



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 29, 2026 – 07:05 PM UTC

PDB ID : 6YF7 / pdb_00006yf7
Title : Virus-like particle of bacteriophage AC
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

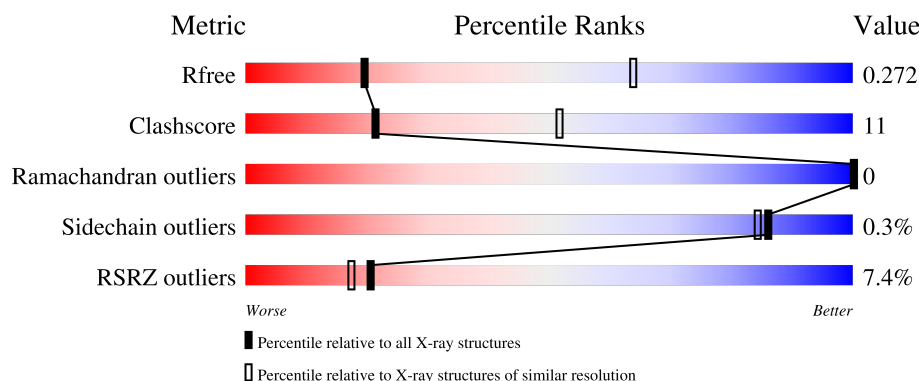
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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

Mol	Chain	Length	Quality of chain
1	AA	115	5% 80% 19% .
1	AB	115	7% 78% 21% .
1	AC	115	9% 78% 21% .
1	AD	115	6% 76% 23% .
1	AE	115	9% 76% 23% .

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Mol	Chain	Length	Quality of chain
1	AF	115	8% 74% 25%
1	AG	115	12% 74% 25%
1	AH	115	5% 81% 18%
1	AI	115	6% 76% 23%
1	AJ	115	3% 77% 23%
1	AK	115	5% 77% 22%
1	AL	115	6% 77% 23%
1	AM	115	9% 72% 27%
1	AN	115	4% 75% 24%
1	AO	115	3% 76% 23%
1	AP	115	19% 76% 23%
1	AQ	115	7% 76% 23%
1	AR	115	14% 77% 23%
1	AS	115	11% 69% 30%
1	AT	115	6% 81% 18%
1	AU	115	13% 67% 32%
1	AV	115	6% 78% 21%
1	AW	115	3% 80% 19%
1	AX	115	4% 75% 24%
1	AY	115	12% 75% 24%
1	AZ	115	15% 80% 19%
1	BA	115	18% 75% 24%
1	BB	115	9% 77% 22%
1	BC	115	3% 73% 26%
1	BD	115	9% 73% 26%

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Mol	Chain	Length	Quality of chain
1	BE	115	
1	BF	115	
1	BG	115	
1	BH	115	
1	BI	115	
1	BJ	115	
1	BK	115	
1	BL	115	
1	BM	115	
1	BN	115	
1	BO	115	
1	BP	115	
1	BQ	115	
1	BR	115	
1	BS	115	
1	BT	115	
1	BU	115	
1	BV	115	
1	BW	115	
1	BX	115	
1	BY	115	
1	BZ	115	
1	CA	115	
1	CB	115	
1	CC	115	

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Mol	Chain	Length	Quality of chain
1	CD	115	3% 77% 22%
1	CE	115	9% 77% 22%
1	CF	115	% 77% 22%
1	CG	115	5% 72% 27%
1	CH	115	10% 68% 31%
1	CI	115	10% 77% 23%
1	CJ	115	11% 75% 24%
1	CK	115	21% 77% 22%
1	CL	115	3% 73% 26%
1	CM	115	5% 77% 22%
1	CN	115	5% 72% 27%
1	CO	115	8% 77% 22%
1	CP	115	10% 80% 19%
1	CQ	115	8% 76% 23%
1	CR	115	3% 76% 23%
1	CS	115	3% 81% 18%
1	CT	115	10% 78% 21%
1	CU	115	9% 78% 21%
1	CV	115	9% 80% 19%
1	CW	115	6% 78% 21%
1	CX	115	3% 79% 20%
1	CY	115	5% 77% 23%
1	CZ	115	7% 74% 25%
1	DA	115	4% 80% 19%
1	DB	115	3% 81% 18%

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Mol	Chain	Length	Quality of chain
1	DC	115	
1	DD	115	
1	DE	115	
1	DF	115	
1	DG	115	
1	DH	115	
1	DI	115	
1	DJ	115	
1	DK	115	
1	DL	115	
1	DM	115	
1	DN	115	
1	DO	115	
1	DP	115	
1	DQ	115	
1	DR	115	
1	DS	115	
1	DT	115	
1	DU	115	
1	DV	115	
1	DW	115	
1	DX	115	
1	DY	115	
1	DZ	115	
1	EA	115	

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Mol	Chain	Length	Quality of chain
1	EB	115	
1	EC	115	
1	ED	115	
1	EE	115	
1	EF	115	
1	EG	115	
1	EH	115	
1	EI	115	
1	EJ	115	
1	EK	115	
1	EL	115	
1	EM	115	
1	EN	115	
1	EO	115	
1	EP	115	
1	EQ	115	
1	ER	115	
1	ES	115	
1	ET	115	
1	EU	115	
1	EV	115	
1	EW	115	
1	EX	115	
1	EY	115	
1	EZ	115	

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Mol	Chain	Length	Quality of chain	
1	FA	115	5%	80% 19%
1	FB	115	10%	77% 23%
1	FC	115	3%	77% 22%
1	FD	115	3%	79% 20%
1	FE	115	3%	78% 21%
1	FF	115	3%	76% 23%
1	FG	115	8%	75% 24%
1	FH	115	10%	77% 22%
1	FI	115	7%	81% 18%
1	FJ	115	11%	70% 30%
1	FK	115	6%	72% 27%
1	FL	115	7%	77% 23%
1	FM	115	6%	77% 23%
1	FN	115	12%	75% 24%
1	FO	115	4%	73% 26%
1	FP	115	3%	79% 20%
1	FQ	115	4%	77% 22%
1	FR	115	8%	71% 28%
1	FS	115	4%	76% 23%
1	FT	115	16%	70% 29%
1	FU	115	9%	72% 27%
1	FV	115	8%	80% 19%
1	FW	115	11%	75% 24%
1	FX	115	3%	77% 22%
1	FY	115	2%	77% 23%

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Mol	Chain	Length	Quality of chain
1	FZ	115	
1	GA	115	
1	GB	115	
1	GC	115	
1	GD	115	
1	GE	115	
1	GF	115	
1	GG	115	
1	GH	115	
1	GI	115	
1	GJ	115	
1	GK	115	
1	GL	115	
1	GM	115	
1	GN	115	
1	GO	115	
1	GP	115	
1	GQ	115	
1	GR	115	
1	GS	115	
1	GT	115	
1	GU	115	
1	GV	115	
1	GW	115	
1	GX	115	

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Mol	Chain	Length	Quality of chain
1	GY	115	
1	GZ	115	
1	HA	115	
1	HB	115	
1	HC	115	
1	HD	115	
1	HE	115	
1	HF	115	
1	HG	115	
1	HH	115	
1	HI	115	
1	HJ	115	
1	HK	115	
1	HL	115	
1	HM	115	
1	HN	115	
1	HO	115	
1	HP	115	
1	HQ	115	
1	HR	115	
1	HS	115	
1	HT	115	
1	HU	115	
1	HV	115	
1	HW	115	

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Mol	Chain	Length	Quality of chain
1	HX	115	
1	HY	115	
1	HZ	115	
1	IA	115	
1	IB	115	
1	IC	115	
1	ID	115	
1	IE	115	
1	IF	115	
1	IG	115	
1	IH	115	
1	II	115	
1	IJ	115	
1	IK	115	
1	IL	115	
1	IM	115	
1	IN	115	
1	IO	115	
1	IP	115	
1	IQ	115	
1	IR	115	
1	IS	115	
1	IT	115	
1	IU	115	
1	IV	115	

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Mol	Chain	Length	Quality of chain
1	IW	115	
1	IX	115	
1	IY	115	
1	IZ	115	
1	JA	115	
1	JB	115	
1	JC	115	
1	JD	115	
1	JE	115	
1	JF	115	
1	JG	115	
1	JH	115	
1	JI	115	
1	JJ	115	
1	JK	115	
1	JL	115	
1	JM	115	
1	JN	115	
1	JO	115	
1	JP	115	
1	JQ	115	
1	JR	115	
1	JS	115	
1	JT	115	
1	JU	115	

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Mol	Chain	Length	Quality of chain
1	JV	115	 6% 78% 21%
1	JW	115	 8% 80% 19%
1	JX	115	 2% 76% 23%
1	JY	115	 8% 79% 20%
1	JZ	115	 17% 81% 18%
1	KA	115	 8% 77% 22%
1	KB	115	 3% 78% 21%
1	KC	115	 4% 79% 20%
1	KD	115	 9% 79% 20%
1	KE	115	 4% 79% 20%
1	KF	115	 2% 81% 18%
1	KG	115	 5% 79% 20%
1	KH	115	 8% 72% 27%
1	KI	115	 3% 78% 21%
1	KJ	115	 3% 77% 23%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 231390 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Coat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AD	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AR	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AS	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AT	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	AZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BD	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BR	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BS	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BT	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	BZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CD	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CR	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CS	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CT	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	CZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DD	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DR	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DS	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DT	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	DZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	ED	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	ER	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	ES	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	ET	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	EZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FD	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	FM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FR	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FS	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FT	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	FZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GD	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	GH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GR	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GS	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GT	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	GZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	HC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HD	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HR	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HS	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HT	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	HX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	HZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	ID	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	II	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IR	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	IS	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IT	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	IZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JD	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JK	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JL	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JM	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	JN	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JO	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JP	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JQ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JR	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JS	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JT	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JU	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JV	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JW	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JX	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JY	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	JZ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	KA	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	KB	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	KC	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	KD	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	KE	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	KF	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	KG	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	KH	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

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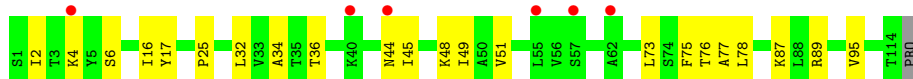
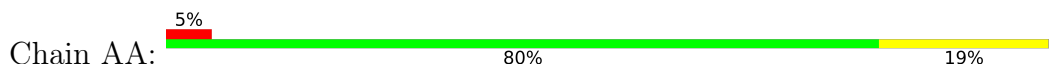
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	KI	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			
1	KJ	114	Total	C	N	O	S	0	0	0
			857	545	141	170	1			

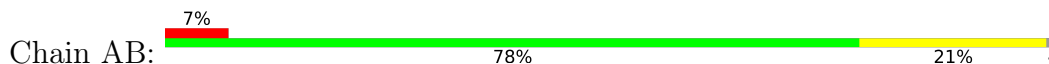
3 Residue-property plots [i](#)

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

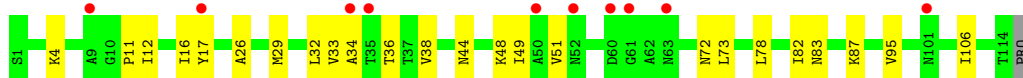
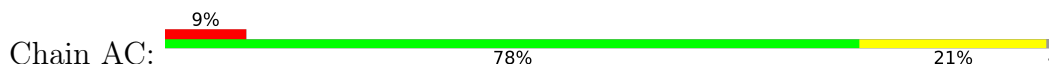
- Molecule 1: Coat protein



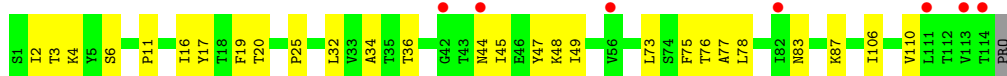
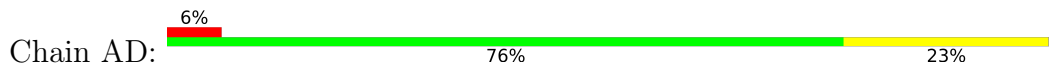
- Molecule 1: Coat protein



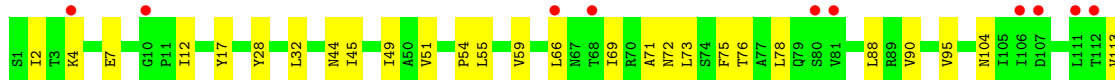
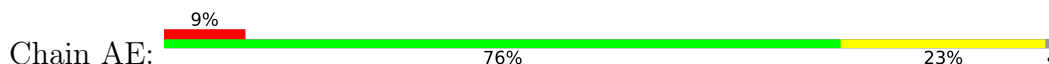
- Molecule 1: Coat protein



- Molecule 1: Coat protein

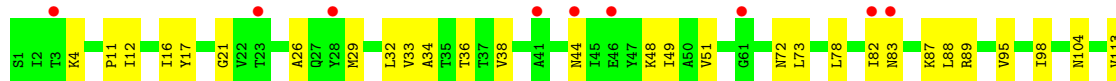
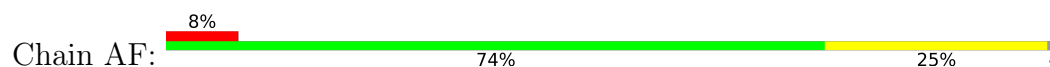


- Molecule 1: Coat protein

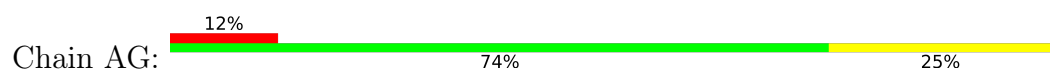




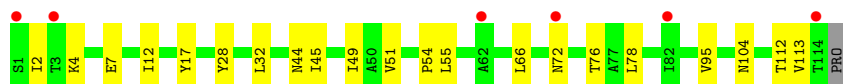
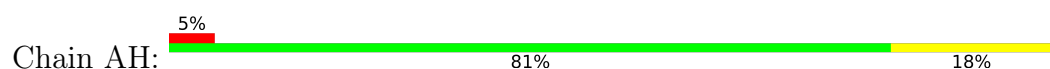
- Molecule 1: Coat protein



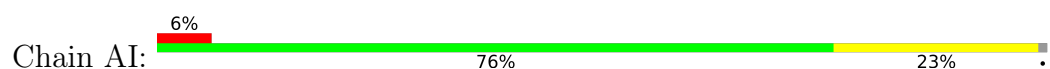
- Molecule 1: Coat protein



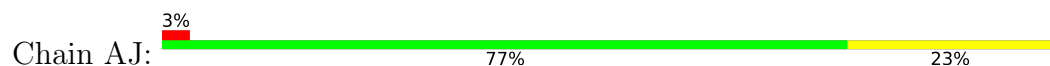
- Molecule 1: Coat protein



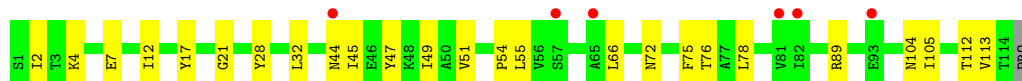
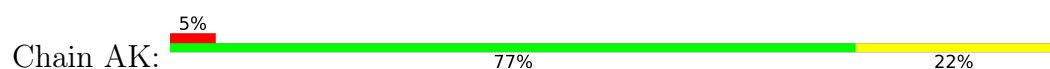
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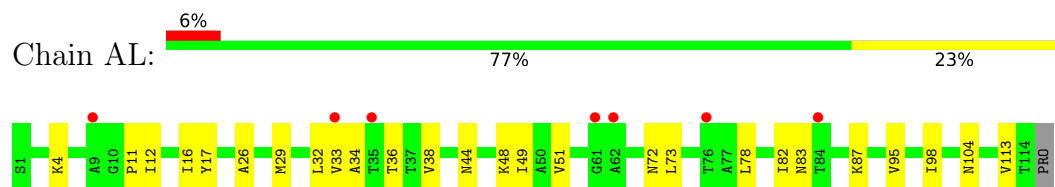
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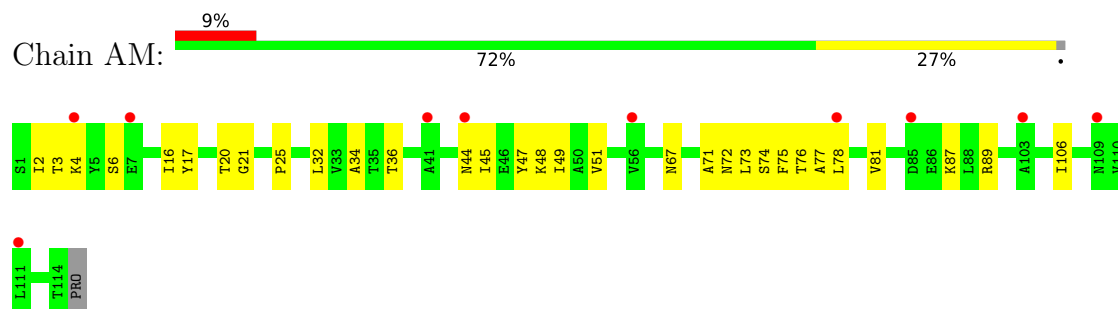
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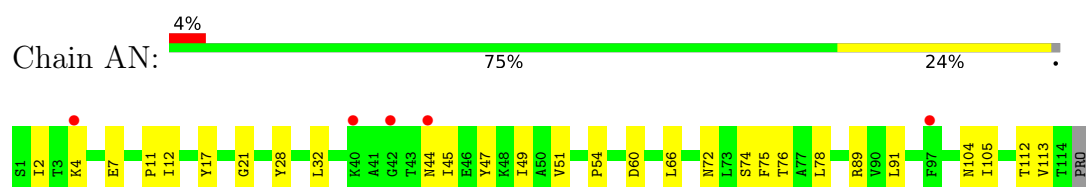
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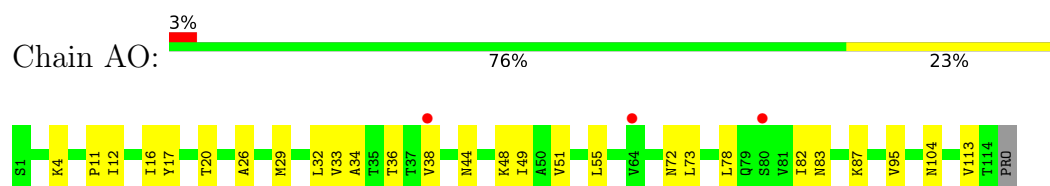
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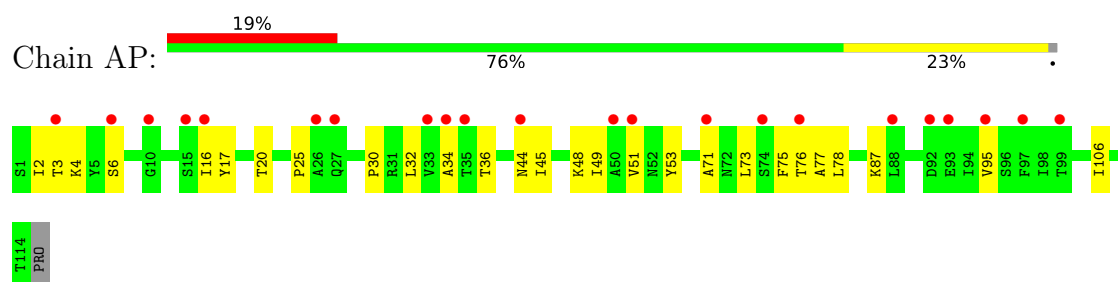
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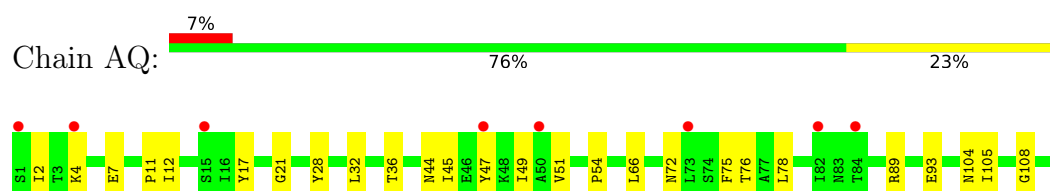
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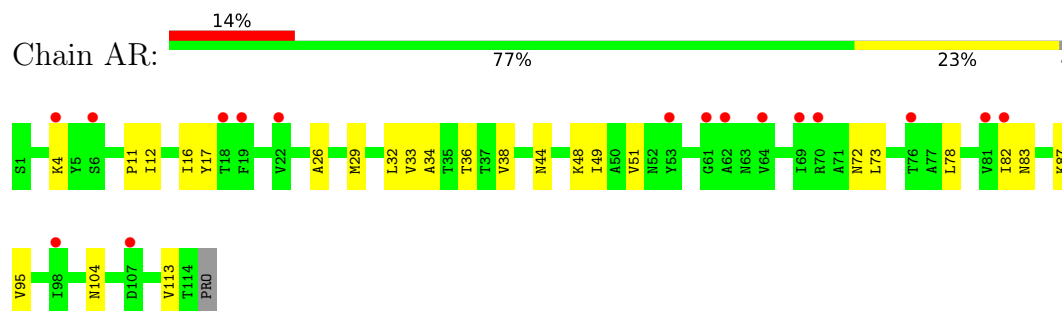
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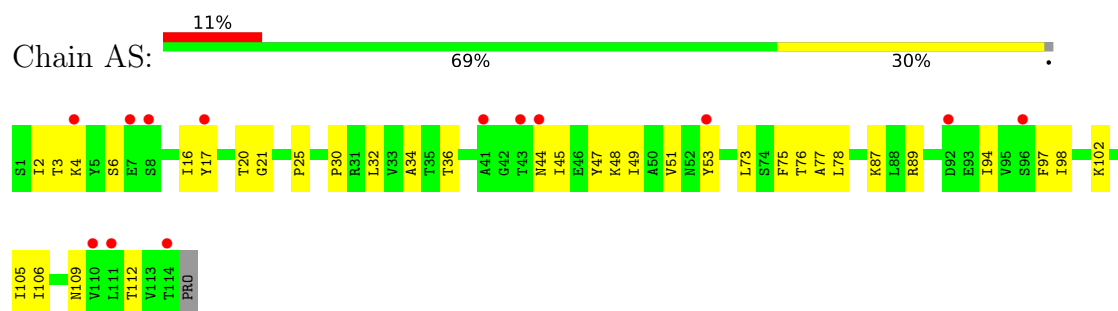
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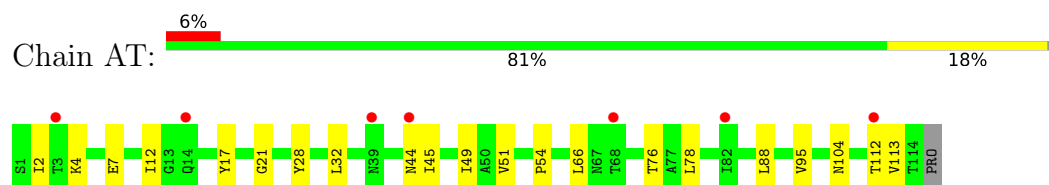
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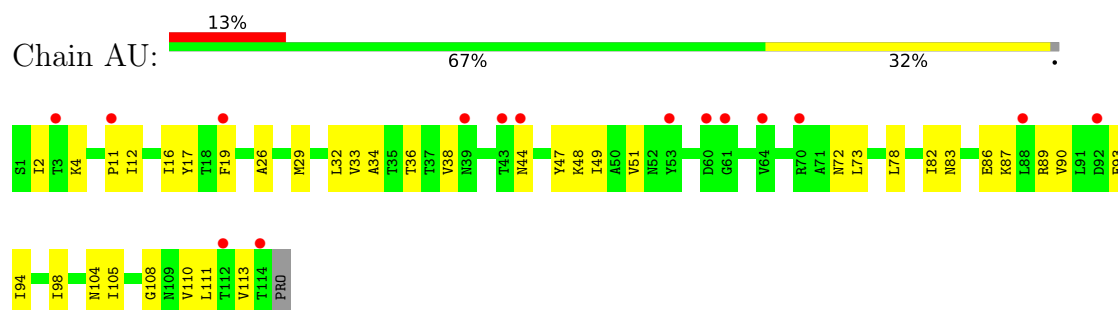
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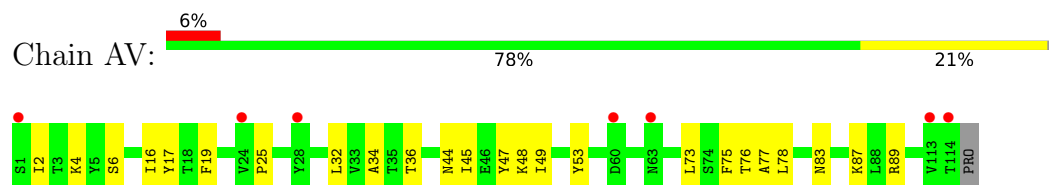
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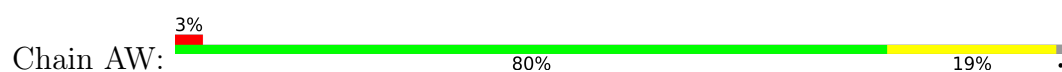
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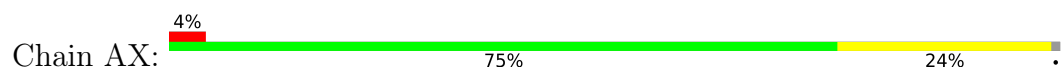
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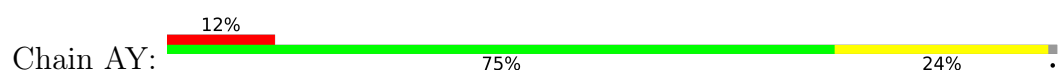
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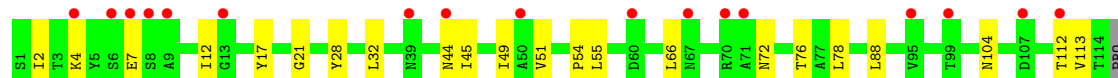
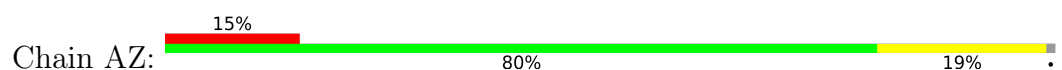
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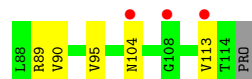
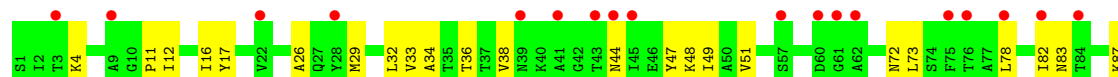
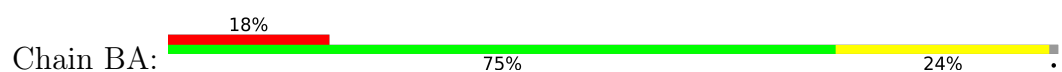
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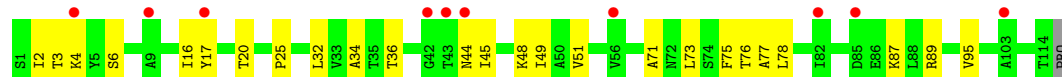
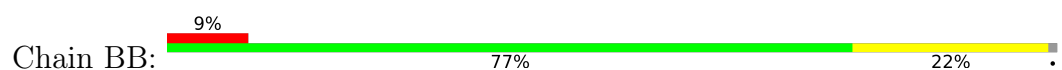
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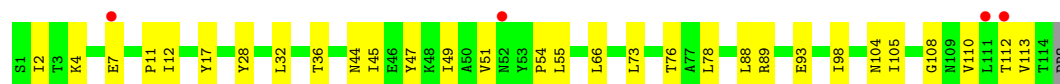


