:MET:HG2	1.80	0.62
1:EA:130:MET:HG3	3:Et:63:VAL:HG21	1.81	0.62
1:GD:166:LYS:HD3	1:HA:194:LYS:HE3	1.82	0.62
1:JB:168:ASN:ND2	1:JB:171:MET:SD	2.73	0.62
1:JC:133:TYR:HB3	1:JC:181:VAL:HG21	1.81	0.62
6:NY:1693:ALA:HB2	6:NY:1725:MET:HG2	1.80	0.62
1:CB:168:ASN:ND2	1:CB:171:MET:SD	2.73	0.62
1:ED:140:THR:HG22	1:ED:166:LYS:HB2	1.81	0.62
1:KE:136:LEU:HB2	1:KE:179:LEU:HB2	1.80	0.62
5:FX:439:ILE:HG12	5:FX:478:LEU:HG	1.82	0.62
1:GD:111:LEU:HD11	1:GE:174:ALA:HB3	1.81	0.62
5:HX:439:ILE:HG12	5:HX:478:LEU:HG	1.82	0.62
2:Im:197:TYR:HB2	2:Im:238:ILE:HG21	1.81	0.62
2:Im:344:LYS:HB3	2:Im:347:MET:HB2	1.81	0.62
1:JD:167:ILE:HB	1:KA:194:LYS:HZ2	1.65	0.62
2:Km:298:LEU:HB2	2:Km:303:LYS:HE3	1.81	0.62
6:EY:1693:ALA:HB2	6:EY:1725:MET:HG2	1.80	0.62
6:FY:1693:ALA:HB2	6:FY:1725:MET:HG2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HE:140:THR:HG23	1:HE:166:LYS:HB2	1.81	0.62
5:KX:439:ILE:HG12	5:KX:478:LEU:HG	1.82	0.62
1:LA:296:VAL:HB	1:LC:164:VAL:HG12	1.82	0.62
1:BE:150:TYR:O	1:BE:154:LYS:HB2	1.98	0.62
6:DY:1693:ALA:HB2	6:DY:1725:MET:HG2	1.80	0.62
3:Dt:217:GLN:HG3	3:ET:273:ILE:HD12	1.81	0.62
6:LY:1693:ALA:HB2	6:LY:1725:MET:HG2	1.80	0.62
6:MY:1693:ALA:HB2	6:MY:1725:MET:HG2	1.80	0.62
1:NE:157:ASN:HD21	1:NE:161:ALA:H	1.47	0.62
2:Nm:344:LYS:HB3	2:Nm:347:MET:HB3	1.82	0.62
1:AA:106:LEU:HD13	3:At:136:SER:HB3	1.81	0.62
5:FX:408:GLU:OE1	3:GT:32:LYS:N	2.32	0.62
1:NB:137:ILE:HD13	1:NB:153:LEU:HD23	1.80	0.62
1:AA:104:THR:HA	3:At:137:ASN:O	1.99	0.62
1:FD:138:ILE:HG12	1:FD:164:VAL:HB	1.80	0.62
2:Lm:215:LYS:NZ	2:Lm:295:ASN:O	2.33	0.62
1:MC:187:PRO:HD3	1:NA:191:THR:HB	1.82	0.62
2:DM:205:SER:OG	2:DM:268:ARG:O	2.18	0.62
1:FA:224:ASP:O	1:FA:231:ARG:NH2	2.33	0.62
5:IX:439:ILE:HG12	5:IX:478:LEU:HG	1.82	0.62
2:NM:189:LYS:HA	2:NM:192:ARG:HG3	1.80	0.62
3:Nt:93:ILE:O	3:Nt:120:PHE:HA	2.00	0.62
3:Et:93:ILE:O	3:Et:120:PHE:HA	2.00	0.62
2:Fm:346:THR:HA	2:Fm:350:GLU:HB2	1.82	0.62
1:HA:296:VAL:HB	1:HC:164:VAL:HG12	1.82	0.62
3:HT:184:GLU:OE1	3:HT:187:ARG:NH1	2.26	0.62
3:Jt:32:LYS:NZ	3:KT:47:TYR:OH	2.33	0.62
1:KB:110:ASP:OD1	3:KT:235:ASN:ND2	2.32	0.62
2:LM:222:TYR:HE1	3:Lt:227:ARG:HD3	1.65	0.62
2:Nm:346:THR:HA	2:Nm:350:GLU:HB2	1.82	0.62
2:Bm:197:TYR:HB2	2:Bm:238:ILE:HG21	1.81	0.61
1:CC:132:THR:HG22	1:CC:156:LEU:HB3	1.81	0.61
5:CX:439:ILE:HG12	5:CX:478:LEU:HG	1.82	0.61
1:ED:95:PHE:HE1	1:EE:128:ARG:HH21	1.46	0.61
5:EX:439:ILE:HG12	5:EX:478:LEU:HG	1.82	0.61
1:GA:224:ASP:O	1:GA:231:ARG:NH2	2.33	0.61
3:Ht:93:ILE:O	3:Ht:120:PHE:HA	2.00	0.61
2:Im:215:LYS:NZ	2:Im:295:ASN:O	2.33	0.61
1:CE:150:TYR:O	1:CE:154:LYS:HB2	2.00	0.61
3:Ft:93:ILE:O	3:Ft:120:PHE:HA	2.00	0.61
3:Gt:217:GLN:HG3	3:HT:273:ILE:HD12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JA:224:ASP:O	1:JA:231:ARG:NH2	2.33	0.61
5:JX:439:ILE:HG12	5:JX:478:LEU:HG	1.82	0.61
3:Kt:93:ILE:O	3:Kt:120:PHE:HA	2.00	0.61
1:MC:169:GLU:OE1	3:Mt:233:ARG:NH2	2.33	0.61
5:MX:439:ILE:HG12	5:MX:478:LEU:HG	1.82	0.61
1:NB:126:LYS:HG2	1:NB:184:ARG:HH12	1.65	0.61
1:ND:114:TYR:HA	1:ND:117:TYR:HB3	1.81	0.61
1:AC:131:GLY:HA3	1:AC:153:LEU:HD22	1.81	0.61
2:Am:215:LYS:NZ	2:Am:295:ASN:O	2.31	0.61
1:DB:110:ASP:OD2	3:DT:235:ASN:ND2	2.33	0.61
1:DB:126:LYS:HG2	1:DB:184:ARG:HH12	1.66	0.61
3:Dt:93:ILE:O	3:Dt:120:PHE:HA	2.00	0.61
1:ID:137:ILE:O	1:ID:163:PHE:HA	2.00	0.61
2:JM:219:ASN:HB3	2:JM:222:TYR:HB3	1.82	0.61
3:KT:184:GLU:OE1	3:KT:187:ARG:NH1	2.26	0.61
4:KU:610:UNK:HA	2:Km:212:LEU:HD21	1.82	0.61
2:Km:197:TYR:HB2	2:Km:238:ILE:HG21	1.82	0.61
1:LA:304:LYS:HZ3	1:LD:79:ASP:HA	1.64	0.61
1:AA:224:ASP:O	1:AA:231:ARG:NH2	2.33	0.61
1:DB:121:GLU:HG3	1:DC:124:ILE:HD12	1.82	0.61
5:DX:439:ILE:HG12	5:DX:478:LEU:HG	1.82	0.61
3:Et:217:GLN:HG3	3:FT:273:ILE:HD12	1.82	0.61
1:KA:224:ASP:O	1:KA:231:ARG:NH2	2.33	0.61
1:LC:137:ILE:HD13	1:LC:163:PHE:HE1	1.65	0.61
2:Mm:346:THR:HA	2:Mm:350:GLU:HB2	1.82	0.61
1:NA:304:LYS:HZ3	1:ND:79:ASP:HA	1.65	0.61
1:AE:140:THR:HG23	1:AE:166:LYS:HB2	1.82	0.61
5:AX:439:ILE:HG12	5:AX:478:LEU:HG	1.82	0.61
2:Gm:344:LYS:HB3	2:Gm:347:MET:HB3	1.81	0.61
1:HD:136:LEU:HG	1:HD:162:LYS:HB3	1.83	0.61
3:It:93:ILE:O	3:It:120:PHE:HA	2.00	0.61
1:JE:150:TYR:O	1:JE:154:LYS:HB2	2.00	0.61
1:KB:126:LYS:HG2	1:KB:184:ARG:HH12	1.65	0.61
1:KD:167:ILE:HB	1:LA:194:LYS:HZ2	1.65	0.61
2:Mm:215:LYS:NZ	2:Mm:295:ASN:O	2.32	0.61
1:ND:111:LEU:HD11	1:NE:174:ALA:HB3	1.83	0.61
3:Gt:93:ILE:O	3:Gt:120:PHE:HA	2.00	0.61
1:ID:166:LYS:HD3	1:JA:194:LYS:HE3	1.83	0.61
5:IX:505:ASN:ND2	5:IX:508:GLU:OE2	2.33	0.61
4:LU:610:UNK:HA	2:Lm:212:LEU:HD21	1.83	0.61
1:MA:224:ASP:O	1:MA:231:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:NE:128:ARG:HE	1:NE:156:LEU:HD11	1.64	0.61
3:Bt:217:GLN:HG3	3:CT:273:ILE:HD12	1.82	0.61
3:Ct:93:ILE:O	3:Ct:120:PHE:HA	2.00	0.61
1:EA:224:ASP:O	1:EA:231:ARG:NH2	2.33	0.61
1:HC:138:ILE:O	1:HC:176:ALA:HA	1.99	0.61
3:Ht:217:GLN:HG3	3:IT:273:ILE:HD12	1.82	0.61
1:IA:224:ASP:O	1:IA:231:ARG:NH2	2.33	0.61
1:KB:121:GLU:HG3	1:KC:124:ILE:HD12	1.82	0.61
1:ED:130:MET:HE1	1:EE:109:MET:HG3	1.83	0.61
6:GY:1706:VAL:HB	6:GY:1871:LYS:HB3	1.83	0.61
1:HA:224:ASP:O	1:HA:231:ARG:NH2	2.33	0.61
2:HM:263:ASN:O	2:HM:267:LEU:HB2	2.01	0.61
2:Jm:215:LYS:NZ	2:Jm:295:ASN:O	2.33	0.61
1:LD:143:LEU:HD23	3:LT:221:LEU:HD22	1.82	0.61
3:Lt:93:ILE:O	3:Lt:120:PHE:HA	2.00	0.61
6:MY:1706:VAL:HB	6:MY:1871:LYS:HB3	1.82	0.61
5:NX:505:ASN:ND2	5:NX:508:GLU:OE2	2.33	0.61
1:MD:138:ILE:HG12	1:MD:164:VAL:HB	1.80	0.61
1:MD:166:LYS:HD3	1:NA:194:LYS:HE3	1.83	0.61
3:Mt:93:ILE:O	3:Mt:120:PHE:HA	2.00	0.61
2:Nm:197:TYR:HB2	2:Nm:238:ILE:HG21	1.83	0.61
1:AA:111:LEU:HD11	3:At:133:MET:HB2	1.80	0.61
1:AE:140:THR:HG21	1:BA:278:PRO:HD3	1.83	0.61
1:BD:137:ILE:O	1:BD:163:PHE:HA	2.01	0.61
2:Dm:197:TYR:HB2	2:Dm:238:ILE:HG21	1.82	0.61
1:EB:121:GLU:HG2	1:EC:124:ILE:HD12	1.83	0.61
1:FE:109:MET:HE1	1:FE:111:LEU:HD13	1.82	0.61
1:NB:126:LYS:HE2	1:NB:184:ARG:HH22	1.65	0.61
6:AY:1706:VAL:HB	6:AY:1871:LYS:HB3	1.83	0.60
3:At:93:ILE:O	3:At:120:PHE:HA	2.01	0.60
1:CA:224:ASP:O	1:CA:231:ARG:NH2	2.33	0.60
1:EA:296:VAL:HB	1:EC:164:VAL:HG12	1.83	0.60
6:EY:1706:VAL:HB	6:EY:1871:LYS:HB3	1.83	0.60
2:FM:263:ASN:O	2:FM:267:LEU:HB2	2.01	0.60
5:GX:439:ILE:HG12	5:GX:478:LEU:HG	1.82	0.60
1:MD:136:LEU:HG	1:MD:162:LYS:HB3	1.82	0.60
1:DD:146:VAL:O	1:DD:150:TYR:HB2	2.02	0.60
5:DX:505:ASN:ND2	5:DX:508:GLU:OE2	2.33	0.60
1:EB:137:ILE:HD13	1:EB:153:LEU:HD23	1.83	0.60
1:HD:129:ALA:O	1:HD:133:TYR:HB2	2.01	0.60
1:NB:182:PRO:HG3	1:NC:107:TYR:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:138:ILE:O	1:AC:176:ALA:HA	2.01	0.60
5:AX:404:TYR:HB3	3:BT:36:TYR:HB3	1.82	0.60
1:BA:224:ASP:O	1:BA:231:ARG:NH2	2.33	0.60
3:BT:209:GLU:HG3	3:BT:218:ARG:HH22	1.67	0.60
4:CU:610:UNK:HA	2:Cm:212:LEU:HD21	1.83	0.60
3:Ct:217:GLN:HG3	3:DT:273:ILE:HD12	1.83	0.60
1:DA:224:ASP:O	1:DA:231:ARG:NH2	2.33	0.60
6:FY:1706:VAL:HB	6:FY:1871:LYS:HB3	1.83	0.60
2:Fm:215:LYS:NZ	2:Fm:295:ASN:O	2.33	0.60
1:ID:167:ILE:HB	1:JA:194:LYS:HZ2	1.66	0.60
3:JT:209:GLU:HG3	3:JT:218:ARG:HH22	1.67	0.60
3:Jt:93:ILE:O	3:Jt:120:PHE:HA	2.00	0.60
3:KT:209:GLU:HG3	3:KT:218:ARG:HH22	1.67	0.60
3:LT:209:GLU:HG3	3:LT:218:ARG:HH22	1.67	0.60
3:AT:209:GLU:HG3	3:AT:218:ARG:HH22	1.67	0.60
3:ET:209:GLU:HG3	3:ET:218:ARG:HH22	1.67	0.60
3:Ft:32:LYS:NZ	3:GT:47:TYR:OH	2.35	0.60
1:GC:146:VAL:HB	1:GC:165:LEU:HD12	1.84	0.60
1:GC:146:VAL:O	1:GC:150:TYR:HB2	2.00	0.60
5:HX:505:ASN:ND2	5:HX:508:GLU:OE2	2.33	0.60
3:Jt:217:GLN:HG3	3:KT:273:ILE:HD12	1.81	0.60
3:At:217:GLN:HG3	3:BT:273:ILE:HD12	1.82	0.60
5:BX:439:ILE:HG12	5:BX:478:LEU:HG	1.82	0.60
1:EE:109:MET:HE1	1:EE:111:LEU:HD13	1.83	0.60
2:Gm:215:LYS:NZ	2:Gm:295:ASN:O	2.34	0.60
1:HA:234:MET:O	1:HB:166:LYS:NZ	2.35	0.60
1:HE:140:THR:HG21	1:IA:278:PRO:HD3	1.82	0.60
6:HY:1706:VAL:HB	6:HY:1871:LYS:HB3	1.83	0.60
2:IM:308:LEU:HD21	3:It:232:MET:HG2	1.83	0.60
3:IT:209:GLU:HG3	3:IT:218:ARG:HH22	1.67	0.60
6:IY:1706:VAL:HB	6:IY:1871:LYS:HB3	1.83	0.60
6:KY:1706:VAL:HB	6:KY:1871:LYS:HB3	1.82	0.60
1:LB:126:LYS:HG2	1:LB:184:ARG:HH12	1.66	0.60
4:NU:610:UNK:HA	2:Nm:212:LEU:HD21	1.84	0.60
2:Em:215:LYS:NZ	2:Em:295:ASN:O	2.33	0.60
3:FT:209:GLU:HG3	3:FT:218:ARG:HH22	1.67	0.60
2:Gm:197:TYR:HB2	2:Gm:238:ILE:HG21	1.83	0.60
3:HT:209:GLU:HG3	3:HT:218:ARG:HH22	1.67	0.60
2:LM:308:LEU:HD21	3:Lt:232:MET:HG2	1.83	0.60
3:MT:209:GLU:HG3	3:MT:218:ARG:HH22	1.67	0.60
1:NA:224:ASP:O	1:NA:231:ARG:NH2	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:DY:1706:VAL:HB	6:DY:1871:LYS:HB3	1.82	0.60
3:GT:184:GLU:OE1	3:GT:187:ARG:NH1	2.26	0.60
3:GT:209:GLU:HG3	3:GT:218:ARG:HH22	1.67	0.60
2:Gm:346:THR:HA	2:Gm:350:GLU:HB2	1.83	0.60
1:LD:140:THR:HG22	1:LD:166:LYS:HB2	1.84	0.60
2:Lm:197:TYR:HB2	2:Lm:238:ILE:HG21	1.84	0.60
1:BB:126:LYS:HD3	1:BB:184:ARG:HH22	1.67	0.60
3:Bt:93:ILE:O	3:Bt:120:PHE:HA	2.00	0.60
3:DT:209:GLU:HG3	3:DT:218:ARG:HH22	1.67	0.60
1:ED:166:LYS:HD3	1:FA:194:LYS:HE3	1.84	0.60
1:GB:138:ILE:HG12	1:GB:164:VAL:HB	1.84	0.60
5:LX:439:ILE:HG12	5:LX:478:LEU:HG	1.82	0.60
1:MA:216:ASN:HA	1:MA:220:CYS:HB2	1.84	0.60
6:NY:1706:VAL:HB	6:NY:1871:LYS:HB3	1.83	0.60
1:CA:295:LEU:HD12	1:CC:163:PHE:HB2	1.84	0.60
3:Dt:210:TYR:O	3:Dt:213:ARG:NH1	2.35	0.60
1:JA:216:ASN:HA	1:JA:220:CYS:HB2	1.84	0.60
2:KM:189:LYS:HA	2:KM:192:ARG:HG3	1.83	0.60
3:Kt:217:GLN:HG3	3:LT:273:ILE:HD12	1.82	0.60
1:LA:224:ASP:O	1:LA:231:ARG:NH2	2.33	0.60
6:LY:1706:VAL:HB	6:LY:1871:LYS:HB3	1.83	0.60
2:MM:205:SER:OG	2:MM:268:ARG:O	2.18	0.60
3:Nt:210:TYR:O	3:Nt:213:ARG:NH1	2.35	0.60
1:CB:182:PRO:HG3	1:CC:107:TYR:HB2	1.84	0.60
1:CC:187:PRO:HD2	1:DA:188:ASN:HA	1.84	0.60
3:CT:209:GLU:HG3	3:CT:218:ARG:HH22	1.67	0.60
5:EX:410:ARG:HH12	5:FX:445:ASP:HA	1.67	0.60
1:GC:169:GLU:OE2	3:Gt:233:ARG:NH2	2.35	0.60
1:HC:187:PRO:HD2	1:IA:188:ASN:HA	1.84	0.60
3:Jt:210:TYR:O	3:Jt:213:ARG:NH1	2.35	0.60
1:KA:216:ASN:HA	1:KA:220:CYS:HB2	1.84	0.60
5:MX:404:TYR:HB3	3:NT:36:TYR:HB3	1.84	0.60
3:NT:209:GLU:HG3	3:NT:218:ARG:HH22	1.67	0.60
5:NX:439:ILE:HG12	5:NX:478:LEU:HG	1.82	0.60
6:CY:1706:VAL:HB	6:CY:1871:LYS:HB3	1.83	0.59
2:DM:189:LYS:HA	2:DM:192:ARG:HG3	1.84	0.59
4:GU:610:UNK:HA	2:Gm:212:LEU:HD21	1.84	0.59
5:MX:505:ASN:ND2	5:MX:508:GLU:OE2	2.33	0.59
3:Mt:210:TYR:O	3:Mt:213:ARG:NH1	2.35	0.59
1:NA:130:MET:HG3	3:Nt:63:VAL:HG21	1.83	0.59
3:At:210:TYR:O	3:At:213:ARG:NH1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:218:VAL:HG23	1:CA:219:ILE:HG13	1.84	0.59
1:FD:114:TYR:HA	1:FD:117:TYR:HB3	1.82	0.59
1:GE:107:TYR:CE2	1:GE:109:MET:HB2	2.37	0.59
1:IA:216:ASN:HA	1:IA:220:CYS:HB2	1.84	0.59
3:AT:273:ILE:HD12	3:Nt:217:GLN:HG3	1.83	0.59
4:BU:610:UNK:HA	2:Bm:212:LEU:HD21	1.84	0.59
1:CC:146:VAL:HB	1:CC:165:LEU:HD12	1.83	0.59
1:DA:216:ASN:HA	1:DA:220:CYS:HB2	1.84	0.59
1:DA:218:VAL:HG23	1:DA:219:ILE:HG13	1.85	0.59
3:Dt:32:LYS:NZ	3:ET:47:TYR:OH	2.35	0.59
3:Et:210:TYR:O	3:Et:213:ARG:NH1	2.35	0.59
1:FB:126:LYS:HG2	1:FB:184:ARG:HH12	1.67	0.59
1:GC:187:PRO:HD2	1:HA:188:ASN:HA	1.84	0.59
3:Gt:210:TYR:O	3:Gt:213:ARG:NH1	2.35	0.59
3:Ht:32:LYS:NZ	3:IT:47:TYR:OH	2.35	0.59
1:IA:295:LEU:HD12	1:IC:163:PHE:HB2	1.84	0.59
1:JB:182:PRO:HG3	1:JC:107:TYR:HB2	1.84	0.59
2:Jm:299:SER:H	2:Jm:302:GLN:HE21	1.48	0.59
2:Km:344:LYS:HB3	2:Km:347:MET:HB2	1.84	0.59
1:LA:216:ASN:HA	1:LA:220:CYS:HB2	1.84	0.59
1:LC:187:PRO:HD2	1:MA:188:ASN:HA	1.85	0.59
2:LM:205:SER:OG	2:LM:268:ARG:O	2.19	0.59
1:AA:188:ASN:HA	1:NC:187:PRO:HD2	1.85	0.59
1:BC:130:MET:HE1	1:BC:182:PRO:HB3	1.83	0.59
1:CA:216:ASN:HA	1:CA:220:CYS:HB2	1.84	0.59
1:CD:167:ILE:HB	1:DA:194:LYS:HZ2	1.67	0.59
1:GA:248:ASN:HA	1:GB:187:PRO:HB2	1.82	0.59
4:IU:610:UNK:HA	2:Im:212:LEU:HD21	1.84	0.59
2:JM:310:VAL:HG21	2:JM:358:PHE:HE1	1.67	0.59
3:Lt:217:GLN:HB3	3:MT:269:LEU:HB3	1.83	0.59
1:NA:216:ASN:HA	1:NA:220:CYS:HB2	1.84	0.59
1:AC:187:PRO:HD2	1:BA:188:ASN:HA	1.85	0.59
1:CD:166:LYS:HD3	1:DA:194:LYS:HE3	1.84	0.59
1:EA:218:VAL:HG23	1:EA:219:ILE:HG13	1.84	0.59
1:GA:107:TYR:CG	3:Gt:44:ILE:HD11	2.37	0.59
2:Im:346:THR:HA	2:Im:350:GLU:HB2	1.84	0.59
3:It:210:TYR:O	3:It:213:ARG:NH1	2.35	0.59
1:JD:171:MET:HE1	3:Jt:254:GLU:HG2	1.84	0.59
6:JY:1706:VAL:HB	6:JY:1871:LYS:HB3	1.83	0.59
1:LC:120:ILE:HD11	3:LT:241:ILE:HG12	1.84	0.59
1:LD:166:LYS:HD3	1:MA:194:LYS:HE3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:NT:184:GLU:OE1	3:NT:187:ARG:NH1	2.26	0.59
1:BA:218:VAL:HG23	1:BA:219:ILE:HG13	1.84	0.59
1:BB:182:PRO:HG3	1:BC:107:TYR:HB2	1.84	0.59
6:BY:1706:VAL:HB	6:BY:1871:LYS:HB3	1.83	0.59
3:Ct:210:TYR:O	3:Ct:213:ARG:NH1	2.35	0.59
1:ED:146:VAL:O	1:ED:150:TYR:HB2	2.02	0.59
1:FE:136:LEU:HB2	1:FE:179:LEU:HB2	1.83	0.59
2:Hm:197:TYR:HB2	2:Hm:238:ILE:HG21	1.84	0.59
1:JD:143:LEU:HD23	3:JT:221:LEU:HD22	1.84	0.59
2:Jm:197:TYR:HB2	2:Jm:238:ILE:HG21	1.84	0.59
1:LB:155:ALA:HA	3:Lt:179:LYS:HE2	1.83	0.59
1:EA:111:LEU:HD11	3:Et:133:MET:HB2	1.85	0.59
1:EA:216:ASN:HA	1:EA:220:CYS:HB2	1.84	0.59
3:Et:32:LYS:NZ	3:FT:47:TYR:OH	2.36	0.59
1:FA:218:VAL:HG23	1:FA:219:ILE:HG13	1.84	0.59
2:FM:187:ASN:ND2	2:FM:251:GLU:OE1	2.35	0.59
1:GC:138:ILE:O	1:GC:176:ALA:HA	2.02	0.59
2:Jm:219:ASN:HB3	2:Jm:222:TYR:HD2	1.67	0.59
1:MD:178:PHE:CE1	1:ME:107:TYR:HB3	2.37	0.59
1:BA:216:ASN:HA	1:BA:220:CYS:HB2	1.84	0.59
1:BD:140:THR:HA	1:BD:166:LYS:O	2.03	0.59
1:HA:216:ASN:HA	1:HA:220:CYS:HB2	1.84	0.59
3:Kt:210:TYR:O	3:Kt:213:ARG:NH1	2.35	0.59
1:MB:146:VAL:HB	1:MB:165:LEU:HD22	1.83	0.59
1:ND:127:THR:HA	1:ND:130:MET:HE2	1.85	0.59
3:At:106:LYS:NZ	3:At:110:GLN:OE1	2.36	0.59
3:Bt:210:TYR:O	3:Bt:213:ARG:NH1	2.35	0.59
5:CX:505:ASN:ND2	5:CX:508:GLU:OE2	2.33	0.59
2:Dm:346:THR:HA	2:Dm:350:GLU:HB2	1.84	0.59
1:ED:177:THR:HA	1:EE:107:TYR:O	2.03	0.59
1:FD:136:LEU:HG	1:FD:162:LYS:HB3	1.83	0.59
5:GX:505:ASN:ND2	5:GX:508:GLU:OE2	2.33	0.59
2:Jm:282:ASP:HB3	2:Jm:285:GLU:H	1.68	0.59
3:Lt:210:TYR:O	3:Lt:213:ARG:NH1	2.35	0.59
2:MM:263:ASN:O	2:MM:267:LEU:HB2	2.02	0.59
1:AA:216:ASN:HA	1:AA:220:CYS:HB2	1.84	0.59
1:AA:218:VAL:HG23	1:AA:219:ILE:HG13	1.84	0.59
2:Bm:215:LYS:NZ	2:Bm:295:ASN:O	2.32	0.59
1:DC:187:PRO:HD2	1:EA:188:ASN:HA	1.85	0.59
3:Dt:106:LYS:NZ	3:Dt:110:GLN:OE1	2.36	0.59
5:HX:408:GLU:OE1	3:IT:32:LYS:N	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Hm:215:LYS:NZ	2:Hm:295:ASN:O	2.32	0.59
2:IM:205:SER:OG	2:IM:268:ARG:O	2.21	0.59
1:JC:187:PRO:HD2	1:KA:188:ASN:HA	1.85	0.59
4:JU:610:UNK:HA	2:Jm:212:LEU:HD21	1.84	0.59
1:LD:178:PHE:CZ	1:LE:107:TYR:HB3	2.37	0.59
3:Lt:217:GLN:HG3	3:MT:273:ILE:HD12	1.82	0.59
1:ME:136:LEU:HB2	1:ME:179:LEU:HB2	1.84	0.59
3:At:32:LYS:NZ	3:BT:47:TYR:OH	2.36	0.58
3:Bt:106:LYS:NZ	3:Bt:110:GLN:OE1	2.36	0.58
3:Ct:106:LYS:NZ	3:Ct:110:GLN:OE1	2.36	0.58
2:FM:205:SER:OG	2:FM:268:ARG:O	2.20	0.58
3:FT:184:GLU:OE1	3:FT:187:ARG:NH1	2.26	0.58
3:FT:237:ILE:O	3:FT:241:ILE:HB	2.03	0.58
1:GA:216:ASN:HA	1:GA:220:CYS:HB2	1.84	0.58
1:GA:218:VAL:HG23	1:GA:219:ILE:HG13	1.84	0.58
1:GA:295:LEU:HD12	1:GC:163:PHE:HB2	1.85	0.58
3:Ht:210:TYR:O	3:Ht:213:ARG:NH1	2.35	0.58
1:IA:106:LEU:HD13	3:It:136:SER:HB3	1.84	0.58
1:JD:178:PHE:CE1	1:JE:107:TYR:HB3	2.37	0.58
5:JX:404:TYR:HB3	3:KT:36:TYR:HB3	1.85	0.58
2:KM:205:SER:OG	2:KM:268:ARG:O	2.21	0.58
1:BA:130:MET:HG3	3:Bt:63:VAL:HG21	1.84	0.58
3:Ft:210:TYR:O	3:Ft:213:ARG:NH1	2.35	0.58
1:GD:129:ALA:O	1:GD:133:TYR:HB2	2.03	0.58
1:HD:122:ASN:OD1	1:HD:126:LYS:NZ	2.25	0.58
2:Hm:282:ASP:HB3	2:Hm:285:GLU:H	1.67	0.58
2:Jm:195:LEU:HD23	2:Jm:198:LYS:HD2	1.85	0.58
1:KC:187:PRO:HD2	1:LA:188:ASN:HA	1.85	0.58
1:LC:138:ILE:O	1:LC:176:ALA:HA	2.02	0.58
1:MB:191:THR:HA	1:MC:158:LYS:HZ1	1.67	0.58
1:ND:125:ILE:HG21	1:NE:128:ARG:HG2	1.84	0.58
1:AD:140:THR:HG22	1:AD:166:LYS:HB2	1.85	0.58
1:BC:131:GLY:HA3	1:BC:153:LEU:HD22	1.84	0.58
1:BD:166:LYS:HD3	1:CA:194:LYS:HE3	1.85	0.58
3:Ct:217:GLN:HB3	3:DT:269:LEU:HB3	1.85	0.58
2:Em:197:TYR:HB2	2:Em:238:ILE:HG21	1.83	0.58
2:Em:346:THR:HA	2:Em:350:GLU:HB2	1.85	0.58
3:GT:237:ILE:O	3:GT:241:ILE:HB	2.03	0.58
2:Gm:264:GLU:HB2	2:Gm:268:ARG:HH21	1.67	0.58
6:HY:1711:THR:HG22	6:HY:1744:SER:H	1.69	0.58
1:IC:187:PRO:HD2	1:JA:188:ASN:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:IT:237:ILE:O	3:IT:241:ILE:HB	2.03	0.58
1:CC:140:THR:HG22	1:CC:166:LYS:HB2	1.84	0.58
6:DY:1711:THR:HG22	6:DY:1744:SER:H	1.69	0.58
1:ED:121:GLU:HG2	1:EE:128:ARG:HE	1.68	0.58
1:FA:216:ASN:HA	1:FA:220:CYS:HB2	1.84	0.58
1:FD:130:MET:HE1	1:FE:109:MET:HG3	1.85	0.58
3:FT:211:THR:O	1:GA:159:ARG:NH2	2.35	0.58
1:HA:218:VAL:HG23	1:HA:219:ILE:HG13	1.84	0.58
3:HT:237:ILE:O	3:HT:241:ILE:HB	2.04	0.58
1:JD:140:THR:HA	1:JD:166:LYS:O	2.04	0.58
1:LD:107:TYR:HE1	1:LE:80:ILE:HB	1.69	0.58
1:MC:146:VAL:HB	1:MC:165:LEU:HD12	1.85	0.58
2:AM:308:LEU:HD21	3:At:232:MET:HG2	1.84	0.58
2:BM:308:LEU:HD21	3:Bt:232:MET:HG2	1.84	0.58
3:Bt:32:LYS:NZ	3:CT:47:TYR:OH	2.36	0.58
6:KY:1711:THR:HG22	6:KY:1744:SER:H	1.69	0.58
1:NA:218:VAL:HG23	1:NA:219:ILE:HG13	1.84	0.58
1:AB:168:ASN:ND2	1:AB:171:MET:SD	2.77	0.58
1:BC:187:PRO:HD2	1:CA:188:ASN:HA	1.85	0.58
1:DB:120:ILE:HG13	3:DT:242:PHE:HE1	1.69	0.58
3:DT:211:THR:O	1:EA:159:ARG:NH2	2.36	0.58
3:DT:237:ILE:O	3:DT:241:ILE:HB	2.03	0.58
4:EU:610:UNK:HA	2:Em:212:LEU:HD21	1.85	0.58
6:EY:1711:THR:HG22	6:EY:1744:SER:H	1.69	0.58
4:HU:610:UNK:HA	2:Hm:212:LEU:HD21	1.85	0.58
1:IA:130:MET:HG3	3:It:63:VAL:HG21	1.85	0.58
3:JT:184:GLU:OE1	3:JT:187:ARG:NH1	2.26	0.58
1:LB:132:THR:HA	1:LB:157:ASN:HA	1.85	0.58
6:LY:1711:THR:HG22	6:LY:1744:SER:H	1.69	0.58
1:MA:218:VAL:HG23	1:MA:219:ILE:HG13	1.84	0.58
2:DM:308:LEU:HD21	3:Dt:232:MET:HG2	1.85	0.58
3:ET:237:ILE:O	3:ET:241:ILE:HB	2.03	0.58
3:Et:106:LYS:NZ	3:Et:110:GLN:OE1	2.36	0.58
3:Gt:106:LYS:NZ	3:Gt:110:GLN:OE1	2.36	0.58
1:HA:295:LEU:HD12	1:HC:163:PHE:HB2	1.86	0.58
1:ID:180:ARG:HH11	1:IE:104:THR:HA	1.69	0.58
3:JT:237:ILE:O	3:JT:241:ILE:HB	2.03	0.58
1:LA:218:VAL:HG23	1:LA:219:ILE:HG13	1.84	0.58
6:AY:1711:THR:HG22	6:AY:1744:SER:H	1.69	0.58
2:Am:203:GLU:O	2:Am:207:ASN:ND2	2.37	0.58
3:CT:237:ILE:O	3:CT:241:ILE:HB	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ED:128:ARG:NH1	1:ED:132:THR:OG1	2.36	0.58
3:Ft:106:LYS:NZ	3:Ft:110:GLN:OE1	2.36	0.58
2:JM:205:SER:OG	2:JM:268:ARG:O	2.21	0.58
6:JY:1711:THR:HG22	6:JY:1744:SER:H	1.69	0.58
2:KM:219:ASN:HB3	2:KM:222:TYR:HB3	1.86	0.58
3:Kt:32:LYS:NZ	3:LT:47:TYR:OH	2.36	0.58
2:Am:197:TYR:HB2	2:Am:238:ILE:HG21	1.86	0.58
2:CM:205:SER:OG	2:CM:268:ARG:O	2.21	0.58
5:CX:404:TYR:HB3	3:DT:36:TYR:HB3	1.85	0.58
6:IY:1711:THR:HG22	6:IY:1744:SER:H	1.69	0.58
1:JA:218:VAL:HG23	1:JA:219:ILE:HG13	1.84	0.58
2:Jm:298:LEU:HB2	2:Jm:303:LYS:HE3	1.86	0.58
3:Jt:106:LYS:NZ	3:Jt:110:GLN:OE1	2.36	0.58
1:KA:218:VAL:HG23	1:KA:219:ILE:HG13	1.84	0.58
5:LX:505:ASN:ND2	5:LX:508:GLU:OE2	2.33	0.58
1:NC:138:ILE:O	1:NC:176:ALA:HA	2.03	0.58
2:FM:358:PHE:HA	2:FM:361:VAL:HG12	1.86	0.58
1:HB:121:GLU:HG3	1:HC:124:ILE:HD12	1.86	0.58
2:HM:308:LEU:HD21	3:Ht:232:MET:HG2	1.85	0.58
2:Hm:346:THR:HA	2:Hm:350:GLU:HB2	1.86	0.58
1:IA:218:VAL:HG23	1:IA:219:ILE:HG13	1.84	0.58
3:Kt:106:LYS:NZ	3:Kt:110:GLN:OE1	2.36	0.58
3:MT:211:THR:O	1:NA:159:ARG:NH2	2.37	0.58
6:NY:1711:THR:HG22	6:NY:1744:SER:H	1.69	0.58
2:Cm:197:TYR:HB2	2:Cm:238:ILE:HG21	1.86	0.57
2:DM:214:ARG:NH2	2:DM:216:GLU:O	2.37	0.57
5:GX:408:GLU:OE1	3:HT:32:LYS:N	2.35	0.57
3:Ht:106:LYS:NZ	3:Ht:110:GLN:OE1	2.36	0.57
1:JA:295:LEU:HD12	1:JC:163:PHE:HB2	1.85	0.57
3:KT:237:ILE:O	3:KT:241:ILE:HB	2.03	0.57
1:MD:114:TYR:HA	1:MD:117:TYR:HB3	1.86	0.57
3:Mt:106:LYS:NZ	3:Mt:110:GLN:OE1	2.36	0.57
1:AE:105:TYR:CE2	1:AE:107:TYR:HB2	2.39	0.57
1:BE:117:TYR:O	1:BE:121:GLU:HB2	2.04	0.57
1:CA:130:MET:HG3	3:Ct:63:VAL:HG21	1.85	0.57
1:DA:130:MET:HG3	3:Dt:63:VAL:HG21	1.85	0.57
1:ID:178:PHE:CE1	1:IE:107:TYR:HB3	2.39	0.57
1:JD:128:ARG:NH1	1:JD:157:ASN:OD1	2.36	0.57
1:LB:150:TYR:OH	1:LB:154:LYS:NZ	2.36	0.57
1:MD:167:ILE:HB	1:NA:194:LYS:HZ2	1.68	0.57
5:MX:349:ALA:O	5:MX:353:ARG:NH2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Mm:197:TYR:HB2	2:Mm:238:ILE:HG21	1.87	0.57
1:AA:192:LEU:HD12	1:NC:126:LYS:HD2	1.86	0.57
6:AY:1736:THR:HG22	6:AY:1765:PRO:HD2	1.86	0.57
5:BX:404:TYR:HB3	3:CT:36:TYR:HB3	1.85	0.57
6:BY:1711:THR:HG22	6:BY:1744:SER:H	1.69	0.57
1:DE:157:ASN:HD21	1:DE:161:ALA:H	1.52	0.57
6:GY:1711:THR:HG22	6:GY:1744:SER:H	1.69	0.57
1:IB:126:LYS:HD3	1:IB:184:ARG:HH22	1.68	0.57
2:JM:308:LEU:HD21	3:Jt:232:MET:HG2	1.85	0.57
5:KX:404:TYR:HB3	3:LT:36:TYR:HB3	1.87	0.57
1:LC:131:GLY:HA3	1:LC:153:LEU:HD22	1.86	0.57
6:MY:1711:THR:HG22	6:MY:1744:SER:H	1.69	0.57
2:Bm:343:ASP:HB2	2:Bm:344:LYS:HB2	1.87	0.57
3:Ct:32:LYS:NZ	3:DT:47:TYR:OH	2.37	0.57
1:EB:132:THR:HA	1:EB:157:ASN:HA	1.85	0.57
2:EM:205:SER:OG	2:EM:268:ARG:O	2.22	0.57
2:Gm:283:ASP:HA	2:Gm:286:LEU:HD13	1.85	0.57
2:HM:310:VAL:HG21	2:HM:358:PHE:HE1	1.69	0.57
3:IT:211:THR:O	1:JA:183:LYS:NZ	2.38	0.57
5:IX:408:GLU:OE1	3:JT:32:LYS:N	2.34	0.57
2:KM:308:LEU:HD21	3:Kt:232:MET:HG2	1.86	0.57
3:LT:237:ILE:O	3:LT:241:ILE:HB	2.03	0.57
6:NY:1736:THR:HG22	6:NY:1765:PRO:HD2	1.86	0.57
5:AX:349:ALA:O	5:AX:353:ARG:NH2	2.35	0.57
2:Am:282:ASP:HB3	2:Am:285:GLU:H	1.68	0.57
1:CD:140:THR:HA	1:CD:166:LYS:O	2.04	0.57
1:EA:295:LEU:HD12	1:EC:163:PHE:HB2	1.87	0.57
3:ET:184:GLU:OE1	3:ET:187:ARG:NH1	2.26	0.57
1:FC:133:TYR:HB3	1:FC:181:VAL:HG21	1.86	0.57
2:FM:308:LEU:HD21	3:Ft:232:MET:HG2	1.86	0.57
2:Hm:203:GLU:O	2:Hm:207:ASN:ND2	2.37	0.57
2:JM:263:ASN:O	2:JM:267:LEU:HB2	2.05	0.57
5:KX:505:ASN:ND2	5:KX:508:GLU:OE2	2.33	0.57
1:LE:140:THR:HG23	1:LE:166:LYS:HB2	1.87	0.57
3:Mt:217:GLN:HB3	3:NT:269:LEU:HB3	1.86	0.57
3:Nt:106:LYS:NZ	3:Nt:110:GLN:OE1	2.36	0.57
6:BY:1736:THR:HG22	6:BY:1765:PRO:HD2	1.86	0.57
2:CM:263:ASN:O	2:CM:267:LEU:HB2	2.03	0.57
2:Cm:346:THR:HA	2:Cm:350:GLU:HB2	1.86	0.57
2:Dm:215:LYS:NZ	2:Dm:295:ASN:O	2.34	0.57
1:HE:126:LYS:O	1:HE:130:MET:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IM:221:ASP:N	2:IM:221:ASP:OD1	2.38	0.57
1:KB:120:ILE:HG13	3:KT:242:PHE:HE1	1.69	0.57
1:LB:124:ILE:HG13	1:LC:124:ILE:HD11	1.87	0.57
1:MD:105:TYR:CE1	1:ME:130:MET:HE1	2.40	0.57
1:ME:109:MET:HE1	1:ME:111:LEU:HD13	1.87	0.57
6:MY:1736:THR:HG22	6:MY:1765:PRO:HD2	1.86	0.57
1:AC:147:ASN:O	1:AC:151:ASN:ND2	2.38	0.57
3:AT:237:ILE:O	3:AT:241:ILE:HB	2.04	0.57
2:CM:308:LEU:HD21	3:Ct:232:MET:HG2	1.85	0.57
6:CY:1711:THR:HG22	6:CY:1744:SER:H	1.69	0.57
1:FA:295:LEU:HD12	1:FC:163:PHE:HB2	1.85	0.57
2:GM:308:LEU:HD21	3:Gt:232:MET:HG2	1.86	0.57
3:MT:237:ILE:O	3:MT:241:ILE:HB	2.03	0.57
1:NC:146:VAL:HB	1:NC:165:LEU:HD12	1.87	0.57
6:CY:1736:THR:HG22	6:CY:1765:PRO:HD2	1.86	0.57
2:DM:358:PHE:HA	2:DM:361:VAL:HG12	1.87	0.57
1:FA:248:ASN:HA	1:FB:187:PRO:HB2	1.86	0.57
1:HA:130:MET:HG3	3:Ht:63:VAL:HG21	1.85	0.57
1:HD:140:THR:HG22	1:HD:166:LYS:HB2	1.86	0.57
2:Hm:343:ASP:HB2	2:Hm:344:LYS:HB2	1.86	0.57
2:IM:192:ARG:HE	2:IM:195:LEU:HD21	1.69	0.57
3:It:106:LYS:NZ	3:It:110:GLN:OE1	2.36	0.57
1:LB:120:ILE:HG13	3:LT:242:PHE:HE1	1.69	0.57
5:LX:404:TYR:HB3	3:MT:36:TYR:HB3	1.87	0.57
3:Lt:106:LYS:NZ	3:Lt:110:GLN:OE1	2.36	0.57
5:MX:435:LEU:HD23	5:MX:480:LYS:HE2	1.87	0.57
2:Mm:203:GLU:O	2:Mm:207:ASN:ND2	2.38	0.57
3:Nt:73:TYR:O	3:Nt:77:ASN:HB2	2.05	0.57
1:AA:295:LEU:HD12	1:AC:163:PHE:HB2	1.86	0.57
2:AM:310:VAL:HG21	2:AM:358:PHE:HE1	1.69	0.57
3:At:73:TYR:O	3:At:77:ASN:HB2	2.05	0.57
1:EC:146:VAL:HB	1:EC:165:LEU:HD12	1.87	0.57
5:FX:505:ASN:ND2	5:FX:508:GLU:OE2	2.33	0.57
3:Gt:32:LYS:NZ	3:HT:47:TYR:OH	2.38	0.57
1:JA:130:MET:HG3	3:Jt:63:VAL:HG21	1.85	0.57
1:KA:130:MET:HG3	3:Kt:63:VAL:HG21	1.85	0.57
6:LY:1736:THR:HG22	6:LY:1765:PRO:HD2	1.86	0.57
2:Mm:195:LEU:HD23	2:Mm:198:LYS:HD2	1.87	0.57
3:NT:237:ILE:O	3:NT:241:ILE:HB	2.04	0.57
2:Nm:215:LYS:NZ	2:Nm:295:ASN:O	2.34	0.57
3:BT:237:ILE:O	3:BT:241:ILE:HB	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BX:435:LEU:HD23	5:BX:480:LYS:HE2	1.87	0.57
6:DY:1736:THR:HG22	6:DY:1765:PRO:HD2	1.86	0.57
1:EA:245:GLN:OE1	1:EB:126:LYS:NZ	2.35	0.57
3:ET:211:THR:O	1:FA:159:ARG:NH2	2.37	0.57
2:GM:189:LYS:HA	2:GM:192:ARG:HG3	1.87	0.57
2:GM:221:ASP:N	2:GM:221:ASP:OD1	2.38	0.57
3:Kt:217:GLN:HB3	3:LT:269:LEU:HB3	1.87	0.57
1:MD:140:THR:HA	1:MD:166:LYS:O	2.04	0.57
1:AA:130:MET:HG3	3:At:63:VAL:HG21	1.86	0.56
1:AD:154:LYS:HA	1:AD:158:LYS:HG3	1.87	0.56
3:AT:47:TYR:OH	3:Nt:32:LYS:NZ	2.37	0.56
5:AX:435:LEU:HD23	5:AX:480:LYS:HE2	1.87	0.56
2:Bm:282:ASP:HB3	2:Bm:285:GLU:H	1.69	0.56
2:DM:263:ASN:O	2:DM:267:LEU:HB2	2.04	0.56
6:DY:1908:SER:O	5:EX:379:GLN:NE2	2.38	0.56
5:EX:455:ILE:HB	6:EY:1765:PRO:HB3	1.86	0.56
6:FY:1711:THR:HG22	6:FY:1744:SER:H	1.69	0.56
1:HD:177:THR:HA	1:HE:107:TYR:O	2.05	0.56
6:HY:1736:THR:HG22	6:HY:1765:PRO:HD2	1.86	0.56
2:Im:299:SER:H	2:Im:302:GLN:HE21	1.53	0.56
6:JY:1736:THR:HG22	6:JY:1765:PRO:HD2	1.86	0.56
6:KY:1736:THR:HG22	6:KY:1765:PRO:HD2	1.86	0.56
3:Kt:73:TYR:O	3:Kt:77:ASN:HB2	2.05	0.56
1:AA:183:LYS:NZ	3:NT:211:THR:O	2.38	0.56
2:AM:240:GLN:O	2:AM:244:ASN:ND2	2.38	0.56
1:BA:295:LEU:HD12	1:BC:163:PHE:HB2	1.85	0.56
1:BD:167:ILE:HB	1:CA:194:LYS:HZ2	1.70	0.56
5:BX:505:ASN:ND2	5:BX:508:GLU:OE2	2.33	0.56
6:EY:1736:THR:HG22	6:EY:1765:PRO:HD2	1.86	0.56
3:Et:217:GLN:HB3	3:FT:269:LEU:HB3	1.86	0.56
1:FC:147:ASN:O	1:FC:151:ASN:HB2	2.05	0.56
2:GM:205:SER:OG	2:GM:268:ARG:O	2.22	0.56
2:GM:338:ASP:HB3	2:GM:341:MET:HG2	1.86	0.56
6:GY:1736:THR:HG22	6:GY:1765:PRO:HD2	1.86	0.56
2:HM:240:GLN:O	2:HM:244:ASN:ND2	2.38	0.56
1:JD:130:MET:HA	1:JD:133:TYR:H	1.70	0.56
1:KC:138:ILE:O	1:KC:176:ALA:HA	2.04	0.56
1:MB:155:ALA:HA	3:Mt:179:LYS:HE2	1.85	0.56
2:NM:205:SER:OG	2:NM:268:ARG:O	2.21	0.56
5:NX:349:ALA:O	5:NX:353:ARG:NH2	2.35	0.56
1:AD:80:ILE:HG13	1:AE:106:LEU:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Bt:217:GLN:HB3	3:CT:269:LEU:HB3	1.86	0.56
5:DX:435:LEU:HD23	5:DX:480:LYS:HE2	1.87	0.56
2:Dm:298:LEU:HB2	2:Dm:303:LYS:HE3	1.87	0.56
3:Dt:73:TYR:O	3:Dt:77:ASN:HB2	2.05	0.56
1:EB:150:TYR:OH	1:EB:154:LYS:NZ	2.37	0.56
2:EM:263:ASN:O	2:EM:267:LEU:HB2	2.06	0.56
2:EM:308:LEU:HD21	3:Et:232:MET:HG2	1.86	0.56
1:FC:140:THR:HG23	1:FC:166:LYS:HB2	1.87	0.56
6:FY:1736:THR:HG22	6:FY:1765:PRO:HD2	1.86	0.56
2:Fm:203:GLU:O	2:Fm:207:ASN:ND2	2.39	0.56
3:HT:54:ASP:HA	3:HT:57:LYS:HE2	1.88	0.56
1:IA:111:LEU:HD11	3:It:133:MET:HB2	1.88	0.56
1:IE:117:TYR:O	1:IE:121:GLU:HB2	2.05	0.56
6:IY:1736:THR:HG22	6:IY:1765:PRO:HD2	1.86	0.56
3:Jt:73:TYR:O	3:Jt:77:ASN:HB2	2.05	0.56
1:KA:175:GLN:NE2	3:Kt:64:GLN:OE1	2.39	0.56
5:KX:349:ALA:O	5:KX:353:ARG:NH2	2.35	0.56
2:Km:346:THR:HA	2:Km:350:GLU:HB2	1.87	0.56
2:LM:263:ASN:O	2:LM:267:LEU:HB2	2.04	0.56
1:MA:80:ILE:O	3:Mt:64:GLN:NE2	2.37	0.56
2:Mm:338:ASP:HB3	2:Mm:340:MET:HE3	1.87	0.56
2:Nm:308:LEU:HD21	3:Nt:232:MET:HG2	1.85	0.56
4:Au:610:UNK:HA	2:Am:212:LEU:HD21	1.87	0.56
2:Am:346:THR:HA	2:Am:350:GLU:HB2	1.87	0.56
5:BX:349:ALA:O	5:BX:353:ARG:NH2	2.35	0.56
3:Et:73:TYR:O	3:Et:77:ASN:HB2	2.05	0.56
3:Ft:73:TYR:O	3:Ft:77:ASN:HB2	2.05	0.56
2:GM:280:VAL:HG23	2:GM:285:GLU:HG2	1.87	0.56
3:HT:211:THR:O	1:IA:183:LYS:NZ	2.39	0.56
3:IT:54:ASP:HA	3:IT:57:LYS:HE2	1.88	0.56
2:Im:203:GLU:O	2:Im:207:ASN:ND2	2.39	0.56
1:KA:295:LEU:HD12	1:KC:163:PHE:HB2	1.86	0.56
3:MT:54:ASP:HA	3:MT:57:LYS:HE2	1.88	0.56
3:NT:54:ASP:HA	3:NT:57:LYS:HE2	1.88	0.56
3:AT:54:ASP:HA	3:AT:57:LYS:HE2	1.88	0.56
2:Cm:203:GLU:O	2:Cm:207:ASN:ND2	2.39	0.56
2:Cm:282:ASP:HB3	2:Cm:285:GLU:H	1.71	0.56
2:Fm:197:TYR:HB2	2:Fm:238:ILE:HG21	1.88	0.56
3:GT:54:ASP:HA	3:GT:57:LYS:HE2	1.88	0.56
3:GT:211:THR:O	1:HA:183:LYS:NZ	2.37	0.56
3:Gt:73:TYR:O	3:Gt:77:ASN:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Ht:73:TYR:O	3:Ht:77:ASN:HB2	2.05	0.56
3:Jt:217:GLN:HB3	3:KT:269:LEU:HB3	1.87	0.56
1:KB:110:ASP:OD2	1:KB:111:LEU:N	2.34	0.56
3:AT:269:LEU:HB3	3:Nt:217:GLN:HB3	1.87	0.56
3:BT:54:ASP:HA	3:BT:57:LYS:HE2	1.88	0.56
1:FA:209:LYS:NZ	1:FA:236:ALA:O	2.39	0.56
3:Gt:217:GLN:HB3	3:HT:269:LEU:HB3	1.86	0.56
3:JT:54:ASP:HA	3:JT:57:LYS:HE2	1.88	0.56
5:KX:435:LEU:HD23	5:KX:480:LYS:HE2	1.87	0.56
5:LX:349:ALA:O	5:LX:353:ARG:NH2	2.35	0.56
1:AA:194:LYS:HZ2	1:ND:167:ILE:HB	1.71	0.56
5:DX:404:TYR:HB3	3:ET:36:TYR:HB3	1.85	0.56
2:Gm:203:GLU:O	2:Gm:207:ASN:ND2	2.38	0.56
1:HA:209:LYS:NZ	1:HA:236:ALA:O	2.39	0.56
1:ID:158:LYS:NZ	1:ID:159:ARG:O	2.38	0.56
2:IM:310:VAL:HG21	2:IM:358:PHE:HE1	1.69	0.56
2:Im:282:ASP:HB3	2:Im:285:GLU:H	1.70	0.56
3:Lt:73:TYR:O	3:Lt:77:ASN:HB2	2.05	0.56
3:MT:184:GLU:OE1	3:MT:187:ARG:NH1	2.26	0.56
3:Mt:73:TYR:O	3:Mt:77:ASN:HB2	2.05	0.56
2:Nm:221:ASP:OD2	2:Nm:222:TYR:N	2.39	0.56
5:NX:435:LEU:HD23	5:NX:480:LYS:HE2	1.87	0.56
2:Nm:203:GLU:O	2:Nm:207:ASN:ND2	2.38	0.56
2:BM:205:SER:OG	2:BM:268:ARG:O	2.23	0.56
3:Bt:73:TYR:O	3:Bt:77:ASN:HB2	2.05	0.56
3:FT:54:ASP:HA	3:FT:57:LYS:HE2	1.88	0.56
1:IB:155:ALA:HA	3:It:179:LYS:HE2	1.87	0.56
2:JM:358:PHE:HA	2:JM:361:VAL:HG12	1.88	0.56
3:LT:54:ASP:HA	3:LT:57:LYS:HE2	1.88	0.56
1:NA:111:LEU:HD11	3:Nt:133:MET:HB2	1.87	0.56
1:CA:209:LYS:NZ	1:CA:236:ALA:O	2.39	0.56
1:CD:143:LEU:HD11	3:DT:268:TYR:CD1	2.40	0.56
1:DA:209:LYS:NZ	1:DA:236:ALA:O	2.39	0.56
2:DM:333:ILE:O	2:DM:337:SER:HB3	2.06	0.56
2:EM:358:PHE:HA	2:EM:361:VAL:HG12	1.88	0.56
2:GM:344:LYS:HB2	2:GM:349:LYS:HE3	1.88	0.56
2:HM:358:PHE:HA	2:HM:361:VAL:HG12	1.88	0.56
2:IM:358:PHE:HA	2:IM:361:VAL:HG12	1.88	0.56
3:JT:211:THR:O	1:KA:183:LYS:NZ	2.39	0.56
3:KT:211:THR:O	1:LA:183:LYS:NZ	2.38	0.56
1:AB:158:LYS:NZ	1:AC:193:ASP:OD2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AX:453:ALA:O	6:AY:1737:LYS:NZ	2.39	0.56
1:CA:175:GLN:NE2	3:Ct:64:GLN:OE1	2.39	0.56
3:CT:54:ASP:HA	3:CT:57:LYS:HE2	1.88	0.56
3:Ct:73:TYR:O	3:Ct:77:ASN:HB2	2.05	0.56
1:DA:295:LEU:HD12	1:DC:163:PHE:HB2	1.86	0.56
3:DT:184:GLU:OE1	3:DT:187:ARG:NH1	2.27	0.56
2:Dm:203:GLU:O	2:Dm:207:ASN:ND2	2.39	0.56
2:Dm:343:ASP:HB2	2:Dm:344:LYS:HB2	1.87	0.56
2:Fm:338:ASP:HB3	2:Fm:340:MET:HE3	1.87	0.56
1:HA:175:GLN:NE2	3:Ht:64:GLN:OE1	2.39	0.56
2:Hm:294:THR:O	2:Hm:303:LYS:NZ	2.38	0.56
1:IA:62:LYS:HG2	1:IA:221:ARG:HH22	1.71	0.56
1:IB:158:LYS:NZ	1:IC:193:ASP:OD2	2.36	0.56
1:ID:130:MET:HG2	1:ID:178:PHE:CE1	2.41	0.56
3:It:73:TYR:O	3:It:77:ASN:HB2	2.05	0.56
3:It:217:GLN:HG3	3:JT:273:ILE:HD12	1.87	0.56
2:JM:240:GLN:O	2:JM:244:ASN:ND2	2.39	0.56
3:KT:54:ASP:HA	3:KT:57:LYS:HE2	1.88	0.56
2:Lm:346:THR:HA	2:Lm:350:GLU:HB2	1.87	0.56
1:MA:209:LYS:NZ	1:MA:236:ALA:O	2.39	0.56
2:MM:308:LEU:HD21	3:Mt:232:MET:HG2	1.86	0.56
1:AB:155:ALA:HA	3:At:179:LYS:HE2	1.88	0.55
1:AD:176:ALA:HB3	1:AE:109:MET:HE3	1.88	0.55
3:At:217:GLN:HB3	3:BT:269:LEU:HB3	1.88	0.55
2:BM:358:PHE:HA	2:BM:361:VAL:HG12	1.88	0.55
1:DC:138:ILE:O	1:DC:176:ALA:HA	2.06	0.55
1:EA:209:LYS:NZ	1:EA:236:ALA:O	2.39	0.55
5:EX:404:TYR:HB3	3:FT:36:TYR:HB3	1.88	0.55
2:GM:358:PHE:HA	2:GM:361:VAL:HG12	1.89	0.55
2:Km:343:ASP:HB2	2:Km:344:LYS:HB2	1.88	0.55
2:LM:240:GLN:O	2:LM:244:ASN:ND2	2.39	0.55
3:LT:234:GLN:HE21	3:LT:238:SER:HG	1.54	0.55
5:LX:435:LEU:HD23	5:LX:480:LYS:HE2	1.87	0.55
1:MB:150:TYR:OH	1:MB:154:LYS:NZ	2.36	0.55
1:NA:209:LYS:NZ	1:NA:236:ALA:O	2.39	0.55
5:AX:505:ASN:ND2	5:AX:508:GLU:OE2	2.33	0.55
2:CM:240:GLN:O	2:CM:244:ASN:ND2	2.39	0.55
2:CM:358:PHE:HA	2:CM:361:VAL:HG12	1.88	0.55
3:CT:59:THR:O	3:CT:137:ASN:ND2	2.40	0.55
1:EA:62:LYS:HG2	1:EA:221:ARG:HH22	1.71	0.55
1:EB:124:ILE:HG13	1:EC:124:ILE:HD11	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:ET:54:ASP:HA	3:ET:57:LYS:HE2	1.88	0.55
1:GE:157:ASN:HD21	1:GE:161:ALA:H	1.54	0.55
3:HT:59:THR:O	3:HT:137:ASN:ND2	2.40	0.55
5:HX:349:ALA:O	5:HX:353:ARG:NH2	2.35	0.55
5:JX:435:LEU:HD23	5:JX:480:LYS:HE2	1.87	0.55
2:Km:203:GLU:O	2:Km:207:ASN:ND2	2.39	0.55
3:MT:59:THR:O	3:MT:137:ASN:ND2	2.40	0.55
5:CX:349:ALA:O	5:CX:353:ARG:NH2	2.35	0.55
3:DT:59:THR:O	3:DT:137:ASN:ND2	2.40	0.55
1:GE:109:MET:HE1	1:GE:111:LEU:HD13	1.89	0.55
3:GT:59:THR:O	3:GT:137:ASN:ND2	2.40	0.55
1:HC:146:VAL:HB	1:HC:165:LEU:HD12	1.87	0.55
1:IA:209:LYS:NZ	1:IA:236:ALA:O	2.39	0.55
1:IC:140:THR:HG22	1:IC:166:LYS:HB2	1.89	0.55
3:KT:59:THR:O	3:KT:137:ASN:ND2	2.40	0.55
1:AA:107:TYR:CG	3:At:44:ILE:HD11	2.42	0.55
1:AA:209:LYS:NZ	1:AA:236:ALA:O	2.39	0.55
3:BT:59:THR:O	3:BT:137:ASN:ND2	2.40	0.55
2:Bm:203:GLU:O	2:Bm:207:ASN:ND2	2.39	0.55
3:DT:54:ASP:HA	3:DT:57:LYS:HE2	1.88	0.55
1:EA:107:TYR:CG	3:Et:44:ILE:HD11	2.41	0.55
2:EM:240:GLN:O	2:EM:244:ASN:ND2	2.39	0.55
5:FX:435:LEU:HD23	5:FX:480:LYS:HE2	1.87	0.55
1:GD:100:LEU:HG	1:GD:101:LYS:HD2	1.87	0.55
5:HX:435:LEU:HD23	5:HX:480:LYS:HE2	1.87	0.55
1:JA:175:GLN:NE2	3:Jt:64:GLN:OE1	2.39	0.55
1:KC:146:VAL:HB	1:KC:165:LEU:HD12	1.88	0.55
1:LA:209:LYS:NZ	1:LA:236:ALA:O	2.39	0.55
3:LT:59:THR:O	3:LT:137:ASN:ND2	2.40	0.55
1:MA:82:ASP:OD1	1:MA:126:LYS:NZ	2.38	0.55
2:MM:341:MET:HG3	2:MM:344:LYS:HZ1	1.71	0.55
1:ND:100:LEU:HG	1:ND:101:LYS:HD2	1.87	0.55
2:AM:358:PHE:HA	2:AM:361:VAL:HG12	1.89	0.55
3:AT:36:TYR:HB3	5:NX:404:TYR:HB3	1.87	0.55
1:FD:178:PHE:CE1	1:FE:107:TYR:HB3	2.41	0.55
1:GA:62:LYS:HG2	1:GA:221:ARG:HH22	1.71	0.55
3:Ht:217:GLN:HB3	3:IT:269:LEU:HB3	1.87	0.55
1:IC:130:MET:HE1	1:IC:182:PRO:HB3	1.88	0.55
1:JA:62:LYS:HG2	1:JA:221:ARG:HH22	1.71	0.55
1:JD:128:ARG:HH22	1:JE:87:ASN:HB3	1.71	0.55
5:JX:408:GLU:OE1	3:KT:32:LYS:N	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KA:209:LYS:NZ	1:KA:236:ALA:O	2.39	0.55
2:Am:294:THR:O	2:Am:303:LYS:NZ	2.39	0.55
5:CX:435:LEU:HD23	5:CX:480:LYS:HE2	1.87	0.55
2:DM:219:ASN:HB3	2:DM:222:TYR:HB3	1.88	0.55
2:Em:203:GLU:O	2:Em:207:ASN:ND2	2.39	0.55
1:GA:209:LYS:NZ	1:GA:236:ALA:O	2.39	0.55
1:GB:136:LEU:HB3	1:GB:179:LEU:HB2	1.87	0.55
5:GX:435:LEU:HD23	5:GX:480:LYS:HE2	1.87	0.55
1:HA:62:LYS:HG2	1:HA:221:ARG:HH22	1.71	0.55
1:ID:140:THR:HA	1:ID:166:LYS:O	2.07	0.55
2:IM:240:GLN:O	2:IM:244:ASN:ND2	2.40	0.55
5:JX:505:ASN:ND2	5:JX:508:GLU:OE2	2.33	0.55
2:LM:358:PHE:HA	2:LM:361:VAL:HG12	1.88	0.55
3:Mt:217:GLN:HG3	3:NT:273:ILE:HD12	1.87	0.55
1:NA:295:LEU:HD12	1:NC:163:PHE:HB2	1.87	0.55
1:NB:155:ALA:HA	3:Nt:179:LYS:HE2	1.88	0.55
3:NT:59:THR:O	3:NT:137:ASN:ND2	2.40	0.55
1:DA:62:LYS:HG2	1:DA:221:ARG:HH22	1.71	0.55
3:Dt:82:LEU:HD23	3:Dt:85:LYS:HE2	1.89	0.55
1:EC:187:PRO:HD2	1:FA:188:ASN:HA	1.88	0.55
1:FA:62:LYS:HG2	1:FA:221:ARG:HH22	1.71	0.55
2:FM:310:VAL:HG21	2:FM:358:PHE:HE1	1.71	0.55
2:FM:333:ILE:O	2:FM:337:SER:HB3	2.07	0.55
2:Hm:198:LYS:HE3	2:Hm:262:ILE:HG12	1.89	0.55
2:JM:280:VAL:HG23	2:JM:285:GLU:HG2	1.88	0.55
5:JX:349:ALA:O	5:JX:353:ARG:NH2	2.35	0.55
2:Km:215:LYS:NZ	2:Km:295:ASN:O	2.33	0.55
2:MM:358:PHE:HA	2:MM:361:VAL:HG12	1.88	0.55
2:Nm:280:VAL:HG23	2:Nm:285:GLU:HG2	1.87	0.55
2:Nm:358:PHE:HA	2:Nm:361:VAL:HG12	1.88	0.55
3:AT:59:THR:O	3:AT:137:ASN:ND2	2.40	0.55
1:BA:175:GLN:NE2	3:Bt:64:GLN:OE1	2.39	0.55
5:BX:408:GLU:OE1	3:CT:32:LYS:N	2.36	0.55
3:Ct:82:LEU:HD23	3:Ct:85:LYS:HE2	1.89	0.55
5:DX:349:ALA:O	5:DX:353:ARG:NH2	2.35	0.55
3:Dt:217:GLN:HB3	3:ET:269:LEU:HB3	1.87	0.55
5:EX:435:LEU:HD23	5:EX:480:LYS:HE2	1.87	0.55
2:FM:240:GLN:O	2:FM:244:ASN:ND2	2.40	0.55
1:GD:173:TYR:O	1:GD:175:GLN:NE2	2.38	0.55
3:IT:59:THR:O	3:IT:137:ASN:ND2	2.40	0.55
5:IX:435:LEU:HD23	5:IX:480:LYS:HE2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JD:126:LYS:O	1:JD:130:MET:HG2	2.07	0.55
3:JT:59:THR:O	3:JT:137:ASN:ND2	2.40	0.55
1:BA:209:LYS:NZ	1:BA:236:ALA:O	2.39	0.55
1:BB:143:LEU:O	1:BB:147:ASN:ND2	2.40	0.55
3:BT:211:THR:O	1:CA:183:LYS:NZ	2.38	0.55
1:EA:80:ILE:O	3:Et:64:GLN:NE2	2.39	0.55
3:Et:82:LEU:HD23	3:Et:85:LYS:HE2	1.89	0.55
1:JA:209:LYS:NZ	1:JA:236:ALA:O	2.39	0.55
2:KM:333:ILE:O	2:KM:337:SER:HB3	2.07	0.55
2:KM:358:PHE:HA	2:KM:361:VAL:HG12	1.88	0.55
2:Bm:298:LEU:HB2	2:Bm:303:LYS:HE3	1.89	0.55
3:CT:234:GLN:HE21	3:CT:238:SER:HG	1.54	0.55
2:DM:205:SER:HA	2:DM:208:VAL:HG12	1.89	0.55
5:EX:505:ASN:ND2	5:EX:508:GLU:OE2	2.33	0.55
3:Ft:82:LEU:HD23	3:Ft:85:LYS:HE2	1.89	0.55
1:GA:133:TYR:HD2	3:Gt:56:LEU:HD22	1.71	0.55
2:Lm:195:LEU:HD23	2:Lm:198:LYS:HD2	1.88	0.55
1:AA:199:ASP:HA	1:AA:203:LEU:HD23	1.89	0.54
1:AB:132:THR:HA	1:AB:157:ASN:HA	1.89	0.54
1:BA:199:ASP:HA	1:BA:203:LEU:HD23	1.89	0.54
2:Bm:195:LEU:HD23	2:Bm:198:LYS:HD2	1.89	0.54
3:Bt:82:LEU:HD23	3:Bt:85:LYS:HE2	1.89	0.54
1:CA:199:ASP:HA	1:CA:203:LEU:HD23	1.89	0.54
1:DA:175:GLN:NE2	3:Dt:64:GLN:OE1	2.39	0.54
1:DA:294:GLN:O	1:DC:162:LYS:NZ	2.40	0.54
3:ET:59:THR:O	3:ET:137:ASN:ND2	2.40	0.54
3:FT:59:THR:O	3:FT:137:ASN:ND2	2.40	0.54
2:KM:240:GLN:O	2:KM:244:ASN:ND2	2.40	0.54
5:KX:408:GLU:OE1	3:LT:32:LYS:N	2.36	0.54
1:NC:140:THR:HG22	1:NC:166:LYS:HB2	1.89	0.54
1:BD:158:LYS:NZ	1:BD:159:ARG:O	2.40	0.54
3:CT:211:THR:O	1:DA:183:LYS:NZ	2.38	0.54
1:DA:143:LEU:HD22	1:DB:150:TYR:CE2	2.42	0.54
1:DA:199:ASP:HA	1:DA:203:LEU:HD23	1.89	0.54
1:DC:146:VAL:HB	1:DC:165:LEU:HD12	1.89	0.54
3:GT:274:ARG:O	3:GT:278:SER:CB	2.56	0.54
3:Gt:82:LEU:HD23	3:Gt:85:LYS:HE2	1.89	0.54
1:HC:169:GLU:OE2	3:Ht:233:ARG:NH2	2.40	0.54
3:IT:184:GLU:OE1	3:IT:187:ARG:NH1	2.27	0.54
3:It:217:GLN:HB3	3:JT:269:LEU:HB3	1.87	0.54
2:Jm:203:GLU:O	2:Jm:207:ASN:ND2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Lm:203:GLU:O	2:Lm:207:ASN:ND2	2.41	0.54
1:MB:182:PRO:HG3	1:MC:107:TYR:HB2	1.90	0.54
2:BM:221:ASP:OD1	2:BM:221:ASP:N	2.39	0.54
2:DM:310:VAL:HG21	2:DM:358:PHE:HE1	1.71	0.54
3:ET:274:ARG:O	3:ET:278:SER:CB	2.56	0.54
3:Ft:217:GLN:HB3	3:GT:269:LEU:HB3	1.88	0.54
3:IT:274:ARG:O	3:IT:278:SER:CB	2.56	0.54
2:JM:212:LEU:HG	2:JM:270:TYR:HB2	1.89	0.54
1:KA:62:LYS:HG2	1:KA:221:ARG:HH22	1.71	0.54
2:Km:282:ASP:HB3	2:Km:285:GLU:H	1.71	0.54
1:NA:199:ASP:HA	1:NA:203:LEU:HD23	1.89	0.54
2:BM:240:GLN:O	2:BM:244:ASN:ND2	2.40	0.54
2:DM:240:GLN:O	2:DM:244:ASN:ND2	2.40	0.54
2:Fm:195:LEU:HD23	2:Fm:198:LYS:HD2	1.89	0.54
3:Ht:82:LEU:HD23	3:Ht:85:LYS:HE2	1.89	0.54
1:IB:136:LEU:HB3	1:IB:179:LEU:HB2	1.88	0.54
5:IX:404:TYR:HB3	3:JT:36:TYR:HB3	1.89	0.54
1:ND:154:LYS:HA	1:ND:158:LYS:HG3	1.88	0.54
2:Am:343:ASP:HB2	2:Am:344:LYS:HB2	1.89	0.54
3:At:82:LEU:HD23	3:At:85:LYS:HE2	1.89	0.54
1:DD:133:TYR:HD1	1:DE:101:LYS:HE2	1.72	0.54
1:EB:182:PRO:HG3	1:EC:107:TYR:HB2	1.89	0.54
1:FC:187:PRO:HD2	1:GA:188:ASN:HA	1.89	0.54
2:Gm:195:LEU:HD23	2:Gm:198:LYS:HD2	1.89	0.54
1:MA:199:ASP:HA	1:MA:203:LEU:HD23	1.89	0.54
2:MM:310:VAL:HG21	2:MM:358:PHE:HE1	1.72	0.54
1:BC:146:VAL:HB	1:BC:165:LEU:HD12	1.90	0.54
1:DA:248:ASN:HA	1:DB:187:PRO:HB2	1.90	0.54
1:DD:80:ILE:HA	1:DE:106:LEU:O	2.08	0.54
1:EA:199:ASP:HA	1:EA:203:LEU:HD23	1.89	0.54
1:EB:122:ASN:O	1:EB:126:LYS:HB2	2.08	0.54
1:FA:107:TYR:CG	3:Ft:44:ILE:HD11	2.43	0.54
1:FB:128:ARG:HA	1:FB:156:LEU:HD21	1.90	0.54
5:FX:349:ALA:O	5:FX:353:ARG:NH2	2.35	0.54
6:IY:1908:SER:O	5:JX:379:GLN:NE2	2.41	0.54
3:It:82:LEU:HD23	3:It:85:LYS:HE2	1.89	0.54
3:JT:234:GLN:HE21	3:JT:238:SER:HG	1.55	0.54
1:MA:62:LYS:HG2	1:MA:221:ARG:HH22	1.71	0.54
1:NA:62:LYS:HG2	1:NA:221:ARG:HH22	1.71	0.54
1:NA:248:ASN:HA	1:NB:187:PRO:HB2	1.89	0.54
2:NM:219:ASN:HB3	2:NM:222:TYR:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Nt:82:LEU:HD23	3:Nt:85:LYS:HE2	1.89	0.54
3:AT:184:GLU:OE1	3:AT:187:ARG:NH1	2.27	0.54
3:AT:211:THR:O	1:BA:183:LYS:NZ	2.39	0.54
1:CA:248:ASN:HA	1:CB:187:PRO:HB2	1.89	0.54
2:Cm:298:LEU:HB2	2:Cm:303:LYS:HE3	1.90	0.54
2:Cm:343:ASP:HB2	2:Cm:344:LYS:HB2	1.89	0.54
1:DD:106:LEU:HB3	1:DE:179:LEU:HD13	1.89	0.54
3:DT:274:ARG:O	3:DT:278:SER:CB	2.56	0.54
5:FX:404:TYR:HB3	3:GT:36:TYR:HB3	1.90	0.54
3:GT:234:GLN:HE21	3:GT:238:SER:HG	1.54	0.54
1:HB:182:PRO:HG3	1:HC:107:TYR:HB2	1.90	0.54
1:HD:105:TYR:CE1	1:HE:130:MET:HE1	2.42	0.54
1:HD:178:PHE:O	1:HE:106:LEU:HA	2.08	0.54
5:IX:349:ALA:O	5:IX:353:ARG:NH2	2.35	0.54
2:JM:221:ASP:N	2:JM:221:ASP:OD1	2.39	0.54
3:JT:274:ARG:O	3:JT:278:SER:CB	2.56	0.54
2:LM:242:ALA:HA	2:LM:245:THR:HG22	1.89	0.54
1:MA:234:MET:HB3	1:MB:138:ILE:HD11	1.90	0.54
2:NM:240:GLN:O	2:NM:244:ASN:ND2	2.41	0.54
1:DA:69:VAL:HG11	1:DA:211:TYR:HE1	1.73	0.54
1:DA:111:LEU:HD11	3:Dt:133:MET:HB2	1.90	0.54
1:DA:296:VAL:HG11	1:DD:80:ILE:HD13	1.89	0.54
2:DM:305:LYS:NZ	3:Dt:231:GLN:O	2.40	0.54
2:GM:205:SER:OG	2:GM:268:ARG:NH1	2.41	0.54
1:JC:130:MET:HE1	1:JC:182:PRO:HB3	1.90	0.54
1:CA:69:VAL:HG11	1:CA:211:TYR:HE1	1.73	0.54
1:CA:111:LEU:HD11	3:Ct:133:MET:HB2	1.90	0.54
1:DD:112:LEU:HD21	1:DD:117:TYR:CD1	2.43	0.54
1:FC:126:LYS:HD2	1:GA:192:LEU:HD12	1.89	0.54
2:Hm:338:ASP:HB3	2:Hm:340:MET:HE3	1.89	0.54
1:IC:138:ILE:O	1:IC:176:ALA:HA	2.07	0.54
1:JA:111:LEU:HD11	3:Jt:133:MET:HB2	1.90	0.54
3:Jt:82:LEU:HD23	3:Jt:85:LYS:HE2	1.89	0.54
3:LT:184:GLU:OE1	3:LT:187:ARG:NH1	2.26	0.54
3:Lt:82:LEU:HD23	3:Lt:85:LYS:HE2	1.89	0.54
3:Mt:82:LEU:HD23	3:Mt:85:LYS:HE2	1.89	0.54
1:AA:62:LYS:HG2	1:AA:221:ARG:HH22	1.71	0.54
1:AB:136:LEU:HB3	1:AB:179:LEU:HB2	1.90	0.54
3:CT:184:GLU:OE1	3:CT:187:ARG:NH1	2.26	0.54
2:Cm:195:LEU:HD23	2:Cm:198:LYS:HD2	1.90	0.54
1:DD:129:ALA:O	1:DD:133:TYR:CB	2.52	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ED:126:LYS:O	1:ED:130:MET:HG3	2.08	0.54
1:ED:137:ILE:O	1:ED:163:PHE:HA	2.07	0.54
1:FC:122:ASN:O	1:FC:126:LYS:HB2	2.07	0.54
2:Fm:273:PHE:HD2	2:Fm:310:VAL:HG11	1.73	0.54
2:GM:240:GLN:O	2:GM:244:ASN:ND2	2.41	0.54
1:HA:248:ASN:HA	1:HB:187:PRO:HB2	1.90	0.54
3:Kt:82:LEU:HD23	3:Kt:85:LYS:HE2	1.89	0.54
1:LA:62:LYS:HG2	1:LA:221:ARG:HH22	1.71	0.54
3:LT:274:ARG:O	3:LT:278:SER:CB	2.56	0.54
1:MA:130:MET:HG3	3:Mt:63:VAL:HG21	1.89	0.54
2:MM:240:GLN:O	2:MM:244:ASN:ND2	2.41	0.54
1:NB:150:TYR:OH	1:NB:154:LYS:NZ	2.39	0.54
3:NT:234:GLN:HE21	3:NT:238:SER:HG	1.54	0.54
1:AA:296:VAL:HB	1:AC:164:VAL:HG12	1.88	0.53
2:Am:220:ILE:HG13	2:Am:224:LEU:HD23	1.90	0.53
3:BT:274:ARG:O	3:BT:278:SER:CB	2.56	0.53
1:CA:62:LYS:HG2	1:CA:221:ARG:HH22	1.71	0.53
1:FA:199:ASP:HA	1:FA:203:LEU:HD23	1.89	0.53
3:FT:274:ARG:O	3:FT:278:SER:CB	2.56	0.53
1:HA:69:VAL:HG11	1:HA:211:TYR:HE1	1.73	0.53
1:HA:111:LEU:HD11	3:Ht:133:MET:HB2	1.90	0.53
1:JA:248:ASN:HA	1:JB:187:PRO:HB2	1.89	0.53
3:KT:234:GLN:HE21	3:KT:238:SER:HG	1.55	0.53
1:LA:199:ASP:HA	1:LA:203:LEU:HD23	1.89	0.53
2:Lm:282:ASP:HB3	2:Lm:285:GLU:H	1.72	0.53
1:NA:107:TYR:CG	3:Nt:44:ILE:HD11	2.43	0.53
2:Nm:195:LEU:HD23	2:Nm:198:LYS:HD2	1.90	0.53
1:BA:111:LEU:HD11	3:Bt:133:MET:HB2	1.90	0.53
3:ET:54:ASP:OD2	5:EX:404:TYR:OH	2.20	0.53
2:Gm:343:ASP:HB2	2:Gm:344:LYS:HB2	1.89	0.53
1:KA:111:LEU:HD11	3:Kt:133:MET:HB2	1.90	0.53
3:KT:274:ARG:O	3:KT:278:SER:CB	2.56	0.53
2:FM:205:SER:HA	2:FM:208:VAL:HG12	1.91	0.53
5:GX:404:TYR:HB3	3:HT:36:TYR:HB3	1.90	0.53
2:KM:280:VAL:HG23	2:KM:285:GLU:HG3	1.90	0.53
3:Kt:207:GLU:OE1	3:Kt:207:GLU:N	2.29	0.53
1:NA:80:ILE:O	3:Nt:64:GLN:NE2	2.39	0.53
1:NB:136:LEU:HB3	1:NB:179:LEU:HB2	1.89	0.53
1:BA:62:LYS:HG2	1:BA:221:ARG:HH22	1.71	0.53
5:CX:453:ALA:O	6:CY:1737:LYS:NZ	2.42	0.53
1:DC:169:GLU:OE2	3:Dt:233:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:69:VAL:HG11	1:EA:211:TYR:HE1	1.73	0.53
1:EE:140:THR:HG23	1:EE:166:LYS:HB2	1.90	0.53
3:Et:207:GLU:OE1	3:Et:207:GLU:N	2.29	0.53
1:GA:69:VAL:HG11	1:GA:211:TYR:HE1	1.73	0.53
2:IM:280:VAL:HG23	2:IM:285:GLU:HG2	1.90	0.53
4:LU:609:UNK:HA	2:Lm:273:PHE:HZ	1.73	0.53
1:AC:130:MET:HE1	1:AC:182:PRO:HB3	1.89	0.53
1:DB:149:TYR:HA	1:DB:152:ILE:HD12	1.90	0.53
5:EX:349:ALA:O	5:EX:353:ARG:NH2	2.35	0.53
1:FA:133:TYR:HD2	3:Ft:56:LEU:HD22	1.73	0.53
6:FY:1722:VAL:HG22	6:FY:1732:LEU:HB2	1.91	0.53
1:GA:175:GLN:NE2	3:Gt:64:GLN:OE1	2.41	0.53
1:GA:199:ASP:HA	1:GA:203:LEU:HD23	1.89	0.53
6:GY:1722:VAL:HG22	6:GY:1732:LEU:HB2	1.91	0.53
5:HX:404:TYR:HB3	3:IT:36:TYR:HB3	1.90	0.53
1:JA:296:VAL:O	1:JC:164:VAL:HA	2.08	0.53
2:Jm:332:ASN:HA	2:Jm:353:LYS:HD3	1.91	0.53
5:MX:408:GLU:OE1	3:NT:32:LYS:N	2.37	0.53
6:MY:1859:LEU:HD22	6:NY:1854:MET:HG2	1.89	0.53
3:NT:89:HIS:HE1	5:NX:401:TYR:CD2	2.27	0.53
1:AB:193:ASP:OD1	1:AB:193:ASP:N	2.42	0.53
3:AT:274:ARG:O	3:AT:278:SER:CB	2.56	0.53
1:BA:69:VAL:HG11	1:BA:211:TYR:HE1	1.73	0.53
1:DD:140:THR:HG22	1:DD:166:LYS:HB2	1.91	0.53
6:DY:1722:VAL:HG22	6:DY:1732:LEU:HB2	1.91	0.53
6:EY:1722:VAL:HG22	6:EY:1732:LEU:HB2	1.91	0.53
1:FA:69:VAL:HG11	1:FA:211:TYR:HE1	1.73	0.53
1:GE:153:LEU:HD13	1:GE:156:LEU:HD13	1.90	0.53
6:HY:1722:VAL:HG22	6:HY:1732:LEU:HB2	1.91	0.53
6:JY:1805:SER:HB2	6:JY:1855:SER:HB2	1.91	0.53
6:JY:1859:LEU:HD22	6:KY:1854:MET:HG2	1.90	0.53
3:MT:274:ARG:O	3:MT:278:SER:CB	2.56	0.53
1:EB:155:ALA:HA	3:Et:179:LYS:HE2	1.90	0.53
3:ET:89:HIS:HE1	5:EX:401:TYR:CD2	2.27	0.53
1:GA:111:LEU:HD11	3:Gt:133:MET:HB2	1.91	0.53
2:Gm:188:LYS:HG3	2:Gm:189:LYS:HD3	1.90	0.53
3:HT:274:ARG:O	3:HT:278:SER:CB	2.56	0.53
1:IA:69:VAL:HG11	1:IA:211:TYR:HE1	1.73	0.53
1:JC:117:TYR:O	1:JC:121:GLU:HB2	2.07	0.53
1:JE:140:THR:HG21	1:KA:278:PRO:HD3	1.90	0.53
1:KA:199:ASP:HA	1:KA:203:LEU:HD23	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:111:LEU:HD11	3:Lt:133:MET:HB2	1.91	0.53
6:LY:1805:SER:HB2	6:LY:1855:SER:HB2	1.91	0.53
2:NM:310:VAL:HG21	2:NM:358:PHE:HE1	1.72	0.53
3:AT:268:TYR:CD1	1:ND:143:LEU:HD11	2.44	0.53
5:AX:454:ALA:HB2	6:AY:1737:LYS:HE2	1.90	0.53
1:BC:140:THR:HG22	1:BC:166:LYS:HB2	1.90	0.53
2:BM:310:VAL:HG21	2:BM:358:PHE:HE1	1.73	0.53
1:CD:123:PRO:HA	1:CD:126:LYS:HE3	1.90	0.53
6:CY:1722:VAL:HG22	6:CY:1732:LEU:HB2	1.91	0.53
1:EC:169:GLU:OE2	3:Et:233:ARG:NH2	2.41	0.53
2:Em:343:ASP:HB2	2:Em:344:LYS:HB2	1.89	0.53
6:HY:1805:SER:HB2	6:HY:1855:SER:HB2	1.91	0.53
1:ID:129:ALA:O	1:ID:133:TYR:CB	2.51	0.53
1:ID:132:THR:OG1	1:ID:157:ASN:ND2	2.42	0.53
6:IY:1805:SER:HB2	6:IY:1855:SER:HB2	1.91	0.53
6:IY:1859:LEU:HD22	6:JY:1854:MET:HG2	1.90	0.53
3:JT:211:THR:O	1:KA:159:ARG:NH2	2.41	0.53
2:KM:247:ILE:O	2:KM:252:ARG:NH1	2.41	0.53
2:KM:305:LYS:NZ	3:Kt:231:GLN:O	2.38	0.53
2:NM:205:SER:OG	2:NM:268:ARG:NH1	2.41	0.53
2:AM:280:VAL:HG23	2:AM:285:GLU:HG2	1.91	0.53
2:Bm:188:LYS:HG3	2:Bm:189:LYS:HD3	1.90	0.53
1:CD:128:ARG:NH1	1:CD:157:ASN:OD1	2.39	0.53
6:IY:1722:VAL:HG22	6:IY:1732:LEU:HB2	1.91	0.53
2:Im:188:LYS:HG3	2:Im:189:LYS:HD3	1.90	0.53
1:JA:199:ASP:HA	1:JA:203:LEU:HD23	1.90	0.53
1:KA:205:GLU:HA	1:KA:208:LYS:HZ3	1.74	0.53
5:NX:453:ALA:O	6:NY:1737:LYS:NZ	2.42	0.53
1:AA:205:GLU:HA	1:AA:208:LYS:HZ3	1.74	0.53
1:BB:138:ILE:HG12	1:BB:164:VAL:HB	1.90	0.53
2:BM:263:ASN:O	2:BM:267:LEU:HB2	2.07	0.53
3:BT:184:GLU:OE1	3:BT:187:ARG:NH1	2.26	0.53
2:CM:221:ASP:OD1	2:CM:221:ASP:N	2.40	0.53
2:Dm:344:LYS:HB3	2:Dm:347:MET:HB2	1.90	0.53
2:HM:280:VAL:HG23	2:HM:285:GLU:HG2	1.91	0.53
1:IA:199:ASP:HA	1:IA:203:LEU:HD23	1.89	0.53
1:KC:133:TYR:HB3	1:KC:181:VAL:HG11	1.90	0.53
1:LC:146:VAL:HB	1:LC:165:LEU:HD12	1.91	0.53
5:MX:454:ALA:HB2	6:MY:1737:LYS:HE2	1.91	0.53
2:Mm:332:ASN:HA	2:Mm:353:LYS:HD3	1.91	0.53
1:AD:140:THR:HA	1:AD:166:LYS:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AM:333:ILE:O	2:AM:337:SER:HB3	2.09	0.52
5:AX:455:ILE:HB	6:AY:1765:PRO:HB3	1.91	0.52
6:BY:1722:VAL:HG22	6:BY:1732:LEU:HB2	1.91	0.52
1:DB:105:TYR:HE2	1:DC:183:LYS:HG3	1.74	0.52
1:DB:136:LEU:HB3	1:DB:179:LEU:HB2	1.90	0.52
6:GY:1805:SER:HB2	6:GY:1855:SER:HB2	1.91	0.52
1:HA:199:ASP:HA	1:HA:203:LEU:HD23	1.89	0.52
2:Hm:188:LYS:HG3	2:Hm:189:LYS:HD3	1.91	0.52
1:IB:138:ILE:HG12	1:IB:164:VAL:HB	1.89	0.52
2:IM:263:ASN:O	2:IM:267:LEU:HB2	2.09	0.52
3:IT:234:GLN:HE21	3:IT:238:SER:HG	1.54	0.52
6:KY:1805:SER:HB2	6:KY:1855:SER:HB2	1.91	0.52
1:MA:69:VAL:HG11	1:MA:211:TYR:HE1	1.73	0.52
5:EX:453:ALA:O	6:EY:1737:LYS:NZ	2.42	0.52
1:GD:154:LYS:HA	1:GD:158:LYS:HG3	1.90	0.52
1:GE:138:ILE:HB	1:GE:177:THR:HB	1.90	0.52
1:JC:140:THR:HG22	1:JC:166:LYS:HB2	1.89	0.52
6:JY:1722:VAL:HG22	6:JY:1732:LEU:HB2	1.91	0.52
1:NA:69:VAL:HG11	1:NA:211:TYR:HE1	1.73	0.52
1:AB:117:TYR:O	1:AB:120:ILE:N	2.42	0.52
2:AM:340:MET:HE2	1:NE:175:GLN:HE21	1.75	0.52
5:AX:410:ARG:HH12	5:BX:445:ASP:HA	1.74	0.52
1:BB:193:ASP:OD1	1:BB:193:ASP:N	2.43	0.52
2:Em:195:LEU:HD23	2:Em:198:LYS:HD2	1.92	0.52
1:FA:175:GLN:NE2	3:Ft:64:GLN:OE1	2.43	0.52
2:GM:199:GLN:HA	2:GM:202:GLU:HG3	1.90	0.52
1:IB:191:THR:HG23	1:IB:192:LEU:HG	1.92	0.52
2:Im:343:ASP:HB2	2:Im:344:LYS:HB2	1.91	0.52
1:LD:129:ALA:O	1:LD:133:TYR:CB	2.53	0.52
2:Mm:343:ASP:HB2	2:Mm:344:LYS:HB2	1.90	0.52
3:Mt:32:LYS:NZ	3:NT:47:TYR:OH	2.42	0.52
3:NT:274:ARG:O	3:NT:278:SER:CB	2.56	0.52
6:AY:1799:GLY:HA2	6:AY:1802:VAL:HG12	1.92	0.52
6:CY:1799:GLY:HA2	6:CY:1802:VAL:HG12	1.92	0.52
2:DM:253:LEU:HG	2:DM:257:MET:HE1	1.91	0.52
6:DY:1799:GLY:HA2	6:DY:1802:VAL:HG12	1.92	0.52
1:EA:255:LEU:HG	1:EC:147:ASN:ND2	2.24	0.52
1:ED:143:LEU:HD23	3:ET:221:LEU:HD22	1.92	0.52
5:GX:349:ALA:O	5:GX:353:ARG:NH2	2.35	0.52
2:Im:195:LEU:HD23	2:Im:198:LYS:HD2	1.90	0.52
1:KE:138:ILE:HB	1:KE:177:THR:HB	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:69:VAL:HG11	1:LA:211:TYR:HE1	1.73	0.52
1:LC:126:LYS:HG3	1:MA:192:LEU:HD12	1.92	0.52
2:LM:310:VAL:HG21	2:LM:358:PHE:HE1	1.75	0.52
5:LX:453:ALA:O	6:LY:1737:LYS:NZ	2.43	0.52
2:Lm:343:ASP:HB2	2:Lm:344:LYS:HB2	1.89	0.52
1:MB:136:LEU:HB3	1:MB:179:LEU:HB2	1.92	0.52