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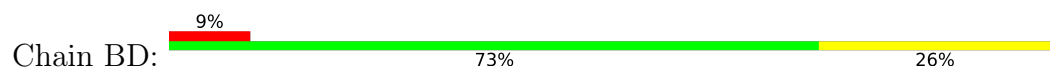


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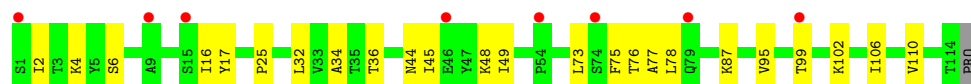
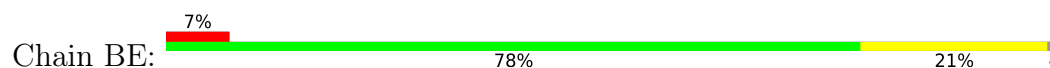




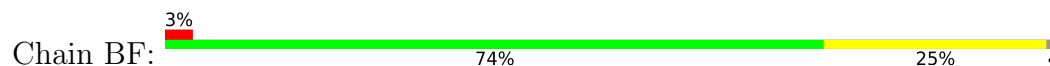
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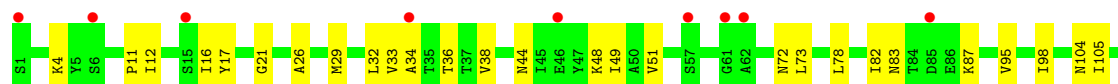
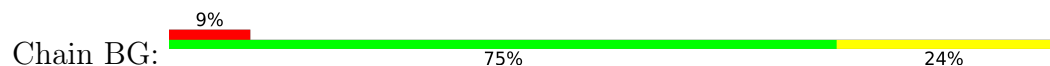
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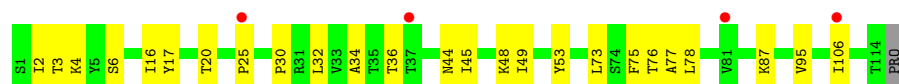
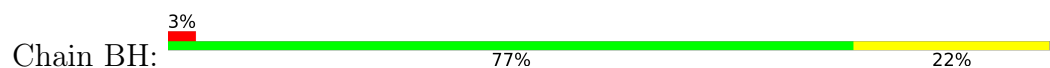
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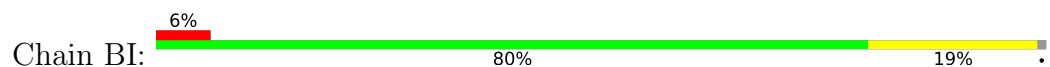
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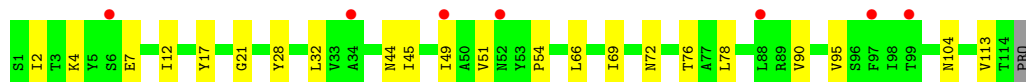


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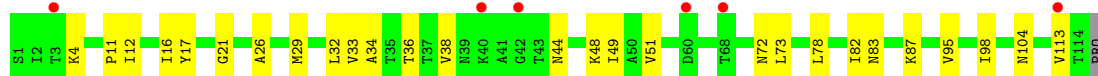
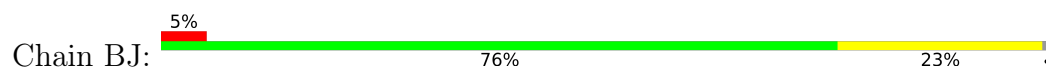


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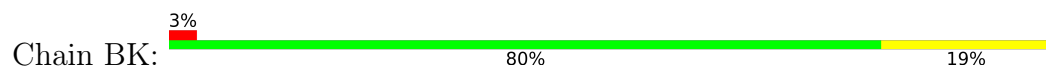




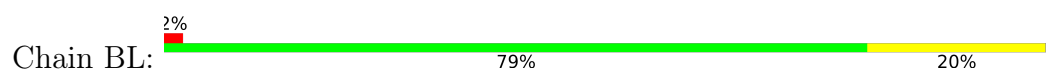
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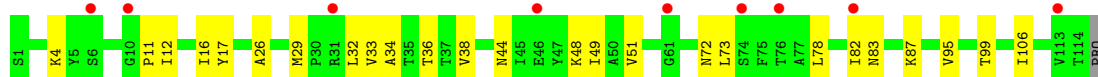
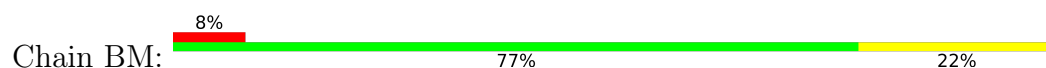
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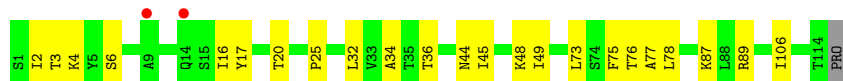
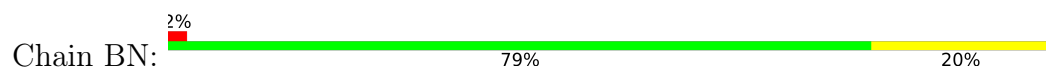
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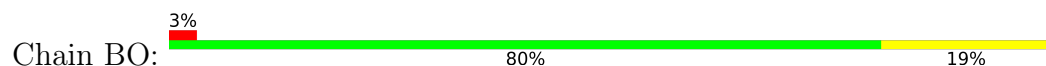
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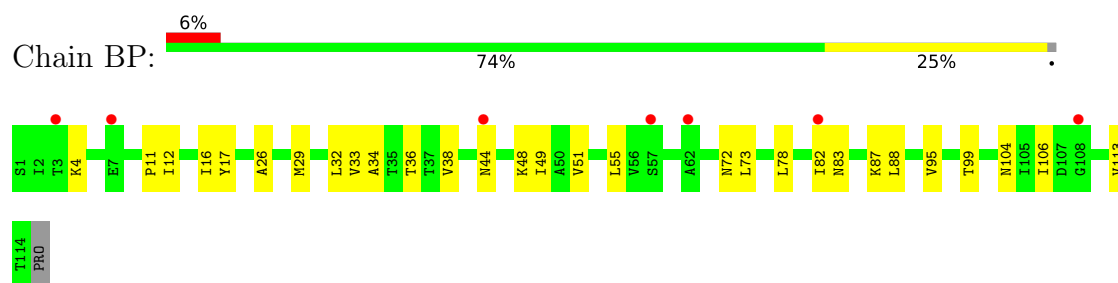
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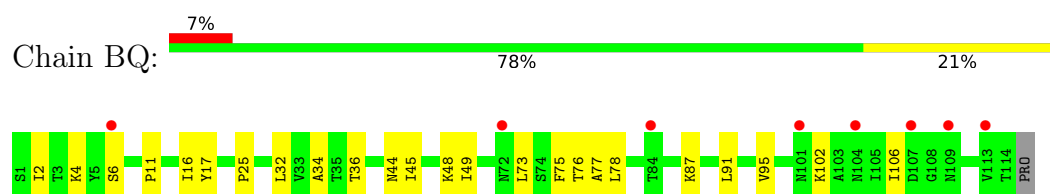
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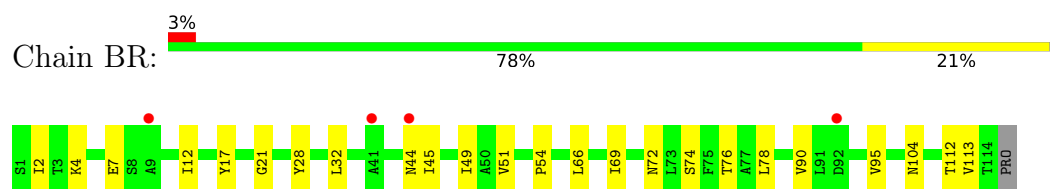
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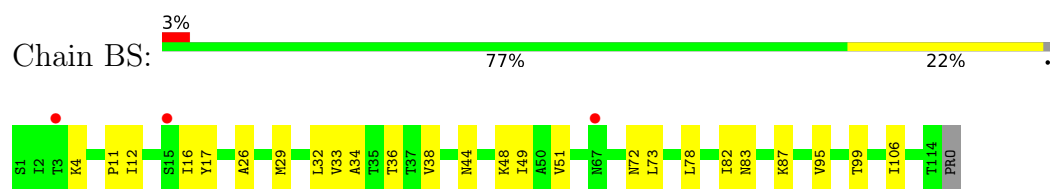
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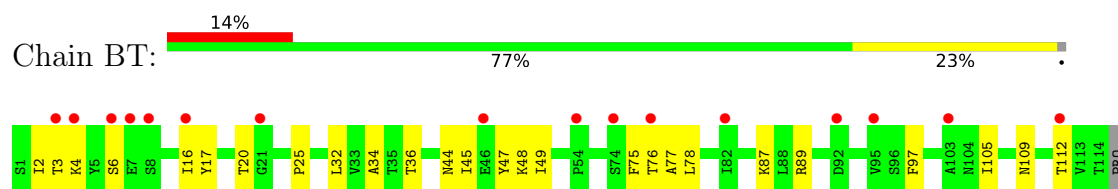
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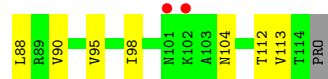
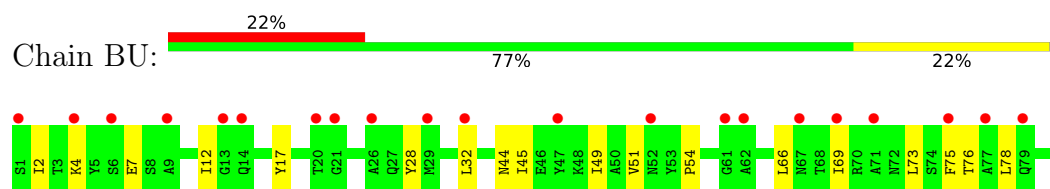
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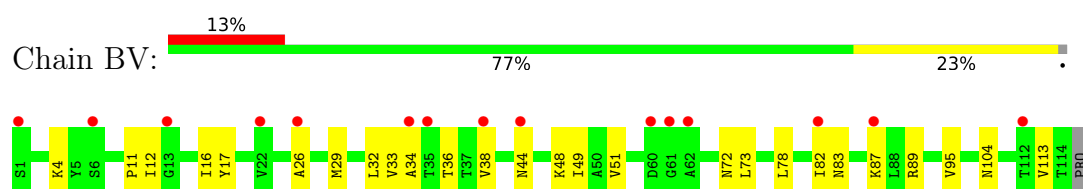
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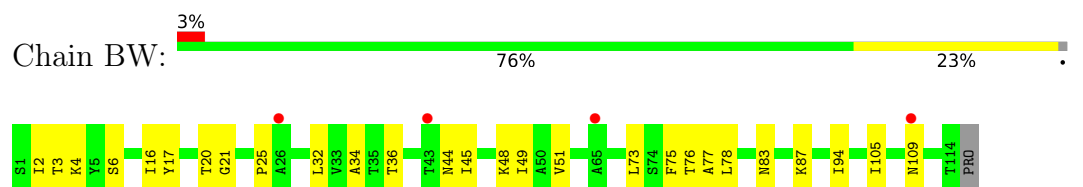
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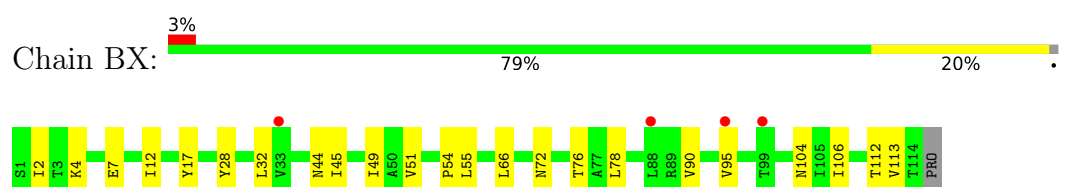
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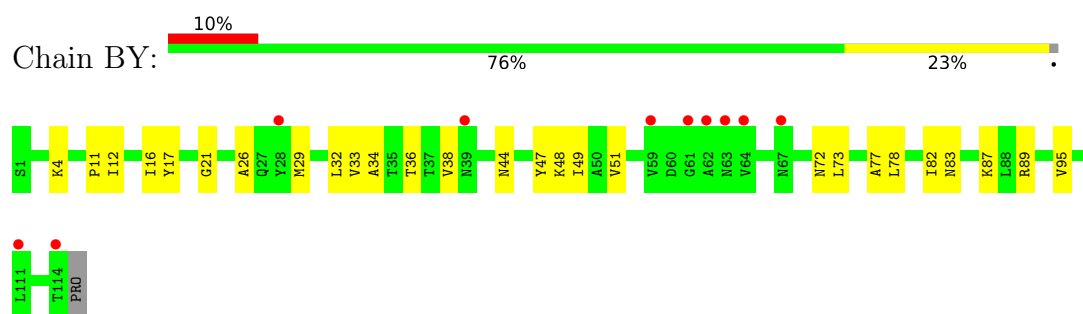
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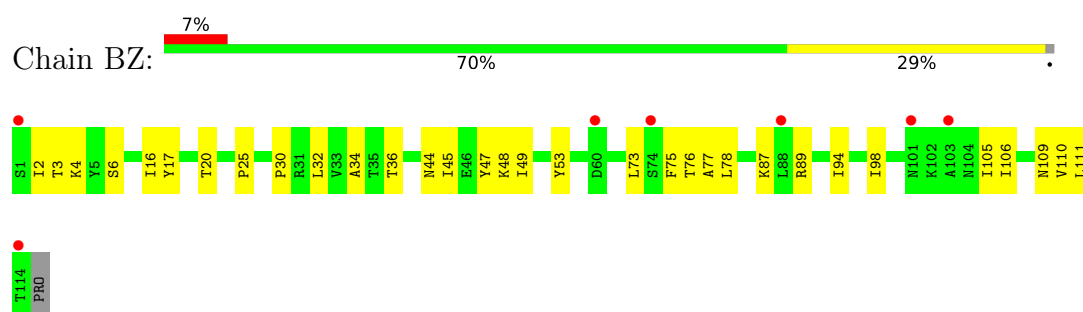
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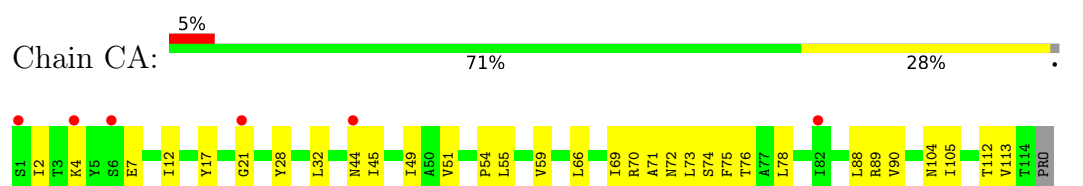
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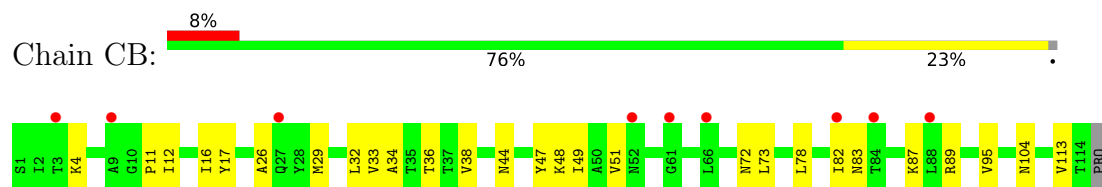
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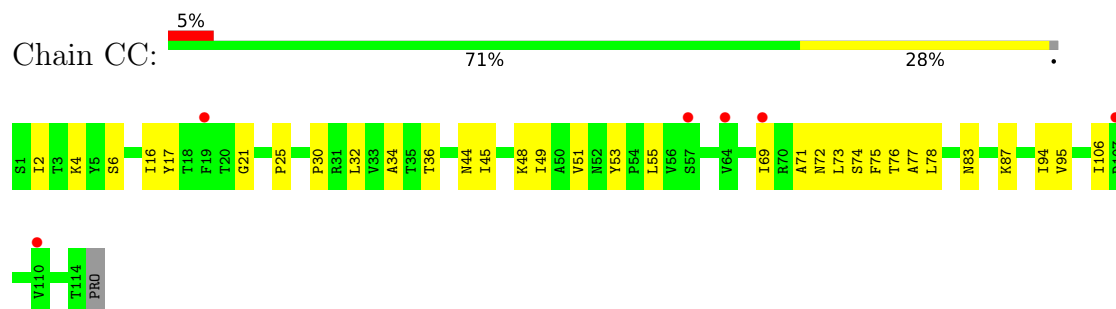
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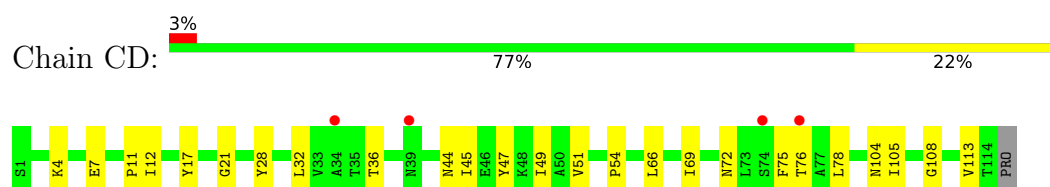
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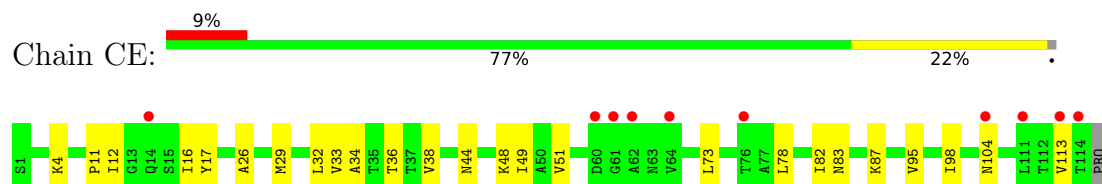
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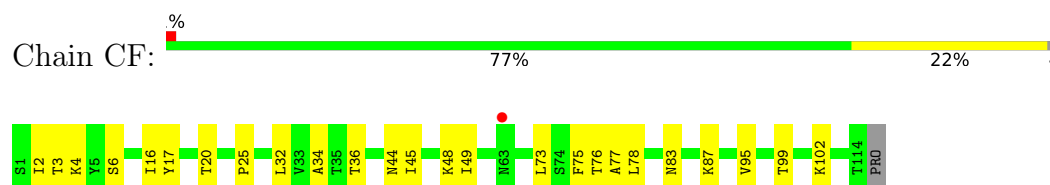
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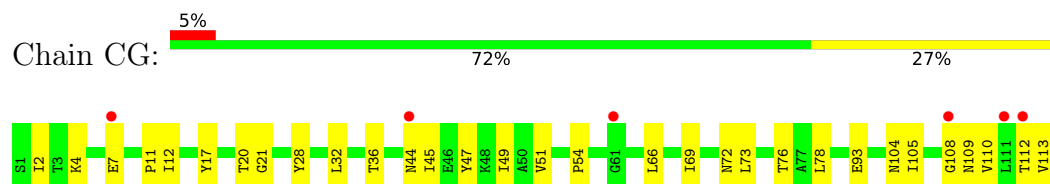
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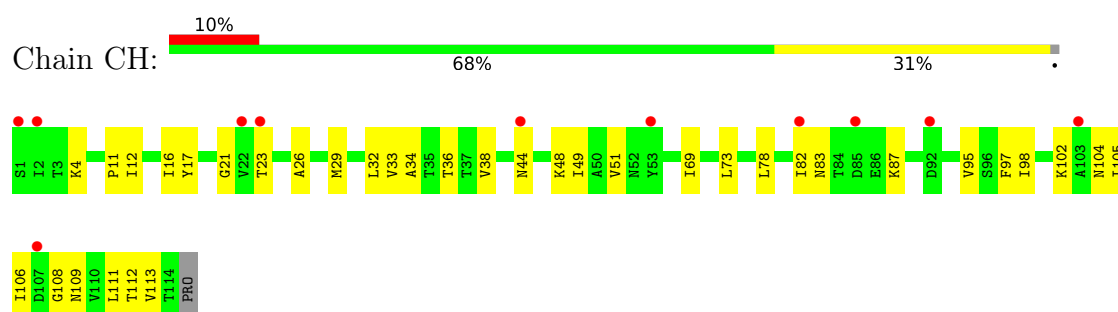
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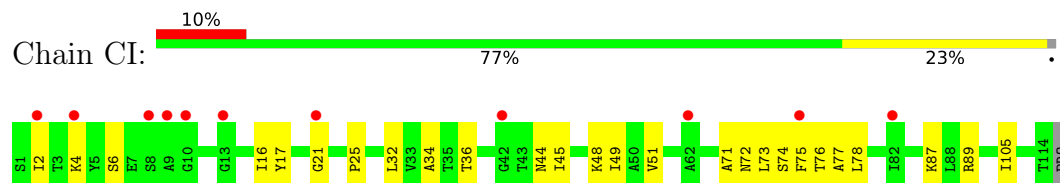
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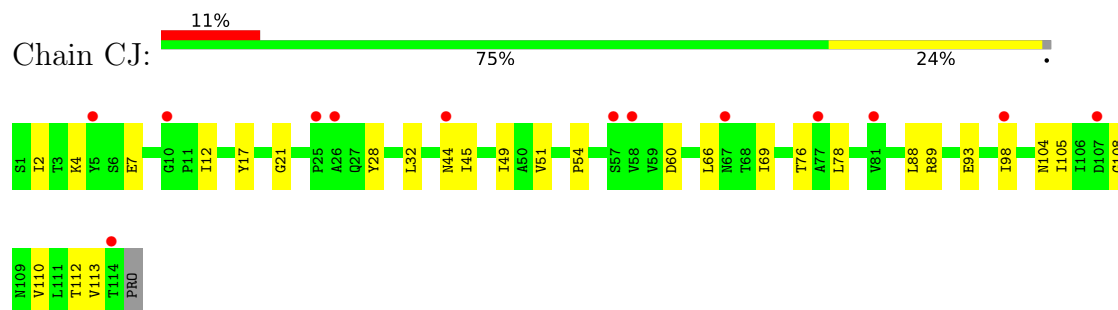
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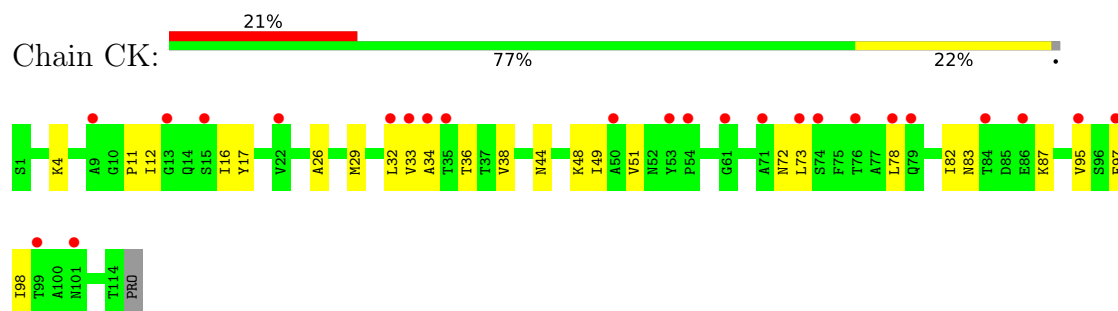
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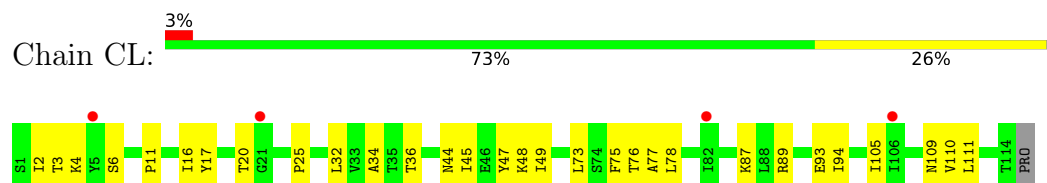
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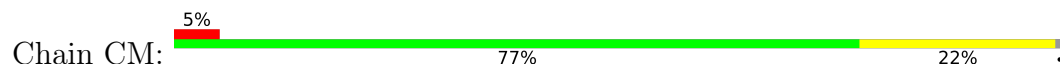
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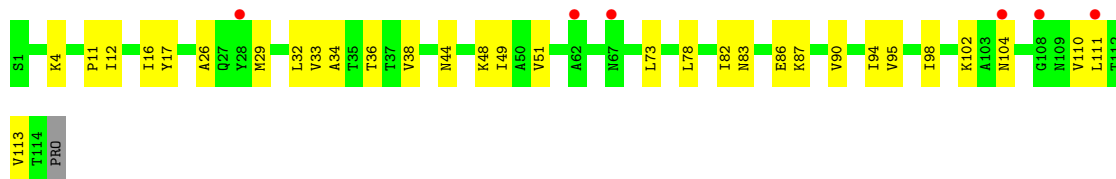
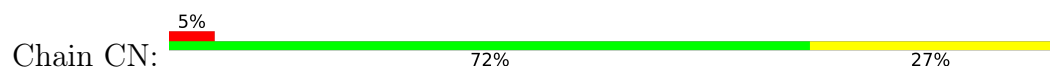


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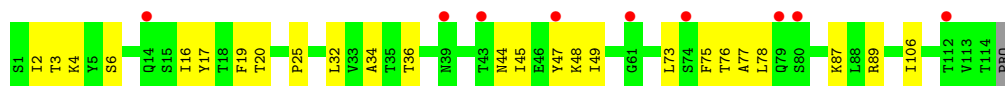
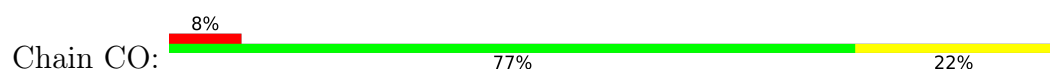




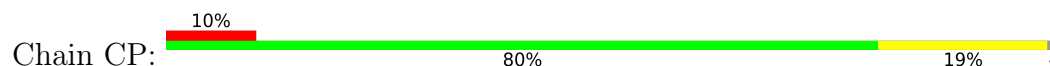
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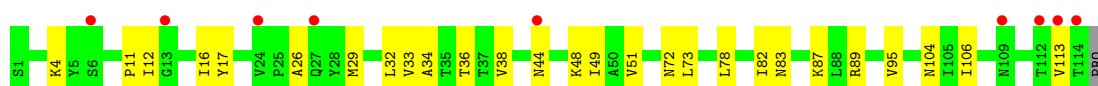
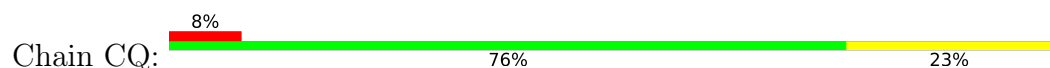
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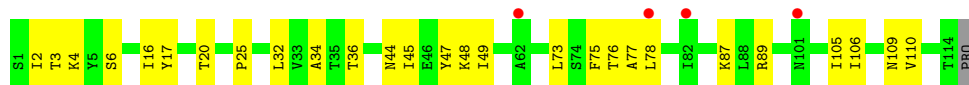
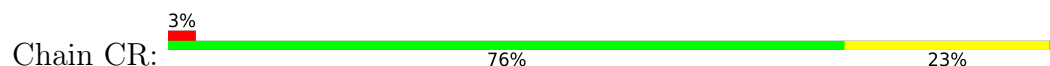
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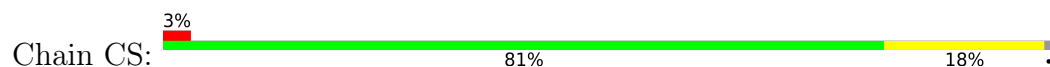
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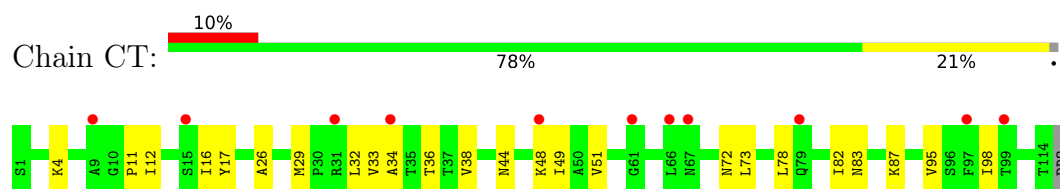
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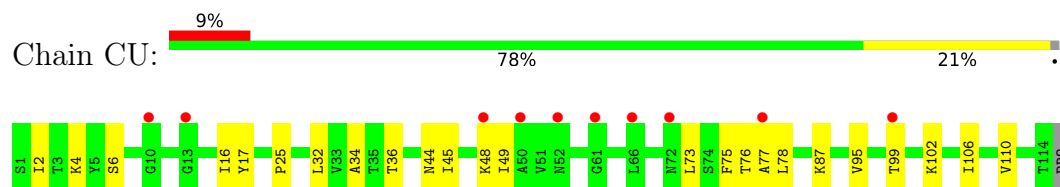
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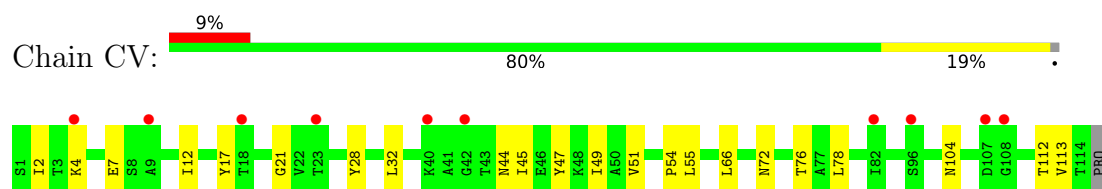
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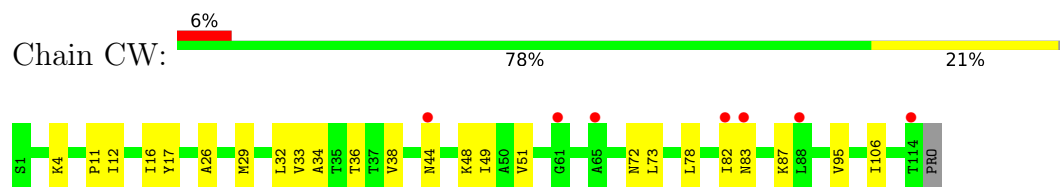
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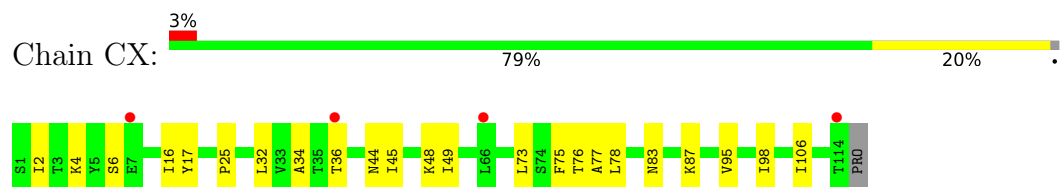
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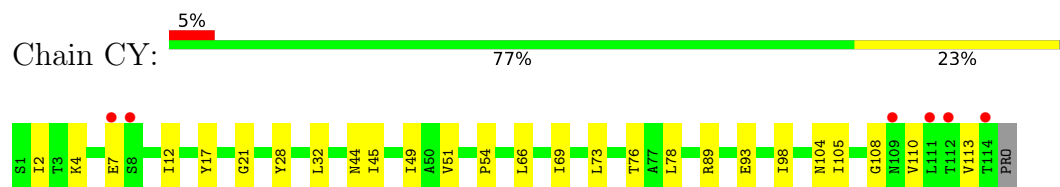
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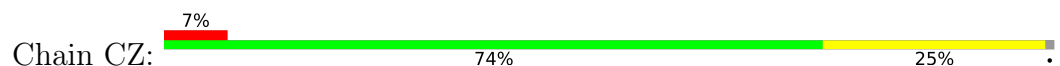
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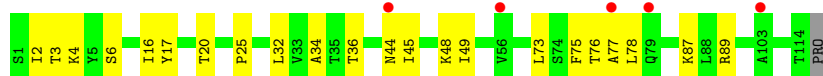
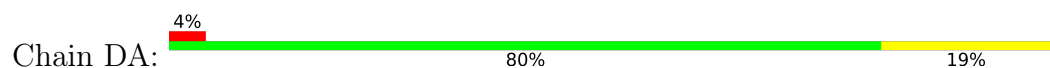