6:MY:1805:SER:HB2	6:MY:1855:SER:HB2	1.91	0.52
5:NX:454:ALA:HB2	6:NY:1737:LYS:HE2	1.91	0.52
6:AY:1722:VAL:HG22	6:AY:1732:LEU:HB2	1.91	0.52
1:CE:140:THR:HG21	1:DA:278:PRO:HD3	1.91	0.52
2:CM:310:VAL:HG21	2:CM:358:PHE:HE1	1.73	0.52
3:CT:274:ARG:O	3:CT:278:SER:CB	2.56	0.52
1:DD:126:LYS:HB3	1:DD:130:MET:HE3	1.91	0.52
2:Em:188:LYS:HG3	2:Em:189:LYS:HD3	1.91	0.52
2:Em:273:PHE:HD2	2:Em:310:VAL:HG11	1.75	0.52
1:FD:166:LYS:HD3	1:GA:194:LYS:HE3	1.92	0.52
3:FT:234:GLN:HE21	3:FT:238:SER:HG	1.56	0.52
6:FY:1805:SER:HB2	6:FY:1855:SER:HB2	1.91	0.52
1:LB:182:PRO:HG3	1:LC:107:TYR:HB2	1.92	0.52
1:NB:117:TYR:O	1:NB:120:ILE:N	2.41	0.52
6:NY:1805:SER:HB2	6:NY:1855:SER:HB2	1.91	0.52
1:AA:69:VAL:HG11	1:AA:211:TYR:HE1	1.73	0.52
1:BB:124:ILE:HG13	1:BC:124:ILE:HD11	1.90	0.52
2:BM:198:LYS:HE2	2:BM:266:TYR:HE2	1.74	0.52
2:Bm:294:THR:O	2:Bm:303:LYS:NZ	2.36	0.52
3:CT:54:ASP:OD1	3:CT:54:ASP:N	2.42	0.52
2:Cm:188:LYS:HG3	2:Cm:189:LYS:HD3	1.91	0.52
1:ED:128:ARG:HH22	1:EE:87:ASN:HB3	1.75	0.52
3:ET:54:ASP:OD1	3:ET:54:ASP:N	2.42	0.52
1:FE:157:ASN:HD21	1:FE:161:ALA:H	1.58	0.52
4:FU:609:UNK:HA	2:Fm:273:PHE:HZ	1.75	0.52
1:GB:155:ALA:HA	3:Gt:179:LYS:HE2	1.90	0.52
4:HU:609:UNK:HA	2:Hm:273:PHE:HZ	1.74	0.52
1:KA:69:VAL:HG11	1:KA:211:TYR:HE1	1.73	0.52
5:MX:453:ALA:O	6:MY:1737:LYS:NZ	2.41	0.52
6:NY:1799:GLY:HA2	6:NY:1802:VAL:HG12	1.92	0.52
2:Nm:343:ASP:HB2	2:Nm:344:LYS:HB2	1.91	0.52
1:AB:182:PRO:HG3	1:AC:107:TYR:HB2	1.91	0.52
1:AD:95:PHE:HE2	1:AE:132:THR:HG21	1.75	0.52
6:EY:1799:GLY:HA2	6:EY:1802:VAL:HG12	1.92	0.52
6:FY:1799:GLY:HA2	6:FY:1802:VAL:HG12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JA:80:ILE:O	3:Jt:64:GLN:NE2	2.42	0.52
1:JB:124:ILE:HG13	1:JC:124:ILE:HD11	1.91	0.52
2:Jm:343:ASP:HB2	2:Jm:344:LYS:HB2	1.92	0.52
1:KA:248:ASN:HA	1:KB:187:PRO:HB2	1.91	0.52
6:KY:1722:VAL:HG22	6:KY:1732:LEU:HB2	1.91	0.52
1:LA:82:ASP:OD1	1:LA:126:LYS:NZ	2.38	0.52
1:AD:117:TYR:O	1:AD:121:GLU:CB	2.55	0.52
6:AY:1859:LEU:HD22	6:BY:1854:MET:HG2	1.91	0.52
2:BM:219:ASN:HB3	2:BM:222:TYR:HB3	1.91	0.52
5:BX:453:ALA:O	6:BY:1737:LYS:NZ	2.42	0.52
6:BY:1799:GLY:HA2	6:BY:1802:VAL:HG12	1.92	0.52
2:CM:338:ASP:HB3	2:CM:341:MET:HG2	1.92	0.52
2:Dm:188:LYS:HG3	2:Dm:189:LYS:HD3	1.92	0.52
3:ET:94:THR:HA	3:ET:121:TYR:O	2.10	0.52
2:FM:280:VAL:HG23	2:FM:285:GLU:HG2	1.91	0.52
3:It:207:GLU:OE1	3:It:207:GLU:N	2.29	0.52
3:JT:102:ILE:HD12	3:JT:122:LEU:HB3	1.92	0.52
1:KD:81:TYR:CD1	1:KE:107:TYR:HB2	2.44	0.52
6:LY:1722:VAL:HG22	6:LY:1732:LEU:HB2	1.91	0.52
3:Lt:207:GLU:OE1	3:Lt:207:GLU:N	2.29	0.52
3:MT:94:THR:HA	3:MT:121:TYR:O	2.10	0.52
1:NE:138:ILE:HB	1:NE:177:THR:HB	1.92	0.52
3:NT:94:THR:HA	3:NT:121:TYR:O	2.10	0.52
6:AY:1805:SER:HB2	6:AY:1855:SER:HB2	1.91	0.52
3:BT:54:ASP:OD1	3:BT:54:ASP:N	2.42	0.52
1:DE:128:ARG:HD3	1:DE:156:LEU:HD21	1.92	0.52
2:Dm:349:LYS:HA	2:Dm:352:TYR:CE2	2.45	0.52
2:EM:199:GLN:HA	2:EM:202:GLU:HG3	1.91	0.52
2:Em:298:LEU:HB2	2:Em:303:LYS:HE3	1.92	0.52
1:FB:104:THR:OG1	1:FB:105:TYR:N	2.42	0.52
3:FT:94:THR:HA	3:FT:121:TYR:O	2.10	0.52
6:FY:1694:GLN:NE2	6:FY:1882:MET:O	2.43	0.52
1:HC:147:ASN:O	1:HC:151:ASN:ND2	2.43	0.52
6:HY:1859:LEU:HD22	6:IY:1854:MET:HG2	1.91	0.52
2:Hm:298:LEU:HB3	2:Hm:302:GLN:NE2	2.24	0.52
1:IB:132:THR:HA	1:IB:157:ASN:HA	1.92	0.52
1:JD:136:LEU:HD12	1:JD:179:LEU:HD11	1.92	0.52
2:Km:302:GLN:HG3	2:Km:305:LYS:HE3	1.92	0.52
1:LA:248:ASN:HA	1:LB:187:PRO:HB2	1.90	0.52
6:NY:1722:VAL:HG22	6:NY:1732:LEU:HB2	1.91	0.52
1:AB:124:ILE:HG13	1:AC:124:ILE:HD11	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AT:102:ILE:HD12	3:AT:122:LEU:HB3	1.92	0.52
1:CB:193:ASP:OD1	1:CB:193:ASP:N	2.43	0.52
3:DT:94:THR:HA	3:DT:121:TYR:O	2.10	0.52
6:DY:1859:LEU:HD22	6:EY:1854:MET:HG2	1.91	0.52
1:HB:191:THR:HG23	1:HB:192:LEU:HG	1.92	0.52
3:HT:102:ILE:HD12	3:HT:122:LEU:HB3	1.92	0.52
3:IT:94:THR:HA	3:IT:121:TYR:O	2.10	0.52
3:JT:94:THR:HA	3:JT:121:TYR:O	2.10	0.52
1:KD:179:LEU:HD13	1:KE:106:LEU:HD12	1.92	0.52
3:KT:102:ILE:HD12	3:KT:122:LEU:HB3	1.92	0.52
2:LM:222:TYR:OH	3:Lt:202:LEU:O	2.17	0.52
3:LT:102:ILE:HD12	3:LT:122:LEU:HB3	1.92	0.52
5:LX:454:ALA:HB2	6:LY:1737:LYS:HE2	1.92	0.52
6:LY:1799:GLY:HA2	6:LY:1802:VAL:HG12	1.92	0.52
1:MC:133:TYR:HB3	1:MC:181:VAL:HG21	1.90	0.52
3:MT:102:ILE:HD12	3:MT:122:LEU:HB3	1.92	0.52
6:MY:1799:GLY:HA2	6:MY:1802:VAL:HG12	1.92	0.52
1:ND:175:GLN:NE2	1:NE:109:MET:H	2.08	0.52
3:NT:102:ILE:HD12	3:NT:122:LEU:HB3	1.92	0.52
1:BB:128:ARG:HA	1:BB:156:LEU:HD21	1.91	0.51
6:BY:1859:LEU:HD22	6:CY:1854:MET:HG2	1.92	0.51
3:CT:211:THR:O	1:DA:159:ARG:NH2	2.43	0.51
6:DY:1805:SER:HB2	6:DY:1855:SER:HB2	1.91	0.51
1:EB:191:THR:HG23	1:EB:192:LEU:HG	1.93	0.51
3:FT:54:ASP:N	3:FT:54:ASP:OD1	2.42	0.51
1:GD:137:ILE:O	1:GD:163:PHE:HA	2.10	0.51
6:GY:1698:ILE:HG12	6:GY:1722:VAL:HG11	1.92	0.51
1:HB:155:ALA:HA	3:Ht:179:LYS:HE2	1.91	0.51
1:HE:109:MET:HE1	1:HE:111:LEU:HD13	1.92	0.51
1:JA:69:VAL:HG11	1:JA:211:TYR:HE1	1.73	0.51
1:JD:137:ILE:O	1:JD:163:PHE:HA	2.11	0.51
2:Nm:188:LYS:HG3	2:Nm:189:LYS:HD3	1.91	0.51
3:AT:234:GLN:HE21	3:AT:238:SER:HG	1.59	0.51
2:Am:298:LEU:HB2	2:Am:303:LYS:HE3	1.93	0.51
1:BB:135:ASP:HB2	1:BB:180:ARG:HB2	1.93	0.51
3:BT:102:ILE:HD12	3:BT:122:LEU:HB3	1.92	0.51
3:CT:58:ASP:O	3:CT:139:ASN:ND2	2.44	0.51
5:DX:453:ALA:O	6:DY:1737:LYS:NZ	2.43	0.51
6:EY:1805:SER:HB2	6:EY:1855:SER:HB2	1.91	0.51
3:HT:94:THR:HA	3:HT:121:TYR:O	2.10	0.51
6:HY:1698:ILE:HG12	6:HY:1722:VAL:HG11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IM:219:ASN:HB3	2:IM:222:TYR:HB3	1.92	0.51
3:IT:102:ILE:HD12	3:IT:122:LEU:HB3	1.92	0.51
2:Jm:219:ASN:HB3	2:Jm:222:TYR:CD2	2.45	0.51
3:LT:94:THR:HA	3:LT:121:TYR:O	2.10	0.51
6:MY:1722:VAL:HG22	6:MY:1732:LEU:HB2	1.91	0.51
1:ND:140:THR:HA	1:ND:166:LYS:O	2.10	0.51
2:Nm:298:LEU:HB2	2:Nm:303:LYS:HE3	1.92	0.51
3:AT:94:THR:HA	3:AT:121:TYR:O	2.10	0.51
1:CB:136:LEU:HB2	1:CB:179:LEU:HB2	1.93	0.51
2:CM:305:LYS:NZ	3:Ct:231:GLN:O	2.38	0.51
1:DE:138:ILE:HB	1:DE:177:THR:HB	1.91	0.51
3:DT:58:ASP:O	3:DT:139:ASN:ND2	2.44	0.51
1:EA:248:ASN:HA	1:EB:187:PRO:HB2	1.91	0.51
2:Em:274:SER:O	2:Em:278:LYS:HB2	2.11	0.51
1:FC:169:GLU:OE2	3:Ft:233:ARG:NH2	2.43	0.51
1:FD:121:GLU:OE2	1:FE:128:ARG:NH2	2.43	0.51
2:Fm:188:LYS:HG3	2:Fm:189:LYS:HD3	1.92	0.51
3:GT:102:ILE:HD12	3:GT:122:LEU:HB3	1.92	0.51
1:IB:136:LEU:HA	1:IB:161:ALA:HB1	1.91	0.51
6:IY:1698:ILE:HG12	6:IY:1722:VAL:HG11	1.93	0.51
2:JM:305:LYS:NZ	3:Jt:231:GLN:O	2.38	0.51
5:KX:454:ALA:HB2	6:KY:1737:LYS:HE2	1.93	0.51
2:Mm:298:LEU:HB2	2:Mm:303:LYS:HE3	1.91	0.51
6:CY:1805:SER:HB2	6:CY:1855:SER:HB2	1.91	0.51
1:DD:166:LYS:HZ3	1:EA:194:LYS:HG2	1.76	0.51
1:EB:193:ASP:N	1:EB:193:ASP:OD1	2.43	0.51
6:FY:1698:ILE:HG12	6:FY:1722:VAL:HG11	1.93	0.51
1:GA:104:THR:HG22	3:Gt:138:TYR:HA	1.91	0.51
1:HB:139:ILE:HG22	1:HB:146:VAL:HG12	1.92	0.51
1:JD:154:LYS:HA	1:JD:158:LYS:HG3	1.93	0.51
1:KA:80:ILE:O	3:Kt:64:GLN:NE2	2.42	0.51
2:Km:188:LYS:HG3	2:Km:189:LYS:HD3	1.91	0.51
1:BA:248:ASN:HA	1:BB:187:PRO:HB2	1.91	0.51
1:BB:146:VAL:HB	1:BB:165:LEU:HD22	1.93	0.51
6:CY:1730:ILE:HD12	5:DX:502:ASN:HA	1.91	0.51
6:CY:1859:LEU:HD22	6:DY:1854:MET:HG2	1.92	0.51
1:DB:110:ASP:OD1	1:DB:111:LEU:N	2.37	0.51
6:DY:1694:GLN:NE2	6:DY:1882:MET:O	2.43	0.51
6:EY:1859:LEU:HD22	6:FY:1854:MET:HG2	1.91	0.51
1:FD:140:THR:HG22	1:FD:166:LYS:HB2	1.92	0.51
1:GA:82:ASP:OD1	1:GA:126:LYS:NZ	2.38	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:GT:94:THR:HA	3:GT:121:TYR:O	2.10	0.51
1:HD:136:LEU:HD22	1:HD:179:LEU:HD11	1.91	0.51
6:HY:1799:GLY:HA2	6:HY:1802:VAL:HG12	1.92	0.51
1:IA:248:ASN:HA	1:IB:187:PRO:HB2	1.91	0.51
5:KX:453:ALA:O	6:KY:1737:LYS:NZ	2.43	0.51
2:NM:199:GLN:HA	2:NM:202:GLU:HG3	1.91	0.51
3:BT:58:ASP:O	3:BT:139:ASN:ND2	2.44	0.51
1:CE:157:ASN:HD21	1:CE:161:ALA:H	1.59	0.51
5:CX:454:ALA:HB2	6:CY:1737:LYS:HE2	1.92	0.51
5:CX:455:ILE:HB	6:CY:1765:PRO:HB3	1.93	0.51
1:DA:296:VAL:O	1:DC:164:VAL:HA	2.11	0.51
3:DT:102:ILE:HD12	3:DT:122:LEU:HB3	1.92	0.51
3:ET:234:GLN:HE21	3:ET:238:SER:HG	1.57	0.51
2:Fm:343:ASP:HB2	2:Fm:344:LYS:HB2	1.90	0.51
2:Gm:298:LEU:HB2	2:Gm:303:LYS:HE3	1.92	0.51
1:HC:122:ASN:O	1:HC:126:LYS:HB2	2.10	0.51
1:IB:124:ILE:HG13	1:IC:124:ILE:HD11	1.92	0.51
6:JY:1698:ILE:HG12	6:JY:1722:VAL:HG11	1.93	0.51
6:JY:1799:GLY:HA2	6:JY:1802:VAL:HG12	1.92	0.51
6:KY:1698:ILE:HG12	6:KY:1722:VAL:HG11	1.93	0.51
6:KY:1859:LEU:HD22	6:LY:1854:MET:HG2	1.93	0.51
1:LA:295:LEU:HD12	1:LC:163:PHE:HB2	1.91	0.51
1:LB:146:VAL:HB	1:LB:165:LEU:HD22	1.92	0.51
1:LC:133:TYR:HB3	1:LC:181:VAL:HG21	1.93	0.51
1:LD:154:LYS:HA	1:LD:158:LYS:HG3	1.92	0.51
2:LM:345:THR:HG23	2:LM:348:GLN:H	1.76	0.51
6:LY:1698:ILE:HG12	6:LY:1722:VAL:HG11	1.93	0.51
1:MA:117:TYR:CE1	3:Mt:80:VAL:HG23	2.45	0.51
1:AC:171:MET:N	1:AC:171:MET:SD	2.83	0.51
3:BT:84:PHE:HA	3:BT:87:VAL:HG22	1.93	0.51
5:BX:454:ALA:HB2	6:BY:1737:LYS:HE2	1.92	0.51
3:CT:84:PHE:HA	3:CT:87:VAL:HG22	1.92	0.51
3:CT:94:THR:HA	3:CT:121:TYR:O	2.10	0.51
1:DC:148:GLY:O	1:DC:151:ASN:N	2.44	0.51
3:DT:54:ASP:N	3:DT:54:ASP:OD1	2.42	0.51
3:ET:102:ILE:HD12	3:ET:122:LEU:HB3	1.92	0.51
1:FA:104:THR:HG22	3:Ft:138:TYR:HA	1.90	0.51
2:FM:212:LEU:HD13	2:FM:270:TYR:HB2	1.92	0.51
6:GY:1799:GLY:HA2	6:GY:1802:VAL:HG12	1.92	0.51
3:Gt:97:GLY:O	3:Gt:125:THR:N	2.37	0.51
2:HM:199:GLN:HA	2:HM:202:GLU:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:JY:1905:ILE:O	6:JY:1908:SER:OG	2.25	0.51
3:KT:94:THR:HA	3:KT:121:TYR:O	2.10	0.51
1:MA:248:ASN:HA	1:MB:187:PRO:HB2	1.93	0.51
1:AA:248:ASN:HA	1:AB:187:PRO:HB2	1.92	0.51
3:AT:84:PHE:HA	3:AT:87:VAL:HG22	1.93	0.51
6:BY:1805:SER:HB2	6:BY:1855:SER:HB2	1.91	0.51
2:CM:276:LEU:HB3	2:CM:289:LEU:HD21	1.91	0.51
3:CT:102:ILE:HD12	3:CT:122:LEU:HB3	1.92	0.51
3:ET:58:ASP:O	3:ET:139:ASN:ND2	2.44	0.51
6:EY:1698:ILE:HG12	6:EY:1722:VAL:HG11	1.93	0.51
1:HC:140:THR:HG22	1:HC:166:LYS:HB2	1.93	0.51
6:HY:1905:ILE:O	6:HY:1908:SER:OG	2.25	0.51
4:KU:609:UNK:HA	2:Km:273:PHE:HZ	1.75	0.51
1:LE:109:MET:HE1	1:LE:111:LEU:HD13	1.93	0.51
1:LE:136:LEU:HD23	1:LE:162:LYS:HB2	1.93	0.51
3:MT:234:GLN:HE21	3:MT:238:SER:HG	1.56	0.51
6:MY:1698:ILE:HG12	6:MY:1722:VAL:HG11	1.93	0.51
2:Am:188:LYS:HG3	2:Am:189:LYS:HD3	1.91	0.51
1:CD:133:TYR:HD1	1:CE:101:LYS:HE3	1.76	0.51
3:DT:84:PHE:HA	3:DT:87:VAL:HG22	1.93	0.51
5:DX:455:ILE:HB	6:DY:1765:PRO:HB3	1.92	0.51
1:EC:138:ILE:O	1:EC:176:ALA:HA	2.10	0.51
2:EM:341:MET:O	2:EM:344:LYS:NZ	2.44	0.51
3:ET:84:PHE:HA	3:ET:87:VAL:HG22	1.93	0.51
1:FA:82:ASP:OD1	1:FA:126:LYS:NZ	2.38	0.51
3:FT:102:ILE:HD12	3:FT:122:LEU:HB3	1.92	0.51
1:GE:140:THR:HG21	1:HA:278:PRO:HD3	1.93	0.51
2:Gm:295:ASN:HA	2:Gm:347:MET:HE1	1.92	0.51
1:HB:137:ILE:HD13	1:HB:153:LEU:HD23	1.92	0.51
1:KB:149:TYR:HA	1:KB:152:ILE:HD12	1.92	0.51
2:KM:310:VAL:HG21	2:KM:358:PHE:HE1	1.75	0.51
6:KY:1799:GLY:HA2	6:KY:1802:VAL:HG12	1.92	0.51
2:LM:199:GLN:HA	2:LM:202:GLU:HG3	1.92	0.51
2:Lm:188:LYS:HG3	2:Lm:189:LYS:HD3	1.92	0.51
1:MB:191:THR:HG23	1:MB:192:LEU:HG	1.93	0.51
1:AB:153:LEU:HA	1:AB:156:LEU:HB2	1.93	0.51
1:AC:169:GLU:OE2	3:At:233:ARG:NH2	2.44	0.51
1:AE:157:ASN:HD21	1:AE:161:ALA:H	1.59	0.51
6:AY:1689:THR:O	6:AY:1724:ASN:ND2	2.41	0.51
1:BB:132:THR:HA	1:BB:157:ASN:HA	1.93	0.51
3:DT:234:GLN:NE2	3:DT:238:SER:OG	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Em:282:ASP:HB3	2:Em:285:GLU:H	1.75	0.51
1:GA:296:VAL:O	1:GC:164:VAL:HA	2.10	0.51
3:GT:58:ASP:O	3:GT:139:ASN:ND2	2.44	0.51
3:HT:54:ASP:OD1	3:HT:54:ASP:N	2.42	0.51
6:HY:1750:PRO:HA	6:HY:1797:ARG:HH22	1.76	0.51
2:Hm:299:SER:O	2:Hm:302:GLN:NE2	2.37	0.51
1:IB:128:ARG:HA	1:IB:156:LEU:HD21	1.92	0.51
3:JT:84:PHE:HA	3:JT:87:VAL:HG22	1.92	0.51
1:LB:138:ILE:HD13	1:LB:164:VAL:HB	1.92	0.51
1:LD:176:ALA:HB3	1:LE:109:MET:HE3	1.92	0.51
6:LY:1694:GLN:NE2	6:LY:1882:MET:O	2.43	0.51
6:LY:1859:LEU:HD22	6:MY:1854:MET:HG2	1.93	0.51
1:NB:136:LEU:HA	1:NB:161:ALA:HB1	1.91	0.51
5:NX:455:ILE:HB	6:NY:1765:PRO:HB3	1.93	0.51
1:AB:191:THR:HG23	1:AB:192:LEU:HG	1.93	0.50
3:BT:94:THR:HA	3:BT:121:TYR:O	2.10	0.50
1:DD:138:ILE:HG13	1:DD:164:VAL:HB	1.91	0.50
1:EC:133:TYR:HB3	1:EC:181:VAL:HG21	1.92	0.50
6:EY:1750:PRO:HA	6:EY:1797:ARG:HH22	1.76	0.50
3:FT:84:PHE:HA	3:FT:87:VAL:HG22	1.92	0.50
6:GY:1859:LEU:HD22	6:HY:1854:MET:HG2	1.92	0.50
3:HT:58:ASP:O	3:HT:139:ASN:ND2	2.44	0.50
6:IY:1799:GLY:HA2	6:IY:1802:VAL:HG12	1.92	0.50
2:MM:205:SER:OG	2:MM:268:ARG:NH1	2.44	0.50
3:MT:89:HIS:HE1	5:MX:401:TYR:CD2	2.29	0.50
3:NT:84:PHE:HA	3:NT:87:VAL:HG22	1.93	0.50
6:NY:1689:THR:O	6:NY:1724:ASN:ND2	2.41	0.50
6:NY:1698:ILE:HG12	6:NY:1722:VAL:HG11	1.93	0.50
6:AY:1750:PRO:HA	6:AY:1797:ARG:HH22	1.76	0.50
3:BT:234:GLN:HE21	3:BT:238:SER:HG	1.55	0.50
6:BY:1750:PRO:HA	6:BY:1797:ARG:HH22	1.76	0.50
1:DB:193:ASP:OD1	1:DB:193:ASP:N	2.44	0.50
1:DD:136:LEU:HG	1:DD:162:LYS:HB3	1.94	0.50
2:Em:344:LYS:HB3	2:Em:347:MET:HB2	1.93	0.50
1:FD:124:ILE:HG23	1:FE:117:TYR:HE1	1.76	0.50
2:Fm:298:LEU:HB2	2:Fm:303:LYS:HE3	1.94	0.50
1:HD:125:ILE:HG21	1:HE:128:ARG:HG2	1.93	0.50
1:IB:146:VAL:HB	1:IB:165:LEU:HD22	1.93	0.50
3:IT:58:ASP:O	3:IT:139:ASN:ND2	2.44	0.50
6:KY:1750:PRO:HA	6:KY:1797:ARG:HH22	1.77	0.50
1:MC:187:PRO:HD2	1:NA:188:ASN:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ME:157:ASN:HD21	1:ME:161:ALA:H	1.59	0.50
1:BB:126:LYS:O	1:BB:130:MET:HB2	2.11	0.50
3:BT:234:GLN:NE2	3:BT:238:SER:OG	2.43	0.50
2:CM:280:VAL:HG23	2:CM:285:GLU:HG2	1.92	0.50
1:DA:80:ILE:O	3:Dt:64:GLN:NE2	2.42	0.50
1:DD:107:TYR:HE2	1:DE:126:LYS:HD2	1.77	0.50
6:DY:1750:PRO:HA	6:DY:1797:ARG:HH22	1.76	0.50
1:GD:176:ALA:O	1:GE:108:ALA:HA	2.11	0.50
3:IT:84:PHE:HA	3:IT:87:VAL:HG22	1.93	0.50
3:JT:58:ASP:O	3:JT:139:ASN:ND2	2.44	0.50
3:KT:84:PHE:HA	3:KT:87:VAL:HG22	1.93	0.50
6:KY:1730:ILE:HD12	5:LX:502:ASN:HA	1.94	0.50
6:LY:1750:PRO:HA	6:LY:1797:ARG:HH22	1.76	0.50
3:MT:58:ASP:O	3:MT:139:ASN:ND2	2.44	0.50
3:NT:54:ASP:N	3:NT:54:ASP:OD1	2.42	0.50
3:NT:58:ASP:O	3:NT:139:ASN:ND2	2.44	0.50
6:NY:1694:GLN:NE2	6:NY:1882:MET:O	2.43	0.50
2:AM:305:LYS:NZ	3:At:231:GLN:O	2.39	0.50
6:BY:1761:LYS:HD3	6:BY:1763:ILE:HD11	1.94	0.50
1:CA:80:ILE:O	3:Ct:64:GLN:NE2	2.42	0.50
1:CA:296:VAL:O	1:CC:164:VAL:HA	2.11	0.50
6:CY:1761:LYS:HD3	6:CY:1763:ILE:HD11	1.94	0.50
6:DY:1761:LYS:HD3	6:DY:1763:ILE:HD11	1.94	0.50
1:FB:150:TYR:OH	1:FB:154:LYS:NZ	2.45	0.50
3:FT:58:ASP:O	3:FT:139:ASN:ND2	2.44	0.50
6:FY:1859:LEU:HD22	6:GY:1854:MET:HG2	1.91	0.50
3:IT:54:ASP:N	3:IT:54:ASP:OD1	2.42	0.50
1:JB:136:LEU:HB2	1:JB:179:LEU:HB2	1.93	0.50
1:JD:140:THR:HG22	1:JD:166:LYS:HB2	1.93	0.50
1:KE:84:LEU:HD21	1:KE:91:PHE:HA	1.94	0.50
6:KY:1905:ILE:O	6:KY:1908:SER:OG	2.25	0.50
1:LB:107:TYR:O	1:LC:177:THR:HA	2.11	0.50
1:LC:175:GLN:HE22	1:LC:177:THR:HG23	1.77	0.50
1:LD:130:MET:HE1	1:LD:134:ALA:HB2	1.92	0.50
5:LX:408:GLU:OE1	3:MT:32:LYS:N	2.40	0.50
5:MX:455:ILE:HB	6:MY:1765:PRO:HB3	1.92	0.50
1:NE:175:GLN:NE2	1:NE:177:THR:OG1	2.37	0.50
3:AT:58:ASP:O	3:AT:139:ASN:ND2	2.44	0.50
6:AY:1698:ILE:HG12	6:AY:1722:VAL:HG11	1.93	0.50
1:BA:80:ILE:O	3:Bt:64:GLN:NE2	2.41	0.50
1:DB:132:THR:HA	1:DB:157:ASN:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DC:131:GLY:HA3	1:DC:153:LEU:HD12	1.93	0.50
1:DE:109:MET:HE1	1:DE:111:LEU:HD13	1.93	0.50
6:DY:1698:ILE:HG12	6:DY:1722:VAL:HG11	1.93	0.50
5:FX:482:LYS:HA	3:GT:29:VAL:HG21	1.94	0.50
3:Ft:207:GLU:OE1	3:Ft:207:GLU:N	2.29	0.50
2:GM:247:ILE:O	2:GM:252:ARG:NH1	2.42	0.50
3:GT:54:ASP:N	3:GT:54:ASP:OD1	2.42	0.50
6:GY:1905:ILE:O	6:GY:1908:SER:OG	2.25	0.50
3:HT:84:PHE:HA	3:HT:87:VAL:HG22	1.92	0.50
1:IB:124:ILE:O	1:IB:127:THR:OG1	2.26	0.50
3:It:97:GLY:O	3:It:125:THR:N	2.37	0.50
1:JD:138:ILE:HG13	1:JD:164:VAL:HB	1.94	0.50
1:LD:107:TYR:CE1	1:LE:80:ILE:HB	2.45	0.50
1:AB:112:LEU:HD21	3:AT:238:SER:HB3	1.93	0.50
1:BD:176:ALA:HB3	1:BE:109:MET:HE3	1.93	0.50
6:BY:1689:THR:O	6:BY:1724:ASN:ND2	2.41	0.50
3:CT:213:ARG:NH2	1:DA:207:GLN:OE1	2.45	0.50
2:DM:205:SER:OG	2:DM:268:ARG:NH1	2.44	0.50
1:EA:205:GLU:HA	1:EA:208:LYS:HZ3	1.77	0.50
6:EY:1761:LYS:HD3	6:EY:1763:ILE:HD11	1.94	0.50
1:FC:136:LEU:HB3	1:FC:179:LEU:HB2	1.94	0.50
2:Fm:332:ASN:HA	2:Fm:353:LYS:HD3	1.94	0.50
1:GB:193:ASP:OD1	1:GB:193:ASP:N	2.42	0.50
3:GT:84:PHE:HA	3:GT:87:VAL:HG22	1.93	0.50
6:GY:1750:PRO:HA	6:GY:1797:ARG:HH22	1.76	0.50
1:HB:193:ASP:OD1	1:HB:193:ASP:N	2.42	0.50
1:HD:154:LYS:HA	1:HD:158:LYS:HG3	1.94	0.50
3:HT:234:GLN:HE21	3:HT:238:SER:HG	1.57	0.50
3:JT:234:GLN:NE2	3:JT:238:SER:OG	2.43	0.50
2:KM:263:ASN:O	2:KM:267:LEU:HB2	2.11	0.50
3:LT:58:ASP:O	3:LT:139:ASN:ND2	2.44	0.50
3:LT:84:PHE:HA	3:LT:87:VAL:HG22	1.93	0.50
2:MM:205:SER:HA	2:MM:208:VAL:HG12	1.92	0.50
3:MT:54:ASP:OD1	3:MT:54:ASP:N	2.42	0.50
3:MT:84:PHE:HA	3:MT:87:VAL:HG22	1.93	0.50
3:AT:54:ASP:N	3:AT:54:ASP:OD1	2.42	0.50
6:BY:1698:ILE:HG12	6:BY:1722:VAL:HG11	1.93	0.50
3:CT:89:HIS:HE1	5:CX:401:TYR:CD2	2.30	0.50
5:DX:454:ALA:HB2	6:DY:1737:LYS:HE2	1.93	0.50
1:FB:124:ILE:HG13	1:FC:124:ILE:HD11	1.93	0.50
3:FT:234:GLN:NE2	3:FT:238:SER:OG	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:FX:454:ALA:HB2	6:FY:1737:LYS:HE2	1.94	0.50
6:GY:1694:GLN:NE2	6:GY:1882:MET:O	2.43	0.50
1:ID:121:GLU:OE2	1:IE:128:ARG:NH1	2.41	0.50
3:KT:58:ASP:O	3:KT:139:ASN:ND2	2.44	0.50
6:KY:1694:GLN:NE2	6:KY:1882:MET:O	2.43	0.50
1:LA:107:TYR:CG	3:Lt:44:ILE:HD11	2.47	0.50
1:LD:130:MET:HE2	1:LD:178:PHE:CD1	2.47	0.50
2:Lm:298:LEU:HB2	2:Lm:303:LYS:HE3	1.93	0.50
3:Lt:97:GLY:O	3:Lt:125:THR:N	2.37	0.50
1:MC:139:ILE:HB	1:MC:165:LEU:HD13	1.93	0.50
3:NT:234:GLN:NE2	3:NT:238:SER:OG	2.43	0.50
6:AY:1761:LYS:HD3	6:AY:1763:ILE:HD11	1.94	0.50
6:AY:1854:MET:HG2	6:NY:1859:LEU:HD22	1.93	0.50
1:BD:177:THR:HA	1:BE:107:TYR:O	2.11	0.50
1:CD:80:ILE:HA	1:CE:106:LEU:O	2.12	0.50
6:CY:1698:ILE:HG12	6:CY:1722:VAL:HG11	1.93	0.50
1:EB:107:TYR:O	1:EC:177:THR:HA	2.12	0.50
3:FT:223:THR:HG22	1:GA:184:ARG:HH21	1.77	0.50
6:FY:1761:LYS:HD3	6:FY:1763:ILE:HD11	1.94	0.50
5:IX:454:ALA:HB2	6:IY:1737:LYS:HE2	1.94	0.50
6:IY:1730:ILE:HD12	5:JX:502:ASN:HA	1.94	0.50
6:IY:1750:PRO:HA	6:IY:1797:ARG:HH22	1.76	0.50
1:KA:296:VAL:O	1:KC:164:VAL:HA	2.11	0.50
6:LY:1730:ILE:HD12	5:MX:502:ASN:HA	1.93	0.50
1:MA:124:ILE:HG13	3:Mt:73:TYR:CE2	2.47	0.50
6:MY:1689:THR:O	6:MY:1724:ASN:ND2	2.42	0.50
1:NB:191:THR:HG23	1:NB:192:LEU:HG	1.94	0.50
2:Nm:247:ILE:O	2:Nm:252:ARG:NH1	2.44	0.50
6:AY:1694:GLN:NE2	6:AY:1882:MET:O	2.43	0.50
1:BB:158:LYS:NZ	1:BC:193:ASP:OD2	2.37	0.50
1:CC:138:ILE:O	1:CC:176:ALA:HA	2.12	0.50
1:DB:118:LEU:HD21	1:DC:152:ILE:HD11	1.93	0.50
1:DE:84:LEU:HD21	1:DE:91:PHE:HA	1.94	0.50
1:EB:146:VAL:HB	1:EB:165:LEU:HD22	1.93	0.50
1:ED:178:PHE:CE1	1:EE:107:TYR:HB3	2.47	0.50
1:FA:80:ILE:O	3:Ft:64:GLN:NE2	2.43	0.50
1:GB:146:VAL:HB	1:GB:165:LEU:HD22	1.92	0.50
5:GX:454:ALA:HB2	6:GY:1737:LYS:HE2	1.94	0.50
1:IC:146:VAL:HB	1:IC:165:LEU:HD12	1.93	0.50
1:JE:157:ASN:HD21	1:JE:161:ALA:H	1.60	0.50
3:Mt:207:GLU:OE1	3:Mt:207:GLU:N	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:NY:1750:PRO:HA	6:NY:1797:ARG:HH22	1.76	0.50
1:AB:135:ASP:HB2	1:AB:180:ARG:HB2	1.94	0.49
1:BB:153:LEU:HD13	1:BB:156:LEU:HD23	1.94	0.49
1:CB:107:TYR:HB3	1:CC:130:MET:HE2	1.94	0.49
2:CM:282:ASP:N	2:CM:285:GLU:OE2	2.45	0.49
1:DB:146:VAL:HB	1:DB:165:LEU:HD22	1.94	0.49
1:FD:140:THR:HA	1:FD:166:LYS:O	2.12	0.49
5:HX:454:ALA:HB2	6:HY:1737:LYS:HE2	1.94	0.49
2:Hm:219:ASN:HB3	2:Hm:222:TYR:CD2	2.47	0.49
1:ID:117:TYR:HE2	1:IE:152:ILE:HG21	1.77	0.49
2:IM:198:LYS:HE2	2:IM:266:TYR:HE2	1.76	0.49
2:Km:220:ILE:HG13	2:Km:224:LEU:HD23	1.94	0.49
1:MC:136:LEU:HB3	1:MC:179:LEU:HB2	1.94	0.49
2:DM:199:GLN:HA	2:DM:202:GLU:HG3	1.93	0.49
1:EB:126:LYS:O	1:EB:130:MET:HB2	2.12	0.49
1:EB:136:LEU:HA	1:EB:161:ALA:HB1	1.93	0.49
2:GM:305:LYS:NZ	3:Gt:231:GLN:O	2.38	0.49
1:HB:136:LEU:HB2	1:HB:179:LEU:HB2	1.92	0.49
1:IA:296:VAL:HB	1:IC:164:VAL:HG12	1.95	0.49
6:JY:1750:PRO:HA	6:JY:1797:ARG:HH22	1.77	0.49
3:KT:54:ASP:OD1	3:KT:54:ASP:N	2.42	0.49
1:LB:168:ASN:ND2	1:LB:171:MET:SD	2.85	0.49
5:LX:455:ILE:HB	6:LY:1765:PRO:HB3	1.95	0.49
1:MA:104:THR:HA	3:Mt:137:ASN:O	2.11	0.49
1:MD:104:THR:OG1	1:ME:181:VAL:O	2.30	0.49
6:MY:1694:GLN:NE2	6:MY:1882:MET:O	2.43	0.49
1:AD:80:ILE:HA	1:AE:106:LEU:O	2.11	0.49
1:BB:139:ILE:HG22	1:BB:146:VAL:HG12	1.95	0.49
3:Et:97:GLY:O	3:Et:125:THR:N	2.37	0.49
2:Fm:294:THR:O	2:Fm:303:LYS:NZ	2.46	0.49
1:GA:149:TYR:OH	3:Gt:68:PRO:O	2.26	0.49
1:IC:139:ILE:HB	1:IC:165:LEU:HD13	1.94	0.49
1:IE:157:ASN:HD21	1:IE:161:ALA:H	1.59	0.49
1:KC:148:GLY:O	1:KC:151:ASN:N	2.45	0.49
5:KX:436:GLN:OE1	5:KX:465:ARG:NE	2.42	0.49
6:NY:1761:LYS:HD3	6:NY:1763:ILE:HD11	1.94	0.49
3:AT:32:LYS:N	5:NX:408:GLU:OE1	2.41	0.49
1:BA:296:VAL:HB	1:BC:164:VAL:HG12	1.94	0.49
2:BM:303:LYS:NZ	2:BM:350:GLU:OE2	2.42	0.49
1:DA:167:ILE:HG21	1:DB:150:TYR:HE1	1.77	0.49
1:ED:121:GLU:HG2	1:EE:128:ARG:HH11	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:193:ASP:OD1	1:FB:193:ASP:N	2.43	0.49
1:HB:117:TYR:O	1:HB:120:ILE:N	2.42	0.49
2:Hm:281:LYS:O	2:Im:219:ASN:ND2	2.46	0.49
1:JA:107:TYR:CG	3:Jt:44:ILE:HD11	2.48	0.49
1:KA:107:TYR:CG	3:Kt:44:ILE:HD11	2.48	0.49
1:NB:139:ILE:HG22	1:NB:146:VAL:HG12	1.94	0.49
3:At:96:ILE:HG12	3:At:123:GLN:HB3	1.95	0.49
1:BA:82:ASP:OD1	1:BA:126:LYS:NZ	2.38	0.49
3:Dt:97:GLY:O	3:Dt:125:THR:N	2.37	0.49
2:EM:242:ALA:HA	2:EM:245:THR:HG22	1.93	0.49
2:FM:242:ALA:HA	2:FM:245:THR:HG22	1.95	0.49
6:FY:1750:PRO:HA	6:FY:1797:ARG:HH22	1.76	0.49
6:GY:1761:LYS:HD3	6:GY:1763:ILE:HD11	1.94	0.49
1:HE:138:ILE:HB	1:HE:177:THR:HB	1.94	0.49
1:JB:193:ASP:N	1:JB:193:ASP:OD1	2.43	0.49
3:LT:54:ASP:N	3:LT:54:ASP:OD1	2.42	0.49
1:MD:106:LEU:HB3	1:ME:179:LEU:HD13	1.93	0.49
3:Mt:96:ILE:HG12	3:Mt:123:GLN:HB3	1.95	0.49
2:Nm:295:ASN:HA	2:Nm:347:MET:HE1	1.95	0.49
1:BA:107:TYR:CG	3:Bt:44:ILE:HD11	2.47	0.49
3:BT:213:ARG:NH2	1:CA:207:GLN:OE1	2.46	0.49
6:BY:1730:ILE:HD12	5:CX:502:ASN:HA	1.95	0.49
1:CC:139:ILE:HB	1:CC:165:LEU:HD13	1.93	0.49
6:CY:1908:SER:O	5:DX:379:GLN:NE2	2.45	0.49
2:Em:294:THR:O	2:Em:303:LYS:NZ	2.43	0.49
1:FB:155:ALA:HA	3:Ft:179:LYS:HE2	1.93	0.49
6:FY:1905:ILE:O	6:FY:1908:SER:OG	2.25	0.49
1:GD:140:THR:HA	1:GD:166:LYS:O	2.13	0.49
2:GM:188:LYS:O	2:GM:191:SER:OG	2.30	0.49
2:GM:310:VAL:HG21	2:GM:358:PHE:HE1	1.78	0.49
6:GY:1730:ILE:HD12	5:HX:502:ASN:HA	1.95	0.49
1:HA:107:TYR:CG	3:Ht:44:ILE:HD11	2.48	0.49
1:IA:82:ASP:OD1	1:IA:126:LYS:NZ	2.38	0.49
1:IA:165:LEU:HD11	1:IB:167:ILE:HD11	1.93	0.49
1:JC:169:GLU:OE2	3:Jt:233:ARG:NH2	2.46	0.49
1:JD:133:TYR:HA	1:JE:101:LYS:HZ3	1.78	0.49
2:KM:199:GLN:HA	2:KM:202:GLU:HG3	1.93	0.49
2:LM:280:VAL:HG23	2:LM:285:GLU:HG2	1.94	0.49
2:LM:305:LYS:NZ	3:Lt:231:GLN:O	2.37	0.49
6:LY:1905:ILE:O	6:LY:1908:SER:OG	2.25	0.49
4:MU:609:UNK:HA	2:Mm:273:PHE:HZ	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:MY:1761:LYS:HD3	6:MY:1763:ILE:HD11	1.94	0.49
1:AB:120:ILE:HD11	1:AC:112:LEU:HD21	1.93	0.49
6:CY:1689:THR:O	6:CY:1724:ASN:ND2	2.41	0.49
1:DB:124:ILE:HG13	1:DC:124:ILE:HD11	1.93	0.49
1:DB:182:PRO:HG3	1:DC:107:TYR:HB2	1.95	0.49
1:ED:138:ILE:HG13	1:ED:164:VAL:HB	1.95	0.49
1:FC:138:ILE:O	1:FC:176:ALA:HA	2.12	0.49
1:GA:80:ILE:O	3:Gt:64:GLN:NE2	2.43	0.49
6:IY:1694:GLN:NE2	6:IY:1882:MET:O	2.43	0.49
6:JY:1694:GLN:NE2	6:JY:1882:MET:O	2.43	0.49
6:MY:1750:PRO:HA	6:MY:1797:ARG:HH22	1.76	0.49
2:Mm:357:PHE:O	2:Mm:360:THR:OG1	2.28	0.49
1:BC:138:ILE:O	1:BC:176:ALA:HA	2.13	0.49
1:CC:171:MET:SD	1:CC:171:MET:N	2.84	0.49
5:EX:436:GLN:OE1	5:EX:465:ARG:NE	2.42	0.49
2:Em:357:PHE:O	2:Em:360:THR:OG1	2.24	0.49
3:HT:211:THR:O	1:IA:159:ARG:NH2	2.44	0.49
1:JB:150:TYR:OH	1:JB:154:LYS:NZ	2.45	0.49
1:KC:139:ILE:HB	1:KC:165:LEU:HD13	1.94	0.49
3:KT:211:THR:O	1:LA:159:ARG:NH2	2.44	0.49
2:Km:357:PHE:O	2:Km:360:THR:OG1	2.26	0.49
1:LD:121:GLU:HG2	1:LE:128:ARG:HH11	1.77	0.49
2:LM:222:TYR:CE1	3:Lt:227:ARG:HD3	2.47	0.49
6:LY:1761:LYS:HD3	6:LY:1763:ILE:HD11	1.94	0.49
2:Lm:259:ILE:HA	2:Lm:262:ILE:HD12	1.95	0.49
1:AE:127:THR:OG1	1:AE:128:ARG:N	2.43	0.49
3:AT:211:THR:O	1:BA:159:ARG:NH2	2.44	0.49
6:CY:1750:PRO:HA	6:CY:1797:ARG:HH22	1.76	0.49
3:Ct:273:ILE:O	2:Dm:261:LYS:NZ	2.41	0.49
1:ED:175:GLN:HA	1:EE:109:MET:O	2.13	0.49
1:FA:234:MET:HB3	1:FB:138:ILE:HD11	1.94	0.49
1:GB:191:THR:HG23	1:GB:192:LEU:HG	1.95	0.49
2:GM:187:ASN:ND2	2:GM:251:GLU:OE1	2.46	0.49
3:GT:213:ARG:NH2	1:HA:207:GLN:OE1	2.45	0.49
1:HB:158:LYS:NZ	1:HC:193:ASP:OD2	2.39	0.49
1:IB:193:ASP:OD1	1:IB:193:ASP:N	2.42	0.49
3:JT:54:ASP:OD1	3:JT:54:ASP:N	2.42	0.49
2:Jm:357:PHE:O	2:Jm:360:THR:OG1	2.27	0.49
1:MD:124:ILE:HG23	1:ME:117:TYR:HE1	1.78	0.49
1:ME:138:ILE:HB	1:ME:177:THR:HB	1.95	0.49
2:Mm:188:LYS:HG3	2:Mm:189:LYS:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:NA:175:GLN:NE2	3:Nt:64:GLN:OE1	2.45	0.49
1:NB:138:ILE:HG12	1:NB:164:VAL:HB	1.93	0.49
2:Nm:332:ASN:HA	2:Nm:353:LYS:HD3	1.93	0.49
3:BT:89:HIS:HE1	5:BX:401:TYR:CD2	2.31	0.49
3:Ct:96:ILE:HG12	3:Ct:123:GLN:HB3	1.95	0.49
1:DC:139:ILE:HB	1:DC:165:LEU:HD13	1.95	0.49
1:ED:140:THR:HA	1:ED:166:LYS:O	2.13	0.49
6:EY:1694:GLN:NE2	6:EY:1882:MET:O	2.43	0.49
2:FM:205:SER:OG	2:FM:268:ARG:NH1	2.45	0.49
5:FX:391:ALA:O	5:FX:505:ASN:ND2	2.41	0.49
6:FY:1700:ILE:HD12	6:FY:1738:VAL:HG11	1.95	0.49
6:HY:1761:LYS:HD3	6:HY:1763:ILE:HD11	1.94	0.49
6:JY:1761:LYS:HD3	6:JY:1763:ILE:HD11	1.94	0.49
1:KA:82:ASP:OD1	1:KA:126:LYS:NZ	2.38	0.49
3:Kt:96:ILE:HG12	3:Kt:123:GLN:HB3	1.95	0.49
1:MA:295:LEU:HD12	1:MC:163:PHE:HB2	1.94	0.49
2:MM:221:ASP:OD2	2:MM:221:ASP:N	2.45	0.49
1:CE:139:ILE:HG12	1:CE:149:TYR:CE2	2.47	0.48
3:DT:89:HIS:HE1	5:DX:401:TYR:CD2	2.31	0.48
1:EB:135:ASP:HB2	1:EB:180:ARG:HB2	1.95	0.48
1:EB:139:ILE:HG22	1:EB:146:VAL:HG12	1.95	0.48
2:EM:280:VAL:HG23	2:EM:285:GLU:HG2	1.94	0.48
1:FC:171:MET:N	1:FC:171:MET:SD	2.84	0.48
1:FD:126:LYS:O	1:FD:130:MET:HG3	2.13	0.48
2:HM:242:ALA:HA	2:HM:245:THR:HG22	1.93	0.48
2:IM:305:LYS:NZ	3:It:231:GLN:O	2.38	0.48
3:IT:211:THR:O	1:JA:159:ARG:NH2	2.44	0.48
1:JC:139:ILE:HB	1:JC:165:LEU:HD13	1.94	0.48
1:KD:132:THR:O	1:KE:101:LYS:NZ	2.36	0.48
6:LY:1689:THR:O	6:LY:1724:ASN:ND2	2.41	0.48
1:AD:137:ILE:O	1:AD:163:PHE:HA	2.13	0.48
5:AX:502:ASN:HA	6:NY:1730:ILE:HD12	1.95	0.48
1:FB:120:ILE:HG13	3:FT:242:PHE:HE1	1.77	0.48
1:FE:138:ILE:HB	1:FE:177:THR:HB	1.95	0.48
1:GD:80:ILE:HG13	1:GE:106:LEU:HB3	1.94	0.48
1:HD:104:THR:OG1	1:HE:181:VAL:O	2.31	0.48
3:IT:213:ARG:NH2	1:JA:207:GLN:OE1	2.46	0.48
6:IY:1761:LYS:HD3	6:IY:1763:ILE:HD11	1.94	0.48
3:KT:213:ARG:NH2	1:LA:207:GLN:OE1	2.46	0.48
6:KY:1761:LYS:HD3	6:KY:1763:ILE:HD11	1.94	0.48
2:Lm:219:ASN:HD22	2:Lm:222:TYR:HE2	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AX:436:GLN:OE1	5:AX:465:ARG:NE	2.42	0.48
1:BD:178:PHE:CE1	1:BE:107:TYR:HB3	2.48	0.48
6:CY:1694:GLN:NE2	6:CY:1882:MET:O	2.43	0.48
2:Em:259:ILE:HA	2:Em:262:ILE:HD12	1.96	0.48
1:FD:104:THR:OG1	1:FE:181:VAL:O	2.30	0.48
1:GA:108:ALA:HA	3:Gt:133:MET:O	2.14	0.48
1:HD:140:THR:HA	1:HD:166:LYS:O	2.13	0.48
2:HM:328:THR:HG21	2:HM:357:PHE:HD1	1.79	0.48
1:JB:139:ILE:HG22	1:JB:146:VAL:HG12	1.95	0.48
1:KB:193:ASP:OD1	1:KB:193:ASP:N	2.43	0.48
3:KT:234:GLN:NE2	3:KT:238:SER:OG	2.43	0.48
1:MC:138:ILE:O	1:MC:176:ALA:HA	2.12	0.48
3:Nt:207:GLU:OE1	3:Nt:207:GLU:N	2.29	0.48
1:AD:149:TYR:OH	1:AE:112:LEU:O	2.27	0.48
1:AE:109:MET:HE1	1:AE:111:LEU:HD13	1.94	0.48
2:EM:310:VAL:HG21	2:EM:358:PHE:HE1	1.77	0.48
1:FA:302:ARG:NH1	1:FA:303:GLU:O	2.47	0.48
2:GM:263:ASN:O	2:GM:267:LEU:HB2	2.13	0.48
5:GX:453:ALA:O	6:GY:1737:LYS:NZ	2.47	0.48
1:IB:139:ILE:HG22	1:IB:146:VAL:HG12	1.94	0.48
2:KM:203:GLU:OE2	2:KM:207:ASN:ND2	2.46	0.48
6:KY:1689:THR:O	6:KY:1724:ASN:ND2	2.41	0.48
1:LB:120:ILE:HG13	3:LT:242:PHE:CE1	2.48	0.48
1:LD:167:ILE:HB	1:MA:194:LYS:HZ2	1.77	0.48
2:Lm:281:LYS:O	2:Mm:219:ASN:ND2	2.47	0.48
1:MB:121:GLU:HG3	1:MC:124:ILE:HD12	1.94	0.48
1:NB:115:ASN:OD1	1:NB:115:ASN:N	2.44	0.48
1:NB:135:ASP:HB2	1:NB:180:ARG:HB2	1.95	0.48
1:AA:80:ILE:O	3:At:64:GLN:NE2	2.41	0.48
3:At:97:GLY:O	3:At:125:THR:N	2.37	0.48
1:BB:126:LYS:HG2	1:BB:184:ARG:HH12	1.79	0.48
6:BY:1694:GLN:NE2	6:BY:1882:MET:O	2.43	0.48
2:Cm:357:PHE:O	2:Cm:360:THR:OG1	2.26	0.48
1:DA:302:ARG:NH1	1:DA:303:GLU:O	2.47	0.48
1:EE:136:LEU:HD23	1:EE:162:LYS:HB2	1.93	0.48
1:FA:111:LEU:HD11	3:Ft:133:MET:HB2	1.96	0.48
1:HB:126:LYS:HG2	1:HB:184:ARG:HH12	1.79	0.48
6:HY:1700:ILE:HD12	6:HY:1738:VAL:HG11	1.95	0.48
1:IA:302:ARG:NH1	1:IA:303:GLU:O	2.47	0.48
5:IX:453:ALA:O	6:IY:1737:LYS:NZ	2.47	0.48
6:IY:1700:ILE:HD12	6:IY:1738:VAL:HG11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KD:149:TYR:OH	1:KE:112:LEU:O	2.27	0.48
1:LB:153:LEU:HA	1:LB:156:LEU:HB2	1.96	0.48
1:MC:130:MET:SD	1:MC:182:PRO:HB3	2.53	0.48
1:MD:176:ALA:HB3	1:ME:109:MET:HE3	1.95	0.48
2:MM:212:LEU:HD13	2:MM:270:TYR:HB2	1.96	0.48
6:MY:1700:ILE:HD12	6:MY:1738:VAL:HG11	1.95	0.48
1:NA:302:ARG:NH1	1:NA:303:GLU:O	2.47	0.48
2:NM:198:LYS:HE2	2:NM:266:TYR:HE2	1.78	0.48
6:NY:1700:ILE:HD12	6:NY:1738:VAL:HG11	1.95	0.48
1:AA:136:LEU:HD22	1:AA:208:LYS:HD3	1.95	0.48
1:AC:146:VAL:HB	1:AC:165:LEU:HD12	1.95	0.48
6:AY:1700:ILE:HD12	6:AY:1738:VAL:HG11	1.95	0.48
1:BC:139:ILE:HB	1:BC:165:LEU:HD13	1.94	0.48
1:DA:107:TYR:CG	3:Dt:44:ILE:HD11	2.48	0.48
2:DM:280:VAL:HG23	2:DM:285:GLU:HG3	1.96	0.48
6:DY:1689:THR:O	6:DY:1724:ASN:ND2	2.41	0.48
3:FT:89:HIS:HE1	5:FX:401:TYR:CD2	2.32	0.48
1:GA:302:ARG:NH1	1:GA:303:GLU:O	2.47	0.48
3:GT:89:HIS:HE1	5:GX:401:TYR:CD2	2.32	0.48
1:HB:124:ILE:HG13	1:HC:124:ILE:HD11	1.95	0.48
1:HD:117:TYR:O	1:HD:121:GLU:CB	2.53	0.48
1:IB:143:LEU:O	1:IB:147:ASN:ND2	2.46	0.48
2:JM:205:SER:HA	2:JM:208:VAL:HG12	1.96	0.48
1:LD:138:ILE:HG13	1:LD:164:VAL:HB	1.96	0.48
6:LY:1700:ILE:HD12	6:LY:1738:VAL:HG11	1.95	0.48
1:MA:205:GLU:HA	1:MA:208:LYS:HZ3	1.78	0.48
1:NE:136:LEU:HD23	1:NE:162:LYS:HB3	1.94	0.48
2:Am:332:ASN:HA	2:Am:353:LYS:HD3	1.95	0.48
1:DB:139:ILE:HG22	1:DB:146:VAL:HG12	1.96	0.48
2:Dm:246:LEU:HD21	2:Dm:251:GLU:HB3	1.96	0.48
1:FB:120:ILE:HD11	3:FT:247:LEU:HB3	1.96	0.48
1:FB:158:LYS:NZ	1:FC:193:ASP:OD2	2.39	0.48
2:GM:198:LYS:HE2	2:GM:266:TYR:HE2	1.78	0.48
1:HA:302:ARG:NH1	1:HA:303:GLU:O	2.47	0.48
2:HM:246:LEU:HD22	2:HM:252:ARG:HG3	1.95	0.48
5:HX:453:ALA:O	6:HY:1737:LYS:NZ	2.47	0.48
1:ID:117:TYR:O	1:ID:121:GLU:CB	2.53	0.48
2:Km:246:LEU:HD21	2:Km:251:GLU:HB3	1.96	0.48
3:Kt:97:GLY:O	3:Kt:125:THR:N	2.37	0.48
1:LA:175:GLN:NE2	3:Lt:64:GLN:OE1	2.46	0.48
2:LM:333:ILE:O	2:LM:337:SER:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MB:193:ASP:OD1	1:MB:193:ASP:N	2.42	0.48
1:NA:136:LEU:HD22	1:NA:208:LYS:HD3	1.95	0.48
1:AE:153:LEU:HD13	1:AE:156:LEU:HD22	1.96	0.48
3:AT:89:HIS:HE1	5:AX:401:TYR:CD2	2.31	0.48
1:BA:136:LEU:HD22	1:BA:208:LYS:HD3	1.95	0.48
3:Bt:97:GLY:O	3:Bt:125:THR:N	2.37	0.48
1:CD:128:ARG:NH1	1:CD:132:THR:OG1	2.44	0.48
1:IB:153:LEU:HD13	1:IB:156:LEU:HD23	1.95	0.48
1:KD:129:ALA:O	1:KD:133:TYR:CB	2.55	0.48
5:KX:391:ALA:O	5:KX:505:ASN:ND2	2.41	0.48
2:Lm:218:ASP:HA	2:Lm:297:LYS:HG2	1.96	0.48
1:ND:137:ILE:O	1:ND:163:PHE:HA	2.13	0.48
2:AM:199:GLN:HA	2:AM:202:GLU:HG3	1.94	0.48
2:AM:246:LEU:HD22	2:AM:252:ARG:HG3	1.96	0.48
1:BE:140:THR:HG21	1:CA:278:PRO:HD3	1.96	0.48
2:Bm:357:PHE:O	2:Bm:360:THR:OG1	2.25	0.48
1:CA:107:TYR:CG	3:Ct:44:ILE:HD11	2.48	0.48
1:CA:136:LEU:HD22	1:CA:208:LYS:HD3	1.95	0.48
3:Ct:97:GLY:O	3:Ct:125:THR:N	2.37	0.48
6:DY:1700:ILE:HD12	6:DY:1738:VAL:HG11	1.95	0.48
6:EY:1905:ILE:O	6:EY:1908:SER:OG	2.25	0.48
1:GB:137:ILE:HD13	1:GB:153:LEU:HD23	1.95	0.48
6:GY:1700:ILE:HD12	6:GY:1738:VAL:HG11	1.95	0.48
1:HE:157:ASN:HD21	1:HE:161:ALA:H	1.61	0.48
5:HX:482:LYS:HA	3:IT:29:VAL:HG21	1.96	0.48
1:JC:138:ILE:O	1:JC:176:ALA:HA	2.13	0.48
2:Jm:218:ASP:HA	2:Jm:297:LYS:HG2	1.96	0.48
1:KD:124:ILE:HD11	1:KE:112:LEU:HD21	1.95	0.48
2:Km:273:PHE:HD2	2:Km:310:VAL:HG11	1.79	0.48
1:MA:302:ARG:NH1	1:MA:303:GLU:O	2.47	0.48
1:NA:205:GLU:HA	1:NA:208:LYS:HZ3	1.79	0.48
2:Nm:259:ILE:HA	2:Nm:262:ILE:HD12	1.96	0.48
1:AE:138:ILE:HB	1:AE:177:THR:HB	1.95	0.48
6:BY:1700:ILE:HD12	6:BY:1738:VAL:HG11	1.95	0.48
3:Bt:96:ILE:HG12	3:Bt:123:GLN:HB3	1.95	0.48
1:CB:124:ILE:HG13	1:CC:124:ILE:HD11	1.96	0.48
1:CC:133:TYR:HB3	1:CC:181:VAL:HG21	1.95	0.48
1:DA:82:ASP:OD1	1:DA:126:LYS:NZ	2.38	0.48
1:DA:136:LEU:HD22	1:DA:208:LYS:HD3	1.95	0.48
3:DT:234:GLN:HE21	3:DT:238:SER:HG	1.59	0.48
3:Dt:96:ILE:HG12	3:Dt:123:GLN:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EX:454:ALA:HB2	6:EY:1737:LYS:HE2	1.95	0.48
1:FD:106:LEU:HB3	1:FE:179:LEU:HD13	1.96	0.48
1:FD:158:LYS:HE3	1:FD:159:ARG:O	2.14	0.48
2:FM:290:THR:HG21	2:FM:355:PHE:HA	1.96	0.48
1:IB:135:ASP:HB2	1:IB:180:ARG:HB2	1.95	0.48
1:IE:139:ILE:HB	1:IE:165:LEU:HD13	1.95	0.48
5:JX:391:ALA:O	5:JX:505:ASN:ND2	2.41	0.48
1:KA:302:ARG:NH1	1:KA:303:GLU:O	2.47	0.48
5:LX:391:ALA:O	5:LX:505:ASN:ND2	2.41	0.48
1:NC:169:GLU:OE2	3:Nt:233:ARG:NH2	2.47	0.48
5:NX:436:GLN:OE1	5:NX:465:ARG:NE	2.42	0.48
3:Nt:96:ILE:HG12	3:Nt:123:GLN:HB3	1.95	0.48
1:AB:146:VAL:HB	1:AB:165:LEU:HD22	1.96	0.47
2:Am:295:ASN:N	2:Am:295:ASN:OD1	2.46	0.47
1:BA:302:ARG:NH1	1:BA:303:GLU:O	2.47	0.47
1:BE:157:ASN:HD21	1:BE:161:ALA:H	1.61	0.47
1:DD:117:TYR:O	1:DD:121:GLU:CB	2.50	0.47
1:DD:133:TYR:HA	1:DE:101:LYS:HE2	1.95	0.47
2:Dm:225:GLN:O	2:Dm:229:ASN:ND2	2.47	0.47
3:Ft:96:ILE:HG12	3:Ft:123:GLN:HB3	1.95	0.47
1:HD:105:TYR:CZ	1:HE:180:ARG:HB2	2.49	0.47
3:HT:213:ARG:NH2	1:IA:207:GLN:OE1	2.47	0.47
1:IE:140:THR:HG21	1:JA:278:PRO:HD3	1.95	0.47
5:IX:391:ALA:O	5:IX:505:ASN:ND2	2.41	0.47
3:It:96:ILE:HG12	3:It:123:GLN:HB3	1.95	0.47
2:JM:276:LEU:HB3	2:JM:289:LEU:HD21	1.96	0.47
6:JY:1730:ILE:HD12	5:KX:502:ASN:HA	1.95	0.47
3:Jt:207:GLU:OE1	3:Jt:207:GLU:N	2.29	0.47
1:KD:108:ALA:HA	1:KE:177:THR:HA	1.95	0.47
1:LA:136:LEU:HD22	1:LA:208:LYS:HD3	1.95	0.47
1:LB:139:ILE:HG22	1:LB:146:VAL:HG12	1.96	0.47
1:LB:193:ASP:OD1	1:LB:193:ASP:N	2.44	0.47
2:LM:328:THR:HG21	2:LM:357:PHE:HD1	1.79	0.47
1:MA:136:LEU:HD22	1:MA:208:LYS:HD3	1.95	0.47
6:MY:1905:ILE:O	6:MY:1908:SER:OG	2.25	0.47
2:Nm:205:SER:HA	2:Nm:208:VAL:HG12	1.96	0.47
5:NX:391:ALA:O	5:NX:505:ASN:ND2	2.41	0.47
2:BM:345:THR:HG23	2:BM:348:GLN:H	1.79	0.47
3:BT:211:THR:O	1:CA:159:ARG:NH2	2.44	0.47
1:CB:139:ILE:HG22	1:CB:146:VAL:HG12	1.95	0.47
2:CM:246:LEU:HD22	2:CM:252:ARG:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:136:LEU:HD22	1:EA:208:LYS:HD3	1.95	0.47
1:EA:302:ARG:NH1	1:EA:303:GLU:O	2.47	0.47
6:EY:1689:THR:O	6:EY:1724:ASN:ND2	2.41	0.47
6:EY:1700:ILE:HD12	6:EY:1738:VAL:HG11	1.95	0.47
1:FC:184:ARG:HH11	1:FC:186:ASP:H	1.62	0.47
2:GM:328:THR:HG21	2:GM:357:PHE:HD1	1.80	0.47
3:HT:89:HIS:HE1	5:HX:401:TYR:CD2	2.32	0.47
6:HY:1694:GLN:NE2	6:HY:1882:MET:O	2.43	0.47
1:IB:128:ARG:HG3	1:IB:156:LEU:HD11	1.96	0.47
2:IM:199:GLN:HA	2:IM:202:GLU:HG3	1.95	0.47
5:IX:482:LYS:HA	3:JT:29:VAL:HG21	1.96	0.47
6:KY:1700:ILE:HD12	6:KY:1738:VAL:HG11	1.95	0.47
2:Km:274:SER:HB2	2:Km:314:PHE:HD1	1.80	0.47
1:LD:146:VAL:O	1:LD:150:TYR:HB2	2.14	0.47
3:LT:89:HIS:HE1	5:LX:401:TYR:CD2	2.32	0.47
2:Lm:344:LYS:HB3	2:Lm:347:MET:HB2	1.96	0.47
5:MX:436:GLN:OE1	5:MX:465:ARG:NE	2.42	0.47
1:NE:172:PRO:HG2	1:NE:173:TYR:HD1	1.79	0.47
1:AA:159:ARG:NH2	3:NT:211:THR:O	2.47	0.47
1:AA:302:ARG:NH1	1:AA:303:GLU:O	2.47	0.47
2:AM:290:THR:HG22	2:AM:358:PHE:HD2	1.80	0.47
3:AT:213:ARG:NH2	1:BA:207:GLN:OE1	2.47	0.47
1:CE:172:PRO:HG2	1:CE:173:TYR:HD1	1.80	0.47
2:FM:221:ASP:OD2	2:FM:221:ASP:N	2.44	0.47
1:GA:136:LEU:HD22	1:GA:208:LYS:HD3	1.95	0.47
3:HT:234:GLN:NE2	3:HT:238:SER:OG	2.43	0.47
2:IM:345:THR:HG23	2:IM:348:GLN:H	1.79	0.47
5:JX:436:GLN:OE1	5:JX:465:ARG:NE	2.42	0.47
6:JY:1689:THR:O	6:JY:1724:ASN:ND2	2.41	0.47
1:KD:138:ILE:HG13	1:KD:164:VAL:HB	1.96	0.47
5:KX:455:ILE:HB	6:KY:1765:PRO:HB3	1.95	0.47
2:Km:225:GLN:O	2:Km:229:ASN:ND2	2.47	0.47
1:LE:140:THR:HG21	1:MA:278:PRO:HD3	1.96	0.47
2:Lm:220:ILE:HG13	2:Lm:224:LEU:HD23	1.97	0.47
3:Lt:96:ILE:HG12	3:Lt:123:GLN:HB3	1.95	0.47
2:Nm:341:MET:HE2	2:Nm:344:LYS:HE2	1.95	0.47
1:BC:179:LEU:HG	1:BC:180:ARG:HB2	1.95	0.47
2:BM:280:VAL:HG23	2:BM:285:GLU:HG3	1.96	0.47
5:BX:455:ILE:HB	6:BY:1765:PRO:HB3	1.95	0.47
1:CA:302:ARG:NH1	1:CA:303:GLU:O	2.47	0.47
1:CE:139:ILE:HB	1:CE:165:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Cm:316:PHE:HE1	2:Cm:365:TYR:HD1	1.63	0.47
1:DB:135:ASP:HB2	1:DB:180:ARG:HB2	1.96	0.47
1:DE:140:THR:HG21	1:EA:278:PRO:HD3	1.97	0.47
1:EC:131:GLY:HA3	1:EC:153:LEU:HD22	1.97	0.47
3:Et:96:ILE:HG12	3:Et:123:GLN:HB3	1.95	0.47
1:FA:136:LEU:HD22	1:FA:208:LYS:HD3	1.95	0.47
1:GC:139:ILE:HG22	1:GC:146:VAL:HG12	1.97	0.47
3:Gt:96:ILE:HG12	3:Gt:123:GLN:HB3	1.95	0.47
1:HA:136:LEU:HD22	1:HA:208:LYS:HD3	1.95	0.47
1:HD:123:PRO:HA	1:HD:126:LYS:HE2	1.96	0.47
1:HE:136:LEU:HB2	1:HE:179:LEU:HB2	1.96	0.47
1:HE:172:PRO:HG2	1:HE:173:TYR:HD1	1.80	0.47
3:Ht:96:ILE:HG12	3:Ht:123:GLN:HB3	1.95	0.47
1:IA:175:GLN:NE2	3:It:64:GLN:OE1	2.46	0.47
1:JA:82:ASP:OD1	1:JA:126:LYS:NZ	2.38	0.47
1:JA:302:ARG:NH1	1:JA:303:GLU:O	2.47	0.47
2:Jm:188:LYS:HG3	2:Jm:189:LYS:HD3	1.95	0.47
1:KA:136:LEU:HD22	1:KA:208:LYS:HD3	1.95	0.47
1:KC:169:GLU:OE2	3:Kt:233:ARG:NH2	2.47	0.47
2:KM:290:THR:HG22	2:KM:358:PHE:HD2	1.79	0.47
2:KM:290:THR:HG21	2:KM:355:PHE:HA	1.97	0.47
1:LA:302:ARG:NH1	1:LA:303:GLU:O	2.47	0.47
1:LD:137:ILE:O	1:LD:163:PHE:HA	2.14	0.47
2:LM:290:THR:HG22	2:LM:358:PHE:HD2	1.79	0.47
3:Lt:32:LYS:NZ	3:MT:47:TYR:OH	2.48	0.47
2:Mm:274:SER:HB2	2:Mm:314:PHE:HD1	1.80	0.47
1:AE:107:TYR:CE2	1:AE:109:MET:HB2	2.49	0.47
1:BB:155:ALA:HA	3:Bt:179:LYS:HE2	1.95	0.47
5:BX:436:GLN:OE1	5:BX:465:ARG:NE	2.42	0.47
6:CY:1700:ILE:HD12	6:CY:1738:VAL:HG11	1.95	0.47
1:DB:153:LEU:HA	1:DB:156:LEU:HB2	1.96	0.47
1:DB:172:PRO:HG3	3:DT:256:VAL:HG21	1.97	0.47
5:FX:453:ALA:O	6:FY:1737:LYS:NZ	2.47	0.47
5:GX:482:LYS:HA	3:HT:29:VAL:HG21	1.96	0.47
2:Gm:259:ILE:HA	2:Gm:262:ILE:HD12	1.97	0.47
5:HX:391:ALA:O	5:HX:505:ASN:ND2	2.41	0.47
1:IA:136:LEU:HD22	1:IA:208:LYS:HD3	1.95	0.47
3:IT:89:HIS:HE1	5:IX:401:TYR:CD2	2.32	0.47
1:JA:136:LEU:HD22	1:JA:208:LYS:HD3	1.95	0.47
1:JD:143:LEU:HD21	3:KT:268:TYR:CD1	2.49	0.47
1:KB:118:LEU:HD21	1:KC:152:ILE:HD11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KB:124:ILE:HG13	1:KC:124:ILE:HD11	1.94	0.47
1:KB:153:LEU:HA	1:KB:156:LEU:HB2	1.96	0.47
3:KT:89:HIS:HE1	5:KX:401:TYR:CD2	2.33	0.47
1:NE:153:LEU:HD13	1:NE:156:LEU:HD13	1.96	0.47
6:AY:1730:ILE:HD12	5:BX:502:ASN:HA	1.96	0.47
3:At:207:GLU:OE1	3:At:207:GLU:N	2.29	0.47
1:BD:133:TYR:HD1	1:BE:101:LYS:HE2	1.78	0.47
2:BM:192:ARG:HA	2:BM:192:ARG:HH11	1.78	0.47
2:BM:199:GLN:HA	2:BM:202:GLU:HG3	1.95	0.47
1:CE:79:ASP:N	1:CE:79:ASP:OD1	2.45	0.47
1:CE:162:LYS:HA	1:CE:162:LYS:HD2	1.71	0.47
1:DD:179:LEU:HD13	1:DE:106:LEU:HD12	1.97	0.47
2:DM:290:THR:HG22	2:DM:358:PHE:HD2	1.78	0.47
3:ET:67:LEU:HB2	3:ET:131:VAL:HG13	1.96	0.47
3:ET:234:GLN:NE2	3:ET:238:SER:OG	2.43	0.47
2:Em:218:ASP:HA	2:Em:297:LYS:HG2	1.97	0.47
3:FT:67:LEU:HB2	3:FT:131:VAL:HG13	1.96	0.47
1:GB:117:TYR:O	1:GB:120:ILE:N	2.44	0.47
1:GE:107:TYR:HE2	1:GE:109:MET:HB2	1.77	0.47
2:GM:205:SER:HA	2:GM:208:VAL:HG12	1.97	0.47
3:GT:211:THR:O	1:HA:159:ARG:NH2	2.46	0.47
1:HD:143:LEU:O	1:HD:147:ASN:HB2	2.15	0.47
2:HM:290:THR:HG22	2:HM:358:PHE:HD2	1.79	0.47
1:ID:158:LYS:HA	1:ID:158:LYS:HD2	1.65	0.47
1:KB:139:ILE:HG22	1:KB:146:VAL:HG12	1.95	0.47
1:KB:182:PRO:HG3	1:KC:107:TYR:HB2	1.97	0.47
1:KB:191:THR:HG23	1:KB:192:LEU:HG	1.96	0.47
1:KD:122:ASN:OD1	1:KD:126:LYS:NZ	2.46	0.47
5:LX:436:GLN:OE1	5:LX:465:ARG:NE	2.42	0.47
5:MX:391:ALA:O	5:MX:505:ASN:ND2	2.41	0.47
2:NM:188:LYS:O	2:NM:191:SER:OG	2.30	0.47
1:AC:139:ILE:HB	1:AC:165:LEU:HD13	1.97	0.47
1:AE:172:PRO:HG2	1:AE:173:TYR:HD1	1.80	0.47
2:AM:324:ILE:HA	2:AM:327:LYS:HE3	1.97	0.47
2:Am:274:SER:O	2:Am:278:LYS:HB2	2.14	0.47
1:BB:136:LEU:HA	1:BB:161:ALA:HB1	1.95	0.47
1:BE:139:ILE:HB	1:BE:165:LEU:HD13	1.97	0.47
1:CB:122:ASN:O	1:CB:126:LYS:HB2	2.14	0.47
2:CM:290:THR:HG21	2:CM:355:PHE:HA	1.97	0.47
3:CT:234:GLN:NE2	3:CT:238:SER:OG	2.43	0.47
1:DB:191:THR:HG23	1:DB:192:LEU:HG	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DE:139:ILE:HG12	1:DE:149:TYR:CE2	2.50	0.47
2:DM:188:LYS:O	2:DM:191:SER:OG	2.33	0.47
3:DT:67:LEU:HB2	3:DT:131:VAL:HG13	1.96	0.47
3:ET:101:LYS:HD2	3:ET:101:LYS:HA	1.72	0.47
5:EX:391:ALA:O	5:EX:505:ASN:ND2	2.41	0.47
5:EX:502:ASN:OD1	5:EX:502:ASN:N	2.48	0.47
3:FT:266:ASN:HB3	3:FT:270:ARG:HH12	1.80	0.47
2:Fm:295:ASN:OD1	2:Fm:295:ASN:N	2.46	0.47
1:GC:122:ASN:O	1:GC:126:LYS:HB2	2.14	0.47
3:GT:67:LEU:HB2	3:GT:131:VAL:HG13	1.96	0.47
3:GT:234:GLN:NE2	3:GT:238:SER:OG	2.43	0.47
3:GT:266:ASN:HB3	3:GT:270:ARG:HH12	1.80	0.47
5:GX:391:ALA:O	5:GX:505:ASN:ND2	2.41	0.47
5:GX:502:ASN:OD1	5:GX:502:ASN:N	2.48	0.47
6:GY:1859:LEU:O	6:GY:1863:MET:HB2	2.15	0.47
1:IB:150:TYR:OH	1:IB:154:LYS:NZ	2.45	0.47
6:IY:1859:LEU:O	6:IY:1863:MET:HB2	2.15	0.47
1:JB:191:THR:HG23	1:JB:192:LEU:HG	1.97	0.47
3:JT:213:ARG:NH2	1:KA:207:GLN:OE1	2.48	0.47
3:Jt:216:ASN:O	3:Jt:220:ILE:HG12	2.15	0.47
2:KM:328:THR:HG21	2:KM:357:PHE:HD1	1.80	0.47
2:KM:344:LYS:HB2	2:KM:344:LYS:HE2	1.62	0.47
1:LD:114:TYR:H	1:LE:145:GLN:HE22	1.63	0.47
1:LE:137:ILE:HA	1:LE:177:THR:O	2.14	0.47
3:LT:266:ASN:HB3	3:LT:270:ARG:HH12	1.80	0.47
3:Lt:100:ASN:N	3:Lt:100:ASN:OD1	2.48	0.47
3:MT:266:ASN:HB3	3:MT:270:ARG:HH12	1.80	0.47
5:MX:419:ILE:HD12	3:NT:39:VAL:HG11	1.97	0.47
2:Mm:274:SER:O	2:Mm:278:LYS:HB2	2.14	0.47
1:NB:193:ASP:OD1	1:NB:193:ASP:N	2.44	0.47
2:NM:324:ILE:HA	2:NM:327:LYS:HE3	1.97	0.47
3:Nt:97:GLY:O	3:Nt:125:THR:N	2.37	0.47
1:AC:140:THR:HG22	1:AC:166:LYS:HB2	1.97	0.47
1:AC:184:ARG:HH11	1:AC:186:ASP:H	1.63	0.47
1:AD:179:LEU:HD11	1:AE:106:LEU:HD12	1.97	0.47
4:AU:609:UNK:HA	2:Am:273:PHE:CZ	2.50	0.47
3:BT:117:ASP:OD1	3:BT:117:ASP:N	2.48	0.47
3:Bt:216:ASN:O	3:Bt:220:ILE:HG12	2.15	0.47
2:CM:328:THR:HG21	2:CM:357:PHE:HD1	1.79	0.47
3:CT:67:LEU:HB2	3:CT:131:VAL:HG13	1.96	0.47
2:DM:242:ALA:HA	2:DM:245:THR:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Dt:216:ASN:O	3:Dt:220:ILE:HG12	2.15	0.47
1:EA:82:ASP:OD1	1:EA:126:LYS:NZ	2.38	0.47
2:EM:214:ARG:NH2	2:EM:216:GLU:O	2.47	0.47
6:EY:1859:LEU:O	6:EY:1863:MET:HB2	2.15	0.47
6:FY:1730:ILE:HD12	5:GX:502:ASN:HA	1.96	0.47
3:Ft:128:GLN:NE2	3:Ft:130:GLY:O	2.48	0.47
1:GE:172:PRO:HG2	1:GE:173:TYR:HD1	1.80	0.47
3:Gt:216:ASN:O	3:Gt:220:ILE:HG12	2.15	0.47
2:Hm:220:ILE:HG13	2:Hm:224:LEU:HD23	1.97	0.47
3:Ht:216:ASN:O	3:Ht:220:ILE:HG12	2.15	0.47
3:It:128:GLN:NE2	3:It:130:GLY:O	2.48	0.47
1:KD:124:ILE:HG23	1:KE:117:TYR:HE1	1.79	0.47
2:KM:345:THR:HG23	2:KM:348:GLN:H	1.80	0.47
1:LA:133:TYR:HD2	3:Lt:56:LEU:HD22	1.79	0.47
1:LC:126:LYS:O	1:LC:130:MET:HG2	2.14	0.47
1:BD:129:ALA:O	1:BD:133:TYR:CB	2.56	0.47
3:BT:266:ASN:HB3	3:BT:270:ARG:HH12	1.80	0.47
3:CT:266:ASN:HB3	3:CT:270:ARG:HH12	1.80	0.47
6:DY:1859:LEU:O	6:DY:1863:MET:HB2	2.15	0.47
6:FY:1859:LEU:O	6:FY:1863:MET:HB2	2.15	0.47
1:GE:113:ASP:HB3	1:GE:116:ASN:HB3	1.96	0.47
1:HC:133:TYR:HB3	1:HC:181:VAL:HG11	1.97	0.47
2:IM:188:LYS:O	2:IM:191:SER:OG	2.32	0.47
2:JM:246:LEU:HD22	2:JM:252:ARG:HG3	1.96	0.47
3:Jt:96:ILE:HG12	3:Jt:123:GLN:HB3	1.95	0.47
1:LC:139:ILE:HB	1:LC:165:LEU:HD13	1.96	0.47
1:LC:171:MET:HE3	1:LC:171:MET:HB3	1.74	0.47
5:MX:410:ARG:HH12	5:NX:445:ASP:HA	1.80	0.47
1:NE:157:ASN:ND2	1:NE:159:ARG:O	2.47	0.47
1:AA:278:PRO:HD3	1:NE:140:THR:HG21	1.96	0.47
1:AB:139:ILE:HG22	1:AB:146:VAL:HG12	1.96	0.47
3:AT:67:LEU:HB2	3:AT:131:VAL:HG13	1.96	0.47
3:At:216:ASN:O	3:At:220:ILE:HG12	2.15	0.47
3:BT:67:LEU:HB2	3:BT:131:VAL:HG13	1.96	0.47
6:CY:1859:LEU:O	6:CY:1863:MET:HB2	2.15	0.47
6:DY:1905:ILE:O	6:DY:1908:SER:OG	2.25	0.47
1:ED:104:THR:OG1	1:EE:181:VAL:O	2.32	0.47
2:EM:305:LYS:NZ	3:Et:231:GLN:O	2.38	0.47
3:HT:266:ASN:HB3	3:HT:270:ARG:HH12	1.80	0.47
3:Ht:128:GLN:NE2	3:Ht:130:GLY:O	2.48	0.47
3:IT:266:ASN:HB3	3:IT:270:ARG:HH12	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:IX:502:ASN:OD1	5:IX:502:ASN:N	2.48	0.47
3:JT:101:LYS:HA	3:JT:101:LYS:HD2	1.72	0.47
3:JT:266:ASN:HB3	3:JT:270:ARG:HH12	1.80	0.47
6:JY:1700:ILE:HD12	6:JY:1738:VAL:HG11	1.95	0.47
3:Mt:100:ASN:OD1	3:Mt:100:ASN:N	2.48	0.47
3:Mt:216:ASN:O	3:Mt:220:ILE:HG12	2.15	0.47
5:CX:502:ASN:OD1	5:CX:502:ASN:N	2.48	0.46
3:Et:128:GLN:NE2	3:Et:130:GLY:O	2.48	0.46
3:Et:216:ASN:O	3:Et:220:ILE:HG12	2.15	0.46
1:FA:149:TYR:OH	3:Ft:68:PRO:O	2.29	0.46
3:Ft:97:GLY:O	3:Ft:125:THR:N	2.37	0.46
1:HC:171:MET:SD	1:HC:171:MET:N	2.88	0.46
1:IC:118:LEU:HB3	3:It:187:ARG:HB2	1.97	0.46
1:IE:109:MET:HE1	1:IE:111:LEU:HD13	1.97	0.46
2:IM:205:SER:HA	2:IM:208:VAL:HG12	1.97	0.46
2:JM:333:ILE:O	2:JM:337:SER:HB3	2.15	0.46
3:Jt:128:GLN:NE2	3:Jt:130:GLY:O	2.48	0.46
1:KB:135:ASP:HB2	1:KB:180:ARG:HB2	1.97	0.46
3:Kt:128:GLN:NE2	3:Kt:130:GLY:O	2.48	0.46
1:LA:199:ASP:OD1	1:LA:199:ASP:N	2.48	0.46
1:MC:126:LYS:HD2	1:NA:192:LEU:HD12	1.95	0.46
2:MM:199:GLN:HA	2:MM:202:GLU:HG3	1.96	0.46
2:NM:187:ASN:ND2	2:NM:251:GLU:OE1	2.46	0.46
3:Nt:216:ASN:O	3:Nt:220:ILE:HG12	2.15	0.46
1:AA:117:TYR:CE1	3:At:80:VAL:HG23	2.50	0.46
3:AT:117:ASP:N	3:AT:117:ASP:OD1	2.48	0.46
1:BB:130:MET:HG2	1:BB:178:PHE:CG	2.50	0.46
1:BD:136:LEU:HD12	1:BD:179:LEU:HD11	1.97	0.46
2:Bm:295:ASN:OD1	2:Bm:295:ASN:N	2.48	0.46
5:CX:436:GLN:OE1	5:CX:465:ARG:NE	2.42	0.46
3:Ct:128:GLN:NE2	3:Ct:130:GLY:O	2.48	0.46
5:DX:436:GLN:OE1	5:DX:465:ARG:NE	2.42	0.46
1:EA:133:TYR:HD2	3:Et:56:LEU:HD22	1.79	0.46
1:EC:139:ILE:HB	1:EC:165:LEU:HD13	1.96	0.46
2:Em:220:ILE:HG13	2:Em:224:LEU:HD23	1.97	0.46
1:FC:158:LYS:HE3	1:FC:158:LYS:HB2	1.77	0.46
1:HA:80:ILE:O	3:Ht:64:GLN:NE2	2.42	0.46
3:HT:67:LEU:HB2	3:HT:131:VAL:HG13	1.96	0.46
1:IA:205:GLU:HA	1:IA:208:LYS:HZ3	1.80	0.46
2:IM:328:THR:HG21	2:IM:357:PHE:HD1	1.80	0.46
1:LA:149:TYR:OH	3:Lt:68:PRO:O	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LB:135:ASP:HB2	1:LB:180:ARG:HB2	1.97	0.46
1:LD:140:THR:HA	1:LD:166:LYS:O	2.15	0.46
3:NT:67:LEU:HB2	3:NT:131:VAL:HG13	1.96	0.46
1:AE:136:LEU:HB2	1:AE:179:LEU:HB2	1.97	0.46
6:BY:1764:THR:HG23	6:BY:1766:ASP:H	1.81	0.46
6:CY:1764:THR:HG23	6:CY:1766:ASP:H	1.81	0.46
3:Ct:100:ASN:N	3:Ct:100:ASN:OD1	2.48	0.46
3:Ct:216:ASN:O	3:Ct:220:ILE:HG12	2.15	0.46
1:EC:120:ILE:HD11	3:ET:241:ILE:HG12	1.97	0.46
6:EY:1730:ILE:HD12	5:FX:502:ASN:HA	1.97	0.46
2:FM:204:TYR:HB2	2:FM:231:PHE:HB2	1.97	0.46
2:Hm:274:SER:HB2	2:Hm:314:PHE:HD1	1.79	0.46
2:JM:187:ASN:ND2	2:JM:251:GLU:OE1	2.48	0.46
1:KD:104:THR:OG1	1:KE:181:VAL:O	2.32	0.46
3:KT:266:ASN:HB3	3:KT:270:ARG:HH12	1.80	0.46
3:Kt:216:ASN:O	3:Kt:220:ILE:HG12	2.15	0.46
3:Lt:216:ASN:O	3:Lt:220:ILE:HG12	2.15	0.46
2:MM:317:ASP:OD2	2:MM:319:GLN:HG3	2.16	0.46
6:MY:1730:ILE:HD12	5:NX:502:ASN:HA	1.98	0.46
3:Mt:128:GLN:NE2	3:Mt:130:GLY:O	2.48	0.46
3:NT:266:ASN:HB3	3:NT:270:ARG:HH12	1.80	0.46
1:BD:140:THR:HG22	1:BD:166:LYS:HB2	1.98	0.46
6:BY:1859:LEU:O	6:BY:1863:MET:HB2	2.15	0.46
2:CM:242:ALA:HA	2:CM:245:THR:HG22	1.98	0.46
2:Cm:225:GLN:O	2:Cm:229:ASN:ND2	2.49	0.46
1:DA:143:LEU:HD13	1:DB:150:TYR:CZ	2.50	0.46
1:EA:304:LYS:HZ3	1:ED:80:ILE:H	1.63	0.46
2:EM:290:THR:HG22	2:EM:358:PHE:HD2	1.81	0.46
3:Gt:207:GLU:OE1	3:Gt:207:GLU:N	2.29	0.46
3:Ht:97:GLY:O	3:Ht:125:THR:N	2.37	0.46
3:KT:67:LEU:HB2	3:KT:131:VAL:HG13	1.96	0.46
1:LB:105:TYR:HB2	1:LC:182:PRO:HD2	1.98	0.46
1:LD:130:MET:HE2	1:LD:178:PHE:CG	2.50	0.46
2:Lm:357:PHE:O	2:Lm:360:THR:OG1	2.25	0.46
5:MX:482:LYS:HA	3:NT:29:VAL:HG21	1.97	0.46
2:Nm:345:THR:HG23	2:Nm:348:GLN:H	1.80	0.46
1:CB:191:THR:HG23	1:CB:192:LEU:HG	1.98	0.46
3:Dt:128:GLN:NE2	3:Dt:130:GLY:O	2.48	0.46
1:EA:104:THR:HG22	3:Et:138:TYR:HA	1.97	0.46
1:EB:177:THR:HA	1:EC:107:TYR:O	2.16	0.46
3:ET:266:ASN:HB3	3:ET:270:ARG:HH12	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FY:1689:THR:O	6:FY:1724:ASN:ND2	2.41	0.46
1:HE:111:LEU:HD12	1:HE:112:LEU:HD23	1.97	0.46
6:HY:1730:ILE:HD12	5:IX:502:ASN:HA	1.96	0.46
6:HY:1859:LEU:O	6:HY:1863:MET:HB2	2.15	0.46
3:Ht:100:ASN:OD1	3:Ht:100:ASN:N	2.48	0.46
1:IA:107:TYR:CG	3:It:44:ILE:HD11	2.51	0.46
1:ID:105:TYR:CE2	1:IE:130:MET:HE1	2.50	0.46
6:JY:1859:LEU:O	6:JY:1863:MET:HB2	2.15	0.46
2:Jm:342:SER:OG	2:Jm:348:GLN:OE1	2.27	0.46
2:Km:332:ASN:HA	2:Km:353:LYS:HD3	1.97	0.46
2:MM:305:LYS:NZ	3:Mt:231:GLN:O	2.38	0.46
1:NA:199:ASP:OD1	1:NA:199:ASP:N	2.49	0.46
5:AX:379:GLN:NE2	6:NY:1908:SER:O	2.48	0.46
6:AY:1859:LEU:O	6:AY:1863:MET:HB2	2.15	0.46
3:At:128:GLN:NE2	3:At:130:GLY:O	2.48	0.46
1:BD:80:ILE:HA	1:BE:106:LEU:O	2.16	0.46
1:DC:133:TYR:HB3	1:DC:181:VAL:HG11	1.98	0.46
2:DM:345:THR:HG23	2:DM:348:GLN:H	1.81	0.46
1:EB:120:ILE:HG13	3:ET:242:PHE:CE1	2.49	0.46
1:GE:111:LEU:HD12	1:GE:112:LEU:HD23	1.97	0.46
6:GY:1764:THR:HG23	6:GY:1766:ASP:H	1.81	0.46
2:Gm:206:ASN:O	2:Gm:209:SER:OG	2.28	0.46
2:Gm:218:ASP:HA	2:Gm:297:LYS:HG2	1.97	0.46
2:Gm:332:ASN:HA	2:Gm:353:LYS:HD3	1.98	0.46
3:Gt:128:GLN:NE2	3:Gt:130:GLY:O	2.48	0.46