- Molecule 1: Coat protein

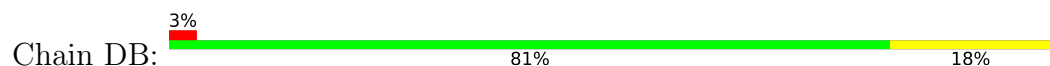




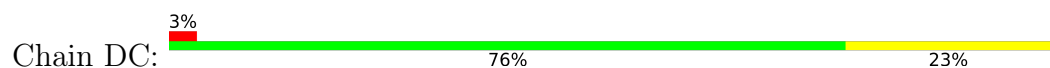
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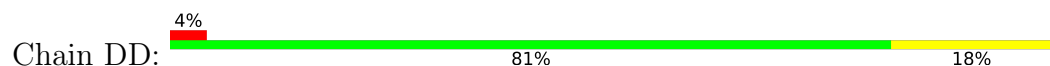
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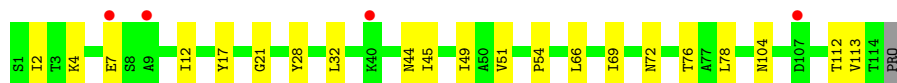
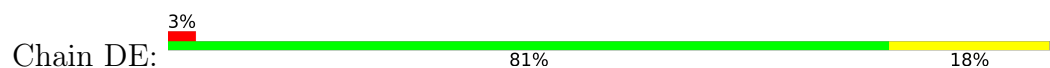
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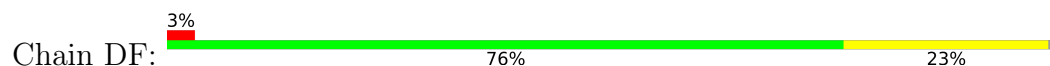
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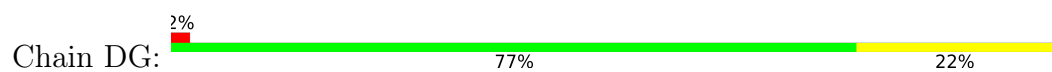
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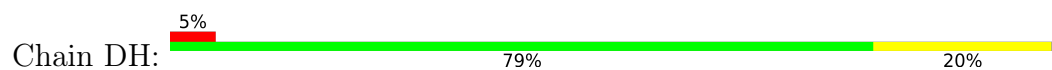
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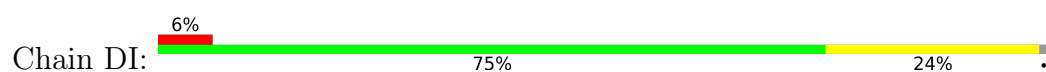
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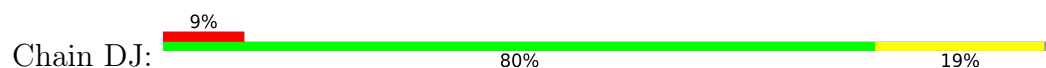
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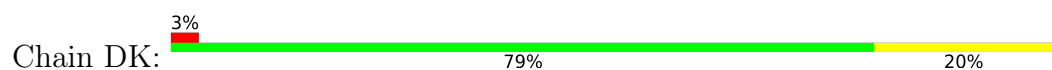
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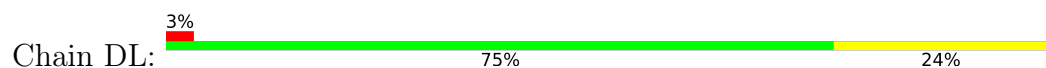
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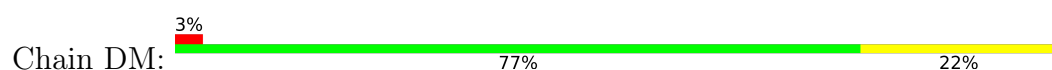
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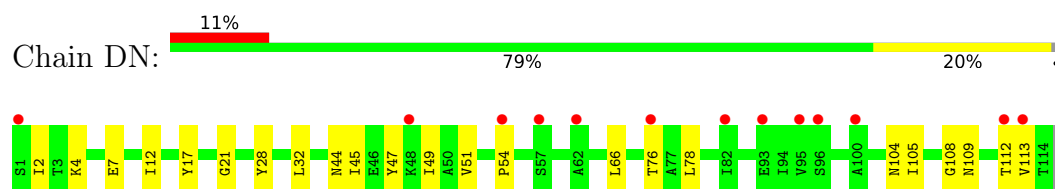
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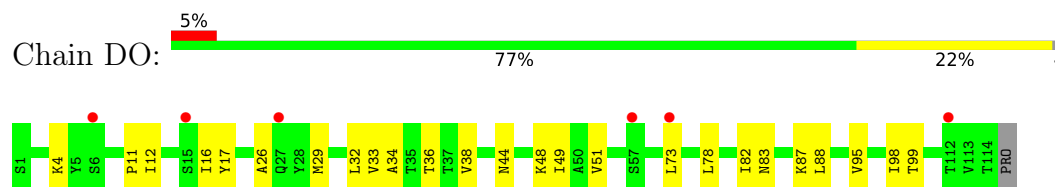
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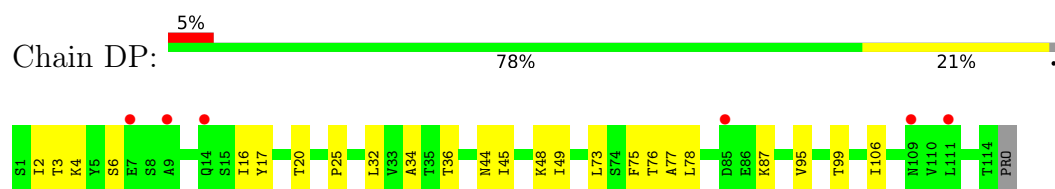
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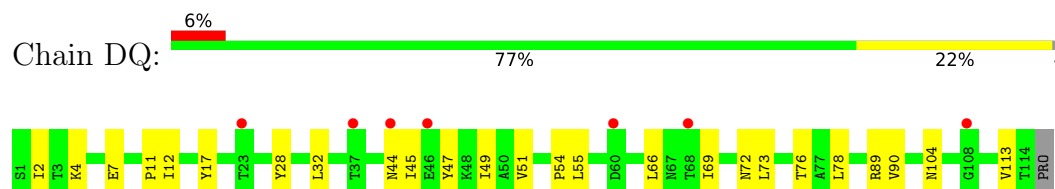
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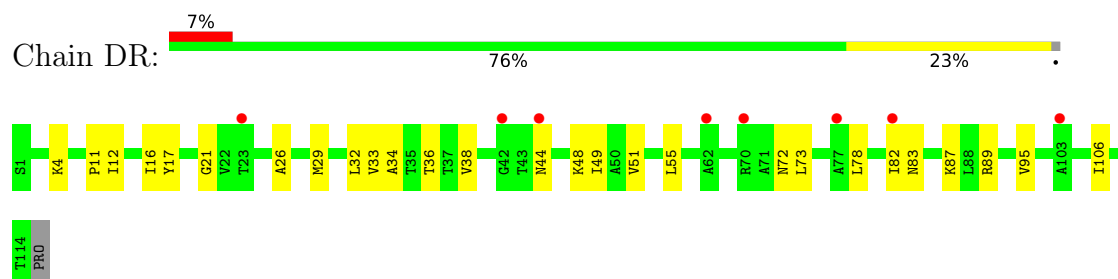
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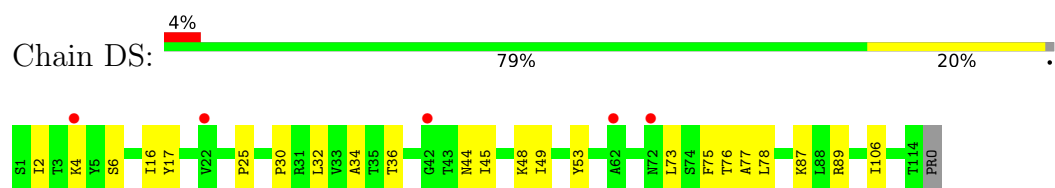
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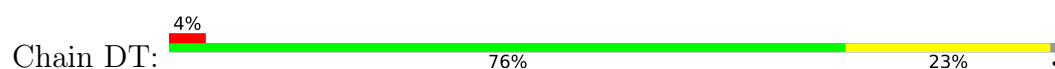
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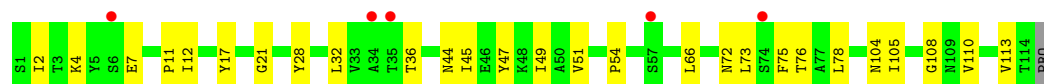


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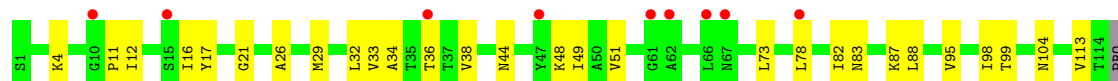
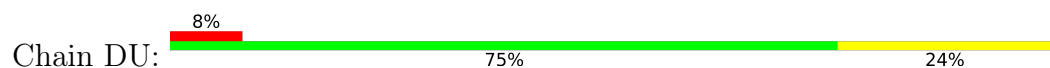


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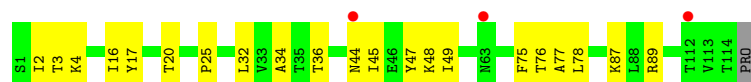
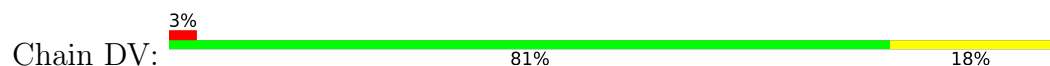




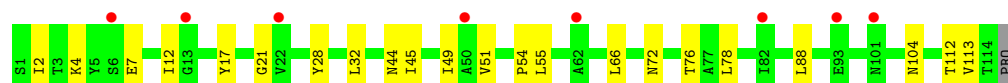
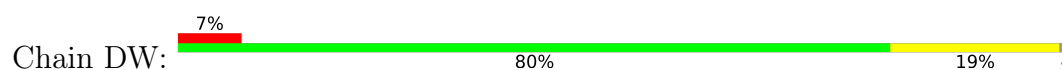
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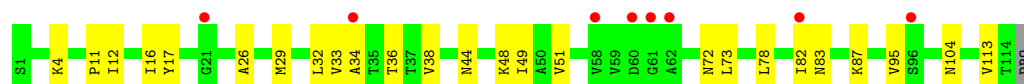
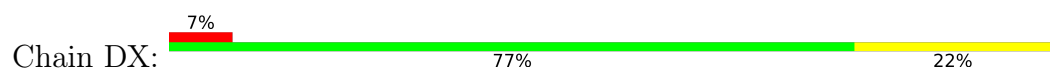
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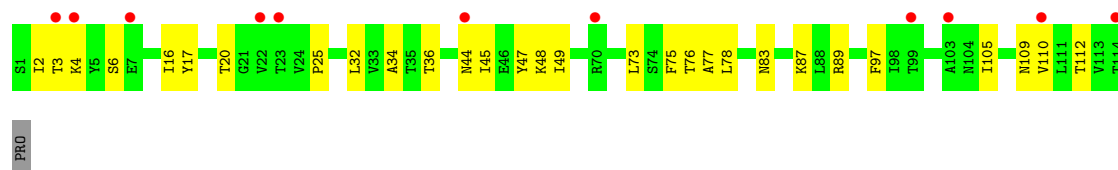
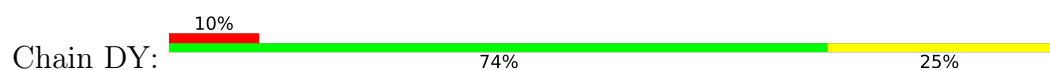
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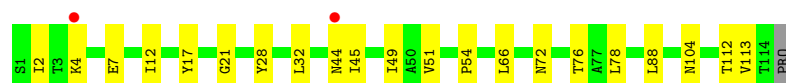
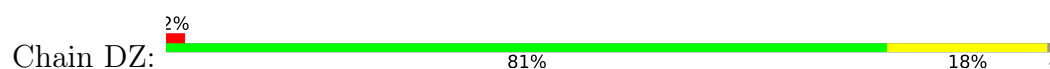
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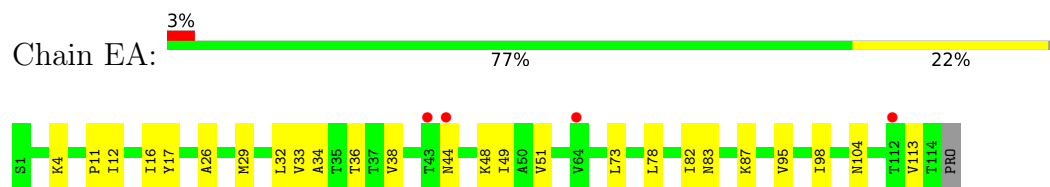
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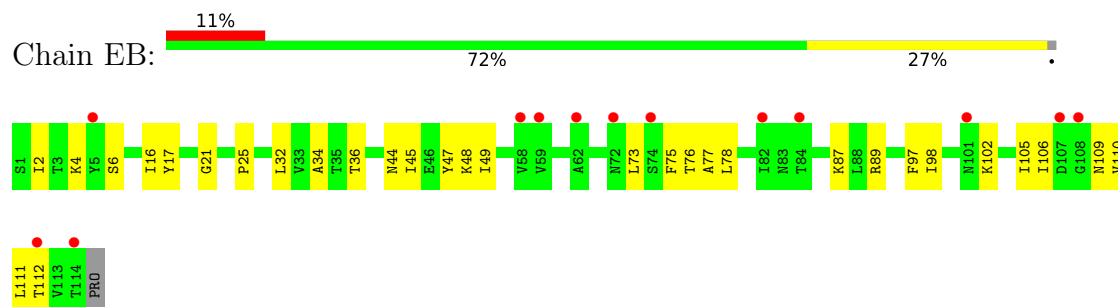
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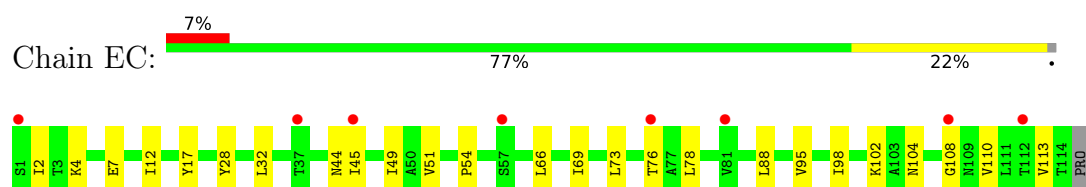
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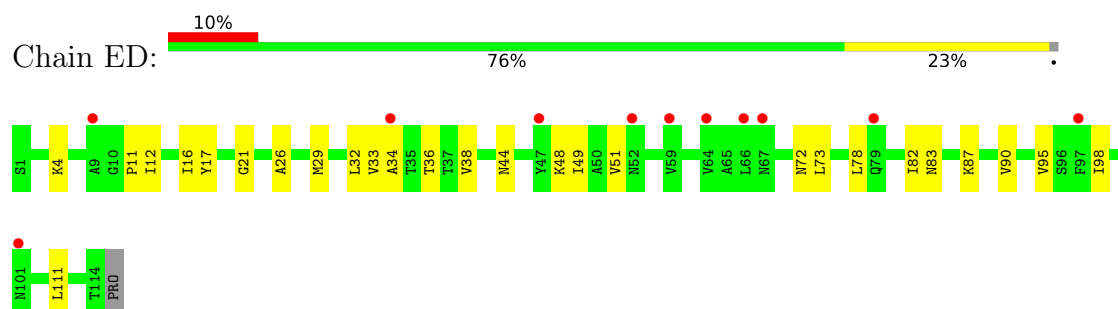
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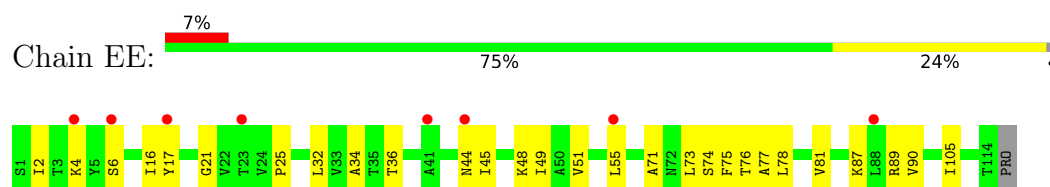
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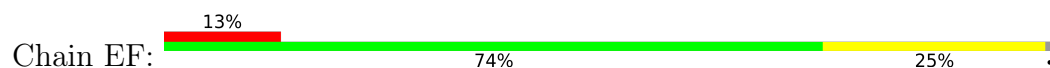
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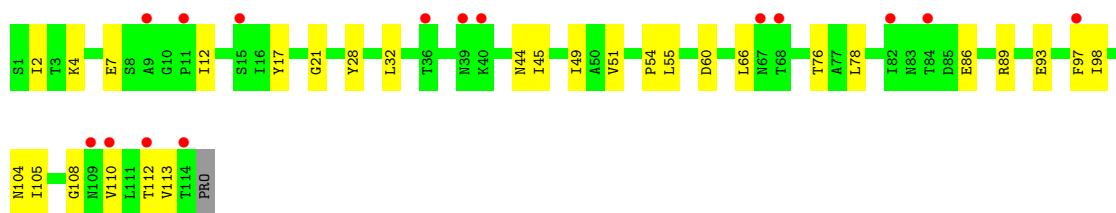


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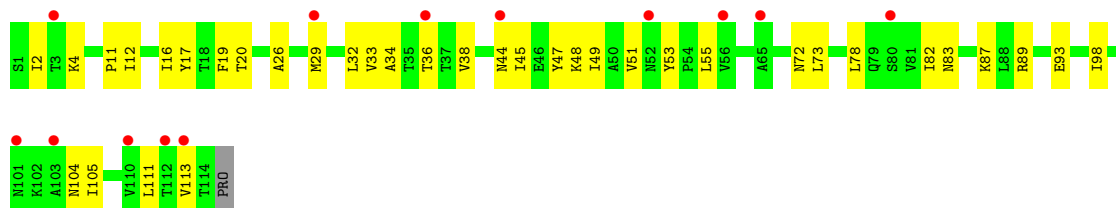


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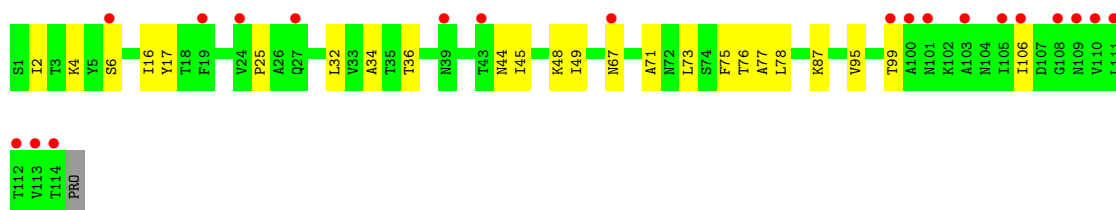
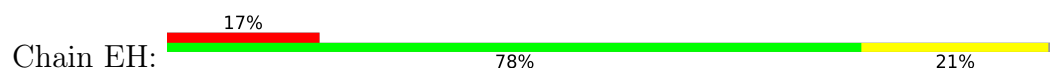




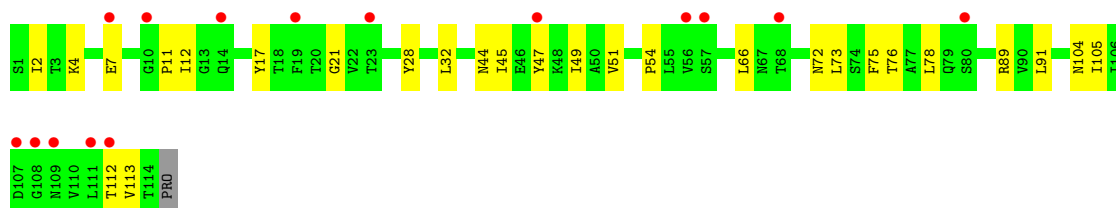
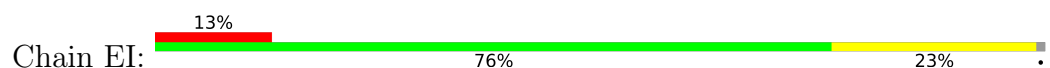
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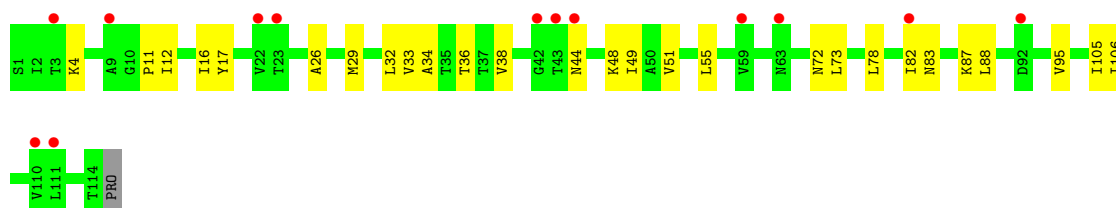
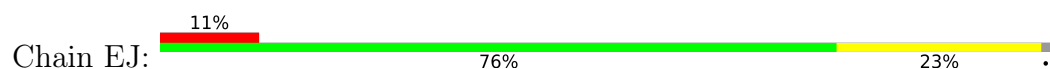
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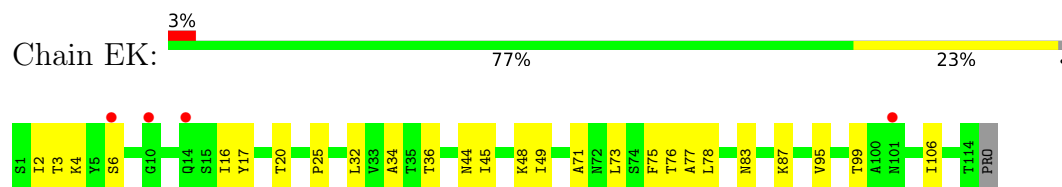
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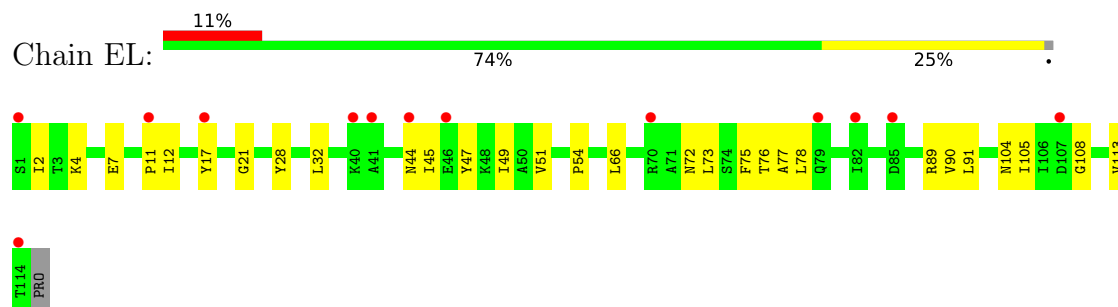
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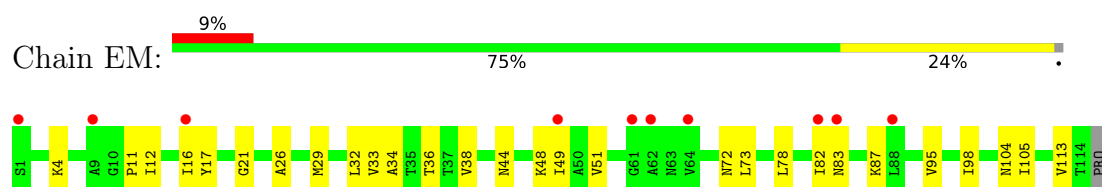
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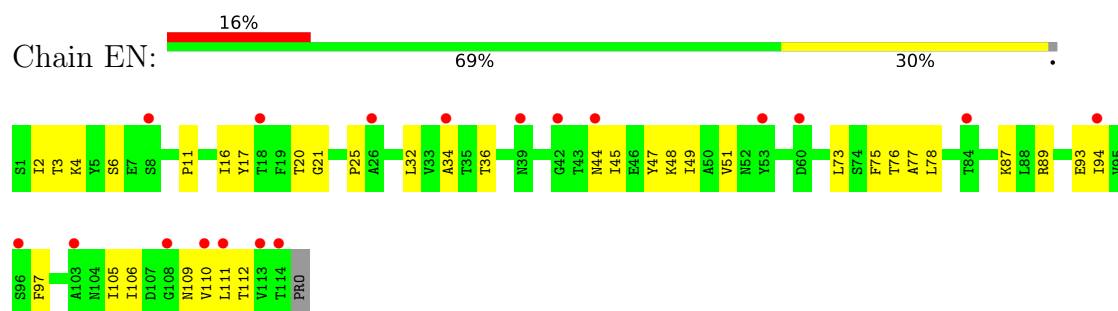
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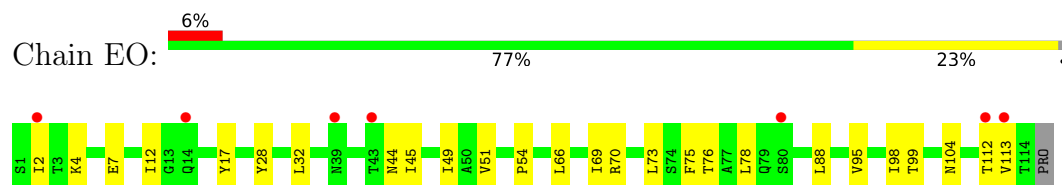
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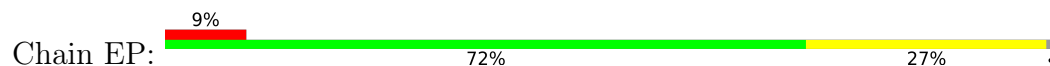
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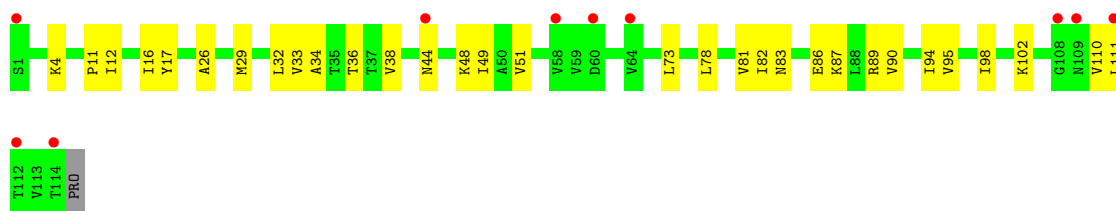


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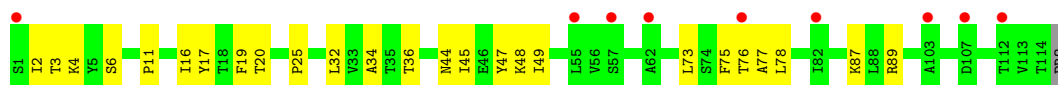
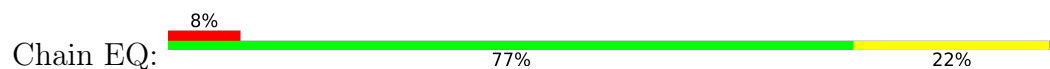


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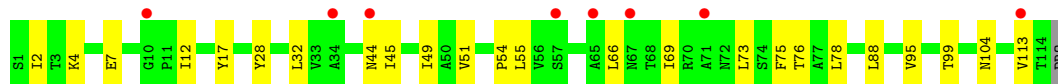
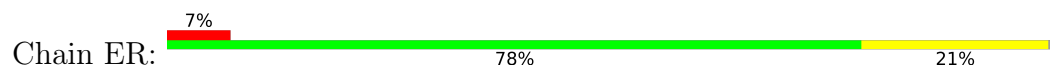




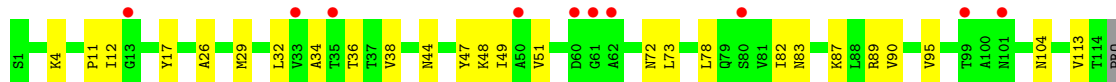
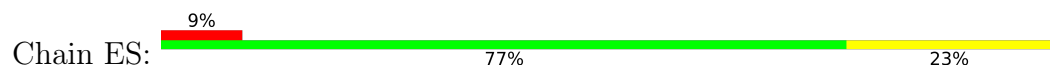
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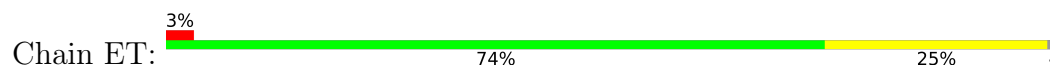
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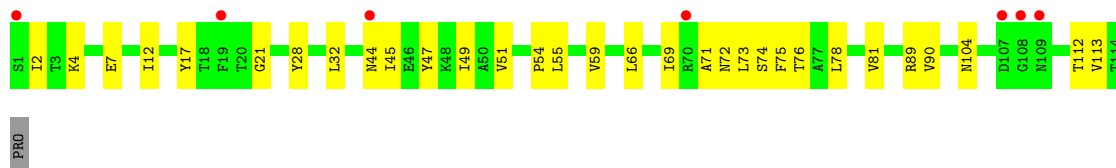
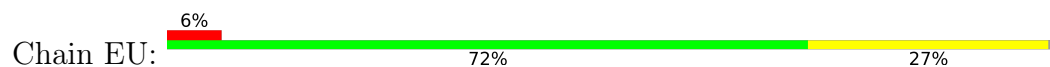
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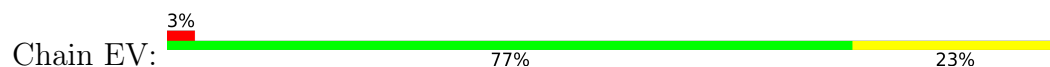
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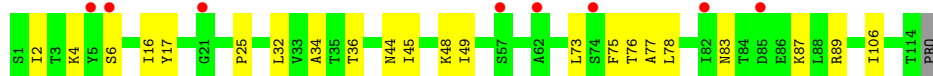
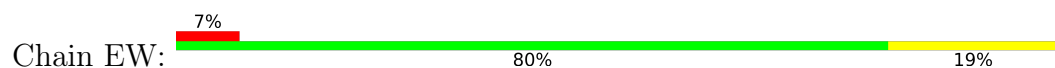


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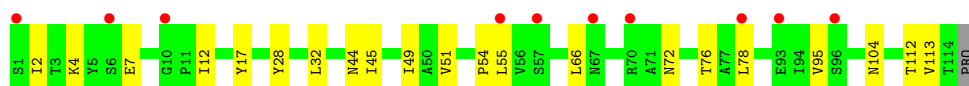
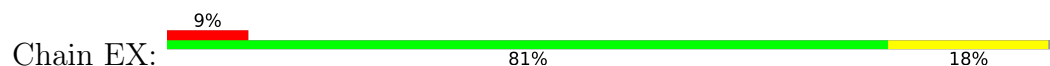




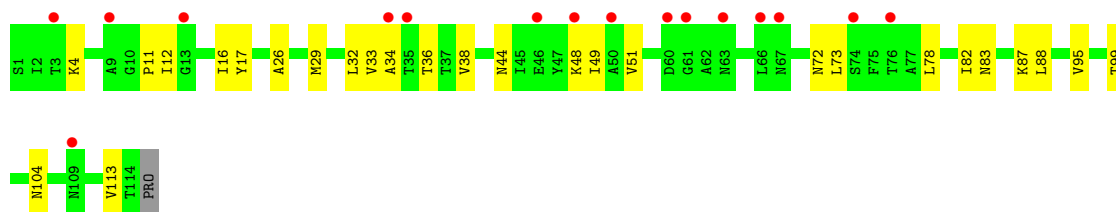
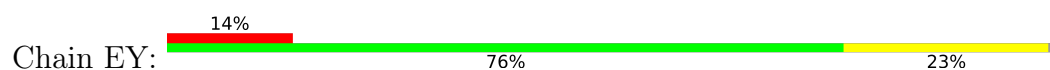
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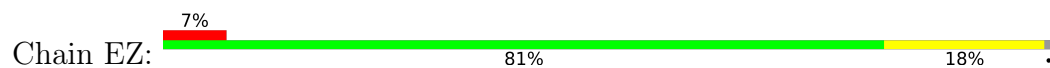
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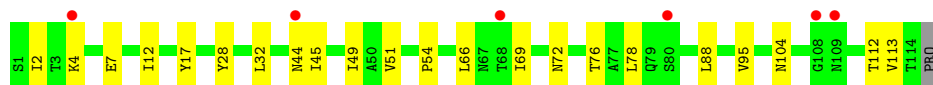
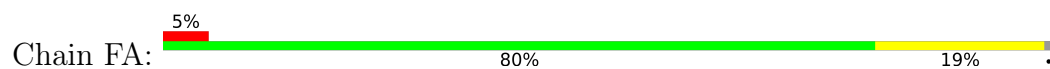
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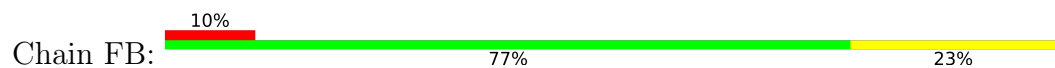
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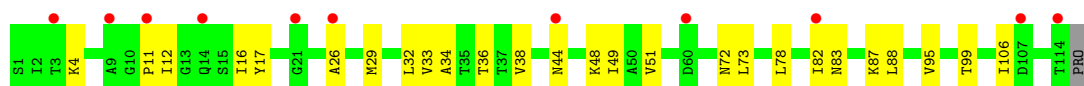


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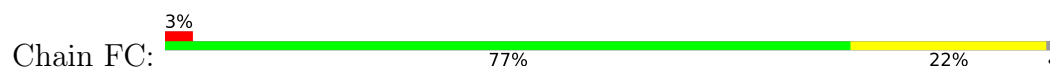


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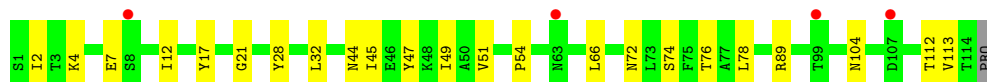
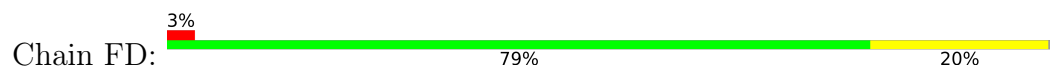




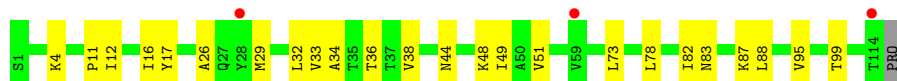
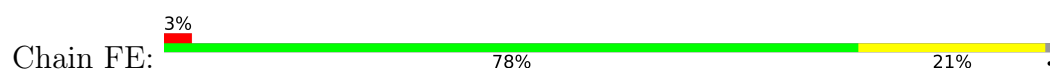
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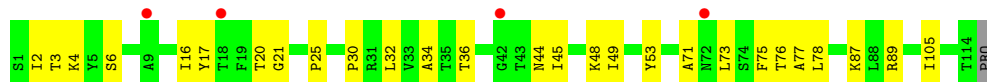
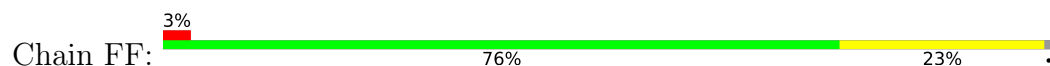
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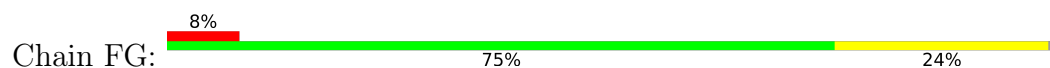
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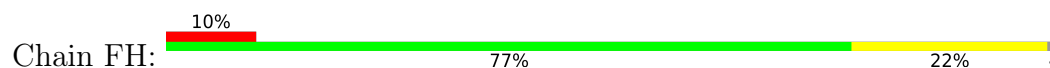
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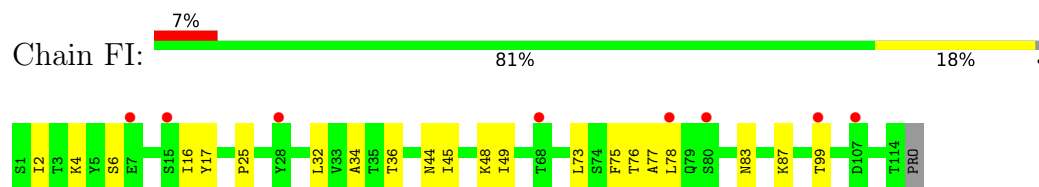
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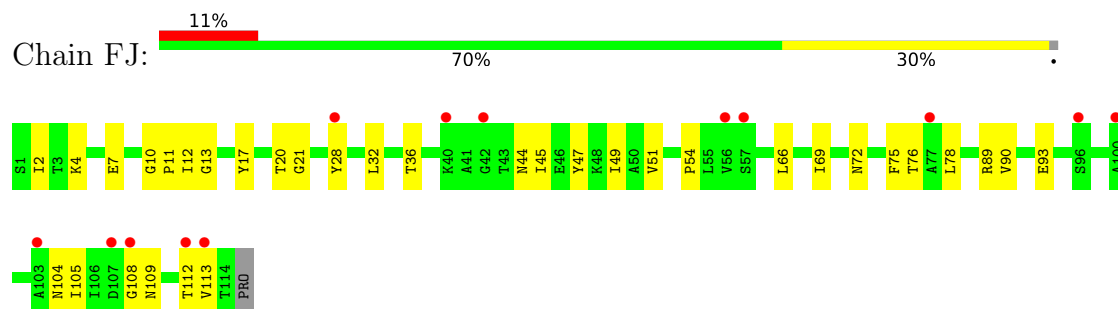
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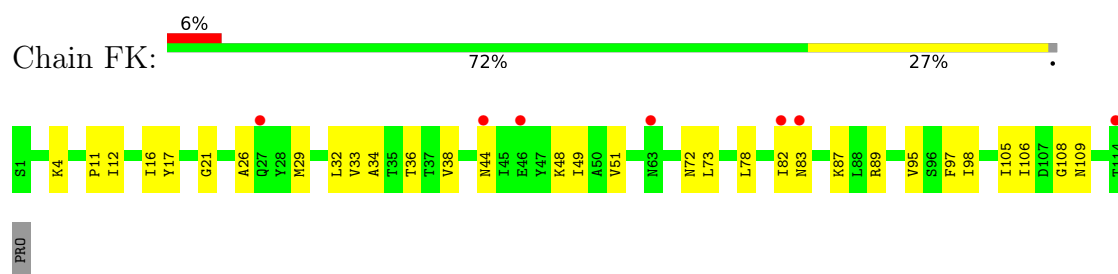
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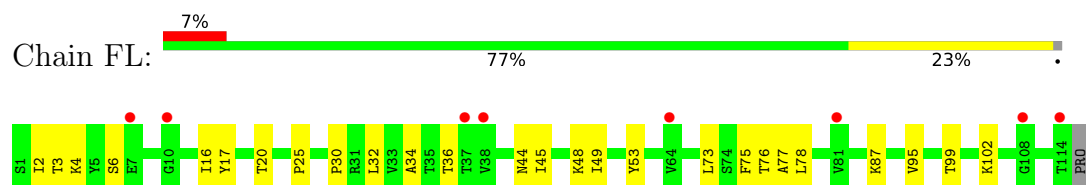
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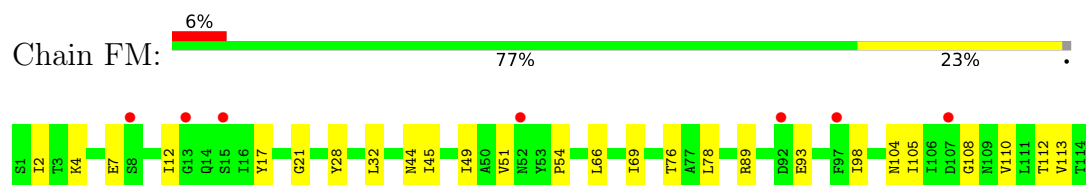
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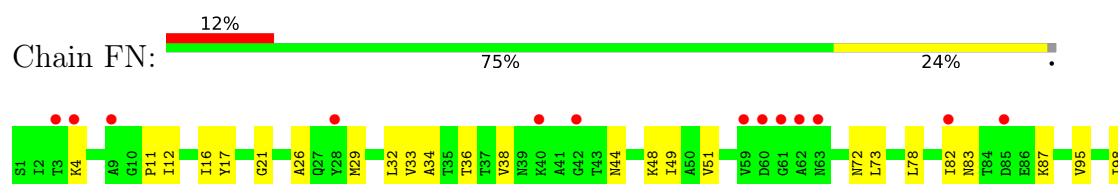
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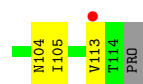


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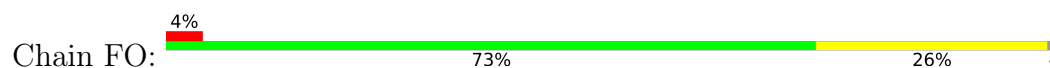


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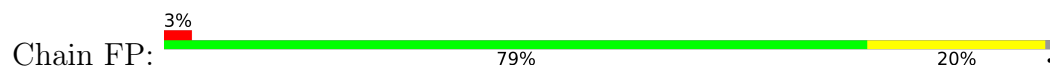




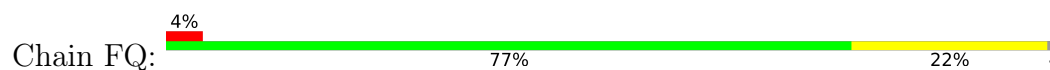
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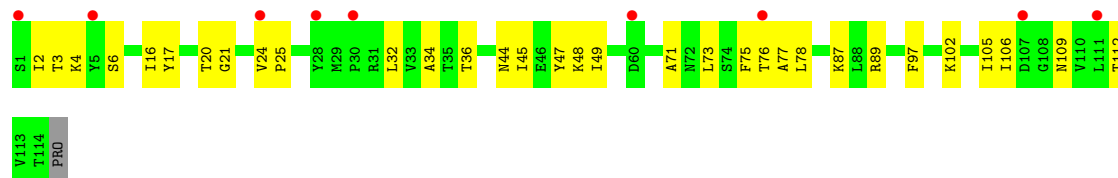
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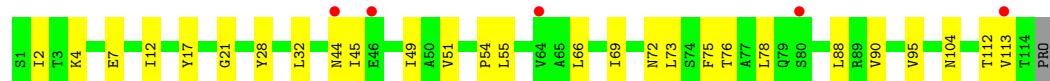
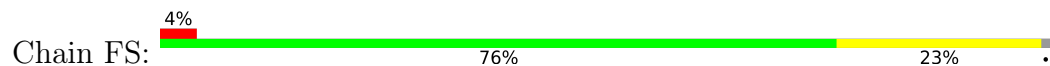
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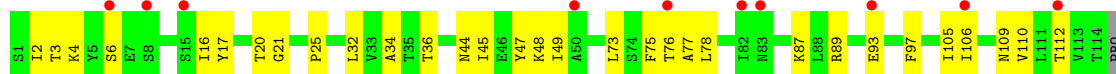
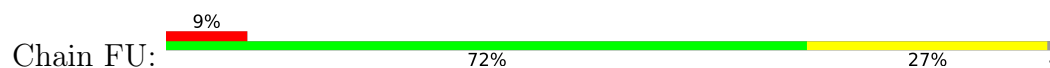


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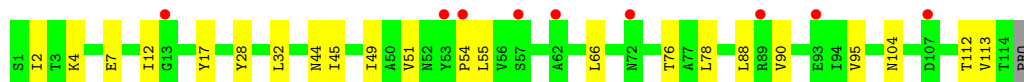
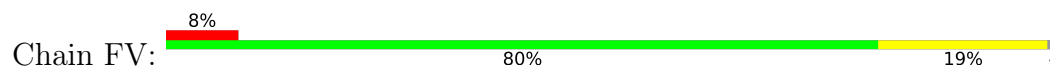




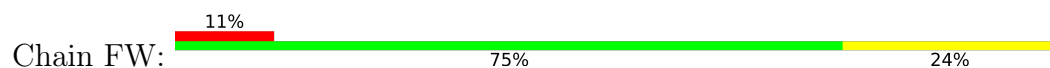
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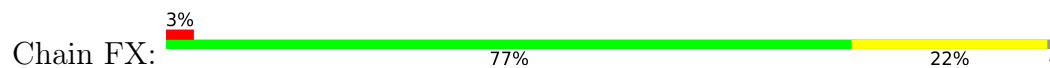
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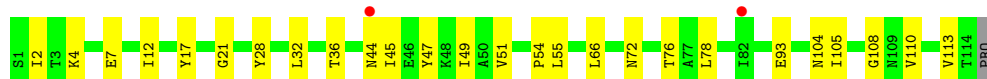
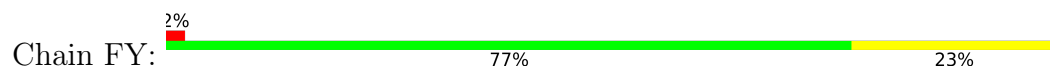
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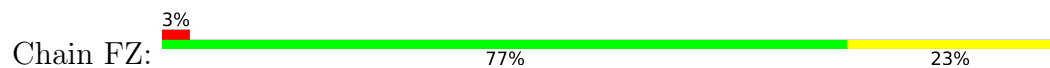
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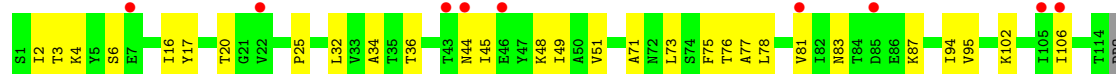
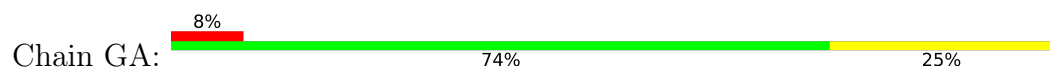