1:HC:184:ARG:HH11	1:HC:186:ASP:H	1.64	0.46
1:ID:114:TYR:HE1	1:IE:149:TYR:HB2	1.81	0.46
3:JT:67:LEU:HB2	3:JT:131:VAL:HG13	1.96	0.46
1:LA:234:MET:HB3	1:LB:138:ILE:HD11	1.98	0.46
3:LT:67:LEU:HB2	3:LT:131:VAL:HG13	1.96	0.46
3:LT:234:GLN:NE2	3:LT:238:SER:OG	2.43	0.46
3:Lt:128:GLN:NE2	3:Lt:130:GLY:O	2.48	0.46
3:MT:67:LEU:HB2	3:MT:131:VAL:HG13	1.96	0.46
2:Nm:263:ASN:O	2:Nm:267:LEU:HB2	2.14	0.46
2:Nm:290:THR:HG22	2:Nm:358:PHE:HD2	1.80	0.46
6:NY:1905:ILE:O	6:NY:1908:SER:OG	2.25	0.46
2:CM:205:SER:HA	2:CM:208:VAL:HG12	1.98	0.46
5:CX:461:ASN:OD1	5:CX:461:ASN:N	2.49	0.46
2:Dm:198:LYS:O	2:Dm:201:ILE:N	2.49	0.46
1:EB:153:LEU:HA	1:EB:156:LEU:HB2	1.97	0.46
1:GA:199:ASP:OD1	1:GA:199:ASP:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Gm:220:ILE:HG13	2:Gm:224:LEU:HD23	1.98	0.46
1:HD:111:LEU:HD13	1:HD:114:TYR:CE2	2.51	0.46
1:HD:114:TYR:H	1:HE:145:GLN:HE22	1.63	0.46
3:IT:67:LEU:HB2	3:IT:131:VAL:HG13	1.96	0.46
3:It:100:ASN:N	3:It:100:ASN:OD1	2.48	0.46
3:It:216:ASN:O	3:It:220:ILE:HG12	2.15	0.46
2:JM:199:GLN:HA	2:JM:202:GLU:HG3	1.97	0.46
1:KB:112:LEU:HD21	3:KT:238:SER:HB3	1.98	0.46
1:KB:115:ASN:OD1	1:KB:115:ASN:N	2.47	0.46
1:KB:136:LEU:HB3	1:KB:179:LEU:HB2	1.98	0.46
2:Km:259:ILE:HA	2:Km:262:ILE:HD12	1.98	0.46
1:LB:112:LEU:HD21	3:LT:238:SER:HB3	1.97	0.46
2:AM:276:LEU:HB3	2:AM:289:LEU:HD21	1.97	0.46
3:BT:90:SER:HB2	3:BT:135:ALA:HB1	1.98	0.46
2:Bm:332:ASN:HA	2:Bm:353:LYS:HD3	1.98	0.46
1:CA:82:ASP:OD1	1:CA:126:LYS:NZ	2.38	0.46
5:DX:461:ASN:OD1	5:DX:461:ASN:N	2.49	0.46
6:DY:1730:ILE:HD12	5:EX:502:ASN:HA	1.98	0.46
6:FY:1764:THR:HG23	6:FY:1766:ASP:H	1.81	0.46
3:Ft:216:ASN:O	3:Ft:220:ILE:HG12	2.15	0.46
1:GB:139:ILE:HG22	1:GB:146:VAL:HG12	1.98	0.46
1:HD:132:THR:O	1:HE:101:LYS:NZ	2.40	0.46
5:IX:436:GLN:OE1	5:IX:465:ARG:NE	2.42	0.46
6:IY:1689:THR:O	6:IY:1724:ASN:ND2	2.41	0.46
1:JD:104:THR:OG1	1:JE:181:VAL:O	2.34	0.46
3:JT:90:SER:HB2	3:JT:135:ALA:HB1	1.98	0.46
2:Jm:206:ASN:O	2:Jm:209:SER:OG	2.27	0.46
2:Jm:259:ILE:HA	2:Jm:262:ILE:HD12	1.97	0.46
6:KY:1859:LEU:O	6:KY:1863:MET:HB2	2.15	0.46
6:LY:1764:THR:HG23	6:LY:1766:ASP:H	1.81	0.46
6:LY:1859:LEU:O	6:LY:1863:MET:HB2	2.15	0.46
1:MB:135:ASP:HB2	1:MB:180:ARG:HB2	1.98	0.46
3:MT:234:GLN:NE2	3:MT:238:SER:OG	2.43	0.46
3:MT:269:LEU:HD23	3:MT:269:LEU:HA	1.81	0.46
3:NT:117:ASP:OD1	3:NT:117:ASP:N	2.48	0.46
6:NY:1859:LEU:O	6:NY:1863:MET:HB2	2.15	0.46
1:AB:149:TYR:HA	1:AB:152:ILE:HD12	1.97	0.46
2:AM:341:MET:O	2:AM:344:LYS:NZ	2.49	0.46
1:BA:199:ASP:OD1	1:BA:199:ASP:N	2.49	0.46
2:Bm:332:ASN:O	2:Bm:353:LYS:NZ	2.48	0.46
1:CD:120:ILE:HG23	1:CD:123:PRO:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:140:THR:HG22	1:CD:166:LYS:HB2	1.97	0.46
2:Dm:332:ASN:HA	2:Dm:353:LYS:HD3	1.98	0.46
2:Fm:218:ASP:HA	2:Fm:297:LYS:HG2	1.98	0.46
2:Fm:274:SER:HB2	2:Fm:314:PHE:HD1	1.80	0.46
1:HA:205:GLU:HA	1:HA:208:LYS:HZ3	1.80	0.46
1:HB:112:LEU:HD21	3:HT:238:SER:HB3	1.96	0.46
1:HC:139:ILE:HB	1:HC:165:LEU:HD13	1.97	0.46
6:HY:1689:THR:O	6:HY:1724:ASN:ND2	2.41	0.46
2:Im:295:ASN:OD1	2:Im:295:ASN:N	2.48	0.46
2:JM:328:THR:HG21	2:JM:357:PHE:HD1	1.81	0.46
5:JX:455:ILE:HB	6:JY:1765:PRO:HB3	1.98	0.46
1:KD:123:PRO:HA	1:KD:126:LYS:HE2	1.98	0.46
1:LC:136:LEU:HB3	1:LC:179:LEU:HB2	1.97	0.46
1:LE:139:ILE:HB	1:LE:165:LEU:HD13	1.98	0.46
1:ME:112:LEU:HD23	1:ME:112:LEU:H	1.81	0.46
2:MM:280:VAL:HG23	2:MM:285:GLU:HG3	1.98	0.46
6:MY:1764:THR:HG23	6:MY:1766:ASP:H	1.81	0.46
6:MY:1859:LEU:O	6:MY:1863:MET:HB2	2.15	0.46
1:ND:140:THR:HG22	1:ND:166:LYS:HB2	1.96	0.46
3:NT:90:SER:HB2	3:NT:135:ALA:HB1	1.98	0.46
1:AA:175:GLN:NE2	3:At:64:GLN:OE1	2.48	0.46
6:AY:1764:THR:HG23	6:AY:1766:ASP:H	1.81	0.46
2:Am:274:SER:HB2	2:Am:314:PHE:HD1	1.81	0.46
3:Bt:207:GLU:OE1	3:Bt:207:GLU:N	2.29	0.46
1:CC:169:GLU:OE1	3:Ct:233:ARG:NH2	2.49	0.46
6:CY:1905:ILE:O	6:CY:1908:SER:OG	2.25	0.46
1:DA:304:LYS:NZ	1:DD:79:ASP:HA	2.29	0.46
1:DE:139:ILE:HB	1:DE:165:LEU:HD13	1.96	0.46
3:DT:90:SER:HB2	3:DT:135:ALA:HB1	1.98	0.46
3:DT:266:ASN:HB3	3:DT:270:ARG:HH12	1.80	0.46
6:DY:1764:THR:HG23	6:DY:1766:ASP:H	1.81	0.46
1:ED:170:ASN:OD1	1:ED:171:MET:N	2.48	0.46
2:Em:219:ASN:HB3	2:Em:222:TYR:CD2	2.51	0.46
5:FX:455:ILE:HB	6:FY:1765:PRO:HB3	1.98	0.46
2:Fm:220:ILE:HG13	2:Fm:224:LEU:HD23	1.98	0.46
1:GB:135:ASP:HB2	1:GB:180:ARG:HB2	1.98	0.46
1:HB:132:THR:HA	1:HB:157:ASN:HA	1.97	0.46
2:HM:305:LYS:NZ	3:Ht:231:GLN:O	2.39	0.46
3:HT:90:SER:HB2	3:HT:135:ALA:HB1	1.98	0.46
5:HX:455:ILE:HB	6:HY:1765:PRO:HB3	1.98	0.46
1:IA:100:LEU:HD22	3:It:44:ILE:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ID:140:THR:HG22	1:ID:166:LYS:HB2	1.98	0.46
1:IE:100:LEU:O	1:IE:105:TYR:OH	2.25	0.46
1:KC:136:LEU:HB3	1:KC:179:LEU:HB2	1.98	0.46
3:KT:117:ASP:OD1	3:KT:117:ASP:N	2.48	0.46
5:KX:502:ASN:OD1	5:KX:502:ASN:N	2.48	0.46
2:Km:198:LYS:O	2:Km:201:ILE:N	2.48	0.46
1:LC:122:ASN:O	1:LC:126:LYS:HG2	2.16	0.46
1:LD:134:ALA:HB3	1:LD:137:ILE:HD11	1.98	0.46
2:LM:253:LEU:HG	2:LM:257:MET:HE1	1.97	0.46
3:LT:90:SER:HB2	3:LT:135:ALA:HB1	1.98	0.46
5:NX:502:ASN:OD1	5:NX:502:ASN:N	2.48	0.46
6:NY:1764:THR:HG23	6:NY:1766:ASP:H	1.81	0.46
3:Nt:100:ASN:N	3:Nt:100:ASN:OD1	2.48	0.46
3:Nt:128:GLN:NE2	3:Nt:130:GLY:O	2.48	0.46
5:BX:461:ASN:N	5:BX:461:ASN:OD1	2.49	0.45
1:CC:129:ALA:HB2	1:CC:192:LEU:HD22	1.98	0.45
5:EX:461:ASN:OD1	5:EX:461:ASN:N	2.49	0.45
1:FE:112:LEU:HD23	1:FE:112:LEU:H	1.81	0.45
4:FU:609:UNK:HA	2:Fm:273:PHE:CZ	2.50	0.45
1:GB:150:TYR:OH	1:GB:154:LYS:NZ	2.39	0.45
2:GM:290:THR:HG22	2:GM:358:PHE:HD2	1.81	0.45
3:GT:101:LYS:HA	3:GT:101:LYS:HD2	1.72	0.45
6:GY:1689:THR:O	6:GY:1724:ASN:ND2	2.41	0.45
2:HM:276:LEU:HB3	2:HM:289:LEU:HD21	1.98	0.45
6:HY:1764:THR:HG23	6:HY:1766:ASP:H	1.81	0.45
1:IA:133:TYR:HD2	3:It:56:LEU:HD22	1.80	0.45
2:Im:332:ASN:O	2:Im:353:LYS:NZ	2.49	0.45
3:JT:89:HIS:HE1	5:JX:401:TYR:CD2	2.34	0.45
1:KC:153:LEU:O	1:KC:157:ASN:HB2	2.16	0.45
3:KT:90:SER:HB2	3:KT:135:ALA:HB1	1.98	0.45
1:ME:152:ILE:HG22	1:ME:153:LEU:HD22	1.98	0.45
2:MM:204:TYR:HB2	2:MM:231:PHE:HB2	1.97	0.45
2:MM:273:PHE:HE1	2:MM:289:LEU:HG	1.81	0.45
1:NE:84:LEU:HD21	1:NE:91:PHE:HA	1.98	0.45
1:AD:104:THR:OG1	1:AE:181:VAL:O	2.32	0.45
2:AM:242:ALA:HA	2:AM:245:THR:HG22	1.98	0.45
3:AT:90:SER:HB2	3:AT:135:ALA:HB1	1.98	0.45
3:AT:234:GLN:NE2	3:AT:238:SER:OG	2.43	0.45
3:AT:266:ASN:HB3	3:AT:270:ARG:HH12	1.80	0.45
2:Am:225:GLN:O	2:Am:229:ASN:ND2	2.49	0.45
6:BY:1908:SER:O	5:CX:379:GLN:NE2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:150:TYR:OH	1:CB:154:LYS:NZ	2.44	0.45
3:CT:90:SER:HB2	3:CT:135:ALA:HB1	1.98	0.45
1:DA:205:GLU:HA	1:DA:208:LYS:HZ3	1.81	0.45
1:DE:117:TYR:O	1:DE:121:GLU:HB2	2.16	0.45
3:Dt:100:ASN:N	3:Dt:100:ASN:OD1	2.48	0.45
1:ED:114:TYR:H	1:EE:145:GLN:HE22	1.63	0.45
1:EE:139:ILE:HB	1:EE:165:LEU:HD13	1.98	0.45
1:FD:158:LYS:HD2	1:FD:158:LYS:HA	1.54	0.45
2:Fm:225:GLN:O	2:Fm:229:ASN:ND2	2.49	0.45
1:GD:138:ILE:HG13	1:GD:164:VAL:HB	1.98	0.45
2:Hm:225:GLN:O	2:Hm:229:ASN:ND2	2.50	0.45
1:ID:170:ASN:OD1	1:ID:171:MET:N	2.48	0.45
2:IM:214:ARG:HG2	2:IM:215:LYS:H	1.81	0.45
1:JC:146:VAL:O	1:JC:150:TYR:HB2	2.17	0.45
2:JM:344:LYS:HE2	2:JM:344:LYS:HB2	1.57	0.45
1:KC:153:LEU:HD13	1:KC:153:LEU:HA	1.76	0.45
1:LB:121:GLU:HG3	1:LC:124:ILE:HD12	1.98	0.45
2:LM:291:LYS:HE2	2:LM:291:LYS:HB2	1.75	0.45
5:LX:461:ASN:N	5:LX:461:ASN:OD1	2.49	0.45
1:MC:184:ARG:HH11	1:MC:186:ASP:H	1.64	0.45
1:NB:146:VAL:HB	1:NB:165:LEU:HD22	1.99	0.45
1:NC:139:ILE:HB	1:NC:165:LEU:HD13	1.97	0.45
1:AA:100:LEU:HD22	3:At:44:ILE:HG22	1.98	0.45
5:AX:461:ASN:N	5:AX:461:ASN:OD1	2.49	0.45
1:BE:85:ASN:OD1	1:BE:87:ASN:ND2	2.50	0.45
1:CB:155:ALA:HA	3:Ct:179:LYS:HE2	1.98	0.45
1:CD:128:ARG:HH22	1:CE:87:ASN:HB3	1.81	0.45
1:DA:108:ALA:HA	3:Dt:133:MET:O	2.17	0.45
1:DD:104:THR:OG1	1:DE:181:VAL:O	2.31	0.45
3:ET:90:SER:HB2	3:ET:135:ALA:HB1	1.98	0.45
3:Et:54:ASP:OD1	3:Et:55:LYS:N	2.50	0.45
1:FA:187:PRO:HD3	1:FA:202:LYS:HG3	1.99	0.45
1:FD:167:ILE:HB	1:GA:194:LYS:HZ2	1.82	0.45
3:Ft:54:ASP:OD1	3:Ft:55:LYS:N	2.50	0.45
1:GB:112:LEU:HD21	3:GT:238:SER:HB3	1.98	0.45
3:GT:90:SER:HB2	3:GT:135:ALA:HB1	1.98	0.45
1:IA:199:ASP:OD1	1:IA:199:ASP:N	2.49	0.45
3:IT:90:SER:HB2	3:IT:135:ALA:HB1	1.98	0.45
1:JA:108:ALA:HA	3:Jt:133:MET:O	2.17	0.45
1:JC:124:ILE:O	1:JC:127:THR:OG1	2.32	0.45
1:KB:172:PRO:HG3	3:KT:256:VAL:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KE:157:ASN:ND2	1:KE:159:ARG:O	2.50	0.45
2:KM:242:ALA:HA	2:KM:245:THR:HG22	1.97	0.45
5:KX:461:ASN:N	5:KX:461:ASN:OD1	2.49	0.45
5:MX:461:ASN:N	5:MX:461:ASN:OD1	2.49	0.45
6:MY:1908:SER:O	5:NX:379:GLN:NE2	2.50	0.45
2:Mm:217:LEU:O	2:Mm:219:ASN:ND2	2.50	0.45
2:BM:328:THR:HG21	2:BM:357:PHE:HD1	1.80	0.45
3:Bt:128:GLN:NE2	3:Bt:130:GLY:O	2.48	0.45
1:CD:120:ILE:HA	1:CD:123:PRO:HD2	1.97	0.45
1:CD:127:THR:HA	1:CD:130:MET:HG2	1.99	0.45
1:CD:137:ILE:O	1:CD:163:PHE:HA	2.16	0.45
2:Dm:283:ASP:HA	2:Dm:286:LEU:HD13	1.99	0.45
3:Dt:54:ASP:OD1	3:Dt:55:LYS:N	2.50	0.45
6:EY:1745:VAL:HG23	6:EY:1866:PRO:HB2	1.99	0.45
3:Et:100:ASN:OD1	3:Et:100:ASN:N	2.48	0.45
1:FA:150:TYR:CZ	1:FB:167:ILE:HD13	2.50	0.45
3:Ft:100:ASN:OD1	3:Ft:100:ASN:N	2.48	0.45
1:GA:187:PRO:HD3	1:GA:202:LYS:HG3	1.99	0.45
1:GC:132:THR:HG22	1:GC:156:LEU:HB3	1.98	0.45
1:HA:187:PRO:HD3	1:HA:202:LYS:HG3	1.99	0.45
1:HB:126:LYS:O	1:HB:130:MET:HB2	2.17	0.45
2:Hm:295:ASN:OD1	2:Hm:295:ASN:N	2.46	0.45
1:IE:114:TYR:CZ	1:IE:118:LEU:HD11	2.52	0.45
3:Jt:100:ASN:OD1	3:Jt:100:ASN:N	2.48	0.45
6:KY:1764:THR:HG23	6:KY:1766:ASP:H	1.81	0.45
3:LT:223:THR:HG22	1:MA:184:ARG:HH21	1.82	0.45
3:MT:90:SER:HB2	3:MT:135:ALA:HB1	1.98	0.45
5:NX:461:ASN:OD1	5:NX:461:ASN:N	2.49	0.45
1:AC:171:MET:HE3	1:AC:171:MET:HB3	1.85	0.45
3:AT:269:LEU:HD23	3:AT:269:LEU:HA	1.81	0.45
1:BE:114:TYR:CZ	1:BE:118:LEU:HD11	2.52	0.45
2:BM:305:LYS:NZ	3:Bt:231:GLN:O	2.38	0.45
1:CA:108:ALA:HA	3:Ct:133:MET:O	2.17	0.45
1:CC:130:MET:HE1	1:CC:182:PRO:HG3	1.98	0.45
2:Cm:344:LYS:HB3	2:Cm:347:MET:HB2	1.98	0.45
1:DA:187:PRO:HD3	1:DA:202:LYS:HG3	1.99	0.45
1:DA:199:ASP:OD1	1:DA:199:ASP:N	2.49	0.45
2:Dm:327:LYS:HD2	2:Dm:327:LYS:HA	1.85	0.45
2:EM:253:LEU:HG	2:EM:257:MET:HE1	1.99	0.45
2:Em:332:ASN:HA	2:Em:353:LYS:HD3	1.99	0.45
1:FD:113:ASP:O	1:FD:117:TYR:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HA:138:ILE:HG13	1:HA:164:VAL:HB	1.99	0.45
1:HE:112:LEU:HD23	1:HE:112:LEU:H	1.81	0.45
1:IA:187:PRO:HD3	1:IA:202:LYS:HG3	1.99	0.45
1:IE:172:PRO:HG2	1:IE:173:TYR:HD1	1.81	0.45
2:IM:290:THR:HG22	2:IM:358:PHE:HD2	1.81	0.45
6:IY:1745:VAL:HG23	6:IY:1866:PRO:HB2	1.99	0.45
1:JA:138:ILE:HG13	1:JA:164:VAL:HB	1.99	0.45
1:JD:156:LEU:HD23	1:JD:156:LEU:HA	1.83	0.45
1:LB:177:THR:HA	1:LC:107:TYR:O	2.17	0.45
3:LT:149:GLN:HB2	3:LT:151:PHE:HE1	1.82	0.45
3:MT:149:GLN:HB2	3:MT:151:PHE:HE1	1.82	0.45
2:Mm:225:GLN:O	2:Mm:229:ASN:ND2	2.49	0.45
1:BA:138:ILE:HG13	1:BA:164:VAL:HB	1.99	0.45
2:Bm:225:GLN:O	2:Bm:229:ASN:ND2	2.50	0.45
1:CA:187:PRO:HD3	1:CA:202:LYS:HG3	1.99	0.45
1:CD:154:LYS:HA	1:CD:158:LYS:HG3	1.98	0.45
2:CM:187:ASN:ND2	2:CM:251:GLU:OE1	2.49	0.45
1:DA:138:ILE:HG13	1:DA:164:VAL:HB	1.99	0.45
1:EA:138:ILE:HG13	1:EA:164:VAL:HB	1.99	0.45
1:EA:187:PRO:HD3	1:EA:202:LYS:HG3	1.99	0.45
1:EC:126:LYS:NZ	1:EC:184:ARG:HH12	2.15	0.45
2:EM:246:LEU:HD22	2:EM:252:ARG:HG3	1.97	0.45
4:EU:609:UNK:HA	2:Em:273:PHE:CZ	2.51	0.45
6:GY:1745:VAL:HG23	6:GY:1866:PRO:HB2	1.99	0.45
3:Gt:54:ASP:OD1	3:Gt:55:LYS:N	2.50	0.45
2:IM:246:LEU:HD22	2:IM:252:ARG:HG3	1.97	0.45
6:IY:1752:MET:HE2	6:IY:1752:MET:HB2	1.72	0.45
5:JX:461:ASN:N	5:JX:461:ASN:OD1	2.49	0.45
6:KY:1745:VAL:HG23	6:KY:1866:PRO:HB2	1.99	0.45
2:Lm:219:ASN:HB3	2:Lm:222:TYR:CD2	2.51	0.45
3:MT:117:ASP:OD1	3:MT:117:ASP:N	2.48	0.45
1:NE:85:ASN:OD1	1:NE:87:ASN:ND2	2.50	0.45
1:AA:82:ASP:OD1	1:AA:126:LYS:NZ	2.38	0.45
2:AM:328:THR:HG21	2:AM:357:PHE:HD1	1.80	0.45
1:BD:114:TYR:HE1	1:BE:149:TYR:HB2	1.81	0.45
2:BM:324:ILE:HA	2:BM:327:LYS:HE3	1.99	0.45
6:BY:1905:ILE:O	6:BY:1908:SER:OG	2.25	0.45
2:Bm:218:ASP:HA	2:Bm:297:LYS:HG2	1.99	0.45
3:CT:213:ARG:NH1	3:CT:219:GLU:OE2	2.50	0.45
3:Ct:54:ASP:OD1	3:Ct:55:LYS:N	2.50	0.45
3:DT:213:ARG:NH1	3:DT:219:GLU:OE2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EB:136:LEU:HB3	1:EB:179:LEU:HB2	1.99	0.45
1:EC:139:ILE:HG22	1:EC:146:VAL:HG12	1.98	0.45
1:FD:176:ALA:HB3	1:FE:109:MET:HE3	1.98	0.45
1:GA:138:ILE:HG13	1:GA:164:VAL:HB	1.99	0.45
1:GC:133:TYR:OH	1:GC:194:LYS:O	2.29	0.45
1:IE:85:ASN:OD1	1:IE:87:ASN:ND2	2.50	0.45
1:JE:117:TYR:O	1:JE:121:GLU:HB2	2.17	0.45
1:KA:108:ALA:HA	3:Kt:133:MET:O	2.17	0.45
1:KA:199:ASP:OD1	1:KA:199:ASP:N	2.49	0.45
1:KE:113:ASP:OD1	1:KE:115:ASN:N	2.50	0.45
1:KE:152:ILE:HG22	1:KE:153:LEU:HD22	1.99	0.45
1:LB:128:ARG:NH1	1:LC:121:GLU:OE2	2.50	0.45
4:LU:609:UNK:HA	2:Lm:273:PHE:CZ	2.52	0.45
2:MM:290:THR:HG21	2:MM:355:PHE:HA	1.99	0.45
1:AD:143:LEU:O	1:AD:147:ASN:HB2	2.16	0.45
6:AY:1905:ILE:O	6:AY:1908:SER:OG	2.25	0.45
2:BM:246:LEU:HD22	2:BM:252:ARG:HG3	1.98	0.45
2:Bm:302:GLN:HG3	2:Bm:305:LYS:HE3	1.99	0.45
1:CA:138:ILE:HG13	1:CA:164:VAL:HB	1.99	0.45
1:CA:304:LYS:HZ3	1:CD:79:ASP:HA	1.81	0.45
1:CD:124:ILE:O	1:CD:127:THR:OG1	2.28	0.45
3:CT:101:LYS:HD2	3:CT:101:LYS:HA	1.72	0.45
1:DD:178:PHE:CE1	1:DE:107:TYR:HB3	2.51	0.45
3:DT:54:ASP:OD2	5:DX:404:TYR:OH	2.26	0.45
3:ET:149:GLN:HB2	3:ET:151:PHE:HE1	1.82	0.45
4:EU:609:UNK:HA	2:Em:273:PHE:HZ	1.82	0.45
6:EY:1764:THR:HG23	6:EY:1766:ASP:H	1.81	0.45
1:FB:114:TYR:CD1	1:FC:145:GLN:HA	2.52	0.45
1:FC:187:PRO:HG3	1:GA:189:ALA:H	1.82	0.45
2:FM:324:ILE:HA	2:FM:327:LYS:HE3	1.98	0.45
3:FT:90:SER:HB2	3:FT:135:ALA:HB1	1.98	0.45
5:FX:461:ASN:OD1	5:FX:461:ASN:N	2.49	0.45
2:Fm:357:PHE:O	2:Fm:360:THR:OG1	2.28	0.45
1:HA:108:ALA:HA	3:Ht:133:MET:O	2.17	0.45
1:HB:153:LEU:HA	1:HB:156:LEU:HB2	1.98	0.45
2:Im:225:GLN:O	2:Im:229:ASN:ND2	2.50	0.45
1:JC:133:TYR:OH	1:JC:194:LYS:O	2.27	0.45
2:JM:290:THR:HG21	2:JM:355:PHE:HA	1.99	0.45
2:JM:290:THR:HG22	2:JM:358:PHE:HD2	1.82	0.45
5:JX:453:ALA:O	6:JY:1737:LYS:NZ	2.50	0.45
2:Jm:225:GLN:O	2:Jm:229:ASN:ND2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LB:136:LEU:HB3	1:LB:179:LEU:HB2	1.97	0.45
1:LC:148:GLY:O	1:LC:151:ASN:N	2.49	0.45
1:LD:170:ASN:OD1	1:LD:171:MET:N	2.48	0.45
2:LM:246:LEU:HD22	2:LM:252:ARG:HG3	1.97	0.45
1:MD:179:LEU:HD13	1:ME:106:LEU:HD12	1.98	0.45
3:NT:149:GLN:HB2	3:NT:151:PHE:HE1	1.82	0.45
1:AB:191:THR:HA	1:AC:158:LYS:HZ1	1.81	0.45
3:AT:101:LYS:HA	3:AT:101:LYS:HD2	1.72	0.45
5:AX:443:GLN:NE2	6:NY:1780:MET:SD	2.90	0.45
2:Am:338:ASP:HB3	2:Am:340:MET:HE3	1.98	0.45
6:CY:1745:VAL:HG23	6:CY:1866:PRO:HB2	1.99	0.45
3:ET:269:LEU:HD23	3:ET:269:LEU:HA	1.81	0.45
2:Em:225:GLN:O	2:Em:229:ASN:ND2	2.50	0.45
1:FE:111:LEU:HD12	1:FE:112:LEU:HD23	1.99	0.45
1:FE:152:ILE:HG22	1:FE:153:LEU:HD22	1.99	0.45
3:Ht:54:ASP:OD1	3:Ht:55:LYS:N	2.50	0.45
1:IA:138:ILE:HG13	1:IA:164:VAL:HB	1.99	0.45
1:JB:155:ALA:HA	3:Jt:179:LYS:HE2	1.98	0.45
1:JE:139:ILE:HG12	1:JE:149:TYR:CZ	2.52	0.45
2:JM:242:ALA:HA	2:JM:245:THR:HG22	1.98	0.45
1:KA:138:ILE:HG13	1:KA:164:VAL:HB	1.99	0.45
3:KT:149:GLN:HB2	3:KT:151:PHE:HE1	1.82	0.45
1:LA:138:ILE:HG13	1:LA:164:VAL:HB	1.99	0.45
3:Lt:54:ASP:OD1	3:Lt:55:LYS:N	2.50	0.45
1:MC:147:ASN:O	1:MC:151:ASN:CB	2.61	0.45
1:MD:117:TYR:O	1:MD:121:GLU:CB	2.47	0.45
1:NA:138:ILE:HG13	1:NA:164:VAL:HB	1.99	0.45
2:Nm:218:ASP:HA	2:Nm:297:LYS:HG2	1.99	0.45
2:BM:246:LEU:O	2:BM:252:ARG:NH2	2.50	0.45
1:ED:179:LEU:HD11	1:EE:106:LEU:HD12	1.99	0.45
1:EE:152:ILE:HG22	1:EE:153:LEU:HD22	1.99	0.45
2:EM:344:LYS:HB3	2:EM:348:GLN:HB2	1.99	0.45
3:Et:90:SER:OG	3:Et:91:LYS:N	2.51	0.45
2:FM:199:GLN:HA	2:FM:202:GLU:HG3	1.98	0.45
3:FT:149:GLN:HB2	3:FT:151:PHE:HE1	1.82	0.45
1:GE:85:ASN:OD1	1:GE:87:ASN:ND2	2.50	0.45
1:HD:140:THR:HG1	1:HD:175:GLN:HB3	1.82	0.45
5:HX:436:GLN:OE1	5:HX:465:ARG:NE	2.42	0.45
1:JA:187:PRO:HD3	1:JA:202:LYS:HG3	1.99	0.45
3:Kt:54:ASP:OD1	3:Kt:55:LYS:N	2.50	0.45
2:Lm:332:ASN:HA	2:Lm:353:LYS:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MD:146:VAL:O	1:MD:150:TYR:HB2	2.17	0.45
2:MM:188:LYS:O	2:MM:191:SER:OG	2.33	0.45
1:NA:104:THR:HG22	3:Nt:138:TYR:HA	1.99	0.45
1:NB:178:PHE:O	1:NC:106:LEU:HA	2.17	0.45
1:NC:130:MET:HE3	1:NC:130:MET:HB3	1.75	0.45
1:NE:113:ASP:HB3	1:NE:116:ASN:HB3	1.99	0.45
6:NY:1745:VAL:HG23	6:NY:1866:PRO:HB2	1.99	0.45
2:Nm:220:ILE:HG13	2:Nm:224:LEU:HD23	1.99	0.45
3:Nt:54:ASP:OD1	3:Nt:55:LYS:N	2.50	0.45
1:AA:138:ILE:HG13	1:AA:164:VAL:HB	1.99	0.44
2:AM:345:THR:HG23	2:AM:348:GLN:H	1.81	0.44
3:At:54:ASP:OD1	3:At:55:LYS:N	2.50	0.44
3:At:96:ILE:HA	3:At:123:GLN:O	2.18	0.44
1:BE:135:ASP:N	1:BE:179:LEU:O	2.46	0.44
2:BM:290:THR:HG22	2:BM:358:PHE:HD2	1.82	0.44
3:Bt:54:ASP:OD1	3:Bt:55:LYS:N	2.50	0.44
1:DC:159:ARG:H	1:DC:159:ARG:HG2	1.62	0.44
3:DT:149:GLN:HB2	3:DT:151:PHE:HE1	1.82	0.44
5:DX:391:ALA:O	5:DX:505:ASN:ND2	2.41	0.44
2:Em:219:ASN:HD22	2:Em:222:TYR:HE2	1.64	0.44
1:FA:138:ILE:HG13	1:FA:164:VAL:HB	1.99	0.44
2:FM:273:PHE:HE1	2:FM:289:LEU:HG	1.82	0.44
1:GC:131:GLY:HA3	1:GC:153:LEU:HD22	1.99	0.44
1:GE:157:ASN:ND2	1:GE:159:ARG:O	2.50	0.44
1:GE:162:LYS:HD2	1:GE:162:LYS:HA	1.71	0.44
2:Gm:357:PHE:O	2:Gm:360:THR:OG1	2.32	0.44
2:HM:218:ASP:OD1	2:HM:219:ASN:N	2.46	0.44
3:Ht:90:SER:OG	3:Ht:91:LYS:N	2.51	0.44
2:Im:357:PHE:O	2:Im:360:THR:OG1	2.26	0.44
3:JT:149:GLN:HB2	3:JT:151:PHE:HE1	1.82	0.44
6:JY:1752:MET:HE2	6:JY:1752:MET:HB2	1.72	0.44
1:KA:187:PRO:HD3	1:KA:202:LYS:HG3	1.99	0.44
2:Lm:295:ASN:OD1	2:Lm:295:ASN:N	2.49	0.44
1:MA:128:ARG:NH2	3:Mt:49:GLU:O	2.34	0.44
1:MA:150:TYR:CZ	1:MB:167:ILE:HD13	2.52	0.44
3:Mt:54:ASP:OD1	3:Mt:55:LYS:N	2.50	0.44
1:ND:175:GLN:HA	1:NE:109:MET:O	2.17	0.44
1:NE:111:LEU:HD12	1:NE:112:LEU:HD23	1.99	0.44
2:AM:344:LYS:HE2	2:AM:344:LYS:HB2	1.65	0.44
2:Am:357:PHE:O	2:Am:360:THR:OG1	2.27	0.44
1:BA:187:PRO:HD3	1:BA:202:LYS:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:170:ASN:OD1	1:BD:171:MET:N	2.47	0.44
3:Bt:90:SER:OG	3:Bt:91:LYS:N	2.51	0.44
2:CM:246:LEU:O	2:CM:252:ARG:NH2	2.51	0.44
3:Ct:96:ILE:HA	3:Ct:123:GLN:O	2.17	0.44
1:DC:150:TYR:O	1:DC:154:LYS:HB2	2.17	0.44
1:DE:128:ARG:HD3	1:DE:128:ARG:HA	1.78	0.44
1:DE:157:ASN:ND2	1:DE:159:ARG:O	2.50	0.44
1:EA:175:GLN:NE2	3:Et:64:GLN:OE1	2.50	0.44
2:FM:328:THR:HG21	2:FM:357:PHE:HD1	1.82	0.44
1:HB:120:ILE:HD11	1:HC:112:LEU:HD21	2.00	0.44
1:HE:139:ILE:HB	1:HE:165:LEU:HD13	2.00	0.44
1:IE:84:LEU:HD21	1:IE:91:PHE:HA	1.98	0.44
6:IY:1764:THR:HG23	6:IY:1766:ASP:H	1.81	0.44
1:KC:132:THR:HG22	1:KC:156:LEU:HB3	1.99	0.44
4:KU:609:UNK:HA	2:Km:273:PHE:CZ	2.50	0.44
6:LY:1745:VAL:HG23	6:LY:1866:PRO:HB2	1.99	0.44
2:Lm:225:GLN:O	2:Lm:229:ASN:ND2	2.50	0.44
2:Lm:294:THR:O	2:Lm:303:LYS:NZ	2.43	0.44
1:MD:114:TYR:H	1:ME:145:GLN:HE22	1.63	0.44
1:NC:130:MET:HE1	1:NC:182:PRO:HG3	1.99	0.44
3:NT:101:LYS:HD2	3:NT:101:LYS:HA	1.72	0.44
3:NT:213:ARG:NH1	3:NT:219:GLU:OE2	2.50	0.44
2:Nm:357:PHE:O	2:Nm:360:THR:OG1	2.28	0.44
3:Nt:96:ILE:HA	3:Nt:123:GLN:O	2.18	0.44
1:AA:187:PRO:HD3	1:AA:202:LYS:HG3	1.99	0.44
1:AB:107:TYR:O	1:AC:177:THR:HA	2.17	0.44
1:AB:126:LYS:O	1:AB:130:MET:HB2	2.17	0.44
2:AM:246:LEU:O	2:AM:252:ARG:NH2	2.50	0.44
5:AX:391:ALA:O	5:AX:505:ASN:ND2	2.41	0.44
1:BB:191:THR:HG23	1:BB:192:LEU:HG	1.99	0.44
6:BY:1745:VAL:HG23	6:BY:1866:PRO:HB2	1.99	0.44
1:DE:113:ASP:OD1	1:DE:115:ASN:N	2.50	0.44
1:ED:129:ALA:O	1:ED:133:TYR:CB	2.54	0.44
6:HY:1752:MET:HE2	6:HY:1752:MET:HB2	1.72	0.44
3:IT:101:LYS:HA	3:IT:101:LYS:HD2	1.72	0.44
3:It:54:ASP:OD1	3:It:55:LYS:N	2.50	0.44
3:It:96:ILE:HA	3:It:123:GLN:O	2.18	0.44
3:Jt:54:ASP:OD1	3:Jt:55:LYS:N	2.50	0.44
1:KC:150:TYR:O	1:KC:154:LYS:HB2	2.17	0.44
2:Lm:273:PHE:HD2	2:Lm:310:VAL:HG11	1.82	0.44
1:MA:199:ASP:OD1	1:MA:199:ASP:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:NE:121:GLU:O	1:NE:125:ILE:HG12	2.17	0.44
1:BC:184:ARG:HH11	1:BC:186:ASP:H	1.64	0.44
1:BD:107:TYR:HE2	1:BE:126:LYS:HD2	1.83	0.44
2:BM:205:SER:HA	2:BM:208:VAL:HG12	1.99	0.44
3:BT:213:ARG:NH1	3:BT:219:GLU:OE2	2.50	0.44
2:Bm:206:ASN:O	2:Bm:209:SER:OG	2.30	0.44
3:Bt:96:ILE:HA	3:Bt:123:GLN:O	2.18	0.44
3:Ct:90:SER:OG	3:Ct:91:LYS:N	2.51	0.44
3:Dt:96:ILE:HA	3:Dt:123:GLN:O	2.17	0.44
3:ET:213:ARG:NH1	3:ET:219:GLU:OE2	2.50	0.44
1:FA:108:ALA:HA	3:Ft:133:MET:O	2.16	0.44
2:FM:290:THR:HG22	2:FM:358:PHE:HD2	1.82	0.44
2:FM:305:LYS:NZ	3:Ft:231:GLN:O	2.37	0.44
2:Fm:197:TYR:CZ	2:Fm:201:ILE:HD11	2.53	0.44
1:GD:140:THR:HG22	1:GD:166:LYS:HB2	2.00	0.44
1:IE:135:ASP:N	1:IE:179:LEU:O	2.47	0.44
3:IT:149:GLN:HB2	3:IT:151:PHE:HE1	1.82	0.44
3:JT:159:PRO:HA	3:KT:44:ILE:HD12	1.99	0.44
6:JY:1745:VAL:HG23	6:JY:1866:PRO:HB2	1.99	0.44
2:Jm:295:ASN:OD1	2:Jm:295:ASN:N	2.50	0.44
3:Jt:96:ILE:HA	3:Jt:123:GLN:O	2.18	0.44
1:KA:132:THR:HA	1:KA:157:ASN:HA	2.00	0.44
1:LB:122:ASN:O	1:LB:126:LYS:HB2	2.17	0.44
1:MA:100:LEU:HD22	3:Mt:44:ILE:HG22	1.99	0.44
1:MA:128:ARG:HH21	3:Mt:49:GLU:C	2.20	0.44
6:MY:1745:VAL:HG23	6:MY:1866:PRO:HB2	1.99	0.44
1:NE:146:VAL:HB	1:NE:165:LEU:HD12	1.99	0.44
1:CD:177:THR:HA	1:CE:107:TYR:O	2.16	0.44
2:DM:221:ASP:OD1	2:DM:222:TYR:N	2.50	0.44
2:EM:205:SER:OG	2:EM:268:ARG:NH1	2.50	0.44
2:Em:327:LYS:HD2	2:Em:327:LYS:HA	1.86	0.44
1:FB:107:TYR:O	1:FC:177:THR:HA	2.16	0.44
1:FD:167:ILE:H	1:GA:194:LYS:NZ	2.15	0.44
2:Fm:196:SER:HA	2:Fm:199:GLN:HG3	2.00	0.44
3:Ft:90:SER:OG	3:Ft:91:LYS:N	2.51	0.44
3:GT:149:GLN:HB2	3:GT:151:PHE:HE1	1.82	0.44
1:HD:157:ASN:OD1	1:HD:157:ASN:N	2.50	0.44
2:Hm:219:ASN:HB3	2:Hm:222:TYR:HD2	1.81	0.44
2:Hm:259:ILE:HA	2:Hm:262:ILE:HD12	2.00	0.44
1:ID:143:LEU:HD21	3:JT:268:TYR:CD1	2.52	0.44
2:IM:246:LEU:O	2:IM:252:ARG:NH2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:IX:455:ILE:HB	6:IY:1765:PRO:HB3	1.98	0.44
1:JA:132:THR:HA	1:JA:157:ASN:HA	2.00	0.44
1:JA:164:VAL:HG11	1:JA:235:VAL:HG12	2.00	0.44
1:JB:153:LEU:HA	1:JB:156:LEU:HB2	1.99	0.44
6:JY:1764:THR:HG23	6:JY:1766:ASP:H	1.81	0.44
6:JY:1908:SER:O	5:KX:379:GLN:NE2	2.51	0.44
1:LA:132:THR:HA	1:LA:157:ASN:HA	1.99	0.44
1:LE:85:ASN:OD1	1:LE:87:ASN:ND2	2.51	0.44
1:MA:138:ILE:HG13	1:MA:164:VAL:HB	1.99	0.44
6:MY:1752:MET:HE2	6:MY:1752:MET:HB2	1.72	0.44
2:Mm:197:TYR:CZ	2:Mm:201:ILE:HD11	2.52	0.44
3:Mt:97:GLY:O	3:Mt:125:THR:N	2.37	0.44
1:AD:138:ILE:HG13	1:AD:164:VAL:HB	2.00	0.44
1:AE:84:LEU:HD21	1:AE:91:PHE:HA	2.00	0.44
2:Am:352:TYR:HA	2:Am:355:PHE:HB3	1.98	0.44
1:BB:128:ARG:HG3	1:BB:156:LEU:HD11	1.99	0.44
1:CB:191:THR:HA	1:CC:158:LYS:HZ2	1.83	0.44
1:DB:117:TYR:O	1:DB:120:ILE:N	2.47	0.44
1:DD:167:ILE:HB	1:EA:194:LYS:HZ2	1.82	0.44
2:DM:328:THR:HG21	2:DM:357:PHE:HD1	1.81	0.44
6:DY:1745:VAL:HG23	6:DY:1866:PRO:HB2	1.99	0.44
2:EM:221:ASP:OD1	2:EM:222:TYR:N	2.50	0.44
1:FA:296:VAL:O	1:FC:164:VAL:HA	2.17	0.44
1:GA:138:ILE:HA	1:GA:164:VAL:O	2.18	0.44
1:GD:127:THR:HA	1:GD:130:MET:HG2	1.99	0.44
5:GX:461:ASN:N	5:GX:461:ASN:OD1	2.49	0.44
1:HE:162:LYS:HD2	1:HE:162:LYS:HA	1.89	0.44
2:HM:246:LEU:O	2:HM:252:ARG:NH2	2.51	0.44
2:HM:345:THR:HG23	2:HM:348:GLN:H	1.82	0.44
1:IA:170:ASN:OD1	1:IA:171:MET:N	2.51	0.44
1:IC:138:ILE:HG23	1:IC:164:VAL:HG23	2.00	0.44
2:Im:259:ILE:HA	2:Im:262:ILE:HD12	2.00	0.44
1:JA:138:ILE:HA	1:JA:164:VAL:O	2.18	0.44
1:JA:170:ASN:OD1	1:JA:171:MET:N	2.51	0.44
5:JX:454:ALA:HB2	6:JY:1737:LYS:HE2	2.00	0.44
2:Lm:274:SER:HB2	2:Lm:314:PHE:HD1	1.83	0.44
1:MA:251:ALA:HB3	1:MC:151:ASN:OD1	2.18	0.44
3:MT:213:ARG:NH1	3:MT:219:GLU:OE2	2.50	0.44
5:MX:502:ASN:OD1	5:MX:502:ASN:N	2.48	0.44
3:Mt:96:ILE:HA	3:Mt:123:GLN:O	2.18	0.44
2:Nm:225:GLN:O	2:Nm:229:ASN:ND2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Nm:332:ASN:O	2:Nm:353:LYS:NZ	2.51	0.44
1:AA:124:ILE:HG13	3:At:73:TYR:CE2	2.52	0.44
3:At:100:ASN:N	3:At:100:ASN:OD1	2.48	0.44
1:BA:138:ILE:HA	1:BA:164:VAL:O	2.18	0.44
2:BM:188:LYS:O	2:BM:191:SER:OG	2.35	0.44
1:CB:153:LEU:HA	1:CB:156:LEU:HB2	1.99	0.44
1:CE:153:LEU:HD13	1:CE:156:LEU:HD22	1.99	0.44
1:DB:115:ASN:N	1:DB:115:ASN:OD1	2.48	0.44
1:ED:108:ALA:HA	1:EE:177:THR:HA	1.99	0.44
1:EE:172:PRO:HG2	1:EE:173:TYR:HD1	1.82	0.44
3:ET:89:HIS:HE1	5:EX:401:TYR:HD2	1.65	0.44
3:Et:96:ILE:HA	3:Et:123:GLN:O	2.18	0.44
1:FA:138:ILE:HA	1:FA:164:VAL:O	2.18	0.44
1:GD:80:ILE:HA	1:GE:106:LEU:O	2.17	0.44
1:GD:104:THR:OG1	1:GE:181:VAL:O	2.32	0.44
3:Gt:100:ASN:OD1	3:Gt:100:ASN:N	2.48	0.44
1:HA:164:VAL:HG11	1:HA:235:VAL:HG12	2.00	0.44
1:HA:267:ALA:HB1	1:HA:269:PRO:HD2	1.99	0.44
1:HB:107:TYR:O	1:HC:177:THR:HA	2.17	0.44
1:HE:80:ILE:HD13	1:HE:84:LEU:HD22	2.00	0.44
6:HY:1745:VAL:HG23	6:HY:1866:PRO:HB2	1.99	0.44
3:It:32:LYS:NZ	3:JT:47:TYR:OH	2.50	0.44
3:It:90:SER:OG	3:It:91:LYS:N	2.51	0.44
1:JE:172:PRO:HG2	1:JE:173:TYR:HD1	1.83	0.44
5:JX:502:ASN:OD1	5:JX:502:ASN:N	2.48	0.44
1:KE:140:THR:HG21	1:LA:278:PRO:HD3	1.99	0.44
3:Kt:90:SER:OG	3:Kt:91:LYS:N	2.50	0.44
3:Kt:100:ASN:N	3:Kt:100:ASN:OD1	2.48	0.44
1:LA:164:VAL:HG11	1:LA:235:VAL:HG12	2.00	0.44
1:LD:77:LEU:HD12	1:LD:78:PHE:H	1.82	0.44
1:MB:120:ILE:HG13	3:MT:242:PHE:CE1	2.47	0.44
1:ND:107:TYR:CE2	1:ND:109:MET:HB3	2.53	0.44
1:AA:138:ILE:HA	1:AA:164:VAL:O	2.18	0.44
3:AT:149:GLN:HB2	3:AT:151:PHE:HE1	1.82	0.44
3:AT:268:TYR:CE1	1:ND:143:LEU:HD11	2.52	0.44
1:BD:104:THR:OG1	1:BE:181:VAL:O	2.34	0.44
2:Bm:259:ILE:HA	2:Bm:262:ILE:HD12	1.99	0.44
1:CD:104:THR:OG1	1:CE:181:VAL:O	2.34	0.44
3:CT:149:GLN:HB2	3:CT:151:PHE:HE1	1.82	0.44
1:DD:140:THR:HG1	1:DD:175:GLN:HB3	1.83	0.44
1:DE:79:ASP:OD1	1:DE:79:ASP:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EC:187:PRO:HB3	1:FA:190:HIS:C	2.43	0.44
1:GA:170:ASN:OD1	1:GA:171:MET:N	2.51	0.44
5:GX:455:ILE:HB	6:GY:1765:PRO:HB3	1.99	0.44
1:HA:199:ASP:OD1	1:HA:199:ASP:N	2.49	0.44
1:HC:129:ALA:HB2	1:HC:192:LEU:HD22	1.99	0.44
1:HC:139:ILE:HG22	1:HC:146:VAL:HG12	1.98	0.44
3:Ht:96:ILE:HA	3:Ht:123:GLN:O	2.18	0.44
1:IC:184:ARG:HH11	1:IC:186:ASP:H	1.65	0.44
5:IX:461:ASN:OD1	5:IX:461:ASN:N	2.49	0.44
1:KA:138:ILE:HA	1:KA:164:VAL:O	2.18	0.44
1:KA:234:MET:HB3	1:KB:138:ILE:HD11	2.00	0.44
1:KB:117:TYR:HD2	1:KB:118:LEU:HD22	1.81	0.44
1:LA:170:ASN:OD1	1:LA:171:MET:N	2.51	0.44
2:LM:205:SER:HA	2:LM:208:VAL:HG12	2.00	0.44
1:MA:164:VAL:HG11	1:MA:235:VAL:HG12	2.00	0.44
1:MA:170:ASN:OD1	1:MA:171:MET:N	2.51	0.44
1:MA:187:PRO:HD3	1:MA:202:LYS:HG3	1.99	0.44
5:MX:392:LEU:HD23	5:MX:392:LEU:HA	1.88	0.44
1:NA:133:TYR:HD2	3:Nt:56:LEU:HD22	1.83	0.44
1:ND:170:ASN:OD1	1:ND:171:MET:N	2.48	0.44
5:NX:434:THR:O	5:NX:465:ARG:NH1	2.44	0.44
1:BD:143:LEU:HD12	1:BD:167:ILE:HD12	2.00	0.44
1:CA:170:ASN:OD1	1:CA:171:MET:N	2.51	0.44
1:CE:85:ASN:OD1	1:CE:87:ASN:ND2	2.51	0.44
2:CM:199:GLN:HA	2:CM:202:GLU:HG3	1.99	0.44
2:CM:290:THR:HG22	2:CM:358:PHE:HD2	1.83	0.44
2:Cm:327:LYS:HD2	2:Cm:327:LYS:HA	1.86	0.44
3:Ct:207:GLU:OE1	3:Ct:207:GLU:N	2.29	0.44
1:ED:114:TYR:HE1	1:EE:149:TYR:HB2	1.82	0.44
1:FA:164:VAL:HG11	1:FA:235:VAL:HG12	2.00	0.44
2:FM:344:LYS:HB2	2:FM:344:LYS:HE2	1.57	0.44
6:FY:1745:VAL:HG23	6:FY:1866:PRO:HB2	1.99	0.44
2:Hm:218:ASP:HA	2:Hm:297:LYS:HG2	1.99	0.44
1:IA:132:THR:HA	1:IA:157:ASN:HA	2.00	0.44
1:IA:164:VAL:HG11	1:IA:235:VAL:HG12	2.00	0.44
1:ID:138:ILE:HG13	1:ID:164:VAL:HB	1.99	0.44
2:IM:218:ASP:OD1	2:IM:219:ASN:N	2.47	0.44
3:Jt:97:GLY:O	3:Jt:125:THR:N	2.37	0.44
1:KA:170:ASN:OD1	1:KA:171:MET:N	2.51	0.44
1:KB:177:THR:HA	1:KC:107:TYR:O	2.17	0.44
1:MA:164:VAL:HG22	1:MB:166:LYS:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ME:139:ILE:HB	1:ME:165:LEU:HD13	1.99	0.44
2:MM:290:THR:HG22	2:MM:358:PHE:HD2	1.83	0.44
1:NA:187:PRO:HD3	1:NA:202:LYS:HG3	1.99	0.44
2:NM:291:LYS:HE2	2:NM:291:LYS:HB2	1.84	0.44
3:Nt:90:SER:OG	3:Nt:91:LYS:N	2.51	0.44
1:AE:126:LYS:O	1:AE:130:MET:HB2	2.18	0.43
1:BA:108:ALA:HA	3:Bt:133:MET:O	2.18	0.43
2:Cm:220:ILE:HG13	2:Cm:224:LEU:HD23	2.00	0.43
1:DA:132:THR:HA	1:DA:157:ASN:HA	2.00	0.43
3:Dt:207:GLU:OE1	3:Dt:207:GLU:N	2.29	0.43
1:EA:138:ILE:HA	1:EA:164:VAL:O	2.18	0.43
2:Fm:274:SER:O	2:Fm:278:LYS:HB2	2.18	0.43
3:Ft:96:ILE:HA	3:Ft:123:GLN:O	2.18	0.43
1:HA:138:ILE:HA	1:HA:164:VAL:O	2.18	0.43
1:HE:85:ASN:OD1	1:HE:87:ASN:ND2	2.51	0.43
2:HM:325:LEU:HD23	2:HM:325:LEU:HA	1.91	0.43
2:Hm:206:ASN:O	2:Hm:209:SER:OG	2.28	0.43
1:IA:149:TYR:OH	3:It:68:PRO:O	2.33	0.43
1:IA:267:ALA:HB1	1:IA:269:PRO:HD2	1.99	0.43
1:ID:114:TYR:H	1:IE:145:GLN:HE22	1.64	0.43
1:IE:157:ASN:ND2	1:IE:159:ARG:O	2.51	0.43
2:Im:206:ASN:O	2:Im:209:SER:OG	2.29	0.43
2:Im:332:ASN:HA	2:Im:353:LYS:HD3	1.99	0.43
1:KB:146:VAL:HB	1:KB:165:LEU:HD22	1.99	0.43
1:KE:79:ASP:N	1:KE:79:ASP:OD1	2.51	0.43
2:KM:218:ASP:OD1	2:KM:219:ASN:N	2.46	0.43
3:Kt:96:ILE:HA	3:Kt:123:GLN:O	2.18	0.43
1:LA:104:THR:HG22	3:Lt:138:TYR:HA	2.00	0.43
1:LA:187:PRO:HD3	1:LA:202:LYS:HG3	1.99	0.43
3:LT:206:LYS:O	1:MA:160:ASN:ND2	2.51	0.43
1:MA:132:THR:HA	1:MA:157:ASN:HA	2.00	0.43
1:MD:143:LEU:HD23	3:MT:221:LEU:HD22	2.00	0.43
2:MM:242:ALA:HA	2:MM:245:THR:HG22	2.00	0.43
2:Nm:264:GLU:OE1	2:Nm:268:ARG:NE	2.50	0.43
1:BE:162:LYS:HD2	1:BE:162:LYS:HA	1.68	0.43
3:BT:134:ILE:HD11	3:Bt:39:VAL:HG21	1.99	0.43
2:CM:188:LYS:O	2:CM:191:SER:OG	2.34	0.43
2:Cm:332:ASN:HA	2:Cm:353:LYS:HD3	2.01	0.43
1:DA:302:ARG:HH22	1:DA:305:LYS:HB2	1.83	0.43
2:Dm:259:ILE:HA	2:Dm:262:ILE:HD12	1.99	0.43
2:Dm:352:TYR:CE2	5:EX:351:ILE:HG12	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Dt:90:SER:OG	3:Dt:91:LYS:N	2.51	0.43
1:EA:132:THR:HA	1:EA:157:ASN:HA	2.00	0.43
1:EE:117:TYR:O	1:EE:121:GLU:HB2	2.18	0.43
2:EM:324:ILE:HA	2:EM:327:LYS:HE3	2.00	0.43
2:Em:357:PHE:O	2:Em:361:VAL:HG23	2.18	0.43
1:FA:170:ASN:OD1	1:FA:171:MET:N	2.51	0.43
1:HE:113:ASP:OD2	1:HE:115:ASN:N	2.51	0.43
2:HM:324:ILE:HA	2:HM:327:LYS:HE3	1.99	0.43
3:HT:149:GLN:HB2	3:HT:151:PHE:HE1	1.82	0.43
3:IT:234:GLN:NE2	3:IT:238:SER:OG	2.43	0.43
1:JA:267:ALA:HB1	1:JA:269:PRO:HD2	2.00	0.43
2:JM:246:LEU:O	2:JM:252:ARG:NH2	2.51	0.43
3:JT:74:LEU:O	3:JT:105:TYR:OH	2.32	0.43
2:Jm:221:ASP:O	2:Jm:225:GLN:HB2	2.18	0.43
1:KA:164:VAL:HG11	1:KA:235:VAL:HG12	2.00	0.43
1:KE:157:ASN:HD21	1:KE:161:ALA:H	1.66	0.43
6:KY:1752:MET:HE2	6:KY:1752:MET:HB2	1.72	0.43
1:LA:80:ILE:O	3:Lt:64:GLN:NE2	2.45	0.43
1:LE:152:ILE:HG22	1:LE:153:LEU:HD22	2.01	0.43
1:MA:82:ASP:CG	3:Mt:65:VAL:HA	2.43	0.43
1:MD:107:TYR:CE2	1:ME:80:ILE:HG23	2.53	0.43
2:MM:328:THR:HG21	2:MM:357:PHE:HD1	1.82	0.43
1:NA:164:VAL:HG11	1:NA:235:VAL:HG12	2.00	0.43
1:AA:267:ALA:HB1	1:AA:269:PRO:HD2	1.99	0.43
1:AE:85:ASN:OD1	1:AE:87:ASN:ND2	2.51	0.43
1:AE:149:TYR:CZ	1:AE:153:LEU:HG	2.53	0.43
1:BD:138:ILE:HG13	1:BD:164:VAL:HB	2.01	0.43
1:CA:132:THR:HA	1:CA:157:ASN:HA	2.00	0.43
1:CE:84:LEU:HD21	1:CE:91:PHE:HA	2.00	0.43
2:Cm:259:ILE:HA	2:Cm:262:ILE:HD12	2.00	0.43
2:Dm:220:ILE:HG13	2:Dm:224:LEU:HD23	2.00	0.43
1:EA:164:VAL:HG11	1:EA:235:VAL:HG12	2.00	0.43
1:EE:140:THR:HB	1:EE:175:GLN:HB3	2.00	0.43
5:EX:481:ASP:HB2	6:EY:1876:SER:H	1.84	0.43
1:GA:164:VAL:HG11	1:GA:235:VAL:HG12	2.00	0.43
3:GT:115:ARG:H	3:GT:115:ARG:HG2	1.66	0.43
1:IA:138:ILE:HA	1:IA:164:VAL:O	2.18	0.43
1:JC:139:ILE:HG22	1:JC:146:VAL:HG12	1.99	0.43
1:KD:111:LEU:HD13	1:KD:114:TYR:CE1	2.54	0.43
3:LT:117:ASP:N	3:LT:117:ASP:OD1	2.48	0.43
6:LY:1908:SER:O	5:MX:379:GLN:NE2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:MM:246:LEU:HD22	2:MM:252:ARG:HG3	2.00	0.43
3:MT:211:THR:O	1:NA:183:LYS:NZ	2.48	0.43
1:NA:132:THR:HA	1:NA:157:ASN:HA	2.00	0.43
1:NA:267:ALA:HB1	1:NA:269:PRO:HD2	1.99	0.43
1:NA:302:ARG:HH22	1:NA:305:LYS:HB2	1.83	0.43
1:AA:170:ASN:OD1	1:AA:171:MET:N	2.51	0.43
6:AY:1734:LYS:HE3	6:AY:1734:LYS:HB2	1.89	0.43
6:AY:1745:VAL:HG23	6:AY:1866:PRO:HB2	1.99	0.43
3:At:90:SER:OG	3:At:91:LYS:N	2.51	0.43
3:At:195:ILE:HD12	3:At:195:ILE:HA	1.88	0.43
1:BA:267:ALA:HB1	1:BA:269:PRO:HD2	1.99	0.43
1:CA:138:ILE:HA	1:CA:164:VAL:O	2.18	0.43
1:DB:117:TYR:HD2	1:DB:118:LEU:HD22	1.82	0.43
1:DD:111:LEU:HD13	1:DD:114:TYR:CE2	2.54	0.43
1:DE:112:LEU:H	1:DE:112:LEU:HD23	1.83	0.43
3:FT:101:LYS:HD2	3:FT:101:LYS:HA	1.72	0.43
3:FT:213:ARG:NH1	3:FT:219:GLU:OE2	2.50	0.43
2:Fm:259:ILE:HA	2:Fm:262:ILE:HD12	2.00	0.43
2:Fm:344:LYS:HB3	2:Fm:347:MET:HB2	2.00	0.43
1:GA:267:ALA:HB1	1:GA:269:PRO:HD2	2.00	0.43
2:GM:324:ILE:HA	2:GM:327:LYS:HE3	2.00	0.43
3:GT:213:ARG:NH1	3:GT:219:GLU:OE2	2.50	0.43
2:Hm:274:SER:O	2:Hm:278:LYS:HB2	2.19	0.43
1:JD:152:ILE:HG21	1:JE:114:TYR:HE1	1.84	0.43
1:KA:267:ALA:HB1	1:KA:269:PRO:HD2	1.99	0.43
2:KM:188:LYS:O	2:KM:191:SER:OG	2.33	0.43
2:Km:274:SER:O	2:Km:278:LYS:HB2	2.18	0.43
3:LT:213:ARG:NH1	3:LT:219:GLU:OE2	2.50	0.43
6:LY:1810:PHE:HD2	6:LY:1811:LEU:HD12	1.84	0.43
2:Lm:197:TYR:CZ	2:Lm:201:ILE:HD11	2.54	0.43
1:ME:85:ASN:OD1	1:ME:87:ASN:ND2	2.51	0.43
1:ME:101:LYS:HA	1:ME:101:LYS:HD2	1.82	0.43
1:NA:138:ILE:HA	1:NA:164:VAL:O	2.18	0.43
2:Nm:206:ASN:O	2:Nm:209:SER:OG	2.32	0.43
1:AA:209:LYS:HE2	1:AA:209:LYS:HB2	1.88	0.43
1:BA:132:THR:HA	1:BA:157:ASN:HA	2.00	0.43
1:BD:99:ALA:N	1:BE:94:TRP:O	2.47	0.43
1:CA:302:ARG:HH22	1:CA:305:LYS:HB2	1.83	0.43
1:CC:166:LYS:HE3	1:CC:166:LYS:HB3	1.86	0.43
2:CM:324:ILE:HA	2:CM:327:LYS:HE3	2.01	0.43
2:DM:341:MET:C	2:DM:344:LYS:HZ2	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:DY:1819:LEU:HD23	6:DY:1819:LEU:HA	1.87	0.43
1:EC:187:PRO:HG3	1:FA:189:ALA:H	1.84	0.43
2:EM:205:SER:HA	2:EM:208:VAL:HG12	2.01	0.43
5:EX:435:LEU:HD21	6:EY:1720:LYS:HE3	2.01	0.43
1:FA:267:ALA:HB1	1:FA:269:PRO:HD2	2.00	0.43
6:GY:1752:MET:HE2	6:GY:1752:MET:HB2	1.72	0.43
1:HA:302:ARG:HH22	1:HA:305:LYS:HB2	1.83	0.43
6:HY:1819:LEU:HD23	6:HY:1819:LEU:HA	1.87	0.43
2:Hm:332:ASN:HA	2:Hm:353:LYS:HD3	1.99	0.43
2:Hm:357:PHE:O	2:Hm:360:THR:OG1	2.27	0.43
1:JB:122:ASN:O	1:JB:126:LYS:HB2	2.18	0.43
1:KE:117:TYR:O	1:KE:121:GLU:HB2	2.18	0.43
1:LA:138:ILE:HA	1:LA:164:VAL:O	2.18	0.43
2:LM:324:ILE:HA	2:LM:327:LYS:HE3	2.01	0.43
6:LY:1734:LYS:HE3	6:LY:1734:LYS:HB2	1.89	0.43
2:Lm:274:SER:O	2:Lm:278:LYS:HB2	2.18	0.43
3:Lt:90:SER:OG	3:Lt:91:LYS:N	2.51	0.43
3:Lt:96:ILE:HA	3:Lt:123:GLN:O	2.18	0.43
1:MA:255:LEU:HD21	1:MC:146:VAL:HG23	2.01	0.43
1:MD:140:THR:HG22	1:MD:166:LYS:HB2	2.00	0.43
1:ME:172:PRO:HG2	1:ME:173:TYR:HD1	1.83	0.43
2:Mm:295:ASN:OD1	2:Mm:295:ASN:N	2.50	0.43
1:ND:104:THR:OG1	1:NE:181:VAL:O	2.33	0.43
6:NY:1734:LYS:HE3	6:NY:1734:LYS:HB2	1.89	0.43
1:AC:129:ALA:HB2	1:AC:192:LEU:HD22	2.01	0.43
1:BB:126:LYS:O	1:BB:130:MET:CB	2.67	0.43
1:BC:171:MET:SD	1:BC:171:MET:N	2.88	0.43
1:BD:143:LEU:HD21	3:CT:268:TYR:CD1	2.54	0.43
2:Cm:218:ASP:HA	2:Cm:297:LYS:HG2	2.00	0.43
1:DD:149:TYR:OH	1:DE:112:LEU:O	2.34	0.43
1:FD:107:TYR:CE2	1:FE:80:ILE:HG23	2.52	0.43
2:Fm:332:ASN:O	2:Fm:353:LYS:NZ	2.51	0.43
1:GA:237:MET:HE1	1:GB:179:LEU:HD21	2.00	0.43
5:GX:419:ILE:HD12	3:HT:39:VAL:HG11	1.99	0.43
1:JA:199:ASP:OD1	1:JA:199:ASP:N	2.48	0.43
1:JA:302:ARG:HH22	1:JA:305:LYS:HB2	1.83	0.43
1:JB:117:TYR:O	1:JB:120:ILE:N	2.49	0.43
1:JE:162:LYS:HD2	1:JE:162:LYS:HA	1.74	0.43
3:Jt:90:SER:OG	3:Jt:91:LYS:N	2.51	0.43
1:KA:302:ARG:HH22	1:KA:305:LYS:HB2	1.83	0.43
6:KY:1810:PHE:HD2	6:KY:1811:LEU:HD12	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MA:267:ALA:HB1	1:MA:269:PRO:HD2	2.00	0.43
1:MB:130:MET:HE2	1:MB:130:MET:HB2	1.92	0.43
1:MD:108:ALA:HA	1:ME:177:THR:HA	2.01	0.43
1:MD:170:ASN:OD1	1:MD:171:MET:N	2.49	0.43
5:MX:434:THR:O	5:MX:465:ARG:NH1	2.44	0.43
6:MY:1734:LYS:HE3	6:MY:1734:LYS:HB2	1.89	0.43
1:NC:131:GLY:HA3	1:NC:153:LEU:HD22	1.99	0.43
1:ND:156:LEU:HD23	1:ND:156:LEU:HA	1.87	0.43
1:AA:164:VAL:HG11	1:AA:235:VAL:HG12	2.00	0.43
1:AA:302:ARG:HH22	1:AA:305:LYS:HB2	1.83	0.43
1:AD:129:ALA:O	1:AD:133:TYR:CB	2.59	0.43
1:BA:257:ARG:HE	1:BA:305:LYS:HZ1	1.67	0.43
1:BA:302:ARG:HH22	1:BA:305:LYS:HB2	1.83	0.43
1:BC:139:ILE:HG22	1:BC:146:VAL:HG12	2.01	0.43
1:BE:84:LEU:HD21	1:BE:91:PHE:HA	2.00	0.43
2:Bm:264:GLU:OE1	2:Bm:268:ARG:NE	2.52	0.43
3:Bt:100:ASN:OD1	3:Bt:100:ASN:N	2.48	0.43
1:CA:164:VAL:HG11	1:CA:235:VAL:HG12	2.00	0.43
1:CA:267:ALA:HB1	1:CA:269:PRO:HD2	1.99	0.43
1:CB:117:TYR:O	1:CB:120:ILE:N	2.50	0.43
6:CY:1810:PHE:HD2	6:CY:1811:LEU:HD12	1.84	0.43
1:DA:164:VAL:HG11	1:DA:235:VAL:HG12	2.00	0.43
1:ED:133:TYR:OH	1:EE:96:GLY:O	2.34	0.43
1:FD:179:LEU:HD13	1:FE:106:LEU:HD12	2.01	0.43
1:GB:124:ILE:O	1:GB:127:THR:OG1	2.34	0.43
3:Gt:96:ILE:HA	3:Gt:123:GLN:O	2.18	0.43
1:HA:82:ASP:OD1	1:HA:126:LYS:NZ	2.38	0.43
5:HX:461:ASN:OD1	5:HX:461:ASN:N	2.49	0.43
1:IA:302:ARG:HH22	1:IA:305:LYS:HB2	1.83	0.43
1:KA:257:ARG:HE	1:KA:305:LYS:HZ1	1.66	0.43
1:KC:130:MET:HB3	1:KC:178:PHE:CG	2.53	0.43
1:KD:140:THR:HG22	1:KD:166:LYS:HB2	2.01	0.43
2:KM:338:ASP:OD1	2:KM:338:ASP:N	2.50	0.43
3:KT:269:LEU:HD23	3:KT:269:LEU:HA	1.81	0.43
1:LE:157:ASN:ND2	1:LE:159:ARG:O	2.51	0.43
1:NA:304:LYS:NZ	1:ND:80:ILE:HD12	2.34	0.43
3:AT:44:ILE:HD12	3:NT:159:PRO:HA	2.01	0.43
1:BB:150:TYR:OH	1:BB:154:LYS:NZ	2.46	0.43
1:BC:138:ILE:HG23	1:BC:164:VAL:HG23	2.00	0.43
3:BT:149:GLN:HB2	3:BT:151:PHE:HE1	1.82	0.43
1:CB:183:LYS:HE2	1:CB:183:LYS:HB2	1.88	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Cm:236:LYS:HD3	2:Cm:236:LYS:HA	1.87	0.43
2:Cm:349:LYS:HA	2:Cm:352:TYR:CE2	2.54	0.43
1:DB:156:LEU:HA	1:DB:156:LEU:HD13	1.88	0.43
6:DY:1810:PHE:HD2	6:DY:1811:LEU:HD12	1.84	0.43
1:EA:302:ARG:HH22	1:EA:305:LYS:HB2	1.83	0.43
1:ED:152:ILE:HG21	1:EE:114:TYR:HE1	1.83	0.43
1:ED:153:LEU:C	1:ED:158:LYS:HZ3	2.26	0.43
1:EE:85:ASN:OD1	1:EE:87:ASN:ND2	2.52	0.43
3:ET:223:THR:HG22	1:FA:184:ARG:HH21	1.84	0.43
2:Em:295:ASN:OD1	2:Em:295:ASN:N	2.49	0.43
1:FA:303:GLU:CD	1:FA:304:LYS:H	2.27	0.43
1:FB:137:ILE:HD13	1:FB:153:LEU:HD23	1.99	0.43
1:FC:130:MET:HA	1:FC:130:MET:HE3	2.00	0.43
1:FD:77:LEU:HD12	1:FD:78:PHE:H	1.84	0.43
2:FM:247:ILE:O	2:FM:252:ARG:NH1	2.46	0.43
1:GA:302:ARG:HH22	1:GA:305:LYS:HB2	1.83	0.43
1:GB:168:ASN:ND2	1:GB:171:MET:SD	2.92	0.43
1:GD:112:LEU:HD21	1:GD:117:TYR:CD1	2.53	0.43
1:GE:146:VAL:O	1:GE:149:TYR:HB3	2.19	0.43
3:GT:134:ILE:HD11	3:Gt:39:VAL:HG21	2.01	0.43
2:Gm:225:GLN:O	2:Gm:229:ASN:ND2	2.52	0.43
1:HA:170:ASN:OD1	1:HA:171:MET:N	2.51	0.43
3:HT:159:PRO:HA	3:IT:44:ILE:HD12	2.00	0.43
3:HT:213:ARG:NH1	3:HT:219:GLU:OE2	2.50	0.43
1:ID:107:TYR:CE2	1:ID:109:MET:HB3	2.53	0.43
1:IE:79:ASP:OD1	1:IE:79:ASP:N	2.51	0.43
1:IE:152:ILE:HG22	1:IE:153:LEU:HD22	2.01	0.43
6:IY:1900:VAL:HG11	5:JX:387:TYR:CZ	2.54	0.43
1:LC:126:LYS:HZ1	1:LC:184:ARG:NH1	2.16	0.43
1:LD:108:ALA:HA	1:LE:177:THR:HA	2.01	0.43
1:LD:126:LYS:HE2	1:LE:109:MET:HG2	2.00	0.43
2:Mm:206:ASN:O	2:Mm:209:SER:OG	2.27	0.43
1:AA:132:THR:HA	1:AA:157:ASN:HA	2.00	0.43
1:AD:111:LEU:HD13	1:AD:114:TYR:CE1	2.54	0.43
1:AE:112:LEU:HD23	1:AE:112:LEU:H	1.82	0.43
2:AM:218:ASP:OD1	2:AM:219:ASN:N	2.46	0.43
3:AT:134:ILE:HD11	3:At:39:VAL:HG21	2.00	0.43
3:AT:213:ARG:NH1	3:AT:219:GLU:OE2	2.50	0.43
1:BA:164:VAL:HG11	1:BA:235:VAL:HG12	2.00	0.43
2:BM:212:LEU:HG	2:BM:270:TYR:HB2	2.01	0.43
1:CE:153:LEU:HA	1:CE:156:LEU:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Cm:323:SER:HA	2:Cm:326:LYS:HE3	2.01	0.43
1:DA:170:ASN:OD1	1:DA:171:MET:N	2.51	0.43
2:DM:338:ASP:OD1	2:DM:338:ASP:N	2.49	0.43
1:EE:157:ASN:ND2	1:EE:159:ARG:O	2.51	0.43
1:FD:146:VAL:O	1:FD:150:TYR:HB2	2.19	0.43
1:FD:170:ASN:OD1	1:FD:171:MET:N	2.49	0.43
2:FM:338:ASP:OD1	2:FM:338:ASP:N	2.51	0.43
3:FT:134:ILE:HD11	3:Ft:39:VAL:HG21	2.01	0.43
2:Fm:327:LYS:HD2	2:Fm:327:LYS:HA	1.87	0.43
1:GA:304:LYS:NZ	1:GD:79:ASP:HA	2.33	0.43
1:GB:107:TYR:O	1:GC:177:THR:HA	2.17	0.43
1:GC:133:TYR:HB3	1:GC:181:VAL:HG11	2.01	0.43
1:GD:95:PHE:HE1	1:GE:128:ARG:HD2	1.83	0.43
1:GE:84:LEU:HD21	1:GE:91:PHE:HA	2.01	0.43
1:GE:118:LEU:HD23	1:GE:118:LEU:HA	1.77	0.43
1:HA:132:THR:HA	1:HA:157:ASN:HA	2.00	0.43
1:IC:139:ILE:HG22	1:IC:146:VAL:HG12	2.00	0.43
5:IX:392:LEU:HD23	5:IX:392:LEU:HA	1.88	0.43
2:Im:198:LYS:O	2:Im:201:ILE:N	2.52	0.43
3:KT:72:ASP:OD1	3:KT:72:ASP:N	2.52	0.43
3:KT:145:LYS:HD2	3:KT:145:LYS:HA	1.88	0.43
1:LA:302:ARG:HH22	1:LA:305:LYS:HB2	1.83	0.43
1:MD:143:LEU:O	1:MD:147:ASN:HB2	2.18	0.43
6:MY:1810:PHE:HD2	6:MY:1811:LEU:HD12	1.84	0.43
1:NA:296:VAL:O	1:NC:164:VAL:HA	2.18	0.43
1:NA:296:VAL:HG11	1:ND:80:ILE:HD13	2.01	0.43
1:NC:129:ALA:HB2	1:NC:192:LEU:HD22	2.01	0.43
5:AX:408:GLU:OE1	3:BT:32:LYS:N	2.39	0.43
1:BA:170:ASN:OD1	1:BA:171:MET:N	2.51	0.43
1:BC:118:LEU:HB3	3:Bt:187:ARG:HB2	2.00	0.43
1:BE:139:ILE:HG12	1:BE:149:TYR:CZ	2.54	0.43
3:BT:269:LEU:HD23	3:BT:269:LEU:HA	1.81	0.43
2:Bm:357:PHE:O	2:Bm:361:VAL:HG23	2.19	0.43
1:CC:130:MET:HE3	1:CC:178:PHE:HB2	2.00	0.43
2:Cm:193:LEU:HD11	2:Cm:242:ALA:HB2	2.01	0.43
1:DA:138:ILE:HA	1:DA:164:VAL:O	2.18	0.43
2:EM:344:LYS:HE2	2:EM:344:LYS:HB2	1.55	0.43
3:ET:134:ILE:HD11	3:Et:39:VAL:HG21	2.01	0.43
1:FA:132:THR:HA	1:FA:157:ASN:HA	2.00	0.43
1:FE:162:LYS:HD2	1:FE:162:LYS:HA	1.87	0.43
6:FY:1729:MET:HE3	5:GX:511:ARG:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FY:1819:LEU:HD23	6:FY:1819:LEU:HA	1.87	0.43
1:GB:142:SER:OG	1:GB:143:LEU:N	2.52	0.43
1:GB:153:LEU:HA	1:GB:156:LEU:HB2	2.01	0.43
1:GD:170:ASN:OD1	1:GD:171:MET:N	2.48	0.43
1:HD:175:GLN:HA	1:HE:109:MET:O	2.19	0.43
2:IM:325:LEU:HD23	2:IM:325:LEU:HA	1.90	0.43
1:JA:186:ASP:HB3	1:JA:189:ALA:HB2	2.01	0.43
1:JA:303:GLU:CD	1:JA:304:LYS:H	2.27	0.43
1:JB:177:THR:HA	1:JC:107:TYR:O	2.18	0.43
1:JC:136:LEU:HB3	1:JC:179:LEU:HB2	2.00	0.43
2:JM:343:ASP:OD1	2:JM:343:ASP:N	2.52	0.43
1:AA:207:GLN:OE1	3:NT:213:ARG:NH2	2.52	0.42
1:AE:80:ILE:HD13	1:AE:84:LEU:HD22	2.01	0.42
5:AX:481:ASP:HB2	6:AY:1876:SER:H	1.84	0.42
2:Am:249:ASN:OD1	2:Am:249:ASN:N	2.52	0.42
1:BE:152:ILE:HG22	1:BE:153:LEU:HD22	2.01	0.42
2:BM:242:ALA:HA	2:BM:245:THR:HG22	2.01	0.42
5:BX:482:LYS:HA	3:CT:29:VAL:HG21	2.01	0.42
2:Bm:198:LYS:O	2:Bm:201:ILE:N	2.52	0.42
1:CD:126:LYS:NZ	1:CE:109:MET:SD	2.81	0.42
5:CX:372:LYS:O	5:CX:376:ILE:HG12	2.19	0.42
3:DT:134:ILE:HD11	3:Dt:39:VAL:HG21	2.01	0.42
5:DX:410:ARG:HH12	5:EX:445:ASP:HA	1.84	0.42
1:EA:117:TYR:CE1	3:Et:80:VAL:HG23	2.53	0.42
2:EM:189:LYS:HA	2:EM:192:ARG:HG3	2.01	0.42
3:Et:273:ILE:O	2:Fm:261:LYS:NZ	2.41	0.42
1:GA:150:TYR:CZ	1:GB:167:ILE:HD13	2.53	0.42
1:GA:303:GLU:CD	1:GA:304:LYS:H	2.27	0.42
1:HD:140:THR:OG1	1:HD:175:GLN:HB3	2.19	0.42
3:HT:134:ILE:HD11	3:Ht:39:VAL:HG21	2.01	0.42
5:HX:372:LYS:O	5:HX:376:ILE:HG12	2.19	0.42
1:IA:186:ASP:HB3	1:IA:189:ALA:HB2	2.01	0.42
1:ID:108:ALA:HA	1:IE:177:THR:HA	2.01	0.42
1:ID:166:LYS:HD3	1:ID:166:LYS:HA	1.87	0.42
6:IY:1905:ILE:O	6:IY:1908:SER:OG	2.25	0.42
1:JC:158:LYS:HE3	1:JC:158:LYS:HB2	1.92	0.42
3:JT:213:ARG:NH1	3:JT:219:GLU:OE2	2.50	0.42
1:KA:186:ASP:HB3	1:KA:189:ALA:HB2	2.01	0.42
2:KM:349:LYS:O	2:KM:353:LYS:HG2	2.19	0.42
3:KT:213:ARG:NH1	3:KT:219:GLU:OE2	2.50	0.42
1:LB:120:ILE:HD11	3:LT:247:LEU:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MA:302:ARG:HH22	1:MA:305:LYS:HB2	1.83	0.42
1:ME:162:LYS:HD2	1:ME:162:LYS:HA	1.83	0.42
5:MX:372:LYS:O	5:MX:376:ILE:HG12	2.19	0.42
1:NE:152:ILE:HG22	1:NE:153:LEU:HD22	2.01	0.42
6:NY:1721:ASP:OD1	6:NY:1721:ASP:N	2.52	0.42
1:AC:136:LEU:HB3	1:AC:179:LEU:HB2	2.00	0.42
3:AT:159:PRO:HA	3:BT:44:ILE:HD12	2.01	0.42
2:Am:197:TYR:CZ	2:Am:201:ILE:HD11	2.54	0.42
1:BE:157:ASN:ND2	1:BE:159:ARG:O	2.51	0.42
3:BT:159:PRO:HA	3:CT:44:ILE:HD12	2.01	0.42
1:CB:177:THR:HA	1:CC:107:TYR:O	2.18	0.42
6:CY:1721:ASP:OD1	6:CY:1721:ASP:N	2.52	0.42
6:DY:1724:ASN:ND2	6:DY:1729:MET:HB3	2.34	0.42
2:Dm:198:LYS:HE3	2:Dm:262:ILE:HG12	2.01	0.42
2:Dm:345:THR:O	2:Dm:349:LYS:HB2	2.19	0.42
1:EA:186:ASP:HB3	1:EA:189:ALA:HB2	2.01	0.42
2:Em:221:ASP:O	2:Em:225:GLN:HB2	2.19	0.42
1:FA:186:ASP:HB3	1:FA:189:ALA:HB2	2.01	0.42
1:FB:136:LEU:HB3	1:FB:179:LEU:HB2	2.01	0.42
1:FB:191:THR:HG23	1:FB:192:LEU:HG	2.00	0.42
1:FE:85:ASN:OD1	1:FE:87:ASN:ND2	2.51	0.42
2:FM:270:TYR:CE2	2:FM:273:PHE:HB3	2.54	0.42
1:GA:186:ASP:HB3	1:GA:189:ALA:HB2	2.01	0.42
1:GD:156:LEU:HD23	1:GD:156:LEU:HA	1.84	0.42
6:GY:1810:PHE:HD2	6:GY:1811:LEU:HD12	1.84	0.42
3:Gt:41:ASN:N	3:Gt:45:GLU:OE2	2.53	0.42
3:Gt:90:SER:OG	3:Gt:91:LYS:N	2.51	0.42
1:HA:186:ASP:HB3	1:HA:189:ALA:HB2	2.01	0.42
1:HD:166:LYS:HD3	1:HD:166:LYS:HA	1.90	0.42
2:HM:341:MET:O	2:HM:344:LYS:NZ	2.51	0.42
1:IB:112:LEU:HD21	3:IT:238:SER:HB3	2.00	0.42
2:IM:324:ILE:HA	2:IM:327:LYS:HE3	2.00	0.42
3:IT:213:ARG:NH1	3:IT:219:GLU:OE2	2.50	0.42
1:JE:138:ILE:HB	1:JE:177:THR:HB	2.00	0.42
2:Jm:193:LEU:HD11	2:Jm:242:ALA:HB2	2.01	0.42
1:KB:157:ASN:OD1	1:KB:159:ARG:N	2.46	0.42
2:Km:198:LYS:HE3	2:Km:262:ILE:HG12	2.01	0.42
1:LA:108:ALA:HA	3:Lt:133:MET:O	2.20	0.42
1:LA:267:ALA:HB1	1:LA:269:PRO:HD2	2.00	0.42
1:LD:156:LEU:HD23	1:LD:156:LEU:HA	1.85	0.42
3:LT:145:LYS:HD2	3:LT:145:LYS:HA	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MC:140:THR:HG22	1:MC:166:LYS:HB2	2.00	0.42
1:NB:107:TYR:HB3	1:NC:130:MET:HE2	1.99	0.42
2:NM:328:THR:HG21	2:NM:357:PHE:HD1	1.83	0.42
6:NY:1810:PHE:HD2	6:NY:1811:LEU:HD12	1.84	0.42
6:AY:1721:ASP:OD1	6:AY:1721:ASP:N	2.52	0.42
6:AY:1810:PHE:HD2	6:AY:1811:LEU:HD12	1.84	0.42
1:BB:126:LYS:HD2	1:BC:109:MET:HE1	2.00	0.42
5:BX:372:LYS:O	5:BX:376:ILE:HG12	2.20	0.42
6:BY:1749:THR:O	6:BY:1797:ARG:NH2	2.52	0.42
1:CC:136:LEU:HB3	1:CC:179:LEU:HB2	2.01	0.42
1:DA:186:ASP:HB3	1:DA:189:ALA:HB2	2.01	0.42
1:DA:267:ALA:HB1	1:DA:269:PRO:HD2	2.00	0.42
1:DB:107:TYR:O	1:DC:177:THR:HA	2.19	0.42
1:DD:176:ALA:HB3	1:DE:109:MET:HE3	2.02	0.42
2:DM:300:PHE:O	2:DM:304:GLN:NE2	2.52	0.42
1:EA:199:ASP:OD1	1:EA:199:ASP:N	2.49	0.42
1:EA:267:ALA:HB1	1:EA:269:PRO:HD2	2.00	0.42
1:EA:303:GLU:CD	1:EA:304:LYS:H	2.27	0.42
6:EY:1724:ASN:ND2	6:EY:1729:MET:HB3	2.35	0.42
1:FA:302:ARG:HH22	1:FA:305:LYS:HB2	1.83	0.42
1:FE:139:ILE:HB	1:FE:165:LEU:HD13	1.99	0.42
6:FY:1724:ASN:ND2	6:FY:1729:MET:HB3	2.35	0.42
2:GM:325:LEU:HD23	2:GM:325:LEU:HA	1.94	0.42
2:Gm:332:ASN:O	2:Gm:353:LYS:NZ	2.52	0.42
1:HD:138:ILE:HG13	1:HD:164:VAL:HB	2.00	0.42
2:HM:344:LYS:HE2	2:HM:344:LYS:HB2	1.66	0.42
6:HY:1810:PHE:HD2	6:HY:1811:LEU:HD12	1.84	0.42
2:Hm:268:ARG:HB2	2:Hm:271:GLU:HG3	2.01	0.42
1:ID:104:THR:OG1	1:IE:181:VAL:O	2.32	0.42
1:ID:143:LEU:HD12	1:ID:167:ILE:HD12	2.00	0.42
1:JA:164:VAL:HG22	1:JB:166:LYS:HG2	2.01	0.42
2:JM:204:TYR:HB2	2:JM:231:PHE:HB2	2.00	0.42
1:KA:303:GLU:CD	1:KA:304:LYS:H	2.27	0.42
5:KX:372:LYS:O	5:KX:376:ILE:HG12	2.20	0.42
6:LY:1780:MET:SD	5:MX:443:GLN:NE2	2.92	0.42
2:Lm:221:ASP:O	2:Lm:225:GLN:HB2	2.19	0.42
1:MA:138:ILE:HA	1:MA:164:VAL:O	2.18	0.42
2:Mm:323:SER:HA	2:Mm:326:LYS:HE3	2.00	0.42
1:NB:168:ASN:ND2	1:NB:171:MET:SD	2.92	0.42
1:AD:114:TYR:HE2	1:AE:149:TYR:HB2	1.84	0.42
6:AY:1749:THR:O	6:AY:1797:ARG:NH2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:303:GLU:CD	1:BA:304:LYS:H	2.27	0.42
1:BC:169:GLU:OE2	3:Bt:233:ARG:NH2	2.53	0.42
1:BD:123:PRO:HA	1:BD:126:LYS:HE2	2.00	0.42
6:BY:1810:PHE:HD2	6:BY:1811:LEU:HD12	1.84	0.42
1:CA:186:ASP:HB3	1:CA:189:ALA:HB2	2.01	0.42
2:DM:204:TYR:HB2	2:DM:231:PHE:HB2	2.00	0.42
2:DM:349:LYS:O	2:DM:353:LYS:HG2	2.20	0.42
3:DT:159:PRO:HA	3:ET:44:ILE:HD12	2.00	0.42
1:EA:170:ASN:OD1	1:EA:171:MET:N	2.51	0.42
1:EA:209:LYS:HE2	1:EA:209:LYS:HB2	1.88	0.42
2:EM:188:LYS:O	2:EM:191:SER:OG	2.37	0.42
2:Fm:323:SER:HA	2:Fm:326:LYS:HE3	2.00	0.42
2:Gm:264:GLU:OE1	2:Gm:268:ARG:NE	2.51	0.42
1:HE:84:LEU:HD21	1:HE:91:PHE:HA	2.01	0.42
1:IA:304:LYS:NZ	1:ID:79:ASP:HA	2.35	0.42
2:Im:362:VAL:HG21	2:Jm:222:TYR:OH	2.19	0.42
1:JD:176:ALA:H	1:JE:109:MET:HB3	1.84	0.42
1:JE:84:LEU:HD21	1:JE:91:PHE:HA	2.02	0.42
5:JX:372:LYS:O	5:JX:376:ILE:HG12	2.19	0.42
6:JY:1810:PHE:HD2	6:JY:1811:LEU:HD12	1.84	0.42
3:Jt:41:ASN:N	3:Jt:45:GLU:OE2	2.53	0.42
1:LA:186:ASP:HB3	1:LA:189:ALA:HB2	2.01	0.42
1:LA:303:GLU:CD	1:LA:304:LYS:H	2.27	0.42
1:LD:114:TYR:HE1	1:LE:149:TYR:HB2	1.84	0.42
6:LY:1721:ASP:OD1	6:LY:1721:ASP:N	2.52	0.42
2:Lm:357:PHE:O	2:Lm:361:VAL:HG23	2.19	0.42
1:MC:130:MET:HE2	1:MC:130:MET:HB2	1.82	0.42
2:Mm:327:LYS:HD2	2:Mm:327:LYS:HA	1.87	0.42
1:NA:170:ASN:OD1	1:NA:171:MET:N	2.51	0.42
1:NC:133:TYR:HB3	1:NC:181:VAL:HG11	2.00	0.42
1:NE:139:ILE:HB	1:NE:165:LEU:HD13	2.00	0.42
1:AA:186:ASP:HB3	1:AA:189:ALA:HB2	2.01	0.42
1:AE:157:ASN:ND2	1:AE:159:ARG:O	2.52	0.42
2:Am:198:LYS:HG2	2:Am:262:ILE:HG12	2.02	0.42
1:BA:186:ASP:HB3	1:BA:189:ALA:HB2	2.01	0.42
1:BD:150:TYR:HE2	1:BD:163:PHE:CG	2.38	0.42
1:CC:132:THR:HA	1:CC:157:ASN:HA	2.01	0.42
1:CE:112:LEU:HD23	1:CE:112:LEU:H	1.84	0.42
5:CX:391:ALA:O	5:CX:505:ASN:ND2	2.41	0.42
6:CY:1724:ASN:ND2	6:CY:1729:MET:HB3	2.35	0.42
2:Cm:295:ASN:OD1	2:Cm:295:ASN:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DC:136:LEU:HB3	1:DC:179:LEU:HB2	2.01	0.42
5:DX:372:LYS:O	5:DX:376:ILE:HG12	2.20	0.42
6:DY:1749:THR:O	6:DY:1797:ARG:NH2	2.52	0.42
1:FD:108:ALA:HA	1:FE:177:THR:HA	2.02	0.42
1:FD:143:LEU:HD23	3:FT:221:LEU:HD22	2.00	0.42
2:FM:273:PHE:HA	2:FM:276:LEU:HB2	2.02	0.42
3:FT:159:PRO:HA	3:GT:44:ILE:HD12	2.00	0.42
5:FX:372:LYS:O	5:FX:376:ILE:HG12	2.20	0.42
2:Fm:318:THR:O	2:Fm:322:LYS:HG3	2.20	0.42
1:GA:132:THR:HA	1:GA:157:ASN:HA	2.00	0.42
1:GD:117:TYR:O	1:GD:121:GLU:CB	2.52	0.42