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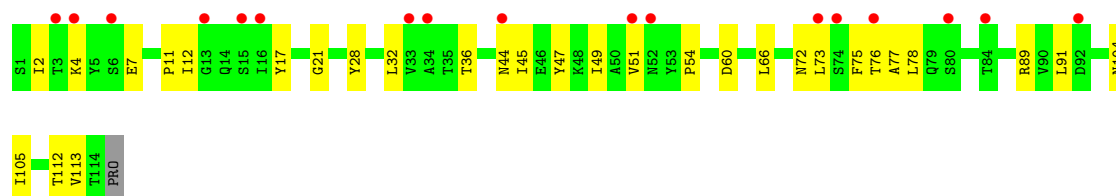
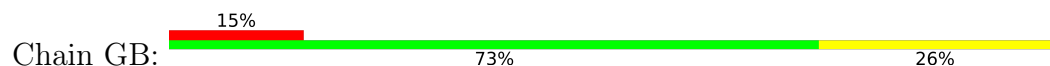




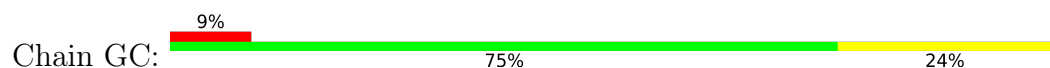
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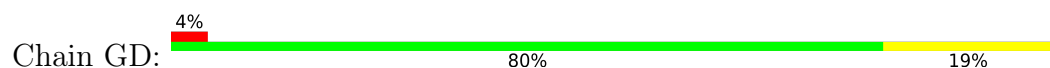
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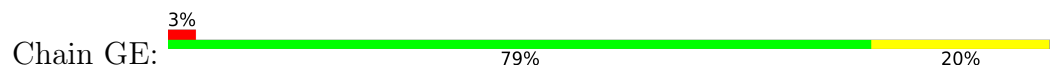
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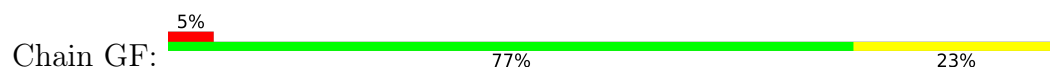
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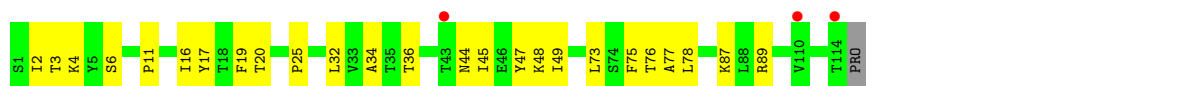
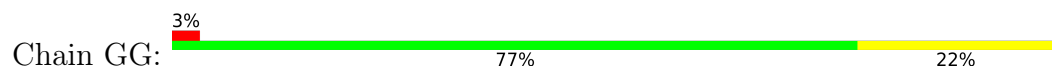
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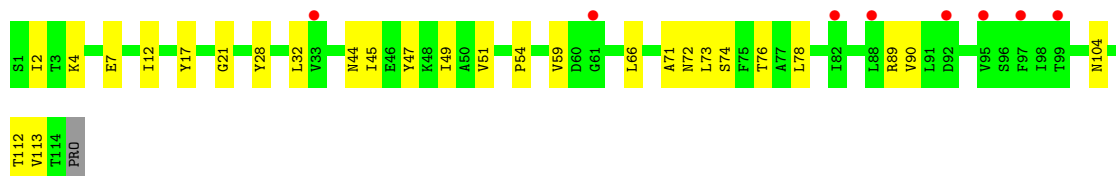
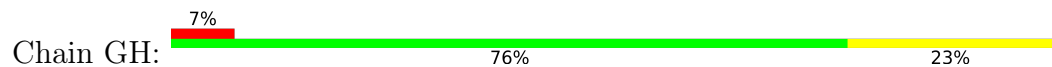
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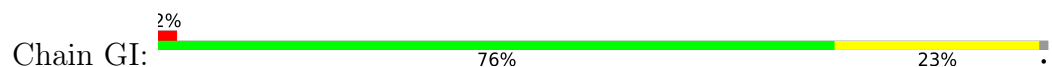
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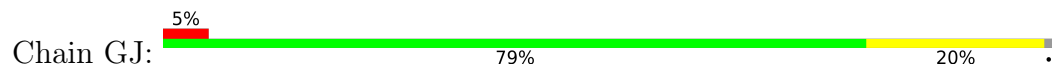
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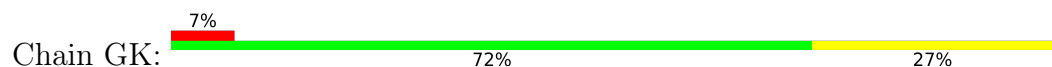
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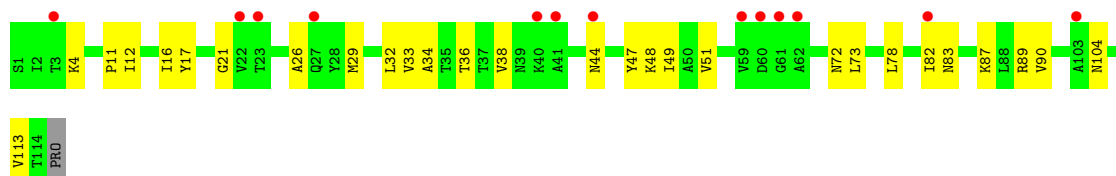
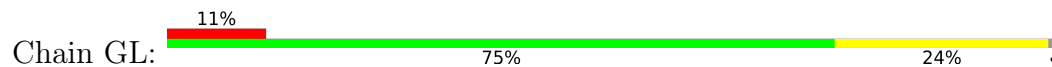
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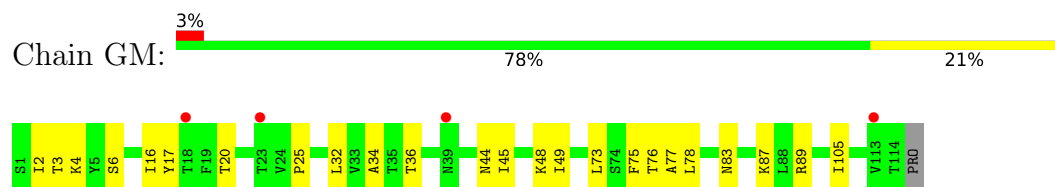
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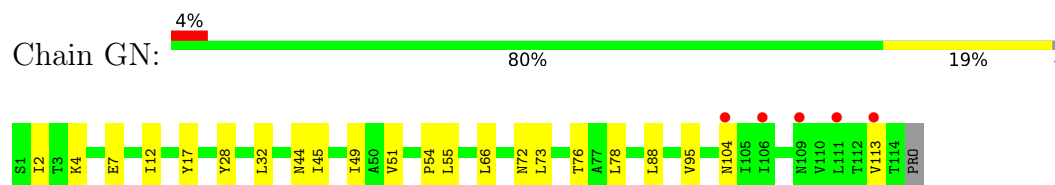
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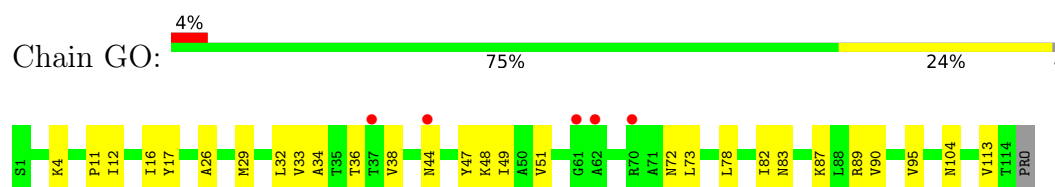
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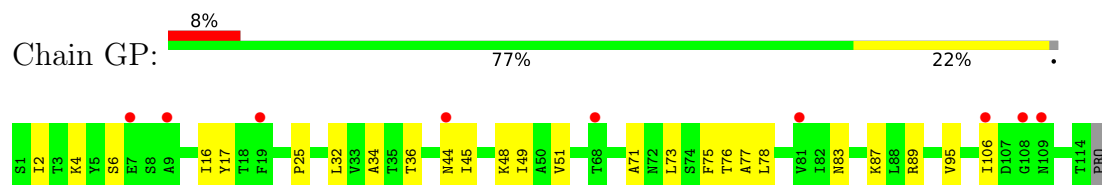
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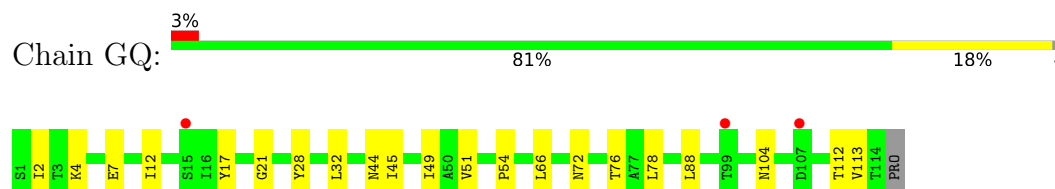
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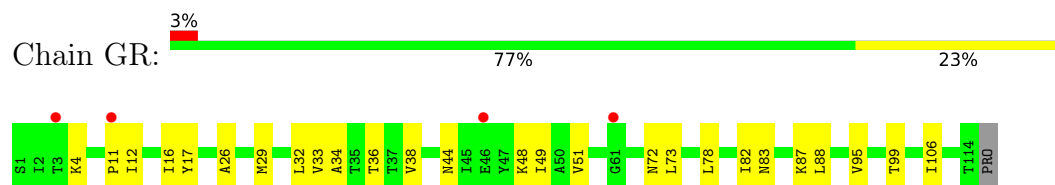
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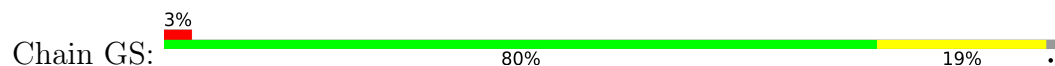
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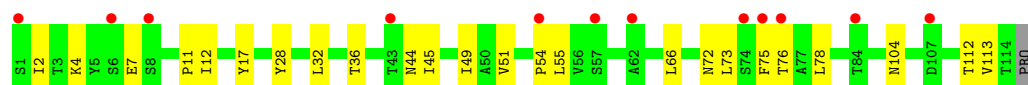
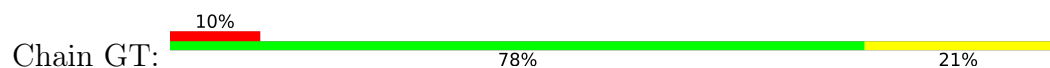


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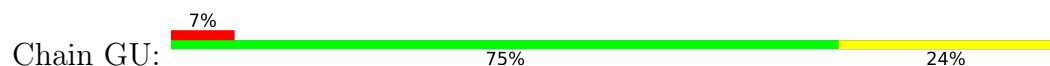




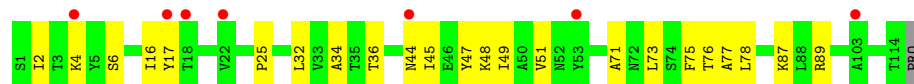
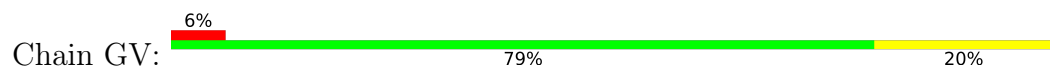
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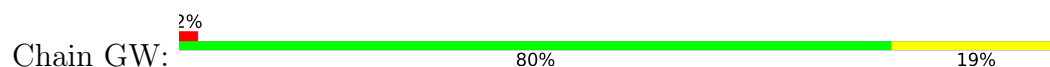
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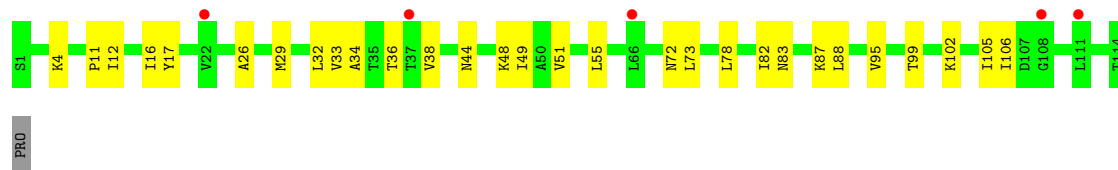
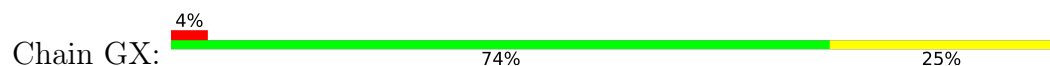
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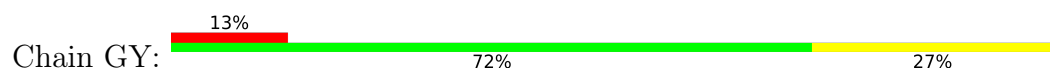
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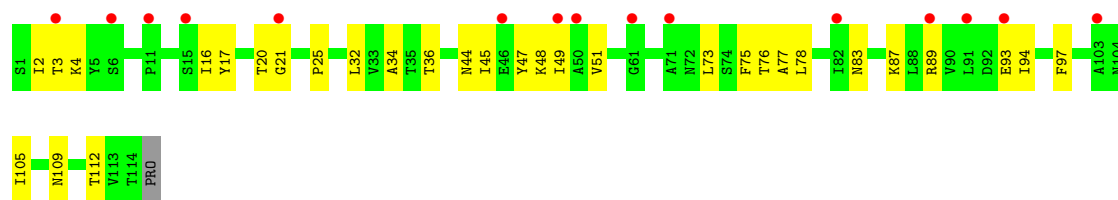


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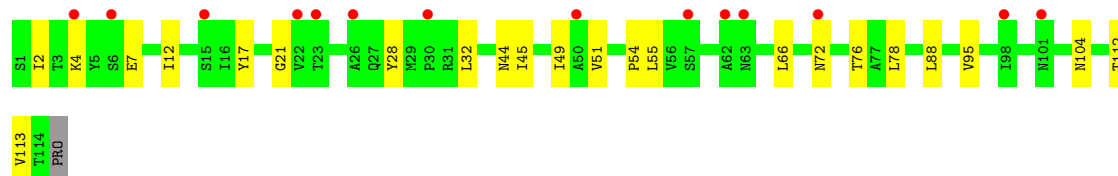
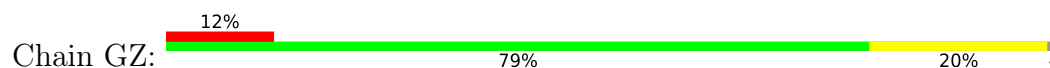


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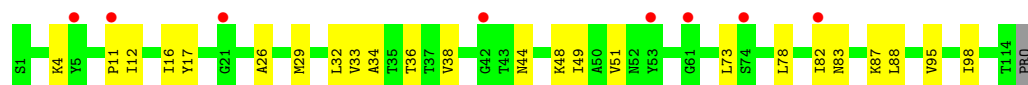
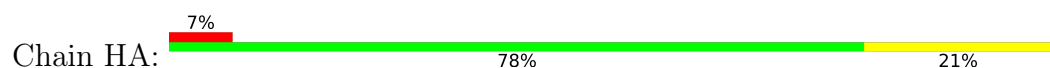




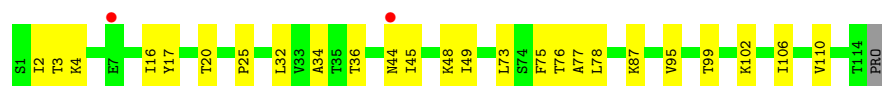
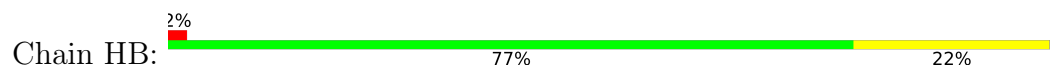
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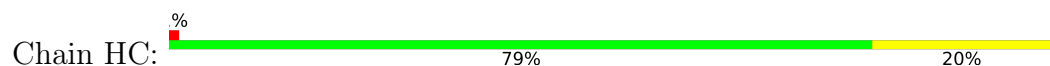
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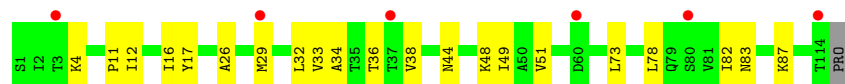
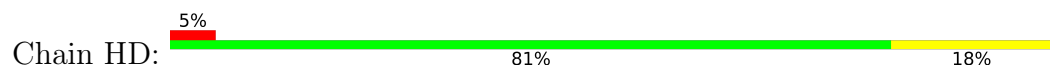
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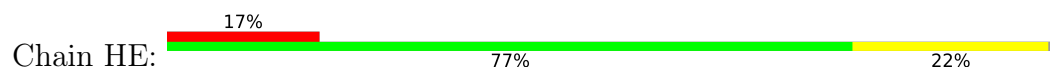
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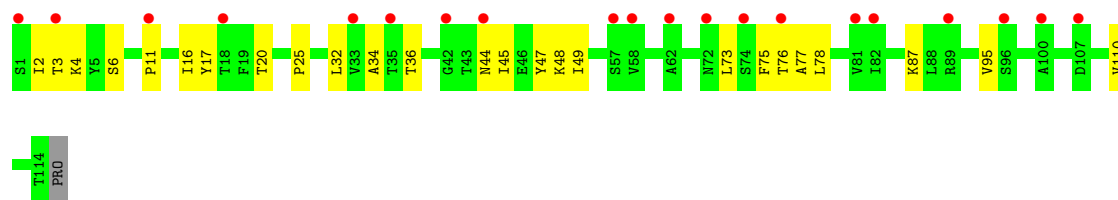


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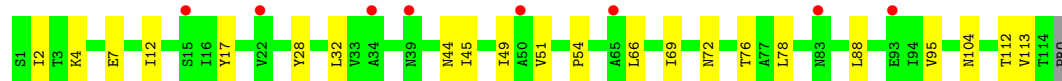
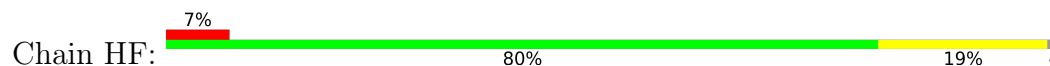


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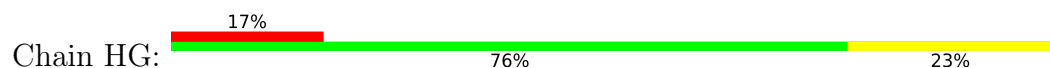




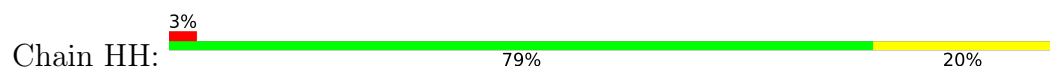
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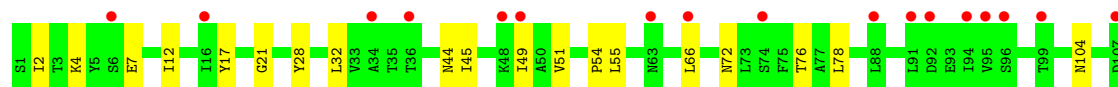
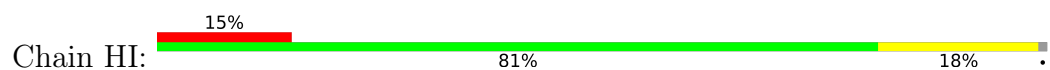
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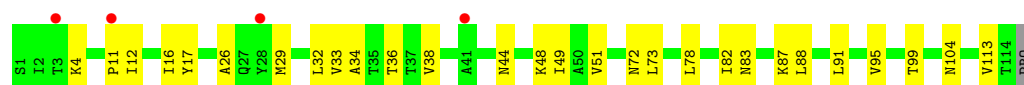
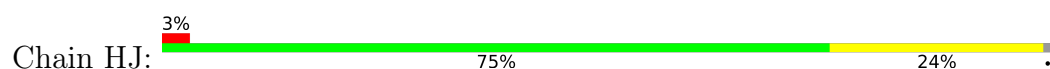
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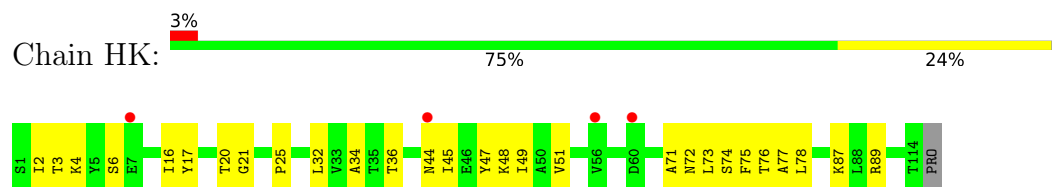
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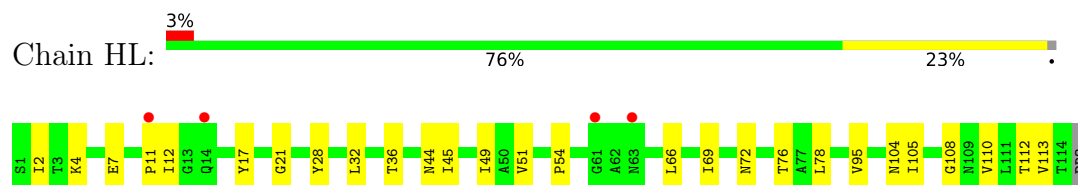
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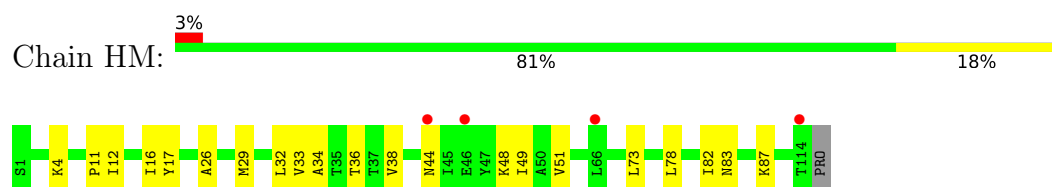
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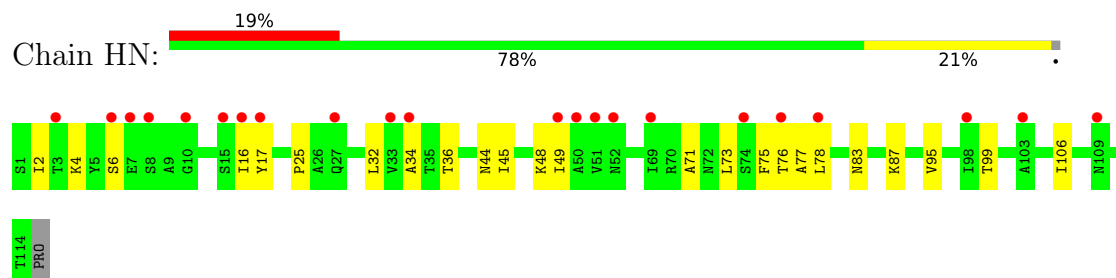
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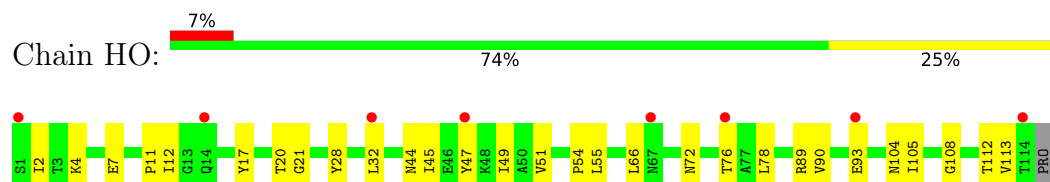
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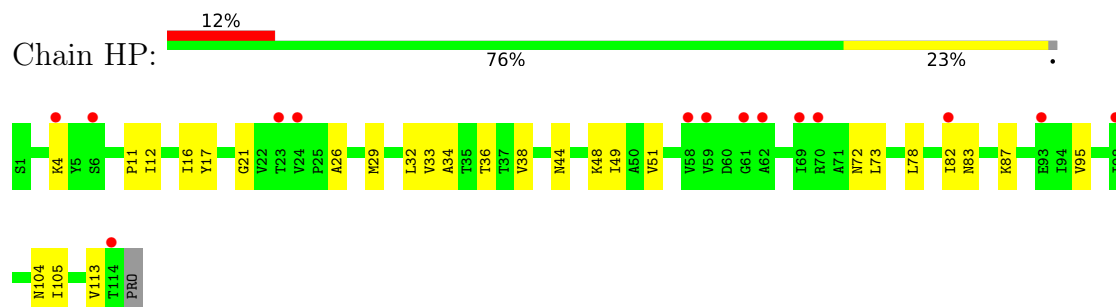
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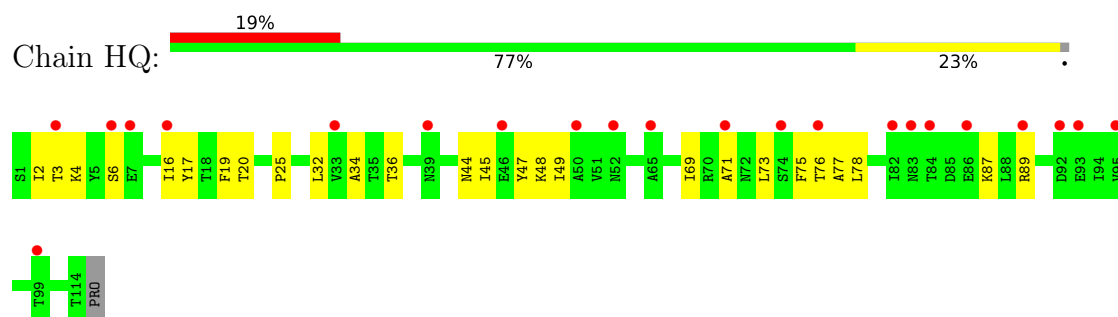
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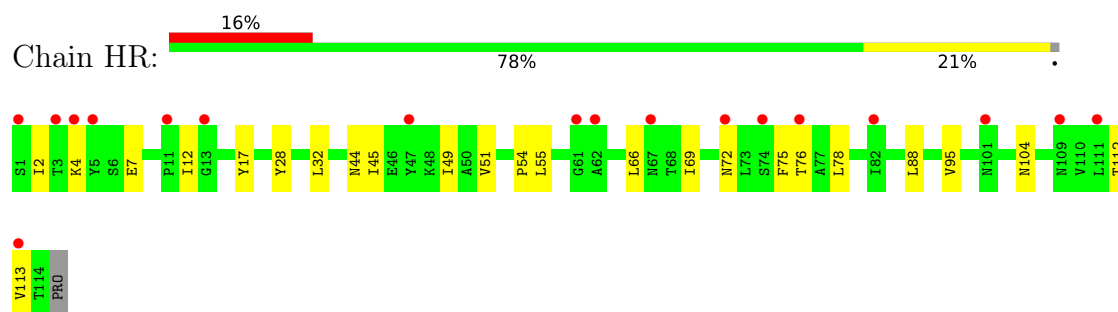
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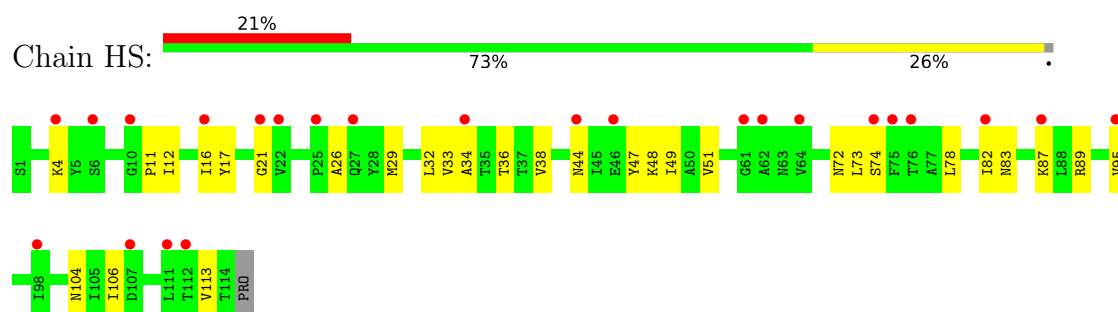
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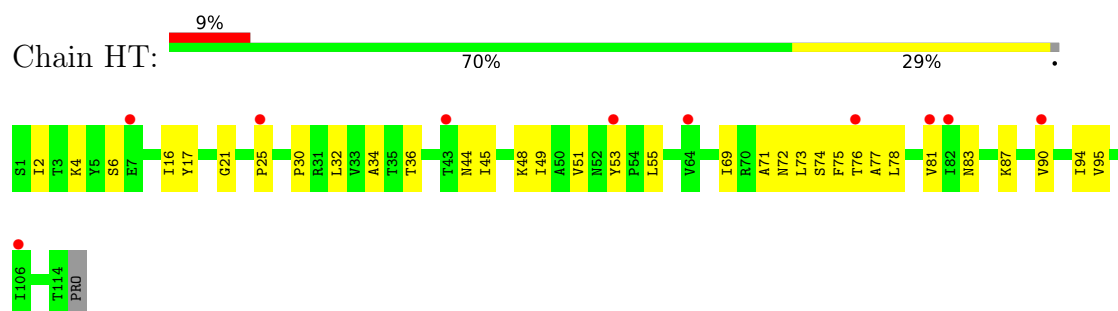
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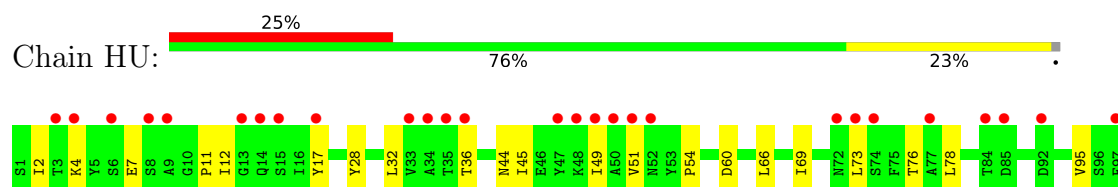
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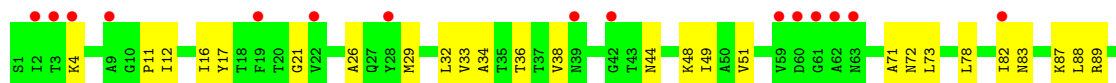
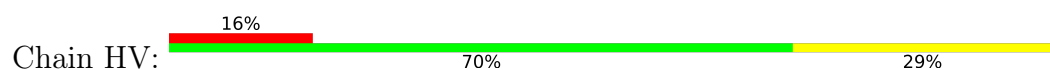


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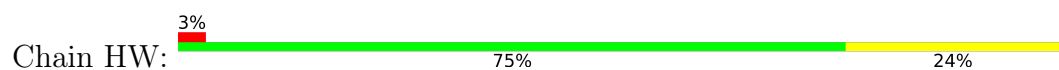




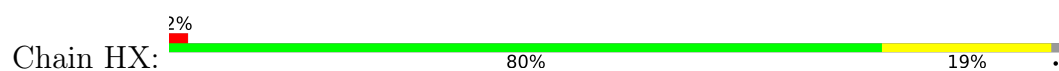
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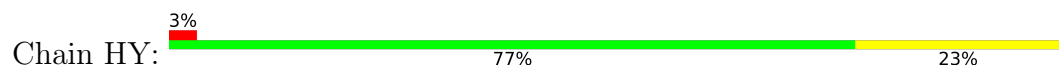
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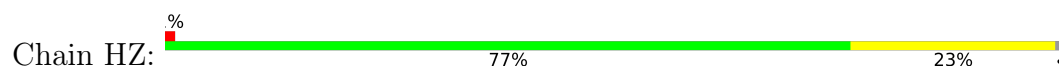
- Molecule 1: Coat protein



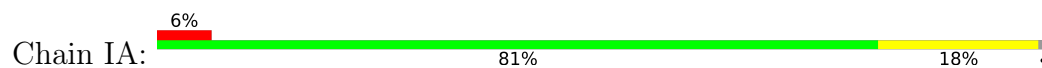
- Molecule 1: Coat protein



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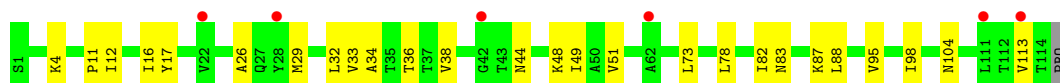
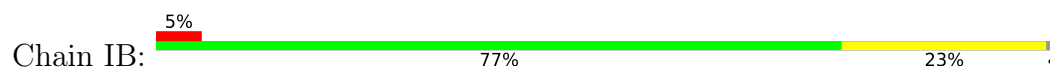


- Molecule 1: Coat protein

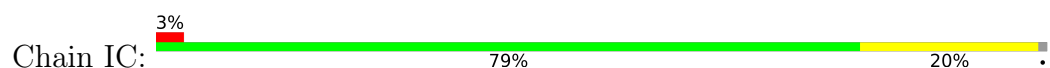




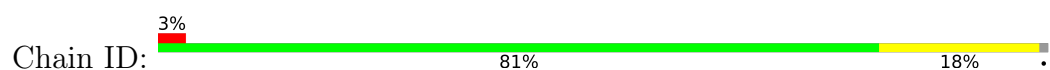
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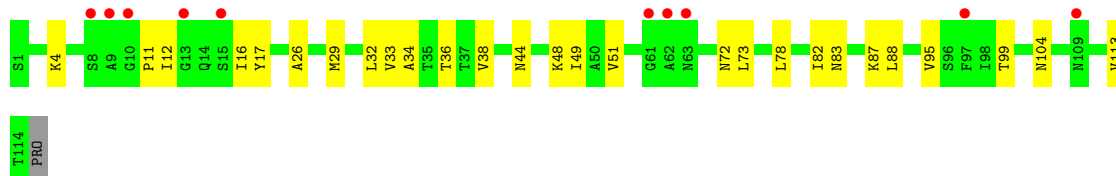
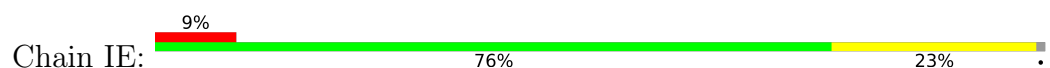
- Molecule 1: Coat protein



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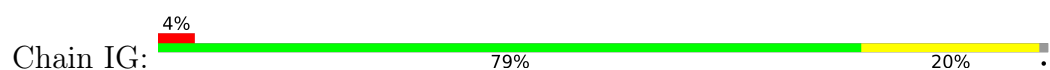
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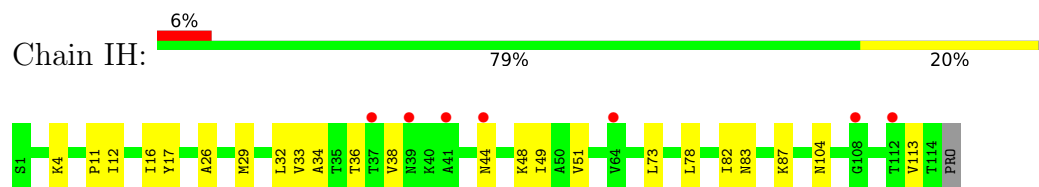
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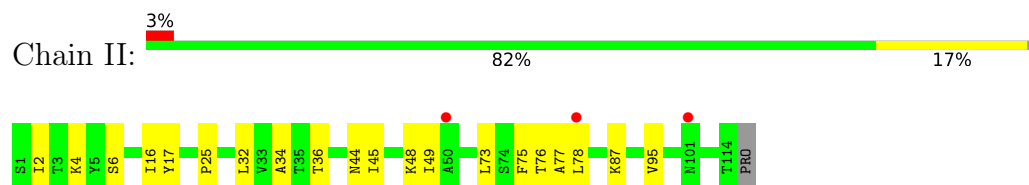
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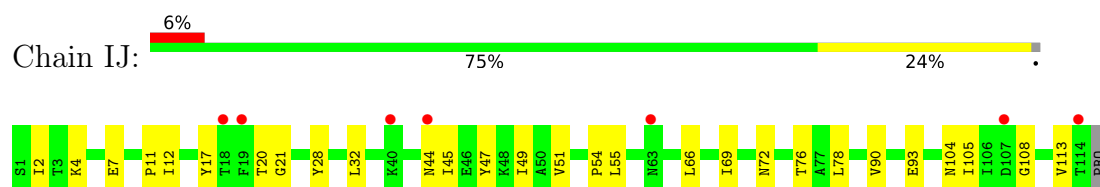
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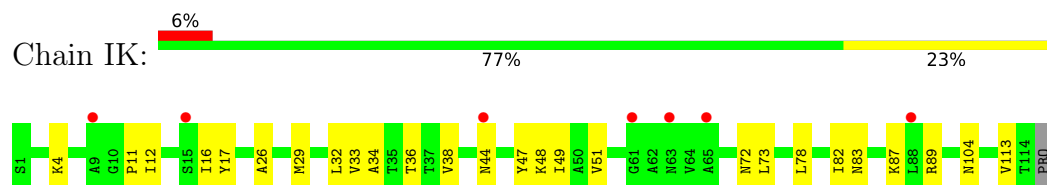
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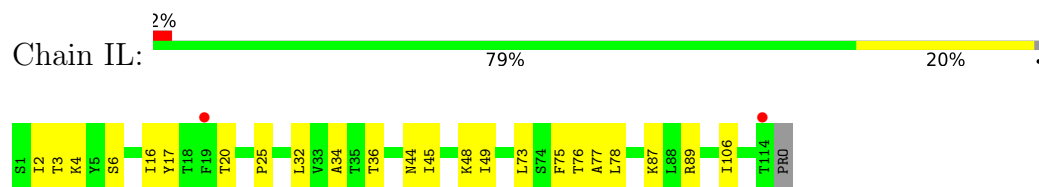
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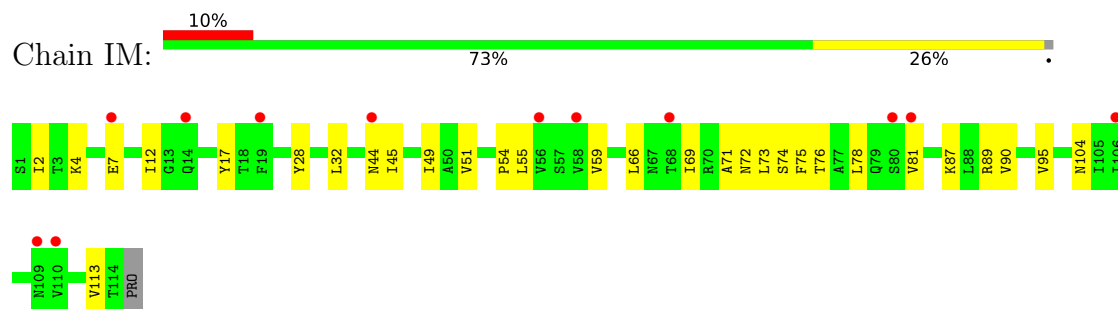
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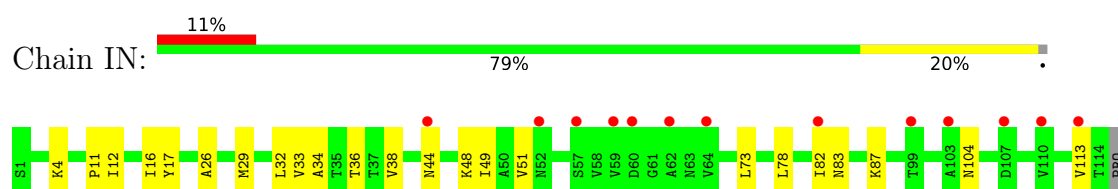
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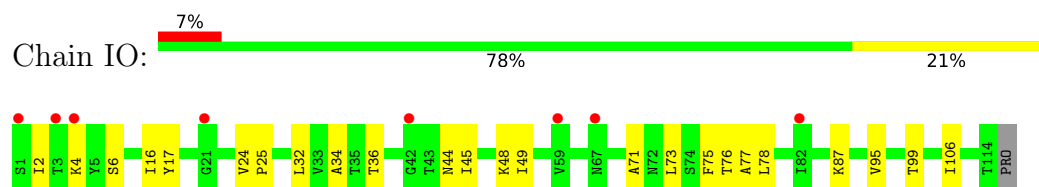
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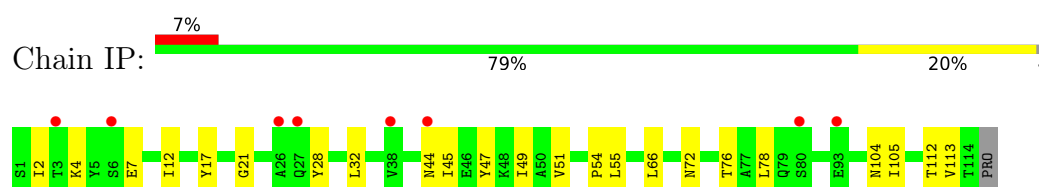
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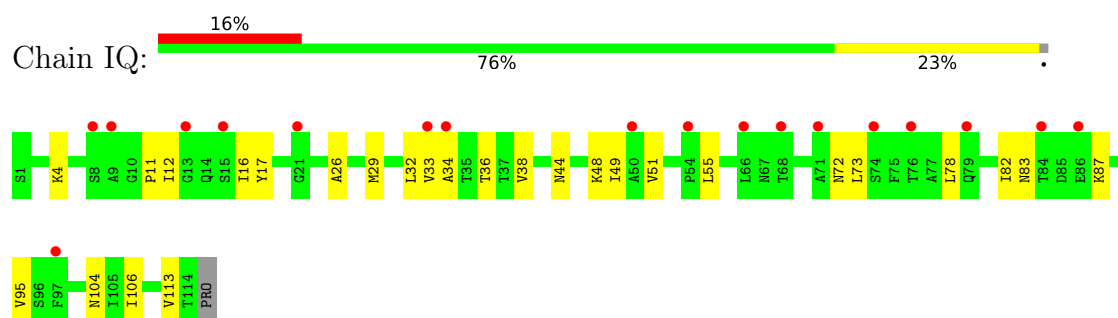
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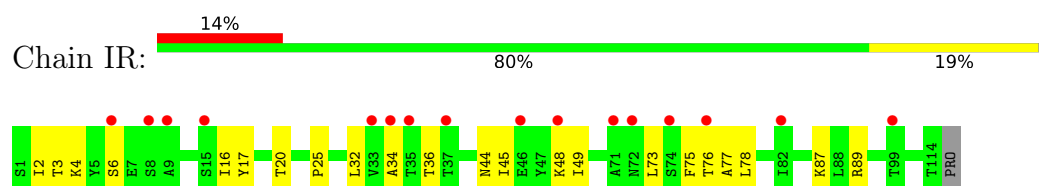
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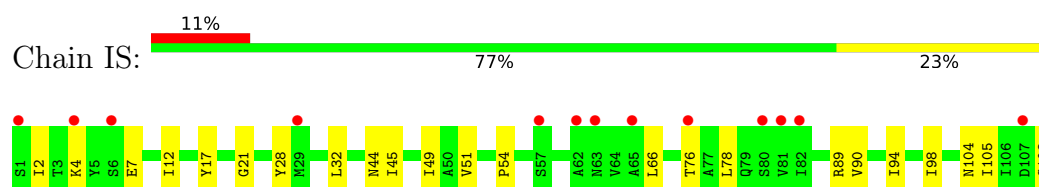
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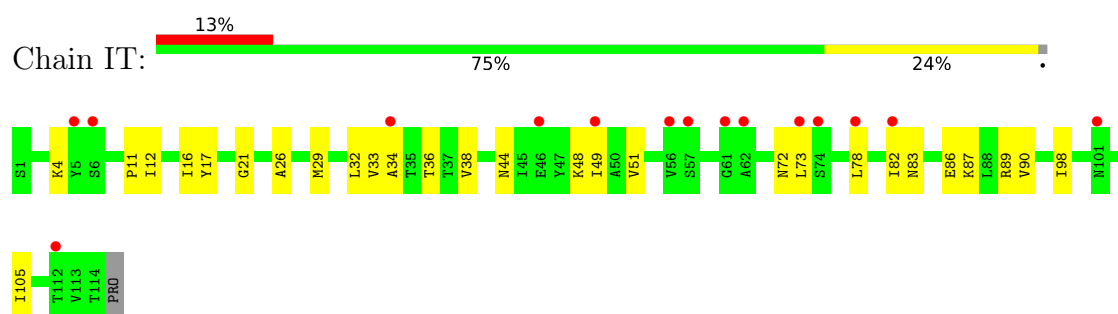