6:GY:1724:ASN:ND2	6:GY:1729:MET:HB3	2.35	0.42
1:HA:296:VAL:HG23	1:HC:162:LYS:NZ	2.34	0.42
1:IA:132:THR:HG21	3:It:51:PRO:HD2	2.02	0.42
2:Im:264:GLU:OE1	2:Im:268:ARG:NE	2.52	0.42
1:JA:295:LEU:HA	1:JC:162:LYS:NZ	2.34	0.42
3:JT:134:ILE:HD11	3:Jt:39:VAL:HG21	2.01	0.42
3:Jt:195:ILE:HD12	3:Jt:195:ILE:HA	1.89	0.42
2:Km:236:LYS:HD3	2:Km:236:LYS:HA	1.85	0.42
1:LC:139:ILE:HG22	1:LC:146:VAL:HG12	2.02	0.42
2:LM:344:LYS:N	2:LM:344:LYS:HD2	2.34	0.42
6:LY:1749:THR:O	6:LY:1797:ARG:NH2	2.52	0.42
1:ME:140:THR:HG21	1:NA:278:PRO:HD3	2.00	0.42
3:Mt:90:SER:OG	3:Mt:91:LYS:N	2.51	0.42
1:NB:142:SER:OG	1:NB:143:LEU:N	2.53	0.42
5:NX:392:LEU:HD23	5:NX:392:LEU:HA	1.88	0.42
6:NY:1749:THR:O	6:NY:1797:ARG:NH2	2.53	0.42
1:AA:303:GLU:CD	1:AA:304:LYS:H	2.27	0.42
5:AX:372:LYS:O	5:AX:376:ILE:HG12	2.19	0.42
1:BE:137:ILE:HA	1:BE:177:THR:O	2.19	0.42
2:Bm:193:LEU:HD11	2:Bm:242:ALA:HB2	2.00	0.42
1:CA:100:LEU:HD22	3:Ct:44:ILE:HG22	2.02	0.42
1:CD:152:ILE:HG21	1:CE:114:TYR:HE1	1.84	0.42
2:CM:288:THR:O	2:CM:291:LYS:HG3	2.20	0.42
3:CT:134:ILE:HD11	3:Ct:39:VAL:HG21	2.01	0.42
2:Cm:294:THR:O	2:Cm:303:LYS:NZ	2.44	0.42
1:DB:132:THR:HG23	1:DB:133:TYR:CD1	2.54	0.42
3:Dt:41:ASN:N	3:Dt:45:GLU:OE2	2.53	0.42
6:EY:1749:THR:O	6:EY:1797:ARG:NH2	2.52	0.42
6:EY:1895:ILE:HG22	6:EY:1897:ASN:H	1.85	0.42
2:Fm:214:ARG:HH22	2:Fm:216:GLU:CD	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Gm:295:ASN:OD1	2:Gm:295:ASN:N	2.52	0.42
1:IA:303:GLU:CD	1:IA:304:LYS:H	2.27	0.42
1:ID:81:TYR:CD2	1:IE:107:TYR:HD1	2.38	0.42
1:JB:115:ASN:HD22	2:JM:300:PHE:HD2	1.67	0.42
1:JD:170:ASN:OD1	1:JD:171:MET:N	2.50	0.42
2:JM:282:ASP:OD1	2:JM:283:ASP:N	2.52	0.42
1:KE:85:ASN:OD1	1:KE:87:ASN:ND2	2.53	0.42
1:KE:139:ILE:HB	1:KE:165:LEU:HD13	2.01	0.42
6:KY:1819:LEU:HD23	6:KY:1819:LEU:HA	1.87	0.42
1:LD:178:PHE:CE1	1:LE:107:TYR:HB3	2.55	0.42
2:LM:205:SER:OG	2:LM:268:ARG:NH1	2.53	0.42
2:LM:218:ASP:OD1	2:LM:219:ASN:N	2.45	0.42
6:NY:1752:MET:HE2	6:NY:1752:MET:HB2	1.72	0.42
2:Am:267:LEU:HD23	2:Am:267:LEU:HA	1.90	0.42
1:BE:79:ASP:N	1:BE:79:ASP:OD1	2.51	0.42
6:BY:1721:ASP:OD1	6:BY:1721:ASP:N	2.52	0.42
6:BY:1724:ASN:ND2	6:BY:1729:MET:HB3	2.35	0.42
2:Bm:327:LYS:HD2	2:Bm:327:LYS:HA	1.87	0.42
1:CA:303:GLU:CD	1:CA:304:LYS:H	2.27	0.42
1:CC:184:ARG:HH11	1:CC:186:ASP:H	1.67	0.42
1:CD:178:PHE:CE1	1:CE:107:TYR:HB3	2.55	0.42
3:CT:97:GLY:O	3:CT:125:THR:N	2.45	0.42
6:CY:1749:THR:O	6:CY:1797:ARG:NH2	2.53	0.42
1:DA:303:GLU:CD	1:DA:304:LYS:H	2.27	0.42
1:DB:107:TYR:CD1	1:EA:193:ASP:HB3	2.54	0.42
1:DD:137:ILE:O	1:DD:163:PHE:HA	2.20	0.42
6:DY:1895:ILE:HG22	6:DY:1897:ASN:H	1.85	0.42
1:EA:124:ILE:HG13	3:Et:73:TYR:CE2	2.54	0.42
1:ED:95:PHE:CD1	1:ED:125:ILE:HD13	2.54	0.42
5:EX:410:ARG:NH1	5:FX:445:ASP:HA	2.33	0.42
2:Fm:193:LEU:HD11	2:Fm:242:ALA:HB2	2.00	0.42
1:HD:143:LEU:HG	1:HD:167:ILE:HD12	2.00	0.42
1:HD:180:ARG:NH2	1:HE:100:LEU:O	2.52	0.42
3:Ht:41:ASN:N	3:Ht:45:GLU:OE2	2.53	0.42
2:Im:357:PHE:O	2:Im:361:VAL:HG23	2.19	0.42
1:JA:139:ILE:O	1:JA:165:LEU:HA	2.20	0.42
2:JM:325:LEU:HD23	2:JM:325:LEU:HA	1.90	0.42
6:JY:1724:ASN:ND2	6:JY:1729:MET:HB3	2.35	0.42
2:KM:341:MET:O	2:KM:344:LYS:NZ	2.52	0.42
3:KT:134:ILE:HD11	3:Kt:39:VAL:HG21	2.01	0.42
5:KX:482:LYS:HA	3:LT:29:VAL:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Km:228:ARG:HD2	2:Km:228:ARG:HA	1.95	0.42
2:Km:295:ASN:N	2:Km:295:ASN:OD1	2.51	0.42
1:LD:152:ILE:HG21	1:LE:114:TYR:HE1	1.84	0.42
1:MA:163:PHE:HB2	1:MB:167:ILE:HG22	2.01	0.42
1:MA:186:ASP:HB3	1:MA:189:ALA:HB2	2.01	0.42
2:MM:309:LEU:HD23	2:MM:309:LEU:HA	1.84	0.42
6:MY:1749:THR:O	6:MY:1797:ARG:NH2	2.53	0.42
2:Mm:218:ASP:HA	2:Mm:297:LYS:HG2	2.02	0.42
1:NA:186:ASP:HB3	1:NA:189:ALA:HB2	2.01	0.42
2:Nm:210:ASN:O	2:Nm:213:SER:OG	2.37	0.42
3:NT:145:LYS:HA	3:NT:145:LYS:HD2	1.88	0.42
1:AD:123:PRO:HA	1:AD:126:LYS:HZ2	1.83	0.42
1:AE:139:ILE:HB	1:AE:165:LEU:HD13	2.01	0.42
1:BE:166:LYS:HB3	1:BE:166:LYS:HE2	1.89	0.42
2:BM:204:TYR:HB2	2:BM:231:PHE:HB2	2.02	0.42
5:BX:391:ALA:O	5:BX:505:ASN:ND2	2.41	0.42
1:CA:209:LYS:HE2	1:CA:209:LYS:HB2	1.88	0.42
1:CA:262:ASN:ND2	1:CA:263:ASN:OD1	2.53	0.42
2:Cm:197:TYR:CZ	2:Cm:201:ILE:HD11	2.55	0.42
2:Cm:264:GLU:OE1	2:Cm:268:ARG:NE	2.52	0.42
1:DA:100:LEU:HD22	3:Dt:44:ILE:HG22	2.02	0.42
6:DY:1900:VAL:HG11	5:EX:387:TYR:CZ	2.54	0.42
3:Et:41:ASN:N	3:Et:45:GLU:OE2	2.53	0.42
1:FA:192:LEU:HD23	1:FA:192:LEU:HA	1.93	0.42
1:FB:135:ASP:HB2	1:FB:180:ARG:HB2	2.02	0.42
1:FE:117:TYR:O	1:FE:121:GLU:HB2	2.20	0.42
1:GA:139:ILE:O	1:GA:165:LEU:HA	2.20	0.42
1:GE:139:ILE:HB	1:GE:165:LEU:HD13	2.01	0.42
1:HA:303:GLU:CD	1:HA:304:LYS:H	2.27	0.42
6:HY:1724:ASN:ND2	6:HY:1729:MET:HB3	2.35	0.42
1:IE:139:ILE:HG12	1:IE:149:TYR:CZ	2.55	0.42
2:IM:204:TYR:HB2	2:IM:231:PHE:HB2	2.00	0.42
6:IY:1896:THR:HG22	5:JX:508:GLU:C	2.44	0.42
1:JA:262:ASN:ND2	1:JA:263:ASN:OD1	2.53	0.42
1:JC:146:VAL:HG21	1:JC:167:ILE:HG13	2.02	0.42
2:JM:188:LYS:O	2:JM:191:SER:OG	2.35	0.42
5:JX:392:LEU:HD23	5:JX:392:LEU:HA	1.88	0.42
2:Jm:323:SER:HA	2:Jm:326:LYS:HE3	2.00	0.42
2:Jm:344:LYS:HB3	2:Jm:347:MET:HB2	2.01	0.42
1:KB:158:LYS:NZ	1:KC:193:ASP:OD2	2.40	0.42
1:KC:130:MET:SD	1:KC:182:PRO:HB3	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KD:156:LEU:HD23	1:KD:156:LEU:HA	1.85	0.42
6:KY:1729:MET:HE3	5:LX:511:ARG:HG3	2.02	0.42
6:KY:1734:LYS:HE3	6:KY:1734:LYS:HB2	1.89	0.42
6:KY:1895:ILE:HG22	6:KY:1897:ASN:H	1.85	0.42
1:MA:262:ASN:ND2	1:MA:263:ASN:OD1	2.53	0.42
1:MA:303:GLU:CD	1:MA:304:LYS:H	2.27	0.42
1:MB:107:TYR:O	1:MC:177:THR:HA	2.20	0.42
2:Mm:193:LEU:HD11	2:Mm:242:ALA:HB2	2.00	0.42
2:Mm:318:THR:O	2:Mm:322:LYS:HG3	2.20	0.42
3:Mt:41:ASN:N	3:Mt:45:GLU:OE2	2.53	0.42
1:NE:166:LYS:HB3	1:NE:166:LYS:HE2	1.91	0.42
2:Nm:198:LYS:O	2:Nm:201:ILE:N	2.52	0.42
1:AA:262:ASN:ND2	1:AA:263:ASN:OD1	2.53	0.42
1:AB:130:MET:O	1:AB:134:ALA:HB2	2.20	0.42
1:AE:117:TYR:O	1:AE:121:GLU:HB2	2.20	0.42
1:AE:166:LYS:HB3	1:AE:166:LYS:HE2	1.89	0.42
2:CM:204:TYR:HB2	2:CM:231:PHE:HB2	2.01	0.42
5:CX:408:GLU:OE1	3:DT:32:LYS:N	2.41	0.42
2:Dm:295:ASN:OD1	2:Dm:295:ASN:N	2.51	0.42
1:EA:257:ARG:HE	1:EA:305:LYS:HZ1	1.68	0.42
6:EY:1810:PHE:HD2	6:EY:1811:LEU:HD12	1.84	0.42
1:FB:182:PRO:HG3	1:FC:107:TYR:HB2	2.01	0.42
2:Fm:219:ASN:HB3	2:Fm:222:TYR:CD2	2.55	0.42
2:Fm:316:PHE:HE1	2:Fm:365:TYR:HD1	1.68	0.42
6:GY:1749:THR:O	6:GY:1797:ARG:NH2	2.52	0.42
1:HA:250:ILE:HG13	1:HA:251:ALA:H	1.85	0.42
1:HE:113:ASP:HB3	1:HE:116:ASN:HB3	2.02	0.42
1:HE:157:ASN:ND2	1:HE:159:ARG:O	2.53	0.42
6:HY:1708:ALA:HB3	6:HY:1869:PHE:HB3	2.02	0.42
2:Hm:228:ARG:HD2	2:Hm:228:ARG:HA	1.92	0.42
1:IC:179:LEU:HG	1:IC:180:ARG:HB2	2.02	0.42
1:ID:156:LEU:HD23	1:ID:156:LEU:HA	1.89	0.42
2:IM:242:ALA:HA	2:IM:245:THR:HG22	2.01	0.42
3:IT:159:PRO:HA	3:JT:44:ILE:HD12	2.02	0.42
3:IT:269:LEU:HD23	3:IT:269:LEU:HA	1.81	0.42
2:Im:221:ASP:O	2:Im:225:GLN:HB2	2.20	0.42
3:JT:145:LYS:HD2	3:JT:145:LYS:HA	1.88	0.42
6:JY:1749:THR:O	6:JY:1797:ARG:NH2	2.52	0.42
1:KD:107:TYR:CE2	1:KD:109:MET:HB3	2.55	0.42
2:Lm:268:ARG:HB2	2:Lm:271:GLU:HG3	2.00	0.42
1:ME:133:TYR:HA	1:ME:159:ARG:HH11	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:MM:349:LYS:O	2:MM:353:LYS:HG2	2.20	0.42
1:NA:303:GLU:CD	1:NA:304:LYS:H	2.27	0.42
1:ND:146:VAL:O	1:ND:150:TYR:HB2	2.19	0.42
1:NE:118:LEU:HD23	1:NE:118:LEU:HA	1.78	0.42
5:NX:372:LYS:O	5:NX:376:ILE:HG12	2.20	0.42
1:AD:167:ILE:H	1:BA:194:LYS:NZ	2.18	0.42
1:BA:100:LEU:HD22	3:Bt:44:ILE:HG22	2.02	0.42
2:BM:276:LEU:HB3	2:BM:289:LEU:HD21	2.01	0.42
1:CA:257:ARG:HE	1:CA:305:LYS:HZ1	1.68	0.42
6:CY:1733:ASP:CG	5:DX:511:ARG:HH12	2.27	0.42
3:Ct:41:ASN:N	3:Ct:45:GLU:OE2	2.53	0.42
3:Ct:86:LEU:HD23	3:Ct:86:LEU:HA	1.90	0.42
1:DC:131:GLY:HA3	1:DC:153:LEU:CD1	2.50	0.42
1:DC:187:PRO:HG3	1:EA:189:ALA:H	1.85	0.42
5:EX:372:LYS:O	5:EX:376:ILE:HG12	2.20	0.42
1:FC:187:PRO:HB3	1:GA:190:HIS:C	2.45	0.42
6:FY:1752:MET:HE2	6:FY:1752:MET:HB2	1.72	0.42
3:Ft:41:ASN:N	3:Ft:45:GLU:OE2	2.53	0.42
2:GM:212:LEU:HG	2:GM:270:TYR:HB2	2.02	0.42
6:GY:1708:ALA:HB3	6:GY:1869:PHE:HB3	2.02	0.42
6:HY:1895:ILE:HG22	6:HY:1897:ASN:H	1.85	0.42
1:IE:130:MET:HB3	1:IE:178:PHE:CD2	2.54	0.42
1:JA:100:LEU:HD22	3:Jt:44:ILE:HG22	2.02	0.42
2:Jm:197:TYR:CZ	2:Jm:201:ILE:HD11	2.55	0.42
6:KY:1721:ASP:OD1	6:KY:1721:ASP:N	2.52	0.42
2:LM:349:LYS:O	2:LM:353:LYS:HG2	2.20	0.42
6:LY:1895:ILE:HG22	6:LY:1897:ASN:H	1.85	0.42
1:MA:139:ILE:O	1:MA:165:LEU:HA	2.20	0.42
1:ME:139:ILE:HG12	1:ME:149:TYR:CE2	2.55	0.42
6:MY:1895:ILE:HG22	6:MY:1897:ASN:H	1.85	0.42
1:NE:146:VAL:O	1:NE:149:TYR:HB3	2.20	0.42
1:NE:162:LYS:HD2	1:NE:162:LYS:HA	1.77	0.42
3:NT:69:ASN:OD1	3:NT:101:LYS:NZ	2.53	0.42
1:AA:160:ASN:ND2	3:NT:206:LYS:O	2.52	0.41
6:AY:1708:ALA:HB3	6:AY:1869:PHE:HB3	2.02	0.41
6:AY:1724:ASN:ND2	6:AY:1729:MET:HB3	2.35	0.41
1:BB:111:LEU:N	1:BC:174:ALA:O	2.51	0.41
1:BC:137:ILE:HA	1:BC:177:THR:O	2.20	0.41
3:BT:69:ASN:OD1	3:BT:101:LYS:NZ	2.53	0.41
2:Bm:221:ASP:O	2:Bm:225:GLN:HB2	2.20	0.41
1:CA:287:GLU:HA	1:CA:290:ILE:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Cm:206:ASN:O	2:Cm:209:SER:OG	2.29	0.41
1:DA:149:TYR:OH	3:Dt:68:PRO:O	2.36	0.41
1:DA:192:LEU:HD23	1:DA:192:LEU:HA	1.93	0.41
1:DC:187:PRO:HB3	1:EA:190:HIS:C	2.45	0.41
2:DM:290:THR:HG21	2:DM:355:PHE:HA	2.02	0.41
2:Dm:332:ASN:O	2:Dm:353:LYS:NZ	2.52	0.41
6:EY:1721:ASP:OD1	6:EY:1721:ASP:N	2.52	0.41
1:FD:143:LEU:O	1:FD:147:ASN:HB2	2.20	0.41
3:FT:69:ASN:OD1	3:FT:101:LYS:NZ	2.53	0.41
6:FY:1708:ALA:HB3	6:FY:1869:PHE:HB3	2.02	0.41
6:FY:1895:ILE:HG22	6:FY:1897:ASN:H	1.85	0.41
1:GA:250:ILE:HG13	1:GA:251:ALA:H	1.85	0.41
5:GX:372:LYS:O	5:GX:376:ILE:HG12	2.20	0.41
5:GX:436:GLN:OE1	5:GX:465:ARG:NE	2.42	0.41
3:Gt:42:GLU:HB2	3:Gt:46:LYS:HE2	2.02	0.41
1:HA:100:LEU:HD22	3:Ht:44:ILE:HG22	2.02	0.41
2:Hm:267:LEU:HD23	2:Hm:267:LEU:HA	1.92	0.41
3:Ht:42:GLU:HB2	3:Ht:46:LYS:HE2	2.03	0.41
3:Ht:207:GLU:OE1	3:Ht:207:GLU:N	2.29	0.41
1:IA:287:GLU:HA	1:IA:290:ILE:HG12	2.02	0.41
3:IT:134:ILE:HD11	3:It:39:VAL:HG21	2.02	0.41
5:IX:372:LYS:O	5:IX:376:ILE:HG12	2.20	0.41
5:IX:416:PRO:HD3	5:IX:478:LEU:HD22	2.02	0.41
2:Im:294:THR:O	2:Im:303:LYS:NZ	2.38	0.41
3:JT:117:ASP:N	3:JT:117:ASP:OD1	2.48	0.41
6:JY:1729:MET:HE3	5:KX:511:ARG:HG3	2.02	0.41
1:KA:209:LYS:HE2	1:KA:209:LYS:HB2	1.88	0.41
1:KC:126:LYS:HD2	1:LA:192:LEU:HD12	2.02	0.41
6:KY:1724:ASN:ND2	6:KY:1729:MET:HB3	2.35	0.41
1:LA:262:ASN:ND2	1:LA:263:ASN:OD1	2.53	0.41
1:LB:191:THR:HG23	1:LB:192:LEU:HG	2.01	0.41
6:LY:1752:MET:HE2	6:LY:1752:MET:HB2	1.72	0.41
2:Lm:321:LYS:HA	2:Lm:321:LYS:HD3	1.88	0.41
1:MA:107:TYR:CD2	3:Mt:44:ILE:HD11	2.55	0.41
1:MB:172:PRO:HG3	3:MT:256:VAL:HG21	2.02	0.41
6:MY:1708:ALA:HB3	6:MY:1869:PHE:HB3	2.02	0.41
1:NA:262:ASN:ND2	1:NA:263:ASN:OD1	2.53	0.41
1:ND:143:LEU:O	1:ND:147:ASN:HB2	2.19	0.41
3:At:86:LEU:HD23	3:At:86:LEU:HA	1.90	0.41
3:CT:206:LYS:O	1:DA:160:ASN:ND2	2.53	0.41
6:CY:1895:ILE:HG22	6:CY:1897:ASN:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DB:147:ASN:O	1:DB:150:TYR:HB3	2.20	0.41
1:DE:85:ASN:OD1	1:DE:87:ASN:ND2	2.53	0.41
6:DY:1721:ASP:OD1	6:DY:1721:ASP:N	2.52	0.41
1:EA:139:ILE:O	1:EA:165:LEU:HA	2.20	0.41
1:EE:79:ASP:N	1:EE:79:ASP:OD1	2.53	0.41
3:Et:42:GLU:HB2	3:Et:46:LYS:HE2	2.02	0.41
1:FA:106:LEU:HD11	3:Ft:134:ILE:HG22	2.01	0.41
1:FC:139:ILE:HB	1:FC:165:LEU:HD13	2.02	0.41
5:FX:436:GLN:OE1	5:FX:465:ARG:NE	2.42	0.41
6:FY:1721:ASP:OD1	6:FY:1721:ASP:N	2.52	0.41
1:GE:175:GLN:HE21	2:HM:340:MET:HE2	1.85	0.41
2:Gm:197:TYR:CZ	2:Gm:201:ILE:HD11	2.55	0.41
2:Gm:246:LEU:HD12	2:Gm:246:LEU:HA	1.92	0.41
1:HA:262:ASN:ND2	1:HA:263:ASN:OD1	2.53	0.41
2:HM:205:SER:OG	2:HM:268:ARG:O	2.34	0.41
1:IA:250:ILE:HG13	1:IA:251:ALA:H	1.85	0.41
6:IY:1724:ASN:ND2	6:IY:1729:MET:HB3	2.35	0.41
3:It:41:ASN:N	3:It:45:GLU:OE2	2.53	0.41
1:JA:287:GLU:HA	1:JA:290:ILE:HG12	2.03	0.41
1:JD:117:TYR:HE2	1:JE:152:ILE:HG21	1.85	0.41
3:JT:227:ARG:NH2	1:KA:188:ASN:HB3	2.36	0.41
5:JX:416:PRO:HD3	5:JX:478:LEU:HD22	2.03	0.41
1:KA:100:LEU:HD22	3:Kt:44:ILE:HG22	2.02	0.41
1:KA:262:ASN:ND2	1:KA:263:ASN:OD1	2.53	0.41
1:KD:80:ILE:HG13	1:KE:106:LEU:HB3	2.02	0.41
2:Km:221:ASP:O	2:Km:225:GLN:HB2	2.21	0.41
3:Kt:41:ASN:N	3:Kt:45:GLU:OE2	2.53	0.41
1:LD:130:MET:HB3	1:LD:130:MET:HE3	1.80	0.41
1:LE:162:LYS:HA	1:LE:162:LYS:HD2	1.84	0.41
3:LT:69:ASN:OD1	3:LT:101:LYS:NZ	2.53	0.41
6:LY:1724:ASN:ND2	6:LY:1729:MET:HB3	2.34	0.41
2:Lm:332:ASN:O	2:Lm:353:LYS:NZ	2.53	0.41
3:Lt:41:ASN:N	3:Lt:45:GLU:OE2	2.53	0.41
6:MY:1724:ASN:ND2	6:MY:1729:MET:HB3	2.35	0.41
3:Mt:86:LEU:HD23	3:Mt:86:LEU:HA	1.90	0.41
2:Nm:305:LYS:NZ	3:Nt:231:GLN:O	2.38	0.41
6:NY:1895:ILE:HG22	6:NY:1897:ASN:H	1.85	0.41
2:Nm:321:LYS:HD3	2:Nm:321:LYS:HA	1.86	0.41
1:AA:287:GLU:HA	1:AA:290:ILE:HG12	2.02	0.41
1:AD:149:TYR:HE2	1:AE:111:LEU:HG	1.85	0.41
1:AE:118:LEU:HA	1:AE:118:LEU:HD13	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AM:188:LYS:O	2:AM:191:SER:OG	2.36	0.41
4:AU:609:UNK:HA	2:Am:273:PHE:HZ	1.85	0.41
5:AX:474:GLU:OE1	5:AX:474:GLU:N	2.38	0.41
2:Am:327:LYS:HD2	2:Am:327:LYS:HA	1.87	0.41
1:BC:150:TYR:O	1:BC:154:LYS:HB2	2.19	0.41
2:Bm:197:TYR:CZ	2:Bm:201:ILE:HD11	2.55	0.41
1:CA:104:THR:HG22	3:Ct:138:TYR:HA	2.02	0.41
1:DA:287:GLU:HA	1:DA:290:ILE:HG12	2.02	0.41
1:DD:126:LYS:O	1:DD:130:MET:HG2	2.20	0.41
1:DD:177:THR:HA	1:DE:107:TYR:O	2.20	0.41
2:DM:341:MET:O	2:DM:344:LYS:NZ	2.53	0.41
3:DT:269:LEU:HD23	3:DT:269:LEU:HA	1.81	0.41
2:Dm:264:GLU:OE1	2:Dm:268:ARG:NE	2.53	0.41
1:EA:262:ASN:ND2	1:EA:263:ASN:OD1	2.53	0.41
1:EA:287:GLU:HA	1:EA:290:ILE:HG12	2.03	0.41
1:ED:77:LEU:HD12	1:ED:78:PHE:H	1.84	0.41
2:EM:311:LEU:HD21	2:EM:321:LYS:HB3	2.01	0.41
2:EM:328:THR:HG21	2:EM:357:PHE:HD1	1.85	0.41
6:EY:1708:ALA:HB3	6:EY:1869:PHE:HB3	2.02	0.41
1:FA:251:ALA:HB3	1:FC:151:ASN:OD1	2.20	0.41
6:FY:1810:PHE:HD2	6:FY:1811:LEU:HD12	1.84	0.41
2:Fm:206:ASN:O	2:Fm:209:SER:OG	2.29	0.41
2:Fm:230:LYS:HB2	2:Fm:230:LYS:HE3	1.94	0.41
6:GY:1729:MET:HE3	5:HX:511:ARG:HG3	2.02	0.41
6:GY:1895:ILE:HG22	6:GY:1897:ASN:H	1.85	0.41
2:HM:333:ILE:O	2:HM:337:SER:HB3	2.19	0.41
5:HX:416:PRO:HD3	5:HX:478:LEU:HD22	2.03	0.41
1:IC:129:ALA:HB2	1:IC:192:LEU:HD22	2.02	0.41
6:IY:1908:SER:HA	5:JX:379:GLN:HE22	1.85	0.41
2:Im:193:LEU:HD11	2:Im:242:ALA:HB2	2.00	0.41
1:JD:124:ILE:HG23	1:JE:117:TYR:HE1	1.84	0.41
1:JD:128:ARG:NH2	1:JE:87:ASN:HB3	2.34	0.41
1:JD:167:ILE:H	1:KA:194:LYS:NZ	2.18	0.41
3:Jt:42:GLU:HB2	3:Jt:46:LYS:HE2	2.02	0.41
1:KB:107:TYR:O	1:KC:177:THR:HA	2.21	0.41
1:KB:114:TYR:O	1:KB:118:LEU:HD23	2.20	0.41
3:Kt:42:GLU:HB2	3:Kt:46:LYS:HE2	2.02	0.41
1:LA:139:ILE:O	1:LA:165:LEU:HA	2.20	0.41
2:LM:204:TYR:HB2	2:LM:231:PHE:HB2	2.03	0.41
3:LT:134:ILE:HD11	3:Lt:39:VAL:HG21	2.02	0.41
3:MT:101:LYS:HD2	3:MT:101:LYS:HA	1.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Mm:236:LYS:HD3	2:Mm:236:LYS:HA	1.86	0.41
1:NA:124:ILE:HG13	3:Nt:73:TYR:CE2	2.55	0.41
1:NC:139:ILE:HG22	1:NC:146:VAL:HG12	2.02	0.41
1:ND:133:TYR:HA	1:NE:101:LYS:HZ1	1.85	0.41
2:AM:282:ASP:N	2:AM:285:GLU:OE2	2.53	0.41
1:BA:287:GLU:HA	1:BA:290:ILE:HG12	2.02	0.41
1:BB:107:TYR:O	1:BC:177:THR:HA	2.19	0.41
1:CD:138:ILE:HG13	1:CD:164:VAL:HB	2.03	0.41
1:CD:170:ASN:OD1	1:CD:171:MET:N	2.49	0.41
1:CD:171:MET:HE1	3:Ct:254:GLU:HG2	2.03	0.41
2:CM:349:LYS:O	2:CM:353:LYS:HG2	2.20	0.41
1:DB:183:LYS:HE2	1:DB:183:LYS:HB2	1.91	0.41
3:DT:69:ASN:OD1	3:DT:101:LYS:NZ	2.53	0.41
6:DY:1752:MET:HE2	6:DY:1752:MET:HB2	1.72	0.41
2:EM:349:LYS:O	2:EM:353:LYS:HG2	2.21	0.41
6:EY:1752:MET:HE2	6:EY:1752:MET:HB2	1.72	0.41
1:FA:250:ILE:HG13	1:FA:251:ALA:H	1.85	0.41
1:FA:287:GLU:HA	1:FA:290:ILE:HG12	2.03	0.41
1:FC:126:LYS:O	1:FC:130:MET:HG2	2.20	0.41
1:FD:112:LEU:HD21	1:FD:117:TYR:CD1	2.56	0.41
2:Fm:268:ARG:HB2	2:Fm:271:GLU:HG3	2.02	0.41
2:Fm:346:THR:O	2:Fm:351:HIS:N	2.48	0.41
1:GA:287:GLU:HA	1:GA:290:ILE:HG12	2.03	0.41
3:GT:69:ASN:OD1	3:GT:101:LYS:NZ	2.53	0.41
3:GT:269:LEU:HD23	3:GT:269:LEU:HA	1.81	0.41
5:GX:416:PRO:HD3	5:GX:478:LEU:HD22	2.02	0.41
1:HA:287:GLU:HA	1:HA:290:ILE:HG12	2.02	0.41
1:HA:296:VAL:HG23	1:HC:162:LYS:HZ1	1.85	0.41
6:HY:1749:THR:O	6:HY:1797:ARG:NH2	2.53	0.41
1:IA:180:ARG:NH2	3:It:56:LEU:O	2.51	0.41
1:IC:175:GLN:HE22	1:IC:177:THR:HG23	1.84	0.41
6:IY:1810:PHE:HD2	6:IY:1811:LEU:HD12	1.84	0.41
3:It:42:GLU:HB2	3:It:46:LYS:HE2	2.03	0.41
1:JC:129:ALA:HB2	1:JC:192:LEU:HD22	2.03	0.41
2:JM:324:ILE:HA	2:JM:327:LYS:HE3	2.01	0.41
5:JX:474:GLU:OE1	5:JX:474:GLU:N	2.38	0.41
1:KA:139:ILE:O	1:KA:165:LEU:HA	2.20	0.41
1:KA:287:GLU:HA	1:KA:290:ILE:HG12	2.02	0.41
1:LA:250:ILE:HG13	1:LA:251:ALA:H	1.85	0.41
1:LA:287:GLU:HA	1:LA:290:ILE:HG12	2.03	0.41
6:MY:1721:ASP:OD1	6:MY:1721:ASP:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:NA:117:TYR:CE1	3:Nt:80:VAL:HG23	2.55	0.41
1:AA:150:TYR:CE1	1:AB:167:ILE:HD11	2.56	0.41
1:AD:81:TYR:HB2	1:AE:107:TYR:CD1	2.55	0.41
1:AD:130:MET:HE1	1:AE:107:TYR:CE2	2.55	0.41
1:AD:136:LEU:HG	1:AD:162:LYS:HB3	2.02	0.41
1:BA:262:ASN:ND2	1:BA:263:ASN:OD1	2.53	0.41
1:CE:166:LYS:HB3	1:CE:166:LYS:HE2	1.88	0.41
2:Cm:352:TYR:CE2	5:DX:351:ILE:HG12	2.55	0.41
1:DA:139:ILE:O	1:DA:165:LEU:HA	2.20	0.41
1:DE:152:ILE:HG22	1:DE:153:LEU:HD22	2.01	0.41
2:DM:240:GLN:NE2	2:DM:241:LYS:HG3	2.36	0.41
3:DT:101:LYS:HA	3:DT:101:LYS:HD2	1.72	0.41
5:DX:350:TYR:HA	5:DX:353:ARG:NE	2.36	0.41
3:Dt:42:GLU:HB2	3:Dt:46:LYS:HE2	2.02	0.41
5:EX:416:PRO:HD3	5:EX:478:LEU:HD22	2.02	0.41
1:FA:163:PHE:HB2	1:FB:167:ILE:HG22	2.02	0.41
5:FX:350:TYR:HA	5:FX:353:ARG:NE	2.36	0.41
5:FX:416:PRO:HD3	5:FX:478:LEU:HD22	2.03	0.41
3:Ft:42:GLU:HB2	3:Ft:46:LYS:HE2	2.02	0.41
1:GC:139:ILE:HB	1:GC:165:LEU:HD13	2.01	0.41
1:HA:139:ILE:O	1:HA:165:LEU:HA	2.20	0.41
1:HC:130:MET:HA	1:HC:130:MET:HE3	2.02	0.41
3:HT:56:LEU:HA	3:HT:59:THR:HG22	2.03	0.41
5:HX:350:TYR:HA	5:HX:353:ARG:NE	2.36	0.41
2:Hm:246:LEU:HD12	2:Hm:246:LEU:HA	1.93	0.41
1:IA:139:ILE:O	1:IA:165:LEU:HA	2.20	0.41
6:IY:1708:ALA:HB3	6:IY:1869:PHE:HB3	2.02	0.41
6:IY:1895:ILE:HG22	6:IY:1897:ASN:H	1.85	0.41
1:JA:149:TYR:OH	3:Jt:68:PRO:O	2.35	0.41
1:JA:250:ILE:HG13	1:JA:251:ALA:H	1.85	0.41
2:JM:263:ASN:O	2:JM:267:LEU:CB	2.69	0.41
5:JX:352:ASN:OD1	5:JX:353:ARG:N	2.54	0.41
2:Jm:346:THR:HA	2:Jm:350:GLU:HB2	2.03	0.41
5:KX:416:PRO:HD3	5:KX:478:LEU:HD22	2.03	0.41
6:KY:1749:THR:O	6:KY:1797:ARG:NH2	2.52	0.41
1:LC:150:TYR:O	1:LC:154:LYS:HB2	2.21	0.41
2:LM:221:ASP:N	2:LM:221:ASP:OD1	2.54	0.41
3:LT:74:LEU:O	3:LT:105:TYR:OH	2.32	0.41
5:LX:372:LYS:O	5:LX:376:ILE:HG12	2.19	0.41
1:ME:126:LYS:O	1:ME:130:MET:HB2	2.20	0.41
3:MT:134:ILE:HD11	3:Mt:39:VAL:HG21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:NT:134:ILE:HD11	3:Nt:39:VAL:HG21	2.01	0.41
5:AX:435:LEU:HD21	6:AY:1720:LYS:HE3	2.02	0.41
3:Bt:41:ASN:N	3:Bt:45:GLU:OE2	2.53	0.41
1:CD:108:ALA:HA	1:CE:177:THR:HA	2.02	0.41
2:Cm:249:ASN:OD1	2:Cm:249:ASN:N	2.53	0.41
3:Ct:195:ILE:HD12	3:Ct:195:ILE:HA	1.89	0.41
5:DX:434:THR:O	5:DX:465:ARG:NH1	2.44	0.41
2:Dm:193:LEU:HD11	2:Dm:242:ALA:HB2	2.03	0.41
2:Dm:357:PHE:O	2:Dm:360:THR:OG1	2.29	0.41
1:ED:95:PHE:CE2	1:EE:132:THR:HG21	2.55	0.41
3:ET:53:ASN:HB2	5:EX:401:TYR:HB3	2.02	0.41
1:FA:262:ASN:ND2	1:FA:263:ASN:OD1	2.53	0.41
5:FX:502:ASN:OD1	5:FX:502:ASN:N	2.48	0.41
6:FY:1749:THR:O	6:FY:1797:ARG:NH2	2.52	0.41
2:Fm:196:SER:O	2:Fm:199:GLN:NE2	2.54	0.41
3:GT:56:LEU:HA	3:GT:59:THR:HG22	2.03	0.41
2:Gm:352:TYR:HA	2:Gm:355:PHE:HB3	2.03	0.41
1:IA:262:ASN:ND2	1:IA:263:ASN:OD1	2.53	0.41
3:IT:56:LEU:HA	3:IT:59:THR:HG22	2.03	0.41
3:IT:69:ASN:OD1	3:IT:101:LYS:NZ	2.53	0.41
5:IX:419:ILE:HD12	3:JT:39:VAL:HG11	2.01	0.41
6:IY:1721:ASP:OD1	6:IY:1721:ASP:N	2.52	0.41
6:IY:1734:LYS:HE3	6:IY:1734:LYS:HB2	1.89	0.41
6:IY:1749:THR:O	6:IY:1797:ARG:NH2	2.52	0.41
6:IY:1780:MET:SD	5:JX:443:GLN:NE2	2.93	0.41
2:Im:197:TYR:CZ	2:Im:201:ILE:HD11	2.55	0.41
1:JB:107:TYR:O	1:JC:177:THR:HA	2.21	0.41
1:JD:143:LEU:HD12	1:JD:167:ILE:HD12	2.02	0.41
6:JY:1708:ALA:HB3	6:JY:1869:PHE:HB3	2.02	0.41
1:KA:167:ILE:HG21	1:KB:150:TYR:CE1	2.55	0.41
2:MM:189:LYS:HA	2:MM:192:ARG:HG2	2.03	0.41
2:MM:270:TYR:CE1	2:MM:273:PHE:HB3	2.56	0.41
2:MM:344:LYS:HB3	2:MM:348:GLN:HB2	2.02	0.41
3:MT:115:ARG:H	3:MT:115:ARG:HG2	1.66	0.41
3:AT:69:ASN:OD1	3:AT:101:LYS:NZ	2.53	0.41
5:AX:392:LEU:HD23	5:AX:392:LEU:HA	1.88	0.41
6:AY:1895:ILE:HG22	6:AY:1897:ASN:H	1.85	0.41
1:CA:250:ILE:HG13	1:CA:251:ALA:H	1.85	0.41
1:CA:294:GLN:O	1:CC:162:LYS:NZ	2.54	0.41
1:CC:146:VAL:HG21	1:CC:167:ILE:HG13	2.03	0.41
1:CD:156:LEU:HD23	1:CD:156:LEU:HA	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CY:1685:LYS:HA	6:CY:1685:LYS:HD3	1.99	0.41
1:DA:71:ASP:OD1	1:DA:72:THR:N	2.53	0.41
1:DD:124:ILE:HG23	1:DE:117:TYR:HE1	1.86	0.41
5:DX:441:VAL:HG23	5:DX:451:THR:HG22	2.03	0.41
6:DY:1708:ALA:HB3	6:DY:1869:PHE:HB3	2.02	0.41
5:EX:441:VAL:HG23	5:EX:451:THR:HG22	2.03	0.41
2:Em:206:ASN:O	2:Em:209:SER:OG	2.33	0.41
2:Em:332:ASN:O	2:Em:353:LYS:NZ	2.53	0.41
1:FA:199:ASP:OD1	1:FA:199:ASP:N	2.48	0.41
1:FD:166:LYS:NZ	1:GA:194:LYS:HG2	2.36	0.41
2:FM:349:LYS:O	2:FM:353:LYS:HG2	2.20	0.41
3:FT:56:LEU:HA	3:FT:59:THR:HG22	2.03	0.41
5:FX:419:ILE:HD12	3:GT:39:VAL:HG11	2.02	0.41
1:GD:166:LYS:HD3	1:GD:166:LYS:HA	1.82	0.41
2:GM:282:ASP:N	2:GM:285:GLU:OE2	2.54	0.41
2:Gm:189:LYS:HE2	2:Gm:189:LYS:HB2	1.95	0.41
2:Gm:193:LEU:HD11	2:Gm:242:ALA:HB2	2.02	0.41
2:HM:282:ASP:N	2:HM:285:GLU:OE2	2.54	0.41
6:HY:1729:MET:HE3	5:IX:511:ARG:HG3	2.03	0.41
2:Hm:197:TYR:CZ	2:Hm:201:ILE:HD11	2.56	0.41
1:IE:161:ALA:HB3	1:IE:163:PHE:HE1	1.86	0.41
1:JB:104:THR:OG1	1:JB:105:TYR:N	2.54	0.41
1:JE:85:ASN:OD1	1:JE:87:ASN:ND2	2.53	0.41
6:JY:1895:ILE:HG22	6:JY:1897:ASN:H	1.85	0.41
2:Jm:294:THR:O	2:Jm:303:LYS:NZ	2.41	0.41
1:LA:150:TYR:CZ	1:LB:167:ILE:HG21	2.55	0.41
1:LB:145:GLN:NE2	1:LC:113:ASP:OD1	2.54	0.41
1:LC:187:PRO:HG3	1:MA:189:ALA:H	1.85	0.41
1:LD:143:LEU:HD21	3:MT:268:TYR:CE1	2.56	0.41
1:LE:166:LYS:HB3	1:LE:166:LYS:HE2	1.90	0.41
2:LM:325:LEU:HD23	2:LM:325:LEU:HA	1.89	0.41
5:LX:416:PRO:HD3	5:LX:478:LEU:HD22	2.02	0.41
1:MA:117:TYR:CD1	3:Mt:80:VAL:HG23	2.55	0.41
3:MT:145:LYS:HD2	3:MT:145:LYS:HA	1.88	0.41
4:MU:609:UNK:HA	2:Mm:273:PHE:CZ	2.55	0.41
2:Mm:357:PHE:O	2:Mm:361:VAL:HG23	2.21	0.41
1:NA:287:GLU:HA	1:NA:290:ILE:HG12	2.02	0.41
3:NT:53:ASN:HB2	5:NX:401:TYR:HB3	2.02	0.41
6:NY:1724:ASN:ND2	6:NY:1729:MET:HB3	2.35	0.41
2:Nm:327:LYS:HD2	2:Nm:327:LYS:HA	1.88	0.41
1:AD:124:ILE:HG13	1:AE:124:ILE:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AM:341:MET:SD	2:AM:344:LYS:NZ	2.89	0.41
4:AU:515:UNK:O	1:NE:162:LYS:HE2	2.20	0.41
5:AX:445:ASP:HA	5:NX:410:ARG:HH12	1.86	0.41
3:At:41:ASN:N	3:At:45:GLU:OE2	2.53	0.41
1:BA:150:TYR:CZ	1:BB:167:ILE:HD13	2.56	0.41
6:BY:1752:MET:HB2	6:BY:1752:MET:HE2	1.72	0.41
3:Bt:195:ILE:HD12	3:Bt:195:ILE:HA	1.88	0.41
1:CD:166:LYS:HD3	1:CD:166:LYS:HA	1.83	0.41
6:CY:1708:ALA:HB3	6:CY:1869:PHE:HB3	2.02	0.41
3:Ct:42:GLU:HB2	3:Ct:46:LYS:HE2	2.02	0.41
1:DB:114:TYR:O	1:DB:118:LEU:HD23	2.20	0.41
1:DB:177:THR:HA	1:DC:107:TYR:O	2.20	0.41
1:DC:171:MET:SD	1:DC:171:MET:N	2.93	0.41
1:DE:146:VAL:HB	1:DE:165:LEU:HD12	2.02	0.41
5:DX:416:PRO:HD3	5:DX:478:LEU:HD22	2.02	0.41
2:Dm:218:ASP:HA	2:Dm:297:LYS:HG2	2.03	0.41
3:ET:159:PRO:HA	3:FT:44:ILE:HD12	2.01	0.41
6:EY:1819:LEU:HD23	6:EY:1819:LEU:HA	1.87	0.41
3:Et:86:LEU:HD23	3:Et:86:LEU:HA	1.90	0.41
1:FA:139:ILE:O	1:FA:165:LEU:HA	2.20	0.41
1:FD:99:ALA:N	1:FE:94:TRP:O	2.49	0.41
1:GD:152:ILE:HG21	1:GE:114:TYR:HE1	1.85	0.41
1:GD:180:ARG:NH2	1:GE:103:LYS:O	2.29	0.41
2:Gm:327:LYS:HD2	2:Gm:327:LYS:HA	1.88	0.41
3:HT:197:GLN:HA	3:HT:200:LYS:HZ3	1.86	0.41
2:Hm:327:LYS:HD2	2:Hm:327:LYS:HA	1.87	0.41
1:IB:107:TYR:O	1:IC:177:THR:HA	2.20	0.41
1:IC:130:MET:HB3	1:IC:178:PHE:CG	2.56	0.41
1:IE:128:ARG:HA	1:IE:128:ARG:HD3	1.88	0.41
2:IM:212:LEU:HG	2:IM:270:TYR:HB2	2.02	0.41
3:IT:115:ARG:H	3:IT:115:ARG:HG2	1.66	0.41
3:IT:197:GLN:HA	3:IT:200:LYS:HZ3	1.86	0.41
2:Im:228:ARG:HD2	2:Im:228:ARG:HA	1.93	0.41
2:Im:246:LEU:HD12	2:Im:246:LEU:HA	1.94	0.41
1:JE:79:ASP:OD1	1:JE:79:ASP:N	2.54	0.41
1:JE:152:ILE:HG22	1:JE:153:LEU:HD22	2.03	0.41
3:JT:56:LEU:HA	3:JT:59:THR:HG22	2.03	0.41
1:KA:250:ILE:HG13	1:KA:251:ALA:H	1.85	0.41
2:KM:204:TYR:HB2	2:KM:231:PHE:HB2	2.02	0.41
2:KM:240:GLN:HA	2:KM:243:THR:HG22	2.03	0.41
3:KT:159:PRO:HA	3:LT:44:ILE:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LE:139:ILE:HG12	1:LE:149:TYR:CZ	2.56	0.41
2:Lm:345:THR:O	2:Lm:349:LYS:HB2	2.20	0.41
1:MA:287:GLU:HA	1:MA:290:ILE:HG12	2.02	0.41
5:MX:352:ASN:OD1	5:MX:353:ARG:N	2.54	0.41
2:Mm:332:ASN:O	2:Mm:353:LYS:NZ	2.54	0.41
1:NA:82:ASP:OD1	1:NA:126:LYS:NZ	2.38	0.41
1:NC:136:LEU:HB3	1:NC:179:LEU:HB2	2.03	0.41
1:ND:130:MET:HE3	1:ND:130:MET:HB2	1.88	0.41
1:ND:138:ILE:HG13	1:ND:164:VAL:HB	2.03	0.41
3:NT:90:SER:OG	3:NT:91:LYS:N	2.54	0.41
1:AA:139:ILE:O	1:AA:165:LEU:HA	2.20	0.41
1:AE:111:LEU:HD12	1:AE:112:LEU:HD23	2.03	0.41
1:AE:162:LYS:HA	1:AE:162:LYS:HD2	1.89	0.41
3:AT:90:SER:OG	3:AT:91:LYS:N	2.54	0.41
2:Am:274:SER:HB2	2:Am:314:PHE:CD1	2.56	0.41
1:BC:130:MET:HB3	1:BC:178:PHE:CG	2.56	0.41
1:BE:162:LYS:HE2	4:CU:516:UNK:HA	2.03	0.41
2:BM:349:LYS:O	2:BM:353:LYS:HG2	2.21	0.41
5:BX:441:VAL:HG23	5:BX:451:THR:HG22	2.03	0.41
5:BX:442:VAL:HG21	5:BX:475:LYS:HD2	2.03	0.41
5:BX:461:ASN:OD1	5:BX:466:TRP:NE1	2.54	0.41
6:BY:1685:LYS:HA	6:BY:1685:LYS:HD3	1.99	0.41
6:BY:1895:ILE:HG22	6:BY:1897:ASN:H	1.85	0.41
3:Bt:117:ASP:OD1	3:Bt:117:ASP:N	2.54	0.41
1:CB:125:ILE:HG12	1:CC:128:ARG:HD2	2.03	0.41
1:CD:121:GLU:HG2	1:CE:128:ARG:HH11	1.86	0.41
1:CE:138:ILE:HB	1:CE:177:THR:HB	2.02	0.41
2:CM:218:ASP:OD1	2:CM:219:ASN:N	2.46	0.41
2:CM:320:SER:O	2:CM:324:ILE:HG12	2.21	0.41
3:CT:166:LYS:HE3	3:CT:170:GLY:HA2	2.03	0.41
5:CX:441:VAL:HG23	5:CX:451:THR:HG22	2.03	0.41
1:DA:104:THR:HG22	3:Dt:138:TYR:HA	2.02	0.41
1:DB:150:TYR:CZ	1:DB:154:LYS:HE2	2.56	0.41
2:DM:324:ILE:HA	2:DM:327:LYS:HE3	2.03	0.41
3:DT:166:LYS:HE3	3:DT:170:GLY:HA2	2.03	0.41
3:DT:237:ILE:HD13	3:DT:237:ILE:HA	1.91	0.41
5:DX:442:VAL:HG21	5:DX:475:LYS:HD2	2.03	0.41
6:DY:1734:LYS:HE3	6:DY:1734:LYS:HB2	1.89	0.41
1:EA:250:ILE:HG13	1:EA:251:ALA:H	1.85	0.41
1:EB:105:TYR:HB2	1:EC:182:PRO:HD2	2.01	0.41
1:EC:117:TYR:O	1:EC:121:GLU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:EM:240:GLN:HA	2:EM:243:THR:HG22	2.02	0.41
2:EM:263:ASN:O	2:EM:267:LEU:CB	2.69	0.41
5:EX:392:LEU:HD23	5:EX:392:LEU:HA	1.88	0.41
1:FC:137:ILE:HA	1:FC:177:THR:O	2.21	0.41
3:FT:115:ARG:H	3:FT:115:ARG:HG2	1.66	0.41
5:FX:441:VAL:HG23	5:FX:451:THR:HG22	2.03	0.41
5:FX:461:ASN:OD1	5:FX:466:TRP:NE1	2.54	0.41
1:GA:71:ASP:OD1	1:GA:72:THR:N	2.53	0.41
1:GA:262:ASN:ND2	1:GA:263:ASN:OD1	2.53	0.41
1:GB:178:PHE:O	1:GC:106:LEU:HA	2.21	0.41
1:GE:152:ILE:HG22	1:GE:153:LEU:HD22	2.02	0.41
2:GM:240:GLN:HA	2:GM:243:THR:HG22	2.02	0.41
3:GT:145:LYS:HA	3:GT:145:LYS:HD2	1.88	0.41
5:GX:441:VAL:HG23	5:GX:451:THR:HG22	2.03	0.41
2:Gm:236:LYS:HD3	2:Gm:236:LYS:HA	1.87	0.41
1:HD:108:ALA:HA	1:HE:177:THR:HA	2.03	0.41
3:HT:69:ASN:OD1	3:HT:101:LYS:NZ	2.53	0.41
5:HX:441:VAL:HG23	5:HX:451:THR:HG22	2.03	0.41
6:HY:1721:ASP:OD1	6:HY:1721:ASP:N	2.52	0.41
2:Hm:340:MET:O	2:Hm:341:MET:HE2	2.21	0.41
1:IC:125:ILE:HA	1:IC:125:ILE:HD12	1.87	0.41
2:IM:273:PHE:HE1	2:IM:289:LEU:HG	1.84	0.41
3:IT:166:LYS:HE3	3:IT:170:GLY:HA2	2.03	0.41
6:IY:1733:ASP:CG	5:JX:511:ARG:HH12	2.29	0.41
1:JE:128:ARG:HA	1:JE:128:ARG:HD3	1.87	0.41
5:JX:432:ASN:ND2	5:KX:497:LEU:O	2.46	0.41
1:KA:104:THR:HG22	3:Kt:138:TYR:HA	2.02	0.41
1:KD:133:TYR:HA	1:KE:101:LYS:HZ3	1.84	0.41
1:KD:146:VAL:O	1:KD:150:TYR:HB2	2.20	0.41
2:KM:309:LEU:HD23	2:KM:309:LEU:HA	1.92	0.41
3:KT:90:SER:OG	3:KT:91:LYS:N	2.54	0.41
3:KT:166:LYS:HE3	3:KT:170:GLY:HA2	2.03	0.41
3:KT:182:ILE:H	3:KT:182:ILE:HG13	1.71	0.41
6:KY:1708:ALA:HB3	6:KY:1869:PHE:HB3	2.02	0.41
3:Kt:195:ILE:HD12	3:Kt:195:ILE:HA	1.88	0.41
3:LT:90:SER:OG	3:LT:91:LYS:N	2.54	0.41
3:LT:182:ILE:H	3:LT:182:ILE:HG13	1.71	0.41
5:LX:434:THR:O	5:LX:465:ARG:NH1	2.44	0.41
2:Lm:228:ARG:HD2	2:Lm:228:ARG:HA	1.93	0.41
2:Lm:340:MET:O	2:Lm:341:MET:HE2	2.21	0.41
3:Lt:42:GLU:HB2	3:Lt:46:LYS:HE2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MA:250:ILE:HG13	1:MA:251:ALA:H	1.85	0.41
1:ME:117:TYR:O	1:ME:121:GLU:HB2	2.20	0.41
3:MT:90:SER:OG	3:MT:91:LYS:N	2.54	0.41
3:Mt:42:GLU:HB2	3:Mt:46:LYS:HE2	2.03	0.41
1:NA:209:LYS:HE2	1:NA:209:LYS:HB2	1.88	0.41
1:NB:152:ILE:HG22	1:NB:153:LEU:HD12	2.03	0.41
1:ND:107:TYR:HD1	1:NE:80:ILE:HG23	1.86	0.41
1:ND:126:LYS:HZ1	1:NE:109:MET:CG	2.32	0.41
5:NX:442:VAL:HG21	5:NX:475:LYS:HD2	2.03	0.41
6:NY:1708:ALA:HB3	6:NY:1869:PHE:HB3	2.02	0.41
1:AD:167:ILE:HB	1:BA:194:LYS:NZ	2.33	0.41
5:AX:350:TYR:HA	5:AX:353:ARG:NE	2.36	0.41
1:BA:250:ILE:HG13	1:BA:251:ALA:H	1.85	0.41
3:BT:166:LYS:HE3	3:BT:170:GLY:HA2	2.03	0.41
3:BT:206:LYS:O	1:CA:160:ASN:ND2	2.54	0.41
1:CA:139:ILE:O	1:CA:165:LEU:HA	2.20	0.41
1:CA:199:ASP:OD1	1:CA:199:ASP:N	2.49	0.41
1:CD:111:LEU:HD13	1:CD:114:TYR:CE1	2.56	0.41
3:CT:159:PRO:HA	3:DT:44:ILE:HD12	2.03	0.41
3:Dt:66:LYS:HD2	3:Dt:66:LYS:HA	1.98	0.41
1:EA:71:ASP:OD1	1:EA:72:THR:N	2.53	0.41
1:EC:157:ASN:OD1	1:EC:159:ARG:N	2.54	0.41
1:ED:166:LYS:NZ	1:FA:194:LYS:HG2	2.36	0.41
3:ET:69:ASN:OD1	3:ET:101:LYS:NZ	2.53	0.41
2:Em:274:SER:HB2	2:Em:314:PHE:HD1	1.86	0.41
3:Et:117:ASP:OD1	3:Et:117:ASP:N	2.54	0.41
1:FA:105:TYR:O	3:Ft:136:SER:HA	2.21	0.41
5:FX:442:VAL:HG21	5:FX:475:LYS:HD2	2.03	0.41
2:Fm:221:ASP:O	2:Fm:225:GLN:HB2	2.21	0.41
1:GC:154:LYS:HA	1:GC:154:LYS:HD3	1.79	0.41
1:GD:167:ILE:H	1:HA:194:LYS:NZ	2.19	0.41
3:GT:166:LYS:HE3	3:GT:170:GLY:HA2	2.03	0.41
2:Hm:249:ASN:OD1	2:Hm:249:ASN:N	2.52	0.41
1:ID:120:ILE:HG21	1:IE:112:LEU:HD13	2.02	0.41
1:JE:135:ASP:N	1:JE:179:LEU:O	2.52	0.41
3:JT:274:ARG:HG3	3:JT:274:ARG:HH11	1.86	0.41
3:KT:56:LEU:HA	3:KT:59:THR:HG22	2.03	0.41
5:KX:352:ASN:OD1	5:KX:353:ARG:N	2.54	0.41
1:LB:126:LYS:O	1:LB:130:MET:HB2	2.21	0.41
1:LB:132:THR:HG23	1:LB:133:TYR:CD2	2.56	0.41
1:LD:166:LYS:NZ	1:MA:194:LYS:HG2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LD:180:ARG:HB3	1:LD:181:VAL:H	1.77	0.41
2:LM:240:GLN:HA	2:LM:243:THR:HG22	2.02	0.41
5:LX:352:ASN:OD1	5:LX:353:ARG:N	2.54	0.41
5:LX:502:ASN:OD1	5:LX:502:ASN:N	2.48	0.41
6:LY:1708:ALA:HB3	6:LY:1869:PHE:HB3	2.02	0.41
1:ME:157:ASN:ND2	1:ME:159:ARG:O	2.53	0.41
3:MT:53:ASN:HB2	5:MX:401:TYR:HB3	2.03	0.41
1:NB:183:LYS:HE2	1:NB:183:LYS:HB2	1.89	0.41
1:ND:124:ILE:HG23	1:NE:117:TYR:HE1	1.85	0.41
2:NM:218:ASP:OD1	2:NM:219:ASN:N	2.46	0.41
5:NX:374:LYS:HE3	5:NX:374:LYS:HB3	1.91	0.41
3:Nt:270:ARG:HE	3:Nt:270:ARG:HB3	1.78	0.41
2:AM:333:ILE:HD13	2:AM:333:ILE:HA	1.88	0.40
5:AX:461:ASN:OD1	5:AX:466:TRP:NE1	2.54	0.40
1:BD:124:ILE:HG23	1:BE:117:TYR:HE1	1.86	0.40
1:BE:161:ALA:HB3	1:BE:163:PHE:HE1	1.87	0.40
1:CD:143:LEU:HD11	3:DT:268:TYR:CE1	2.56	0.40
1:CE:149:TYR:CZ	1:CE:153:LEU:HG	2.56	0.40
5:CX:416:PRO:HD3	5:CX:478:LEU:HD22	2.02	0.40
1:DA:250:ILE:HG13	1:DA:251:ALA:H	1.85	0.40
1:DA:262:ASN:ND2	1:DA:263:ASN:OD1	2.53	0.40
2:DM:246:LEU:HD22	2:DM:252:ARG:HG3	2.02	0.40
5:DX:474:GLU:OE1	5:DX:474:GLU:N	2.38	0.40
3:ET:56:LEU:HA	3:ET:59:THR:HG22	2.03	0.40
3:ET:117:ASP:OD1	3:ET:117:ASP:N	2.48	0.40
3:ET:166:LYS:HE3	3:ET:170:GLY:HA2	2.03	0.40
3:ET:182:ILE:H	3:ET:182:ILE:HG13	1.71	0.40
5:EX:461:ASN:OD1	5:EX:466:TRP:NE1	2.54	0.40
2:Fm:357:PHE:O	2:Fm:361:VAL:HG23	2.21	0.40
2:GM:349:LYS:O	2:GM:353:LYS:HG2	2.20	0.40
3:GT:178:ASN:HD22	3:GT:181:VAL:HG22	1.87	0.40
3:GT:274:ARG:HG3	3:GT:274:ARG:HH11	1.87	0.40
1:HD:167:ILE:HB	1:IA:194:LYS:NZ	2.32	0.40
3:HT:166:LYS:HE3	3:HT:170:GLY:HA2	2.03	0.40
1:IB:126:LYS:O	1:IB:130:MET:HB2	2.21	0.40
1:ID:126:LYS:O	1:ID:129:ALA:N	2.54	0.40
3:IT:145:LYS:HD2	3:IT:145:LYS:HA	1.88	0.40
1:JC:184:ARG:HH11	1:JC:186:ASP:H	1.69	0.40
1:JD:143:LEU:O	1:JD:147:ASN:HB2	2.21	0.40
2:JM:282:ASP:N	2:JM:285:GLU:OE2	2.54	0.40
3:JT:166:LYS:HE3	3:JT:170:GLY:HA2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:JY:1685:LYS:HA	6:JY:1685:LYS:HD3	1.98	0.40
6:JY:1721:ASP:OD1	6:JY:1721:ASP:N	2.52	0.40
2:Jm:264:GLU:OE1	2:Jm:268:ARG:NE	2.53	0.40
1:KD:170:ASN:OD1	1:KD:171:MET:N	2.49	0.40
3:Kt:66:LYS:HD2	3:Kt:66:LYS:HA	1.98	0.40
1:LC:141:GLY:HA2	1:LC:171:MET:SD	2.62	0.40
1:LC:187:PRO:HG3	1:MA:190:HIS:H	1.86	0.40
1:LD:143:LEU:HD11	3:MT:268:TYR:CZ	2.57	0.40
3:LT:101:LYS:HA	3:LT:101:LYS:HD2	1.72	0.40
5:LX:350:TYR:HA	5:LX:353:ARG:NE	2.36	0.40
1:MD:112:LEU:HD21	1:MD:117:TYR:CD1	2.55	0.40
3:MT:274:ARG:HH11	3:MT:274:ARG:HG3	1.86	0.40
2:Mm:281:LYS:N	2:Mm:285:GLU:OE1	2.54	0.40
2:Nm:221:ASP:OD1	2:Nm:302:GLN:HG2	2.21	0.40
3:NT:166:LYS:HE3	3:NT:170:GLY:HA2	2.03	0.40
5:NX:350:TYR:HA	5:NX:353:ARG:NE	2.36	0.40
1:AC:150:TYR:O	1:AC:154:LYS:HB2	2.21	0.40
3:AT:166:LYS:HE3	3:AT:170:GLY:HA2	2.03	0.40
3:At:42:GLU:HB2	3:At:46:LYS:HE2	2.02	0.40
1:BA:104:THR:HG22	3:Bt:138:TYR:HA	2.03	0.40
1:BA:139:ILE:O	1:BA:165:LEU:HA	2.20	0.40
1:BB:183:LYS:HE2	1:BB:183:LYS:HB2	1.89	0.40
1:BC:129:ALA:HB2	1:BC:192:LEU:HD22	2.03	0.40
1:BC:171:MET:HB3	1:BC:171:MET:HE3	1.86	0.40
3:BT:90:SER:OG	3:BT:91:LYS:N	2.54	0.40
3:BT:178:ASN:HD22	3:BT:181:VAL:HG22	1.87	0.40
5:BX:350:TYR:HA	5:BX:353:ARG:NE	2.36	0.40
6:BY:1708:ALA:HB3	6:BY:1869:PHE:HB3	2.02	0.40
3:Bt:42:GLU:HB2	3:Bt:46:LYS:HE2	2.03	0.40
5:CX:350:TYR:HA	5:CX:353:ARG:NE	2.36	0.40
1:DD:140:THR:OG1	1:DD:175:GLN:HB3	2.22	0.40
3:DT:117:ASP:OD1	3:DT:117:ASP:N	2.48	0.40
2:Dm:249:ASN:OD1	2:Dm:249:ASN:N	2.53	0.40
1:EE:113:ASP:OD2	1:EE:115:ASN:N	2.55	0.40
1:EE:139:ILE:HG12	1:EE:149:TYR:CZ	2.56	0.40
2:EM:240:GLN:NE2	2:EM:241:LYS:HG3	2.37	0.40
1:FA:71:ASP:OD1	1:FA:72:THR:N	2.53	0.40
1:FD:107:TYR:HE1	1:FE:126:LYS:HD2	1.85	0.40
3:FT:274:ARG:HG3	3:FT:274:ARG:HH11	1.86	0.40
5:GX:352:ASN:OD1	5:GX:353:ARG:N	2.54	0.40
5:GX:474:GLU:OE1	5:GX:474:GLU:N	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:GY:1721:ASP:N	6:GY:1721:ASP:OD1	2.52	0.40
1:HC:146:VAL:O	1:HC:150:TYR:HB2	2.21	0.40
1:HC:153:LEU:O	1:HC:157:ASN:HB2	2.21	0.40
5:HX:352:ASN:OD1	5:HX:353:ARG:N	2.54	0.40
2:Hm:189:LYS:HE2	2:Hm:189:LYS:HB2	1.97	0.40
2:Hm:274:SER:HB2	2:Hm:314:PHE:CD1	2.55	0.40
1:IE:138:ILE:HB	1:IE:177:THR:HB	2.03	0.40
5:IX:432:ASN:HD21	5:JX:497:LEU:C	2.30	0.40
1:JD:111:LEU:HD13	1:JD:114:TYR:CE1	2.57	0.40
2:JM:240:GLN:NE2	2:JM:241:LYS:HG3	2.37	0.40
2:JM:320:SER:O	2:JM:324:ILE:HG12	2.21	0.40
2:KM:341:MET:C	2:KM:344:LYS:HZ2	2.28	0.40
6:KY:1756:MET:HE1	6:KY:1776:GLN:HB2	2.03	0.40
1:LC:187:PRO:HB3	1:MA:190:HIS:C	2.46	0.40
3:LT:166:LYS:HE3	3:LT:170:GLY:HA2	2.03	0.40
6:LY:1756:MET:HE1	6:LY:1776:GLN:HB2	2.03	0.40
5:MX:416:PRO:HD3	5:MX:478:LEU:HD22	2.02	0.40
6:MY:1756:MET:HE1	6:MY:1776:GLN:HB2	2.03	0.40
2:Mm:268:ARG:HB2	2:Mm:271:GLU:HG3	2.02	0.40
1:NA:62:LYS:HD2	1:NA:62:LYS:HA	1.93	0.40
1:NC:184:ARG:HH11	1:NC:186:ASP:H	1.69	0.40
1:ND:107:TYR:CD1	1:NE:80:ILE:HG23	2.56	0.40
2:Nm:240:GLN:HA	2:Nm:243:THR:HG22	2.03	0.40
2:Nm:349:LYS:O	2:Nm:353:LYS:HG2	2.20	0.40
3:NT:274:ARG:HH11	3:NT:274:ARG:HG3	1.86	0.40
2:Nm:193:LEU:HD11	2:Nm:242:ALA:HB2	2.02	0.40
3:AT:151:PHE:CD2	3:AT:159:PRO:HD3	2.57	0.40
5:AX:441:VAL:HG23	5:AX:451:THR:HG22	2.03	0.40
6:AY:1685:LYS:HA	6:AY:1685:LYS:HD3	1.99	0.40
6:AY:1780:MET:SD	5:BX:443:GLN:NE2	2.94	0.40
5:BX:416:PRO:HD3	5:BX:478:LEU:HD22	2.02	0.40
2:Bm:249:ASN:OD1	2:Bm:249:ASN:N	2.53	0.40
1:CB:115:ASN:OD1	1:CB:116:ASN:N	2.55	0.40
1:CC:139:ILE:HG22	1:CC:146:VAL:HG12	2.04	0.40
6:CY:1865:ILE:HD13	6:CY:1865:ILE:HG21	1.92	0.40
2:Cm:268:ARG:HB2	2:Cm:271:GLU:HG3	2.03	0.40
2:Cm:321:LYS:HA	2:Cm:321:LYS:HD3	1.83	0.40
6:DY:1908:SER:HA	5:EX:379:GLN:HE22	1.86	0.40
1:EA:62:LYS:HD2	1:EA:62:LYS:HA	1.93	0.40
1:ED:80:ILE:HG23	1:EE:106:LEU:HD22	2.03	0.40
2:Em:249:ASN:OD1	2:Em:249:ASN:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:144:GLU:OE2	1:FB:145:GLN:NE2	2.46	0.40
2:FM:246:LEU:O	2:FM:252:ARG:NH2	2.54	0.40
1:GE:139:ILE:HG12	1:GE:149:TYR:CE2	2.56	0.40
2:Gm:230:LYS:HB2	2:Gm:230:LYS:HE3	1.94	0.40
2:Hm:236:LYS:HD3	2:Hm:236:LYS:HA	1.86	0.40
3:IT:227:ARG:NH2	1:JA:188:ASN:HB3	2.36	0.40
5:IX:441:VAL:HG23	5:IX:451:THR:HG22	2.03	0.40
1:JA:132:THR:HG21	3:Jt:51:PRO:HD2	2.04	0.40
1:JA:257:ARG:HE	1:JA:305:LYS:HZ1	1.69	0.40
2:JM:240:GLN:HA	2:JM:243:THR:HG22	2.03	0.40
5:JX:482:LYS:HA	3:KT:29:VAL:HG21	2.03	0.40
6:JY:1756:MET:HE1	6:JY:1776:GLN:HB2	2.03	0.40
2:KM:220:ILE:HD12	2:KM:220:ILE:HA	1.90	0.40
3:KT:274:ARG:HG3	3:KT:274:ARG:HH11	1.86	0.40
5:KX:350:TYR:HA	5:KX:353:ARG:NE	2.36	0.40
2:Km:218:ASP:HA	2:Km:297:LYS:HG2	2.04	0.40
2:LM:263:ASN:O	2:LM:267:LEU:CB	2.69	0.40
3:LT:56:LEU:HA	3:LT:59:THR:HG22	2.03	0.40
3:LT:274:ARG:HH11	3:LT:274:ARG:HG3	1.86	0.40
3:Lt:56:LEU:HD23	3:Lt:56:LEU:HA	1.92	0.40
1:MB:144:GLU:OE2	1:MB:145:GLN:NE2	2.46	0.40
1:MD:111:LEU:HD13	1:MD:114:TYR:CE1	2.57	0.40
1:ME:111:LEU:HD12	1:ME:112:LEU:HD23	2.03	0.40
3:MT:166:LYS:HE3	3:MT:170:GLY:HA2	2.03	0.40
5:MX:350:TYR:HA	5:MX:353:ARG:NE	2.36	0.40
1:NA:139:ILE:O	1:NA:165:LEU:HA	2.20	0.40
3:NT:54:ASP:OD2	5:NX:404:TYR:OH	2.24	0.40
3:Nt:42:GLU:HB2	3:Nt:46:LYS:HE2	2.03	0.40
1:AD:124:ILE:HG23	1:AE:117:TYR:HE1	1.85	0.40
3:AT:53:ASN:HB2	5:AX:401:TYR:HB3	2.04	0.40
3:AT:178:ASN:HD22	3:AT:181:VAL:HG22	1.87	0.40
5:AX:416:PRO:HD3	5:AX:478:LEU:HD22	2.02	0.40
6:AY:1752:MET:HE2	6:AY:1752:MET:HB2	1.72	0.40
2:Am:268:ARG:HB2	2:Am:271:GLU:HG3	2.04	0.40
2:Am:321:LYS:HD3	2:Am:321:LYS:HA	1.86	0.40
1:BA:71:ASP:OD1	1:BA:72:THR:N	2.53	0.40
1:BA:205:GLU:HA	1:BA:208:LYS:HZ3	1.86	0.40
1:BD:124:ILE:O	1:BD:127:THR:OG1	2.31	0.40
1:CE:121:GLU:O	1:CE:125:ILE:HG12	2.21	0.40
3:CT:69:ASN:OD1	3:CT:101:LYS:NZ	2.53	0.40
3:CT:274:ARG:HG3	3:CT:274:ARG:HH11	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CX:461:ASN:OD1	5:CX:466:TRP:NE1	2.54	0.40
5:DX:461:ASN:OD1	5:DX:466:TRP:NE1	2.54	0.40
2:Dm:197:TYR:CZ	2:Dm:201:ILE:HD11	2.57	0.40
2:Dm:228:ARG:HD2	2:Dm:228:ARG:HA	1.94	0.40
1:EA:243:VAL:O	1:EA:245:GLN:NE2	2.55	0.40
3:ET:84:PHE:CD2	5:EX:397:VAL:HG13	2.56	0.40
6:EY:1729:MET:HE3	5:FX:511:ARG:HG3	2.02	0.40
3:FT:90:SER:OG	3:FT:91:LYS:N	2.54	0.40
3:FT:166:LYS:HE3	3:FT:170:GLY:HA2	2.03	0.40
2:Fm:274:SER:HB2	2:Fm:314:PHE:CD1	2.56	0.40
1:GA:163:PHE:HB2	1:GB:167:ILE:HG22	2.03	0.40
3:GT:72:ASP:OD1	3:GT:72:ASP:N	2.52	0.40
3:GT:206:LYS:O	1:HA:160:ASN:ND2	2.54	0.40
6:GY:1756:MET:HE1	6:GY:1776:GLN:HB2	2.03	0.40
1:HD:124:ILE:HG23	1:HE:117:TYR:HE1	1.86	0.40
2:HM:345:THR:OG1	2:HM:346:THR:N	2.55	0.40
3:HT:227:ARG:NH2	1:IA:188:ASN:HB3	2.37	0.40
5:HX:434:THR:O	5:HX:465:ARG:NH1	2.44	0.40
5:HX:442:VAL:HG21	5:HX:475:LYS:HD2	2.03	0.40
6:HY:1756:MET:HE1	6:HY:1776:GLN:HB2	2.03	0.40
1:IA:177:THR:HG22	3:It:64:GLN:HG2	2.03	0.40
1:ID:176:ALA:HB3	1:IE:109:MET:HE3	2.02	0.40
2:IM:282:ASP:N	2:IM:285:GLU:OE2	2.54	0.40
5:IX:352:ASN:OD1	5:IX:353:ARG:N	2.54	0.40
6:IY:1756:MET:HE1	6:IY:1776:GLN:HB2	2.03	0.40
1:JA:71:ASP:OD1	1:JA:72:THR:N	2.53	0.40
1:JE:80:ILE:HD13	1:JE:84:LEU:HD22	2.03	0.40
3:JT:90:SER:OG	3:JT:91:LYS:N	2.54	0.40
2:KM:240:GLN:NE2	2:KM:241:LYS:HG3	2.36	0.40
2:KM:325:LEU:HD23	2:KM:325:LEU:HA	1.91	0.40
3:KT:227:ARG:NH2	1:LA:188:ASN:HB3	2.37	0.40
5:KX:392:LEU:HD23	5:KX:392:LEU:HA	1.88	0.40
2:Mm:259:ILE:HA	2:Mm:262:ILE:HD12	2.02	0.40
1:NA:243:VAL:O	1:NA:245:GLN:NE2	2.55	0.40
1:ND:124:ILE:O	1:ND:127:THR:OG1	2.28	0.40
1:NE:135:ASP:N	1:NE:179:LEU:O	2.53	0.40
5:NX:416:PRO:HD3	5:NX:478:LEU:HD22	2.02	0.40
6:NY:1756:MET:HE1	6:NY:1776:GLN:HB2	2.03	0.40
2:Nm:249:ASN:OD1	2:Nm:249:ASN:N	2.54	0.40
1:AD:180:ARG:NH2	1:AE:103:LYS:O	2.50	0.40
2:Am:198:LYS:HE3	2:Am:262:ILE:HG12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:164:VAL:HG22	1:BB:166:LYS:HG2	2.03	0.40
3:BT:151:PHE:CD2	3:BT:159:PRO:HD3	2.57	0.40
1:CA:243:VAL:O	1:CA:245:GLN:NE2	2.55	0.40
1:CB:107:TYR:CD1	1:DA:193:ASP:HB3	2.56	0.40
1:CB:121:GLU:HB3	1:CB:125:ILE:HD13	2.03	0.40
1:CC:124:ILE:O	1:CC:127:THR:OG1	2.35	0.40
1:CE:157:ASN:ND2	1:CE:159:ARG:O	2.54	0.40
3:CT:84:PHE:HA	3:CT:84:PHE:HD1	1.77	0.40
3:CT:178:ASN:HD22	3:CT:181:VAL:HG22	1.87	0.40
2:DM:240:GLN:HA	2:DM:243:THR:HG22	2.03	0.40
3:DT:56:LEU:HA	3:DT:59:THR:HG22	2.03	0.40
1:EA:211:TYR:HD1	1:EA:211:TYR:HA	1.75	0.40
1:EE:140:THR:HG21	1:FA:278:PRO:HD3	2.03	0.40
3:ET:90:SER:OG	3:ET:91:LYS:N	2.54	0.40
3:FT:151:PHE:CD2	3:FT:159:PRO:HD3	2.57	0.40
6:FY:1756:MET:HE1	6:FY:1776:GLN:HB2	2.03	0.40
1:HA:132:THR:HG21	3:Ht:51:PRO:HD2	2.04	0.40
3:HT:145:LYS:HD2	3:HT:145:LYS:HA	1.88	0.40
3:Ht:86:LEU:HD23	3:Ht:86:LEU:HA	1.90	0.40
3:IT:206:LYS:O	1:JA:160:ASN:ND2	2.54	0.40
5:JX:350:TYR:HA	5:JX:353:ARG:NE	2.36	0.40
5:JX:419:ILE:HD12	3:KT:39:VAL:HG11	2.02	0.40
5:JX:441:VAL:HG23	5:JX:451:THR:HG22	2.03	0.40
1:KA:132:THR:HG21	3:Kt:51:PRO:HD2	2.04	0.40
1:KA:143:LEU:HD22	1:KB:150:TYR:CE2	2.57	0.40
1:KB:105:TYR:H	1:KC:180:ARG:HA	1.85	0.40
1:KD:105:TYR:HB2	1:KE:78:PHE:HD2	1.87	0.40
1:KD:179:LEU:HD22	1:KE:106:LEU:HD12	2.03	0.40
3:LT:197:GLN:HA	3:LT:200:LYS:HZ3	1.87	0.40
3:MT:69:ASN:OD1	3:MT:101:LYS:NZ	2.53	0.40
2:Mm:249:ASN:OD1	2:Mm:249:ASN:N	2.53	0.40
1:ND:126:LYS:HD2	1:ND:127:THR:N	2.37	0.40
2:Nm:295:ASN:OD1	2:Nm:295:ASN:N	2.52	0.40
3:Nt:41:ASN:N	3:Nt:45:GLU:OE2	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	AA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	AB	79/433 (18%)	79 (100%)	0	100	100
1	AC	80/433 (18%)	80 (100%)	0	100	100
1	AD	83/433 (19%)	83 (100%)	0	100	100
1	AE	91/433 (21%)	91 (100%)	0	100	100
1	BA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	BB	79/433 (18%)	79 (100%)	0	100	100
1	BC	80/433 (18%)	80 (100%)	0	100	100
1	BD	83/433 (19%)	82 (99%)	1 (1%)	63	72
1	BE	91/433 (21%)	91 (100%)	0	100	100
1	CA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	CB	79/433 (18%)	79 (100%)	0	100	100
1	CC	80/433 (18%)	80 (100%)	0	100	100
1	CD	83/433 (19%)	83 (100%)	0	100	100
1	CE	91/433 (21%)	91 (100%)	0	100	100
1	DA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	DB	79/433 (18%)	79 (100%)	0	100	100
1	DC	80/433 (18%)	80 (100%)	0	100	100
1	DD	83/433 (19%)	83 (100%)	0	100	100
1	DE	91/433 (21%)	91 (100%)	0	100	100
1	EA	220/433 (51%)	214 (97%)	6 (3%)	39	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	EB	79/433 (18%)	79 (100%)	0	100	100
1	EC	80/433 (18%)	80 (100%)	0	100	100
1	ED	83/433 (19%)	83 (100%)	0	100	100
1	EE	91/433 (21%)	91 (100%)	0	100	100
1	FA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	FB	79/433 (18%)	79 (100%)	0	100	100
1	FC	80/433 (18%)	80 (100%)	0	100	100
1	FD	83/433 (19%)	82 (99%)	1 (1%)	63	72
1	FE	91/433 (21%)	91 (100%)	0	100	100
1	GA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	GB	79/433 (18%)	79 (100%)	0	100	100
1	GC	80/433 (18%)	80 (100%)	0	100	100
1	GD	83/433 (19%)	83 (100%)	0	100	100
1	GE	91/433 (21%)	91 (100%)	0	100	100
1	HA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	HB	79/433 (18%)	79 (100%)	0	100	100
1	HC	80/433 (18%)	80 (100%)	0	100	100
1	HD	83/433 (19%)	83 (100%)	0	100	100
1	HE	91/433 (21%)	91 (100%)	0	100	100
1	IA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	IB	79/433 (18%)	79 (100%)	0	100	100
1	IC	80/433 (18%)	80 (100%)	0	100	100
1	ID	83/433 (19%)	83 (100%)	0	100	100
1	IE	91/433 (21%)	91 (100%)	0	100	100
1	JA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	JB	79/433 (18%)	79 (100%)	0	100	100
1	JC	80/433 (18%)	80 (100%)	0	100	100
1	JD	83/433 (19%)	83 (100%)	0	100	100
1	JE	91/433 (21%)	91 (100%)	0	100	100
1	KA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	KB	79/433 (18%)	79 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	KC	80/433 (18%)	80 (100%)	0	100	100
1	KD	83/433 (19%)	83 (100%)	0	100	100
1	KE	91/433 (21%)	90 (99%)	1 (1%)	65	74
1	LA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	LB	79/433 (18%)	79 (100%)	0	100	100
1	LC	80/433 (18%)	80 (100%)	0	100	100
1	LD	83/433 (19%)	83 (100%)	0	100	100
1	LE	91/433 (21%)	91 (100%)	0	100	100
1	MA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	MB	79/433 (18%)	79 (100%)	0	100	100
1	MC	80/433 (18%)	80 (100%)	0	100	100
1	MD	83/433 (19%)	83 (100%)	0	100	100
1	ME	91/433 (21%)	91 (100%)	0	100	100
1	NA	220/433 (51%)	214 (97%)	6 (3%)	39	60
1	NB	79/433 (18%)	79 (100%)	0	100	100
1	NC	80/433 (18%)	80 (100%)	0	100	100
1	ND	83/433 (19%)	83 (100%)	0	100	100
1	NE	91/433 (21%)	91 (100%)	0	100	100
2	AM	168/342 (49%)	168 (100%)	0	100	100
2	Am	167/342 (49%)	167 (100%)	0	100	100
2	BM	168/342 (49%)	168 (100%)	0	100	100
2	Bm	167/342 (49%)	167 (100%)	0	100	100
2	CM	168/342 (49%)	168 (100%)	0	100	100
2	Cm	167/342 (49%)	167 (100%)	0	100	100
2	DM	168/342 (49%)	168 (100%)	0	100	100
2	Dm	167/342 (49%)	167 (100%)	0	100	100
2	EM	168/342 (49%)	168 (100%)	0	100	100
2	Em	167/342 (49%)	167 (100%)	0	100	100
2	FM	168/342 (49%)	168 (100%)	0	100	100
2	Fm	167/342 (49%)	167 (100%)	0	100	100
2	GM	168/342 (49%)	168 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Gm	167/342 (49%)	167 (100%)	0	100	100
2	HM	168/342 (49%)	168 (100%)	0	100	100
2	Hm	167/342 (49%)	167 (100%)	0	100	100
2	IM	168/342 (49%)	168 (100%)	0	100	100
2	Im	167/342 (49%)	167 (100%)	0	100	100
2	JM	168/342 (49%)	168 (100%)	0	100	100
2	Jm	167/342 (49%)	167 (100%)	0	100	100
2	KM	168/342 (49%)	168 (100%)	0	100	100
2	Km	167/342 (49%)	167 (100%)	0	100	100
2	LM	168/342 (49%)	168 (100%)	0	100	100
2	Lm	167/342 (49%)	167 (100%)	0	100	100
2	MM	168/342 (49%)	168 (100%)	0	100	100
2	Mm	167/342 (49%)	167 (100%)	0	100	100
2	NM	168/342 (49%)	168 (100%)	0	100	100
2	Nm	167/342 (49%)	167 (100%)	0	100	100
3	AT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	At	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	BT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Bt	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	CT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Ct	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	DT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Dt	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	ET	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Et	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	FT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Ft	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	GT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Gt	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	HT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Ht	181/255 (71%)	175 (97%)	6 (3%)	33	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	IT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	It	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	JT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Jt	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	KT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Kt	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	LT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Lt	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	MT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Mt	181/255 (71%)	175 (97%)	6 (3%)	33	57
3	NT	234/255 (92%)	227 (97%)	7 (3%)	36	59
3	Nt	181/255 (71%)	175 (97%)	6 (3%)	33	57
5	AX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	BX	148/470 (32%)	139 (94%)	9 (6%)	17	43
5	CX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	DX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	EX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	FX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	GX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	HX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	IX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	JX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	KX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	LX	148/470 (32%)	139 (94%)	9 (6%)	17	43
5	MX	148/470 (32%)	140 (95%)	8 (5%)	20	47
5	NX	148/470 (32%)	140 (95%)	8 (5%)	20	47
6	AY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	BY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	CY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	DY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	EY	171/1724 (10%)	166 (97%)	5 (3%)	37	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	FY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	GY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	HY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	IY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	JY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	KY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	LY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	MY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
6	NY	171/1724 (10%)	166 (97%)	5 (3%)	37	60
All	All	22708/77742 (29%)	22255 (98%)	453 (2%)	48	65

All (453) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AA	130	MET
1	AA	159	ARG
1	AA	184	ARG
1	AA	210	MET
1	AA	225	GLU
1	AA	226	VAL
3	AT	45	GLU
3	AT	103	LEU
3	AT	187	ARG
3	AT	220	ILE
3	AT	249	MET
3	AT	267	GLU
3	AT	274	ARG
5	AX	356	MET
5	AX	365	LYS
5	AX	384	GLU
5	AX	393	LYS
5	AX	408	GLU
5	AX	410	ARG
5	AX	418	GLU
5	AX	474	GLU
6	AY	1691	VAL
6	AY	1739	TYR
6	AY	1752	MET
6	AY	1780	MET

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Mol	Chain	Res	Type
6	AY	1907	GLN
3	At	37	THR
3	At	207	GLU
3	At	213	ARG
3	At	223	THR
3	At	230	TYR
3	At	233	ARG
1	BA	130	MET
1	BA	159	ARG
1	BA	184	ARG
1	BA	210	MET
1	BA	225	GLU
1	BA	226	VAL
1	BD	157	ASN
3	BT	45	GLU
3	BT	103	LEU
3	BT	187	ARG
3	BT	220	ILE
3	BT	249	MET
3	BT	267	GLU
3	BT	274	ARG
5	BX	356	MET
5	BX	365	LYS
5	BX	379	GLN
5	BX	384	GLU
5	BX	393	LYS
5	BX	408	GLU
5	BX	410	ARG
5	BX	418	GLU
5	BX	474	GLU
6	BY	1691	VAL
6	BY	1739	TYR
6	BY	1752	MET
6	BY	1780	MET
6	BY	1907	GLN
3	Bt	37	THR
3	Bt	207	GLU
3	Bt	213	ARG
3	Bt	223	THR
3	Bt	230	TYR
3	Bt	233	ARG
1	CA	130	MET

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Mol	Chain	Res	Type
1	CA	159	ARG
1	CA	184	ARG
1	CA	210	MET
1	CA	225	GLU
1	CA	226	VAL
3	CT	45	GLU
3	CT	103	LEU
3	CT	187	ARG
3	CT	220	ILE
3	CT	249	MET
3	CT	267	GLU
3	CT	274	ARG
5	CX	356	MET
5	CX	365	LYS
5	CX	384	GLU
5	CX	393	LYS
5	CX	408	GLU
5	CX	410	ARG
5	CX	418	GLU
5	CX	474	GLU
6	CY	1691	VAL
6	CY	1739	TYR
6	CY	1752	MET
6	CY	1780	MET
6	CY	1907	GLN
3	Ct	37	THR
3	Ct	207	GLU
3	Ct	213	ARG
3	Ct	223	THR
3	Ct	230	TYR
3	Ct	233	ARG
1	DA	130	MET
1	DA	159	ARG
1	DA	184	ARG
1	DA	210	MET
1	DA	225	GLU
1	DA	226	VAL
3	DT	45	GLU
3	DT	103	LEU
3	DT	187	ARG
3	DT	220	ILE
3	DT	249	MET

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Mol	Chain	Res	Type
3	DT	267	GLU
3	DT	274	ARG
5	DX	356	MET
5	DX	365	LYS
5	DX	384	GLU
5	DX	393	LYS
5	DX	408	GLU
5	DX	410	ARG
5	DX	418	GLU
5	DX	474	GLU
6	DY	1691	VAL
6	DY	1739	TYR
6	DY	1752	MET
6	DY	1780	MET
6	DY	1907	GLN
3	Dt	37	THR
3	Dt	207	GLU
3	Dt	213	ARG
3	Dt	223	THR
3	Dt	230	TYR
3	Dt	233	ARG
1	EA	130	MET
1	EA	159	ARG
1	EA	184	ARG
1	EA	210	MET
1	EA	225	GLU
1	EA	226	VAL
3	ET	45	GLU
3	ET	103	LEU
3	ET	187	ARG
3	ET	220	ILE
3	ET	249	MET
3	ET	267	GLU
3	ET	274	ARG
5	EX	356	MET
5	EX	365	LYS
5	EX	384	GLU
5	EX	393	LYS
5	EX	408	GLU
5	EX	410	ARG
5	EX	418	GLU
5	EX	474	GLU

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Mol	Chain	Res	Type
6	EY	1691	VAL
6	EY	1739	TYR
6	EY	1752	MET
6	EY	1780	MET
6	EY	1907	GLN
3	Et	37	THR
3	Et	207	GLU
3	Et	213	ARG
3	Et	223	THR
3	Et	230	TYR
3	Et	233	ARG
1	FA	130	MET
1	FA	159	ARG
1	FA	184	ARG
1	FA	210	MET
1	FA	225	GLU
1	FA	226	VAL
1	FD	157	ASN
3	FT	45	GLU
3	FT	103	LEU
3	FT	187	ARG
3	FT	220	ILE
3	FT	249	MET
3	FT	267	GLU
3	FT	274	ARG
5	FX	356	MET
5	FX	365	LYS
5	FX	384	GLU
5	FX	393	LYS
5	FX	408	GLU
5	FX	410	ARG
5	FX	418	GLU
5	FX	474	GLU
6	FY	1691	VAL
6	FY	1739	TYR
6	FY	1752	MET
6	FY	1780	MET
6	FY	1907	GLN
3	Ft	37	THR
3	Ft	207	GLU
3	Ft	213	ARG
3	Ft	223	THR

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Mol	Chain	Res	Type
3	Ft	230	TYR
3	Ft	233	ARG
1	GA	130	MET
1	GA	159	ARG
1	GA	184	ARG
1	GA	210	MET
1	GA	225	GLU
1	GA	226	VAL
3	GT	45	GLU
3	GT	103	LEU
3	GT	187	ARG
3	GT	220	ILE
3	GT	249	MET
3	GT	267	GLU
3	GT	274	ARG
5	GX	356	MET
5	GX	365	LYS
5	GX	384	GLU
5	GX	393	LYS
5	GX	408	GLU
5	GX	410	ARG
5	GX	418	GLU
5	GX	474	GLU
6	GY	1691	VAL
6	GY	1739	TYR
6	GY	1752	MET
6	GY	1780	MET
6	GY	1907	GLN
3	Gt	37	THR
3	Gt	207	GLU
3	Gt	213	ARG
3	Gt	223	THR
3	Gt	230	TYR
3	Gt	233	ARG
1	HA	130	MET
1	HA	159	ARG
1	HA	184	ARG
1	HA	210	MET
1	HA	225	GLU
1	HA	226	VAL
3	HT	45	GLU
3	HT	103	LEU

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Mol	Chain	Res	Type
3	HT	187	ARG
3	HT	220	ILE
3	HT	249	MET
3	HT	267	GLU
3	HT	274	ARG
5	HX	356	MET
5	HX	365	LYS
5	HX	384	GLU
5	HX	393	LYS
5	HX	408	GLU
5	HX	410	ARG
5	HX	418	GLU
5	HX	474	GLU
6	HY	1691	VAL
6	HY	1739	TYR
6	HY	1752	MET
6	HY	1780	MET
6	HY	1907	GLN
3	Ht	37	THR
3	Ht	207	GLU
3	Ht	213	ARG
3	Ht	223	THR
3	Ht	230	TYR
3	Ht	233	ARG
1	IA	130	MET
1	IA	159	ARG
1	IA	184	ARG
1	IA	210	MET
1	IA	225	GLU
1	IA	226	VAL
3	IT	45	GLU
3	IT	103	LEU
3	IT	187	ARG
3	IT	220	ILE
3	IT	249	MET
3	IT	267	GLU
3	IT	274	ARG
5	IX	356	MET
5	IX	365	LYS
5	IX	384	GLU
5	IX	393	LYS
5	IX	408	GLU

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Mol	Chain	Res	Type
5	IX	410	ARG
5	IX	418	GLU
5	IX	474	GLU
6	IY	1691	VAL
6	IY	1739	TYR
6	IY	1752	MET
6	IY	1780	MET
6	IY	1907	GLN
3	It	37	THR
3	It	207	GLU
3	It	213	ARG
3	It	223	THR
3	It	230	TYR
3	It	233	ARG
1	JA	130	MET
1	JA	159	ARG
1	JA	184	ARG
1	JA	210	MET
1	JA	225	GLU
1	JA	226	VAL
3	JT	45	GLU
3	JT	103	LEU
3	JT	187	ARG
3	JT	220	ILE
3	JT	249	MET
3	JT	267	GLU
3	JT	274	ARG
5	JX	356	MET
5	JX	365	LYS
5	JX	384	GLU
5	JX	393	LYS
5	JX	408	GLU
5	JX	410	ARG
5	JX	418	GLU
5	JX	474	GLU
6	JY	1691	VAL
6	JY	1739	TYR
6	JY	1752	MET
6	JY	1780	MET
6	JY	1907	GLN
3	Jt	37	THR
3	Jt	207	GLU

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Mol	Chain	Res	Type
3	Jt	213	ARG
3	Jt	223	THR
3	Jt	230	TYR
3	Jt	233	ARG
1	KA	130	MET
1	KA	159	ARG
1	KA	184	ARG
1	KA	210	MET
1	KA	225	GLU
1	KA	226	VAL
1	KE	175	GLN
3	KT	45	GLU
3	KT	103	LEU
3	KT	187	ARG
3	KT	220	ILE
3	KT	249	MET
3	KT	267	GLU
3	KT	274	ARG
5	KX	356	MET
5	KX	365	LYS
5	KX	384	GLU
5	KX	393	LYS
5	KX	408	GLU
5	KX	410	ARG
5	KX	418	GLU
5	KX	474	GLU
6	KY	1691	VAL
6	KY	1739	TYR
6	KY	1752	MET
6	KY	1780	MET
6	KY	1907	GLN
3	Kt	37	THR
3	Kt	207	GLU
3	Kt	213	ARG
3	Kt	223	THR
3	Kt	230	TYR
3	Kt	233	ARG
1	LA	130	MET
1	LA	159	ARG
1	LA	184	ARG
1	LA	210	MET
1	LA	225	GLU

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Mol	Chain	Res	Type
1	LA	226	VAL
3	LT	45	GLU
3	LT	103	LEU
3	LT	187	ARG
3	LT	220	ILE
3	LT	249	MET
3	LT	267	GLU
3	LT	274	ARG
5	LX	356	MET
5	LX	365	LYS
5	LX	379	GLN
5	LX	384	GLU
5	LX	393	LYS
5	LX	408	GLU
5	LX	410	ARG
5	LX	418	GLU
5	LX	474	GLU
6	LY	1691	VAL
6	LY	1739	TYR
6	LY	1752	MET
6	LY	1780	MET
6	LY	1907	GLN
3	Lt	37	THR
3	Lt	207	GLU
3	Lt	213	ARG
3	Lt	223	THR
3	Lt	230	TYR
3	Lt	233	ARG
1	MA	130	MET
1	MA	159	ARG
1	MA	184	ARG
1	MA	210	MET
1	MA	225	GLU
1	MA	226	VAL
3	MT	45	GLU
3	MT	103	LEU
3	MT	187	ARG
3	MT	220	ILE
3	MT	249	MET
3	MT	267	GLU
3	MT	274	ARG
5	MX	356	MET

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Mol	Chain	Res	Type
5	MX	365	LYS
5	MX	384	GLU
5	MX	393	LYS
5	MX	408	GLU
5	MX	410	ARG
5	MX	418	GLU
5	MX	474	GLU
6	MY	1691	VAL
6	MY	1739	TYR
6	MY	1752	MET
6	MY	1780	MET
6	MY	1907	GLN
3	Mt	37	THR
3	Mt	207	GLU
3	Mt	213	ARG
3	Mt	223	THR
3	Mt	230	TYR
3	Mt	233	ARG
1	NA	130	MET
1	NA	159	ARG
1	NA	184	ARG
1	NA	210	MET
1	NA	225	GLU
1	NA	226	VAL
3	NT	45	GLU
3	NT	103	LEU
3	NT	187	ARG
3	NT	220	ILE
3	NT	249	MET
3	NT	267	GLU
3	NT	274	ARG
5	NX	356	MET
5	NX	365	LYS
5	NX	384	GLU
5	NX	393	LYS
5	NX	408	GLU
5	NX	410	ARG
5	NX	418	GLU
5	NX	474	GLU
6	NY	1691	VAL
6	NY	1739	TYR
6	NY	1752	MET

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Mol	Chain	Res	Type
6	NY	1780	MET
6	NY	1907	GLN
3	Nt	37	THR
3	Nt	207	GLU
3	Nt	213	ARG
3	Nt	223	THR
3	Nt	230	TYR
3	Nt	233	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (345) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	75	GLN
1	AA	116	ASN
1	AB	122	ASN
1	AB	147	ASN
1	AD	151	ASN
1	AE	87	ASN
1	AE	116	ASN
1	AE	157	ASN
2	AM	244	ASN
2	AM	279	ASN
2	AM	295	ASN
2	AM	315	ASN
3	AT	34	HIS
3	AT	64	GLN
3	AT	104	GLN
3	AT	226	ASN
5	AX	379	GLN
2	Am	187	ASN
2	Am	207	ASN
2	Am	210	ASN
2	Am	229	ASN
2	Am	275	ASN
3	At	217	GLN
3	At	266	ASN
3	At	272	GLN
1	BA	75	GLN
1	BA	116	ASN
1	BC	157	ASN
1	BE	87	ASN
1	BE	115	ASN

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Mol	Chain	Res	Type
1	BE	145	GLN
1	BE	157	ASN
2	BM	244	ASN
2	BM	296	GLN
2	BM	315	ASN
3	BT	34	HIS
3	BT	64	GLN
3	BT	226	ASN
6	BY	1857	GLN
2	Bm	187	ASN
2	Bm	207	ASN
2	Bm	225	GLN
2	Bm	229	ASN
2	Bm	332	ASN
3	Bt	41	ASN
3	Bt	217	GLN
3	Bt	266	ASN
3	Bt	272	GLN
1	CA	75	GLN
1	CA	116	ASN
1	CA	245	GLN
1	CC	151	ASN
1	CC	160	ASN
1	CD	175	GLN
1	CE	87	ASN
1	CE	157	ASN
2	CM	244	ASN
2	CM	295	ASN
2	CM	296	GLN
2	CM	315	ASN
3	CT	34	HIS
3	CT	226	ASN
5	CX	379	GLN
2	Cm	187	ASN
2	Cm	207	ASN
2	Cm	210	ASN
2	Cm	225	GLN
2	Cm	229	ASN
2	Cm	332	ASN
3	Ct	41	ASN
3	Ct	217	GLN
3	Ct	266	ASN

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Mol	Chain	Res	Type
3	Ct	272	GLN
1	DA	75	GLN
1	DA	116	ASN
1	DA	245	GLN
1	DD	157	ASN
1	DE	87	ASN
1	DE	116	ASN
1	DE	157	ASN
1	DE	168	ASN
1	DE	175	GLN
2	DM	244	ASN
2	DM	292	ASN
2	DM	296	GLN
3	DT	34	HIS
3	DT	226	ASN
3	DT	231	GLN
5	DX	379	GLN
2	Dm	187	ASN
2	Dm	207	ASN
2	Dm	225	GLN
2	Dm	229	ASN
2	Dm	332	ASN
3	Dt	41	ASN
3	Dt	266	ASN
3	Dt	272	GLN
1	EA	75	GLN
1	EA	116	ASN
1	EB	122	ASN
1	EB	175	GLN
1	EE	87	ASN
1	EE	145	GLN
1	EE	168	ASN
2	EM	225	GLN
2	EM	244	ASN
2	EM	296	GLN
2	EM	304	GLN
3	ET	34	HIS
3	ET	231	GLN
5	EX	379	GLN
6	EY	1857	GLN
2	Em	187	ASN
2	Em	207	ASN

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Mol	Chain	Res	Type
2	Em	225	GLN
2	Em	229	ASN
3	Et	217	GLN
3	Et	266	ASN
3	Et	272	GLN
1	FA	75	GLN
1	FA	116	ASN
1	FA	245	GLN
1	FB	122	ASN
1	FC	157	ASN
1	FE	87	ASN
1	FE	115	ASN
1	FE	116	ASN
1	FE	157	ASN
1	FE	168	ASN
2	FM	225	GLN
2	FM	244	ASN
2	FM	292	ASN
2	FM	295	ASN
2	FM	296	GLN
2	FM	315	ASN
3	FT	34	HIS
3	FT	64	GLN
3	FT	226	ASN
6	FY	1857	GLN
2	Fm	187	ASN
2	Fm	207	ASN
2	Fm	210	ASN
2	Fm	225	GLN
2	Fm	229	ASN
2	Fm	275	ASN
3	Ft	41	ASN
3	Ft	139	ASN
3	Ft	217	GLN
3	Ft	266	ASN
3	Ft	272	GLN
1	GA	75	GLN
1	GA	116	ASN
1	GA	245	GLN
1	GB	190	HIS
1	GC	122	ASN
1	GE	87	ASN

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Mol	Chain	Res	Type
1	GE	157	ASN
1	GE	175	GLN
2	GM	244	ASN
2	GM	296	GLN
2	GM	315	ASN
3	GT	34	HIS
3	GT	64	GLN
3	GT	226	ASN
6	GY	1857	GLN
2	Gm	187	ASN
2	Gm	207	ASN
2	Gm	210	ASN
2	Gm	229	ASN
3	Gt	41	ASN
3	Gt	139	ASN
3	Gt	266	ASN
3	Gt	272	GLN
1	HA	75	GLN
1	HA	116	ASN
1	HB	122	ASN
1	HE	87	ASN
1	HE	97	ASN
1	HE	115	ASN
1	HE	116	ASN
1	HE	145	GLN
1	HE	157	ASN
2	HM	244	ASN
2	HM	292	ASN
2	HM	295	ASN
2	HM	315	ASN
3	HT	34	HIS
3	HT	64	GLN
3	HT	226	ASN
6	HY	1857	GLN
2	Hm	187	ASN
2	Hm	207	ASN
2	Hm	210	ASN
2	Hm	229	ASN
3	Ht	41	ASN
3	Ht	217	GLN
3	Ht	266	ASN
3	Ht	272	GLN

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Mol	Chain	Res	Type
1	IA	75	GLN
1	IA	116	ASN
1	IC	157	ASN
1	IC	175	GLN
1	ID	157	ASN
1	IE	87	ASN
1	IE	115	ASN
1	IE	145	GLN
1	IE	157	ASN
2	IM	244	ASN
2	IM	296	GLN
2	IM	315	ASN
3	IT	34	HIS
3	IT	226	ASN
6	IY	1857	GLN
2	Im	187	ASN
2	Im	207	ASN
2	Im	225	GLN
2	Im	229	ASN
2	Im	332	ASN
3	It	217	GLN
3	It	266	ASN
1	JA	75	GLN
1	JA	116	ASN
1	JA	245	GLN
1	JE	87	ASN
1	JE	157	ASN
2	JM	219	ASN
2	JM	244	ASN
2	JM	295	ASN
2	JM	296	GLN
2	JM	315	ASN
3	JT	34	HIS
3	JT	64	GLN
3	JT	226	ASN
5	JX	379	GLN
6	JY	1857	GLN
2	Jm	187	ASN
2	Jm	207	ASN
2	Jm	225	GLN
2	Jm	229	ASN
3	Jt	217	GLN

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Mol	Chain	Res	Type
3	Jt	266	ASN
3	Jt	272	GLN
1	KA	75	GLN
1	KA	116	ASN
1	KA	245	GLN
1	KB	151	ASN
1	KB	190	HIS
1	KE	87	ASN
1	KE	116	ASN
1	KE	157	ASN
1	KE	168	ASN
2	KM	244	ASN
2	KM	296	GLN
2	KM	315	ASN
3	KT	34	HIS
3	KT	64	GLN
3	KT	226	ASN
5	KX	379	GLN
6	KY	1857	GLN
2	Km	187	ASN
2	Km	207	ASN
2	Km	210	ASN
2	Km	225	GLN
2	Km	229	ASN
2	Km	275	ASN
3	Kt	217	GLN
3	Kt	266	ASN
3	Kt	272	GLN
1	LA	75	GLN
1	LA	116	ASN
1	LC	160	ASN
1	LC	175	GLN
1	LE	87	ASN
1	LE	122	ASN
1	LE	145	GLN
1	LE	168	ASN
2	LM	244	ASN
2	LM	292	ASN
2	LM	296	GLN
2	LM	315	ASN
3	LT	34	HIS
3	LT	64	GLN

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Mol	Chain	Res	Type
3	LT	231	GLN
2	Lm	187	ASN
2	Lm	207	ASN
2	Lm	210	ASN
2	Lm	225	GLN
2	Lm	229	ASN
3	Lt	41	ASN
3	Lt	217	GLN
3	Lt	266	ASN
3	Lt	272	GLN
1	MA	75	GLN
1	MA	116	ASN
1	MB	122	ASN
1	MB	168	ASN
1	ME	87	ASN
1	ME	116	ASN
1	ME	145	GLN
1	ME	157	ASN
1	ME	168	ASN
2	MM	225	GLN
2	MM	244	ASN
2	MM	292	ASN
2	MM	295	ASN
2	MM	296	GLN
2	MM	315	ASN
3	MT	34	HIS
3	MT	64	GLN
3	MT	226	ASN
5	MX	379	GLN
2	Mm	187	ASN
2	Mm	207	ASN
2	Mm	225	GLN
2	Mm	229	ASN
2	Mm	275	ASN
2	Mm	351	HIS
3	Mt	217	GLN
3	Mt	266	ASN
3	Mt	272	GLN
1	NA	75	GLN
1	NA	116	ASN
1	NA	245	GLN
1	NC	122	ASN

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Mol	Chain	Res	Type
1	NE	87	ASN
1	NE	157	ASN
1	NE	175	GLN
2	NM	244	ASN
2	NM	292	ASN
2	NM	296	GLN
2	NM	315	ASN
3	NT	34	HIS
3	NT	104	GLN
3	NT	110	GLN
3	NT	226	ASN
5	NX	379	GLN
6	NY	1857	GLN
2	Nm	187	ASN
2	Nm	207	ASN
2	Nm	229	ASN
2	Nm	275	ASN
3	Nt	41	ASN
3	Nt	217	GLN
3	Nt	266	ASN
3	Nt	272	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	AU	8
4	BU	8
4	CU	8
4	DU	8
4	EU	8
4	FU	8
4	GU	8
4	HU	8
4	IU	8
4	JU	8
4	KU	8
4	LU	8
4	MU	8
4	NU	8

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AU	723:UNK	C	801:UNK	N	98.58
1	BU	723:UNK	C	801:UNK	N	98.58
1	CU	723:UNK	C	801:UNK	N	98.58
1	DU	723:UNK	C	801:UNK	N	98.58
1	EU	723:UNK	C	801:UNK	N	98.58
1	FU	723:UNK	C	801:UNK	N	98.58
1	GU	723:UNK	C	801:UNK	N	98.58
1	HU	723:UNK	C	801:UNK	N	98.58
1	IU	723:UNK	C	801:UNK	N	98.58
1	JU	723:UNK	C	801:UNK	N	98.58
1	KU	723:UNK	C	801:UNK	N	98.58
1	LU	723:UNK	C	801:UNK	N	98.58
1	MU	723:UNK	C	801:UNK	N	98.58
1	NU	723:UNK	C	801:UNK	N	98.58
1	AU	523:UNK	C	601:UNK	N	87.28
1	BU	523:UNK	C	601:UNK	N	87.28
1	CU	523:UNK	C	601:UNK	N	87.28

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	DU	523:UNK	C	601:UNK	N	87.28
1	EU	523:UNK	C	601:UNK	N	87.28
1	FU	523:UNK	C	601:UNK	N	87.28
1	GU	523:UNK	C	601:UNK	N	87.28
1	HU	523:UNK	C	601:UNK	N	87.28
1	IU	523:UNK	C	601:UNK	N	87.28
1	JU	523:UNK	C	601:UNK	N	87.28
1	KU	523:UNK	C	601:UNK	N	87.28
1	LU	523:UNK	C	601:UNK	N	87.28
1	MU	523:UNK	C	601:UNK	N	87.28
1	NU	523:UNK	C	601:UNK	N	87.28
1	AU	422:UNK	C	501:UNK	N	75.39
1	BU	422:UNK	C	501:UNK	N	75.39
1	CU	422:UNK	C	501:UNK	N	75.39
1	DU	422:UNK	C	501:UNK	N	75.39
1	EU	422:UNK	C	501:UNK	N	75.39
1	FU	422:UNK	C	501:UNK	N	75.39
1	GU	422:UNK	C	501:UNK	N	75.39
1	HU	422:UNK	C	501:UNK	N	75.39
1	IU	422:UNK	C	501:UNK	N	75.39
1	JU	422:UNK	C	501:UNK	N	75.39
1	KU	422:UNK	C	501:UNK	N	75.39
1	LU	422:UNK	C	501:UNK	N	75.39
1	MU	422:UNK	C	501:UNK	N	75.39
1	NU	422:UNK	C	501:UNK	N	75.39
1	AU	620:UNK	C	701:UNK	N	74.33
1	BU	620:UNK	C	701:UNK	N	74.33
1	CU	620:UNK	C	701:UNK	N	74.33
1	DU	620:UNK	C	701:UNK	N	74.33
1	EU	620:UNK	C	701:UNK	N	74.33
1	FU	620:UNK	C	701:UNK	N	74.33
1	GU	620:UNK	C	701:UNK	N	74.33
1	HU	620:UNK	C	701:UNK	N	74.33
1	IU	620:UNK	C	701:UNK	N	74.33
1	JU	620:UNK	C	701:UNK	N	74.33
1	KU	620:UNK	C	701:UNK	N	74.33
1	LU	620:UNK	C	701:UNK	N	74.33
1	MU	620:UNK	C	701:UNK	N	74.33
1	NU	620:UNK	C	701:UNK	N	74.33
1	AU	10:UNK	C	101:UNK	N	40.07
1	BU	10:UNK	C	101:UNK	N	40.07
1	CU	10:UNK	C	101:UNK	N	40.07

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	DU	10:UNK	C	101:UNK	N	40.07
1	EU	10:UNK	C	101:UNK	N	40.07
1	FU	10:UNK	C	101:UNK	N	40.07
1	GU	10:UNK	C	101:UNK	N	40.07
1	HU	10:UNK	C	101:UNK	N	40.07
1	IU	10:UNK	C	101:UNK	N	40.07
1	JU	10:UNK	C	101:UNK	N	40.07
1	KU	10:UNK	C	101:UNK	N	40.07
1	LU	10:UNK	C	101:UNK	N	40.07
1	MU	10:UNK	C	101:UNK	N	40.07
1	NU	10:UNK	C	101:UNK	N	40.07
1	AU	217:UNK	C	301:UNK	N	29.34
1	BU	217:UNK	C	301:UNK	N	29.34
1	CU	217:UNK	C	301:UNK	N	29.34
1	DU	217:UNK	C	301:UNK	N	29.34
1	EU	217:UNK	C	301:UNK	N	29.34
1	FU	217:UNK	C	301:UNK	N	29.34
1	GU	217:UNK	C	301:UNK	N	29.34
1	HU	217:UNK	C	301:UNK	N	29.34
1	IU	217:UNK	C	301:UNK	N	29.34
1	JU	217:UNK	C	301:UNK	N	29.34
1	KU	217:UNK	C	301:UNK	N	29.34
1	LU	217:UNK	C	301:UNK	N	29.34
1	MU	217:UNK	C	301:UNK	N	29.34
1	NU	217:UNK	C	301:UNK	N	29.34
1	AU	120:UNK	C	201:UNK	N	28.69
1	BU	120:UNK	C	201:UNK	N	28.69
1	CU	120:UNK	C	201:UNK	N	28.69
1	DU	120:UNK	C	201:UNK	N	28.69
1	EU	120:UNK	C	201:UNK	N	28.69
1	FU	120:UNK	C	201:UNK	N	28.69
1	GU	120:UNK	C	201:UNK	N	28.69
1	HU	120:UNK	C	201:UNK	N	28.69
1	IU	120:UNK	C	201:UNK	N	28.69
1	JU	120:UNK	C	201:UNK	N	28.69
1	KU	120:UNK	C	201:UNK	N	28.69
1	LU	120:UNK	C	201:UNK	N	28.69
1	MU	120:UNK	C	201:UNK	N	28.69
1	NU	120:UNK	C	201:UNK	N	28.69
1	AU	314:UNK	C	401:UNK	N	17.39
1	BU	314:UNK	C	401:UNK	N	17.39
1	CU	314:UNK	C	401:UNK	N	17.39

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	DU	314:UNK	C	401:UNK	N	17.39
1	EU	314:UNK	C	401:UNK	N	17.39
1	FU	314:UNK	C	401:UNK	N	17.39
1	GU	314:UNK	C	401:UNK	N	17.39
1	HU	314:UNK	C	401:UNK	N	17.39
1	IU	314:UNK	C	401:UNK	N	17.39
1	JU	314:UNK	C	401:UNK	N	17.39
1	KU	314:UNK	C	401:UNK	N	17.39
1	LU	314:UNK	C	401:UNK	N	17.39
1	MU	314:UNK	C	401:UNK	N	17.39
1	NU	314:UNK	C	401:UNK	N	17.39

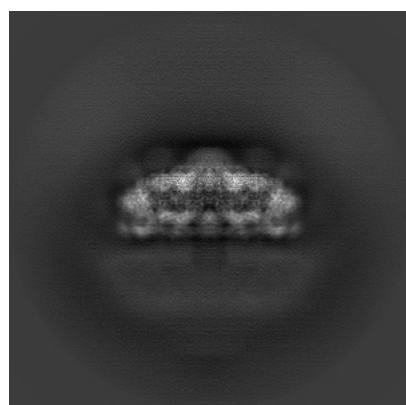
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22081. These allow visual inspection of the internal detail of the map and identification of artifacts.

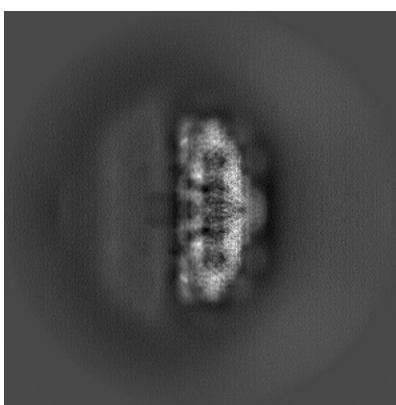
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

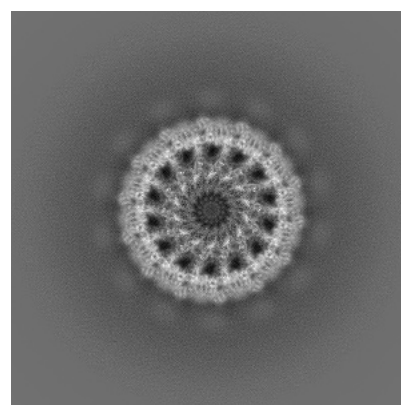
6.1.1 Primary map



X



Y

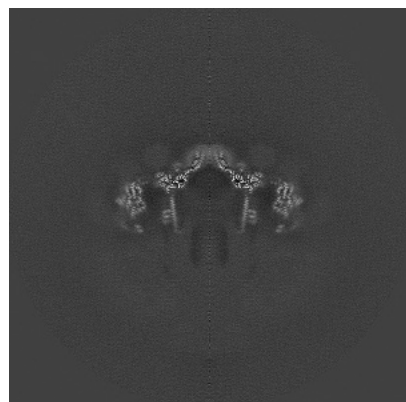


Z

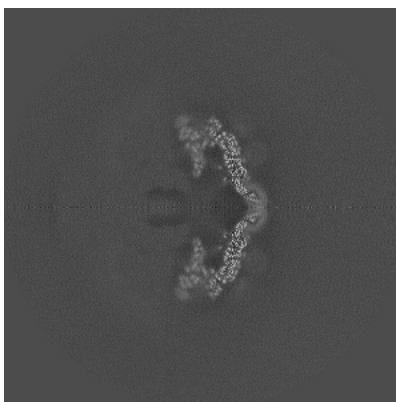
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

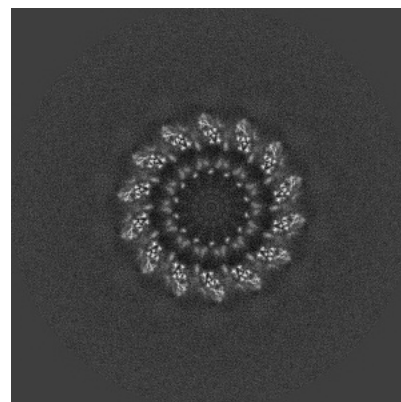
6.2.1 Primary map



X Index: 255



Y Index: 255



Z Index: 255

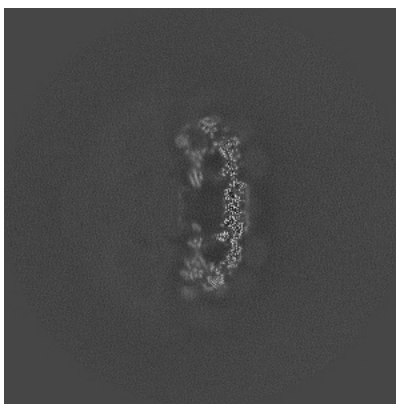
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

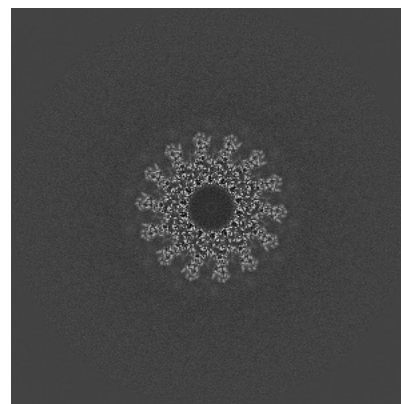
6.3.1 Primary map



X Index: 241



Y Index: 289

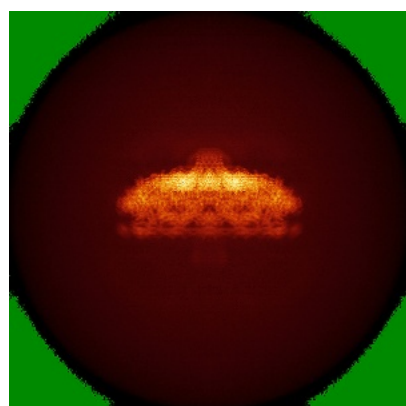


Z Index: 291

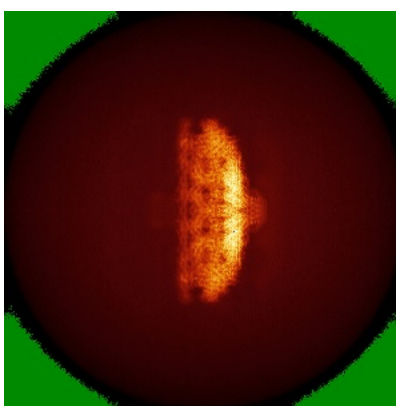
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

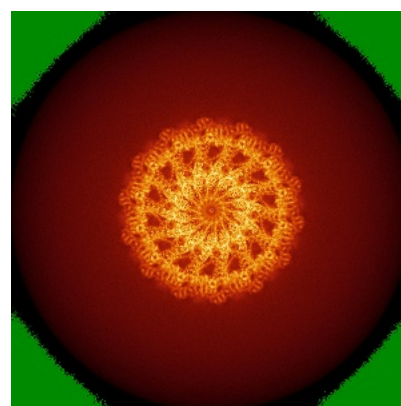
6.4.1 Primary map



X



Y

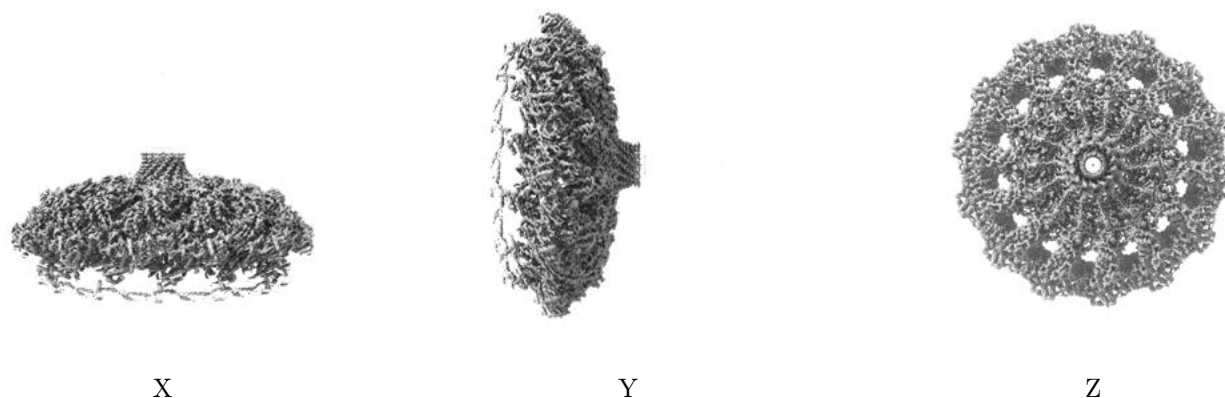


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

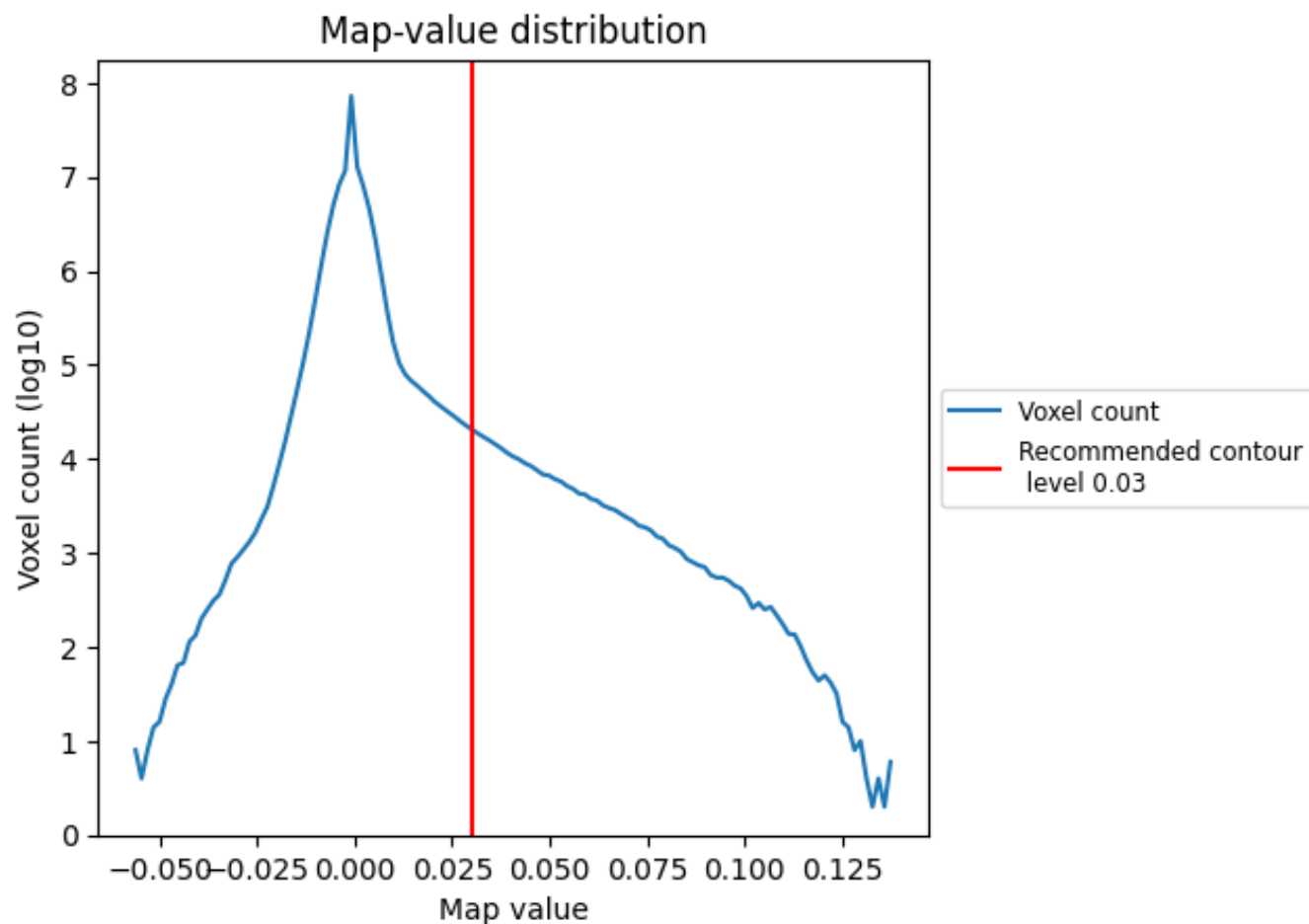
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

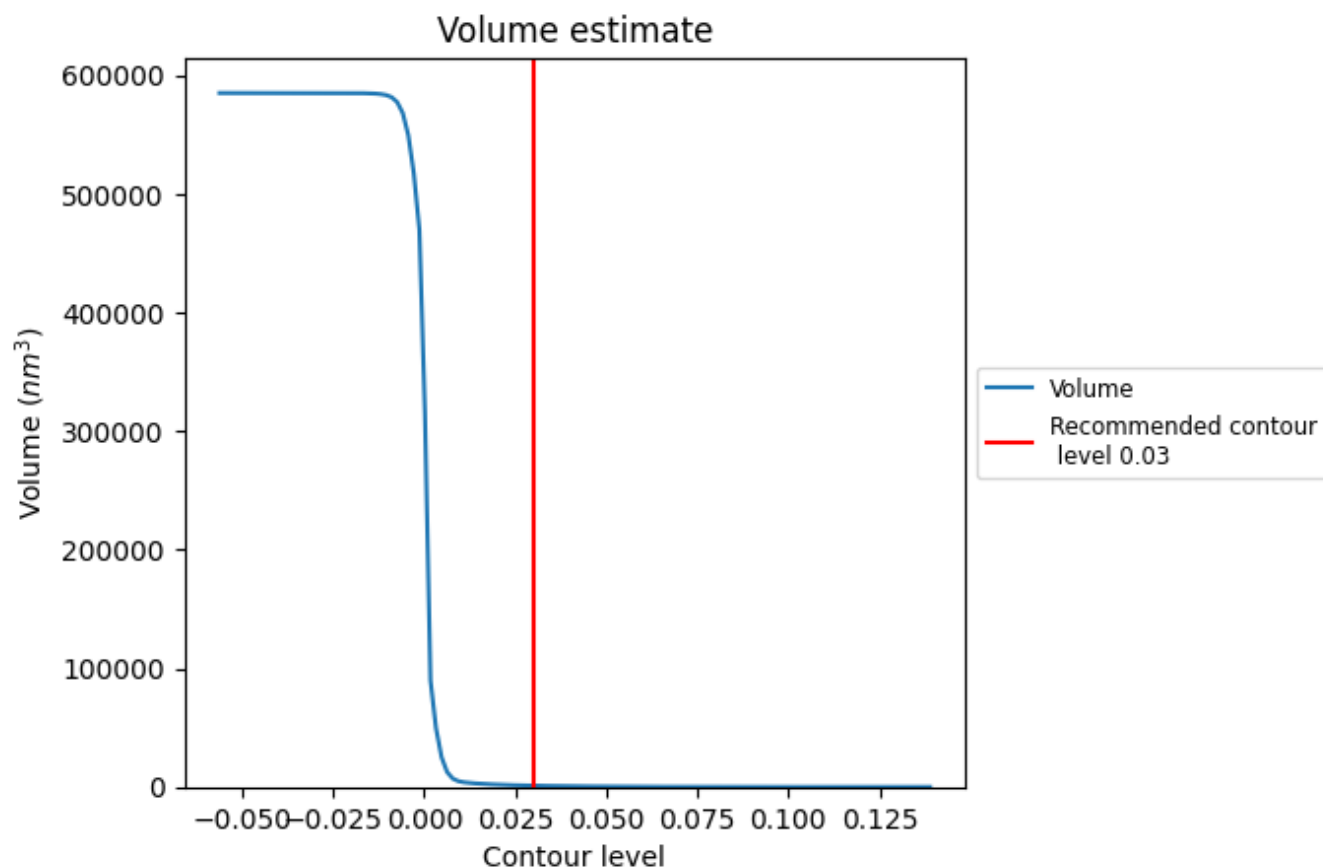
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

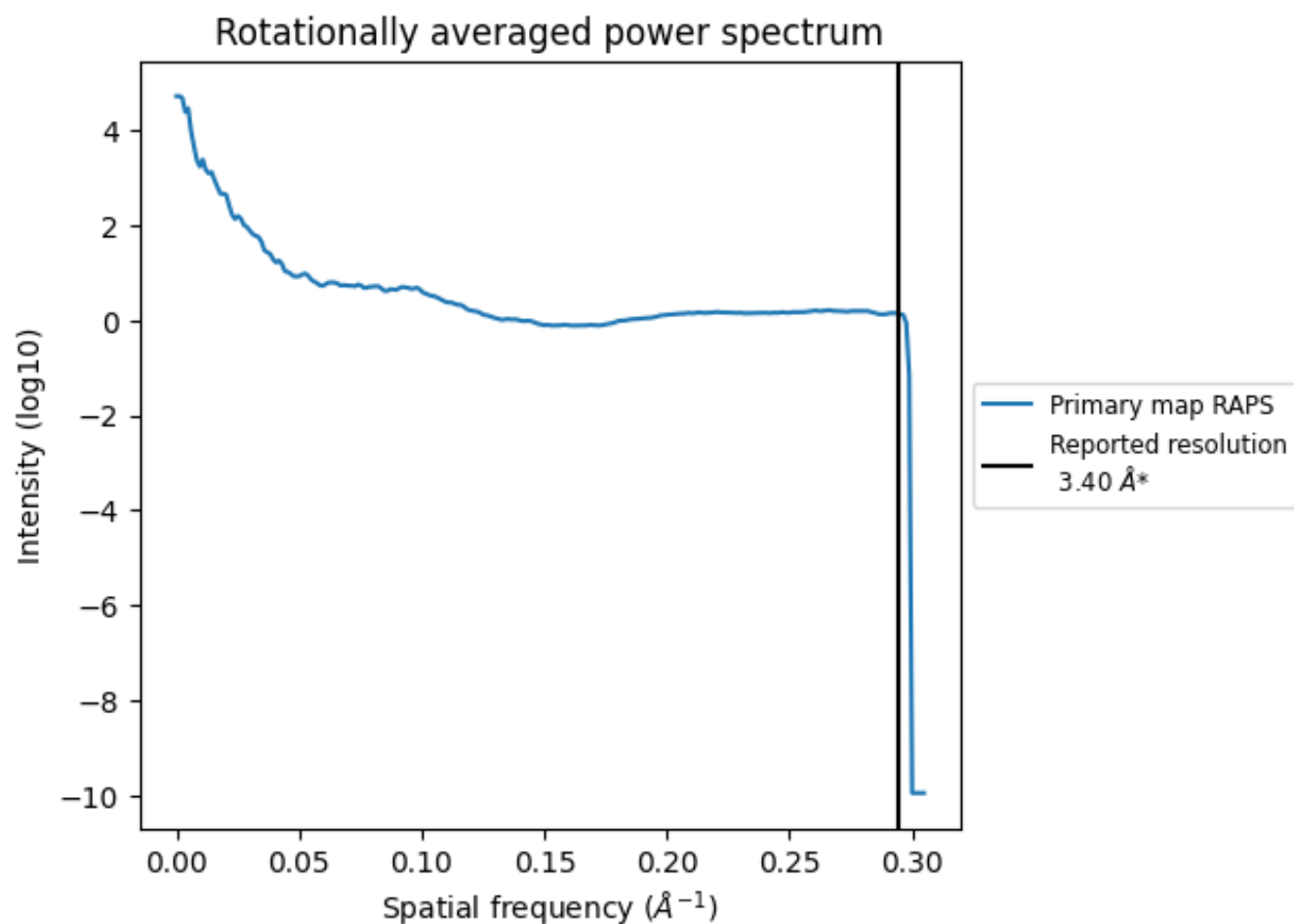
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1078 nm^3 ; this corresponds to an approximate mass of 974 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

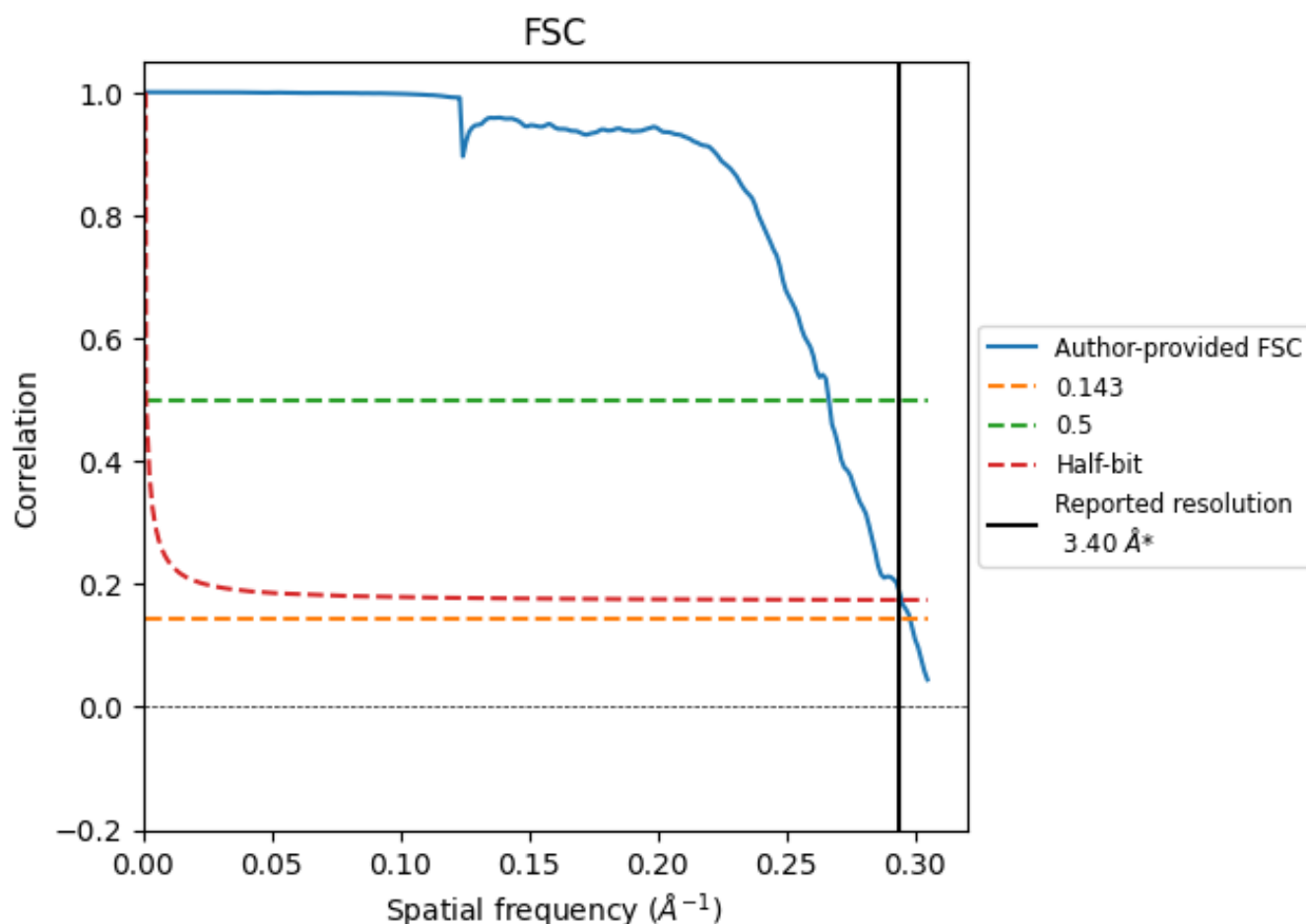


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

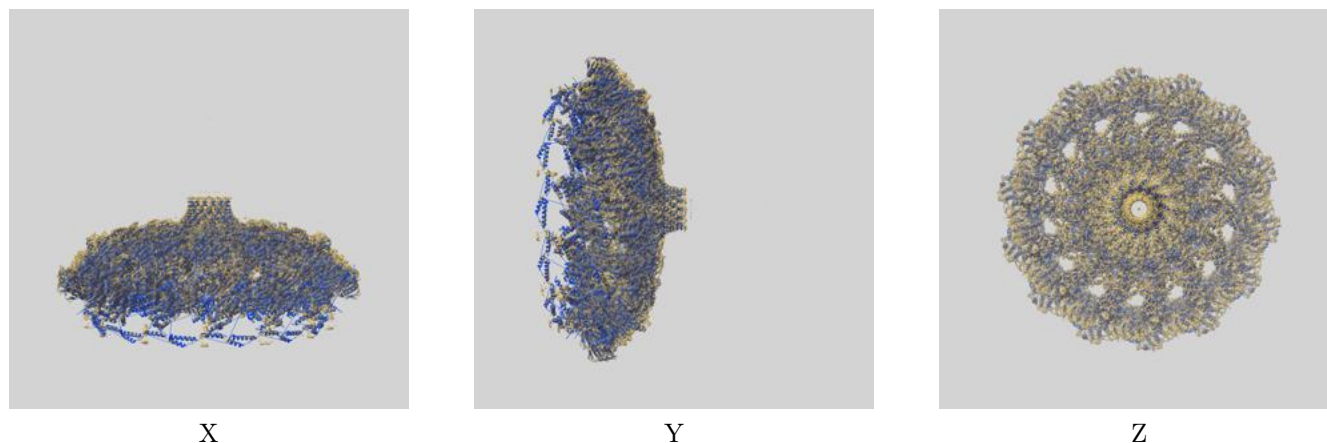
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.35	3.75	3.39
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

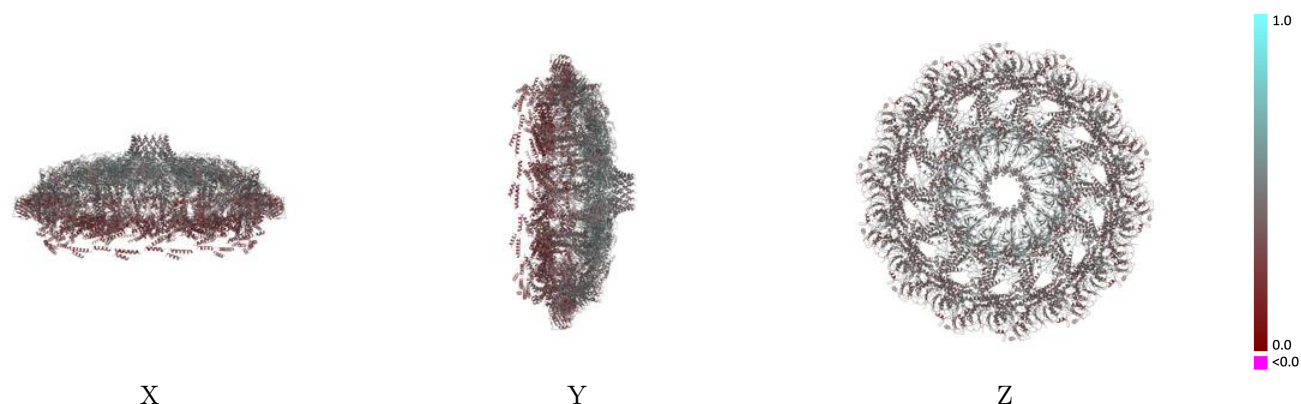
This section contains information regarding the fit between EMDB map EMD-22081 and PDB model 6X6S. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



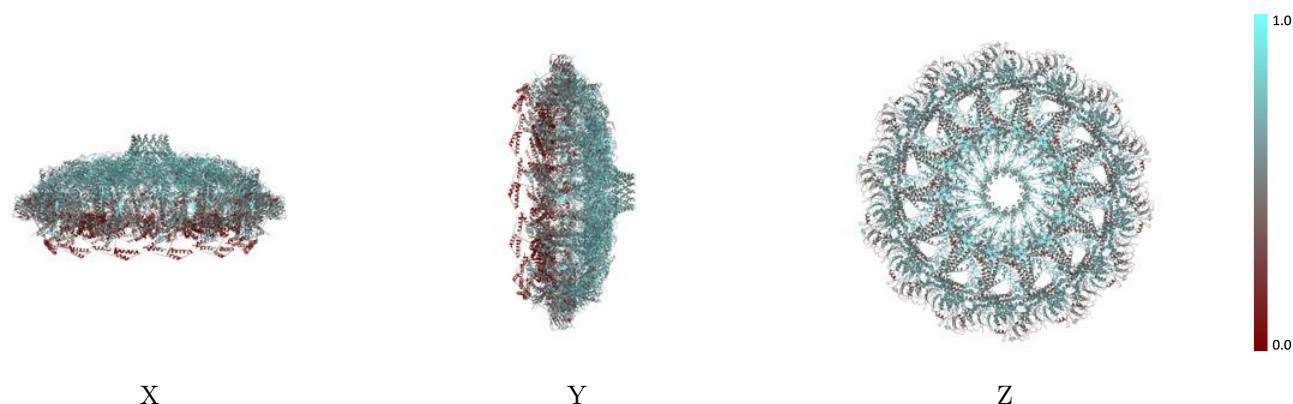
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



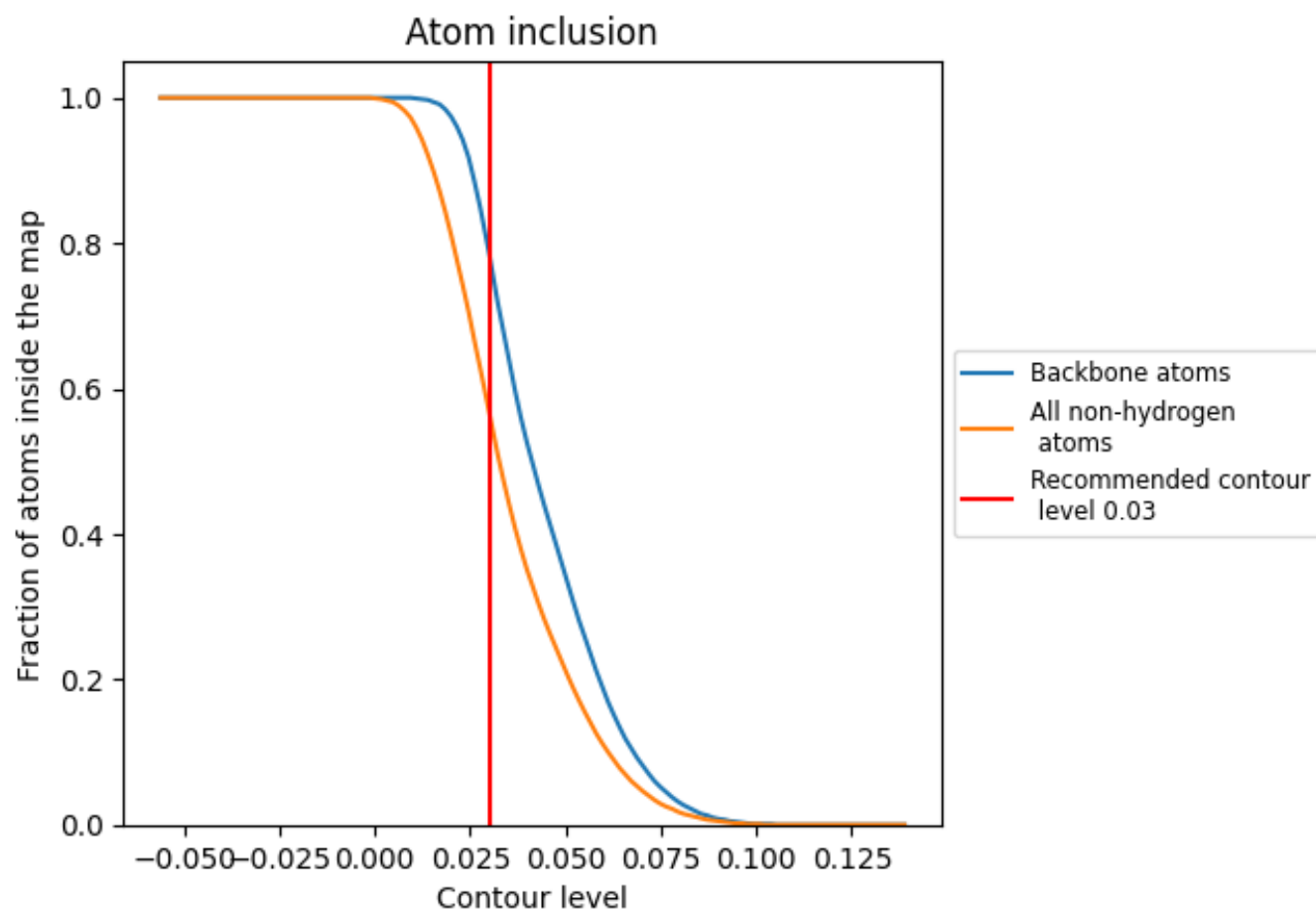
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 57% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5680	 0.4030
AA	 0.5830	 0.4110
AB	 0.6710	 0.4540
AC	 0.6500	 0.4320
AD	 0.4750	 0.3500
AE	 0.4190	 0.3380
AM	 0.5260	 0.3640
AT	 0.6750	 0.4620
AU	 0.4120	 0.3410
AX	 0.7080	 0.4760
AY	 0.7460	 0.5050
Am	 0.2610	 0.2510
At	 0.5610	 0.4120
BA	 0.5780	 0.4100
BB	 0.6740	 0.4410
BC	 0.6360	 0.4250
BD	 0.4840	 0.3550
BE	 0.4220	 0.3390
BM	 0.5250	 0.3670
BT	 0.6780	 0.4630
BU	 0.4110	 0.3360
BX	 0.7080	 0.4750
BY	 0.7390	 0.5020
Bm	 0.2600	 0.2460
Bt	 0.5670	 0.4100
CA	 0.5820	 0.4110
CB	 0.6660	 0.4380
CC	 0.6370	 0.4250
CD	 0.4650	 0.3530
CE	 0.4260	 0.3360
CM	 0.5210	 0.3620
CT	 0.6750	 0.4620
CU	 0.4170	 0.3380
CX	 0.7070	 0.4750
CY	 0.7480	 0.5020



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Chain	Atom inclusion	Q-score
Cm	 0.2610	 0.2470
Ct	 0.5660	 0.4090
DA	 0.5840	 0.4090
DB	 0.6590	 0.4340
DC	 0.6410	 0.4330
DD	 0.4790	 0.3550
DE	 0.4300	 0.3380
DM	 0.5150	 0.3640
DT	 0.6770	 0.4600
DU	 0.4120	 0.3350
DX	 0.7100	 0.4760
DY	 0.7420	 0.5020
Dm	 0.2570	 0.2480
Dt	 0.5650	 0.4100
EA	 0.5780	 0.4050
EB	 0.6600	 0.4390
EC	 0.6500	 0.4230
ED	 0.4720	 0.3520
EE	 0.4220	 0.3280
EM	 0.5190	 0.3620
ET	 0.6810	 0.4620
EU	 0.4140	 0.3370
EX	 0.7000	 0.4730
EY	 0.7410	 0.5030
Em	 0.2600	 0.2470
Et	 0.5740	 0.4100
FA	 0.5790	 0.4050
FB	 0.6740	 0.4380
FC	 0.6430	 0.4240
FD	 0.4840	 0.3660
FE	 0.4260	 0.3340
FM	 0.5220	 0.3640
FT	 0.6830	 0.4610
FU	 0.4040	 0.3350
FX	 0.7060	 0.4730
FY	 0.7390	 0.4990
Fm	 0.2650	 0.2470
Ft	 0.5700	 0.4110
GA	 0.5770	 0.4050
GB	 0.6640	 0.4380
GC	 0.6440	 0.4280
GD	 0.4710	 0.3550

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Chain	Atom inclusion	Q-score
GE	 0.4240	 0.3330
GM	 0.5190	 0.3660
GT	 0.6810	 0.4620
GU	 0.4110	 0.3310
GX	 0.7080	 0.4750
GY	 0.7440	 0.4980
Gm	 0.2620	 0.2470
Gt	 0.5700	 0.4140
HA	 0.5830	 0.4120
HB	 0.6740	 0.4520
HC	 0.6510	 0.4250
HD	 0.4740	 0.3540
HE	 0.4200	 0.3390
HM	 0.5260	 0.3650
HT	 0.6750	 0.4610
HU	 0.4030	 0.3370
HX	 0.7050	 0.4760
HY	 0.7480	 0.5030
Hm	 0.2570	 0.2480
Ht	 0.5620	 0.4100
IA	 0.5780	 0.4090
IB	 0.6680	 0.4390
IC	 0.6410	 0.4290
ID	 0.4790	 0.3520
IE	 0.4220	 0.3440
IM	 0.5240	 0.3650
IT	 0.6770	 0.4640
IU	 0.4110	 0.3360
IX	 0.7040	 0.4770
IY	 0.7390	 0.5000
Im	 0.2610	 0.2450
It	 0.5640	 0.4050
JA	 0.5830	 0.4130
JB	 0.6700	 0.4380
JC	 0.6450	 0.4210
JD	 0.4690	 0.3580
JE	 0.4210	 0.3330
JM	 0.5200	 0.3610
JT	 0.6750	 0.4620
JU	 0.4220	 0.3370
JX	 0.7080	 0.4750
JY	 0.7470	 0.5010

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Chain	Atom inclusion	Q-score
Jm	 0.2630	 0.2460
Jt	 0.5670	 0.4080
KA	 0.5820	 0.4100
KB	 0.6610	 0.4390
KC	 0.6480	 0.4310
KD	 0.4750	 0.3550
KE	 0.4270	 0.3370
KM	 0.5120	 0.3630
KT	 0.6780	 0.4600
KU	 0.4070	 0.3370
KX	 0.7170	 0.4770
KY	 0.7420	 0.5020
Km	 0.2580	 0.2480
Kt	 0.5670	 0.4090
LA	 0.5770	 0.4090
LB	 0.6660	 0.4440
LC	 0.6540	 0.4280
LD	 0.4740	 0.3490
LE	 0.4210	 0.3410
LM	 0.5200	 0.3600
LT	 0.6800	 0.4640
LU	 0.4070	 0.3330
LX	 0.7080	 0.4750
LY	 0.7370	 0.5050
Lm	 0.2580	 0.2450
Lt	 0.5720	 0.4110
MA	 0.5810	 0.4080
MB	 0.6670	 0.4320
MC	 0.6400	 0.4310
MD	 0.4820	 0.3650
ME	 0.4250	 0.3410
MM	 0.5200	 0.3620
MT	 0.6810	 0.4630
MU	 0.3990	 0.3380
MX	 0.7080	 0.4720
MY	 0.7390	 0.5000
Mm	 0.2630	 0.2500
Mt	 0.5690	 0.4120
NA	 0.5810	 0.4120
NB	 0.6700	 0.4380
NC	 0.6470	 0.4280
ND	 0.4820	 0.3560

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Chain	Atom inclusion	Q-score
NE	 0.4250	 0.3380
NM	 0.5190	 0.3630
NT	 0.6750	 0.4620
NU	 0.4170	 0.3350
NX	 0.7080	 0.4750
NY	 0.7420	 0.5010
Nm	 0.2630	 0.2460
Nt	 0.5710	 0.4130