• Molecule 1: Coat protein

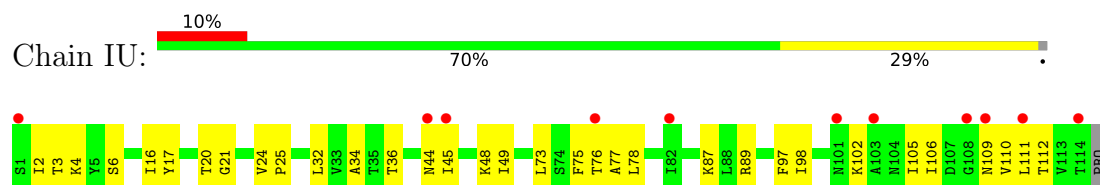


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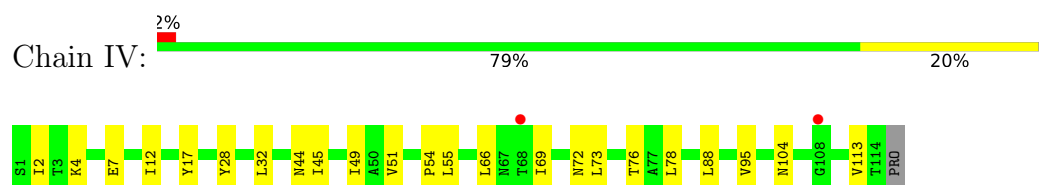
• Molecule 1: Coat protein



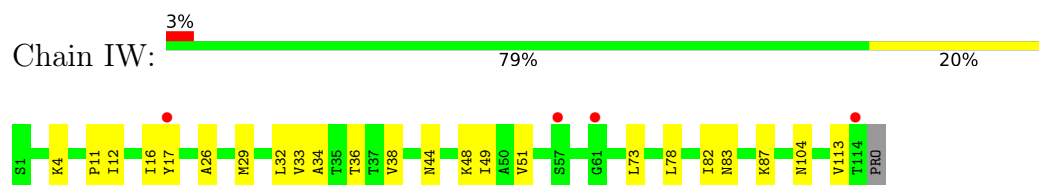
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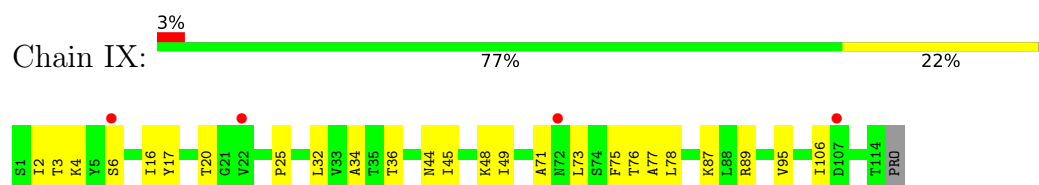
- Molecule 1: Coat protein



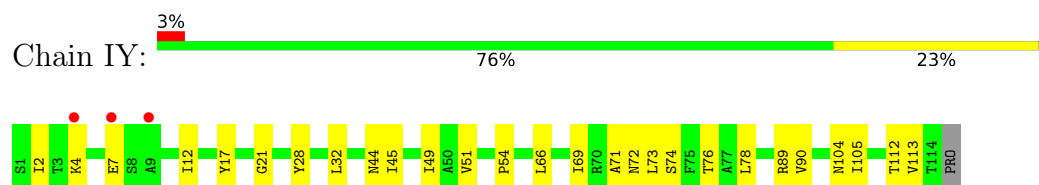
- Molecule 1: Coat protein



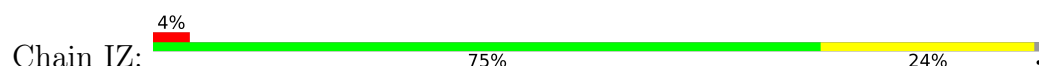
- Molecule 1: Coat protein



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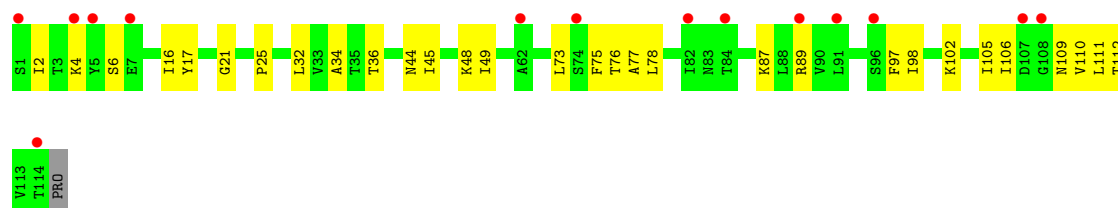
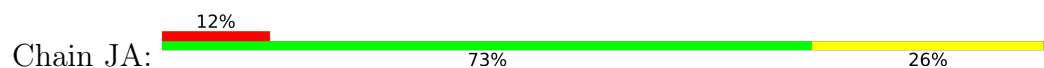


- Molecule 1: Coat protein

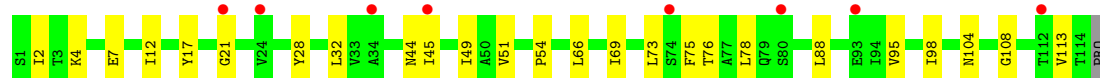
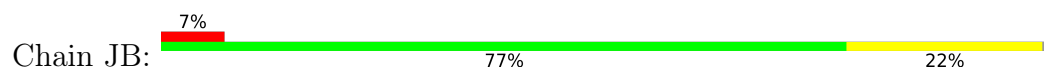




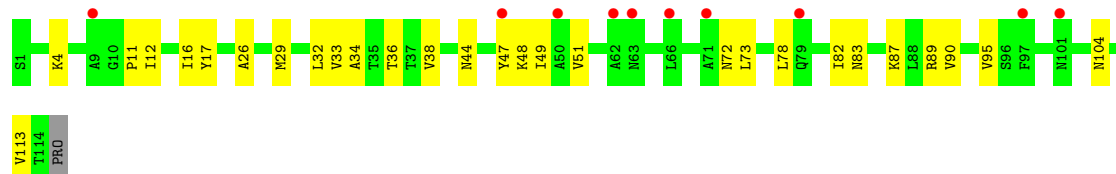
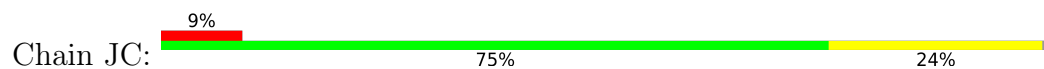
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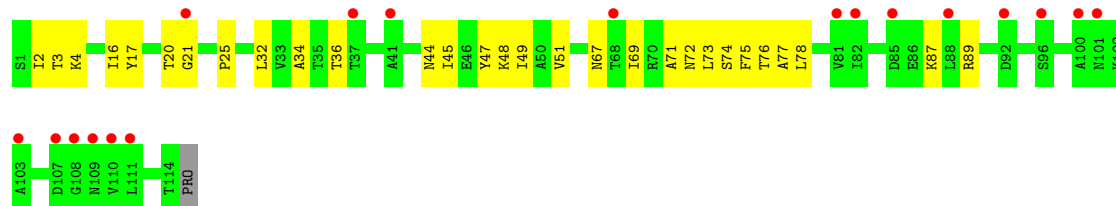
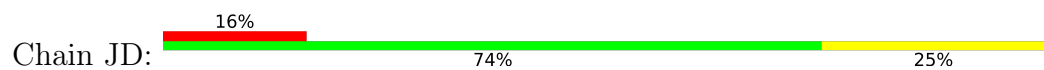
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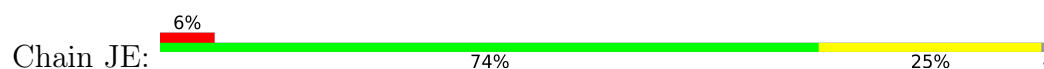
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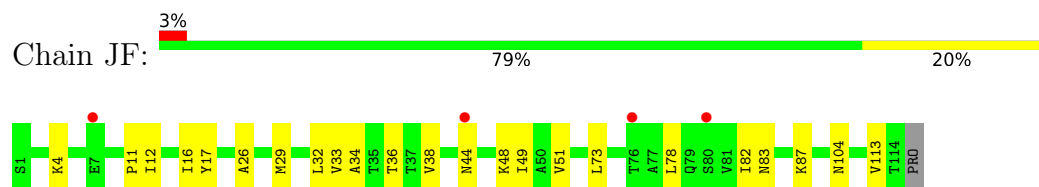
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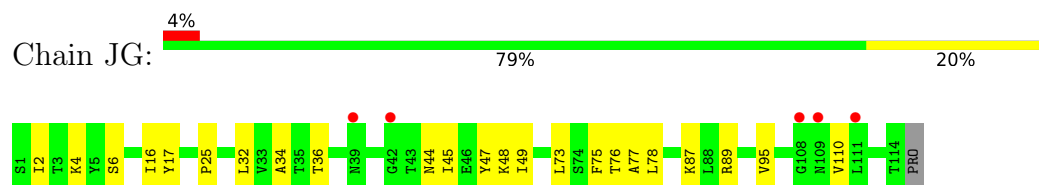
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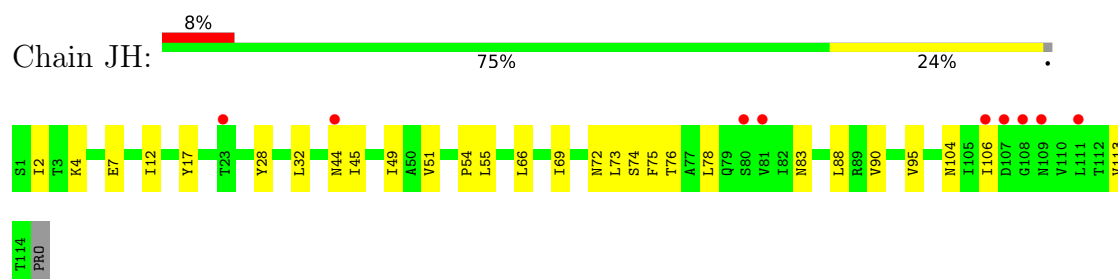
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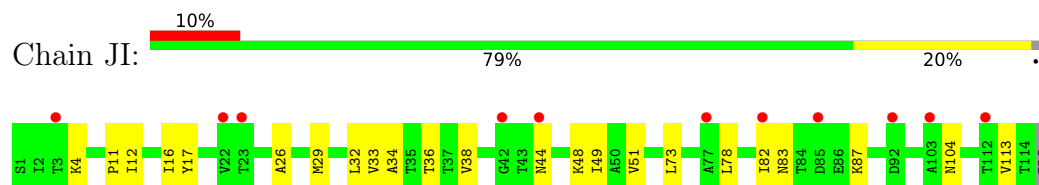
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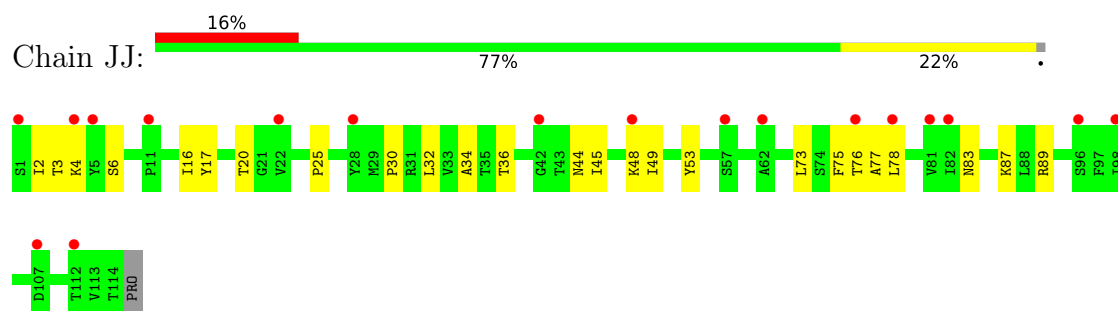
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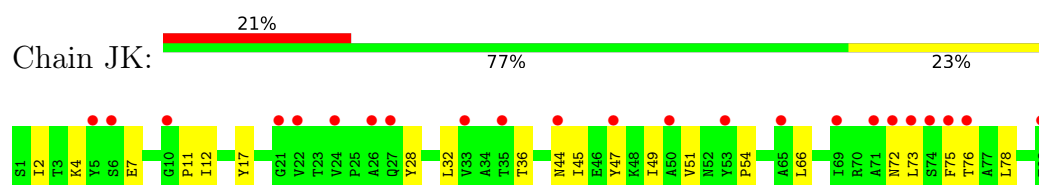
- Molecule 1: Coat protein



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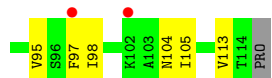
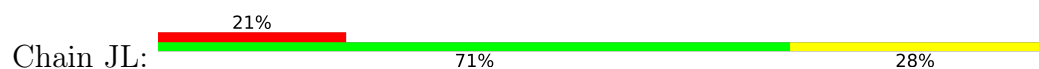


- Molecule 1: Coat protein

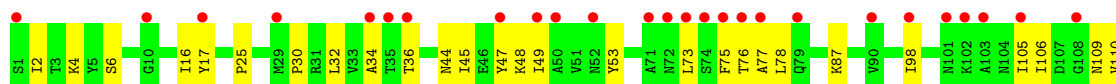
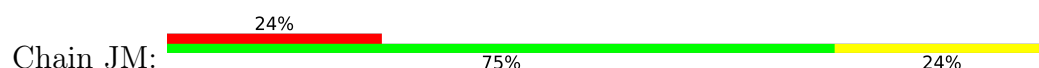




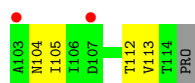
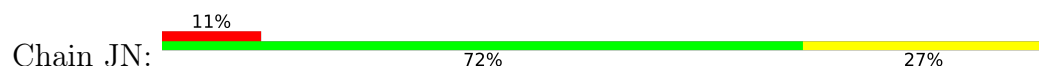
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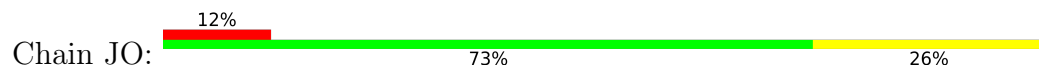
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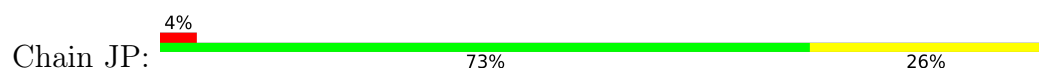
- Molecule 1: Coat protein



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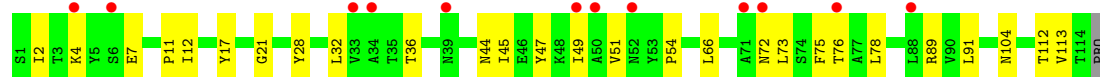
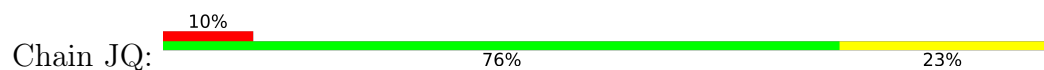


- Molecule 1: Coat protein





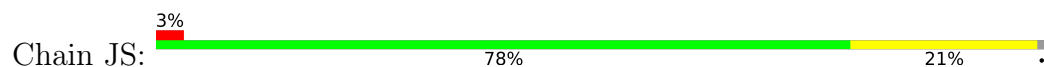
- Molecule 1: Coat protein



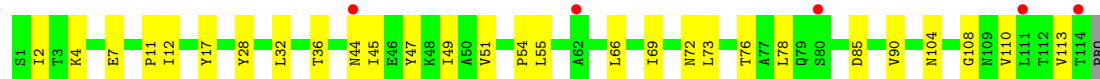
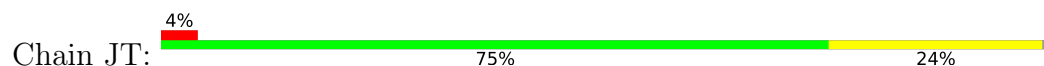
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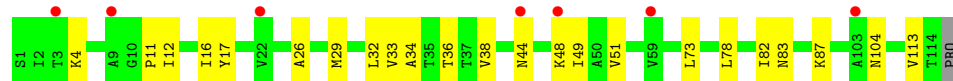
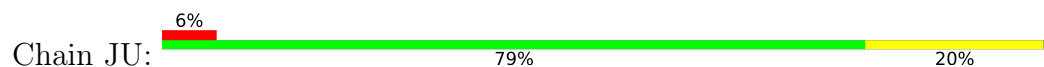
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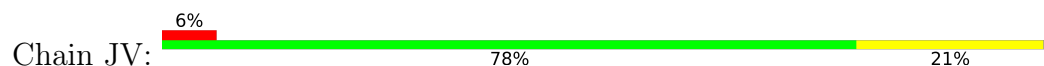
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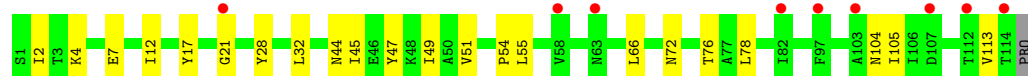
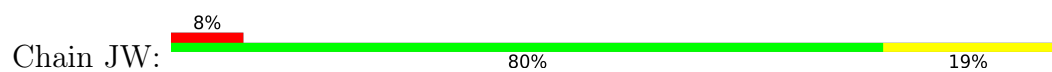
- Molecule 1: Coat protein



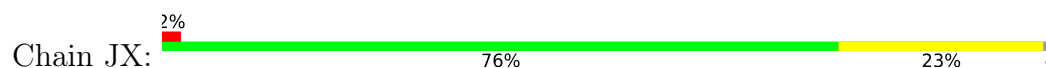
- Molecule 1: Coat protein



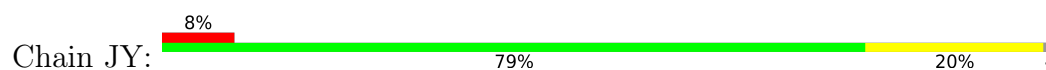
- Molecule 1: Coat protein



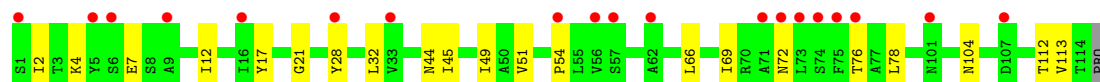
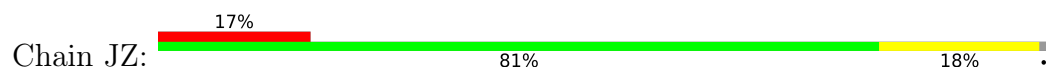
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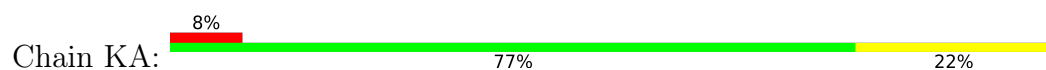
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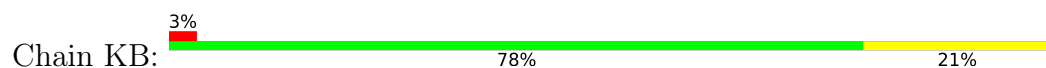
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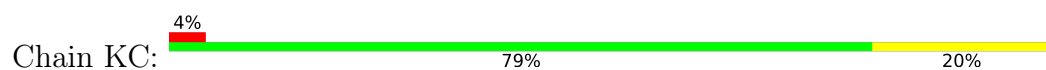
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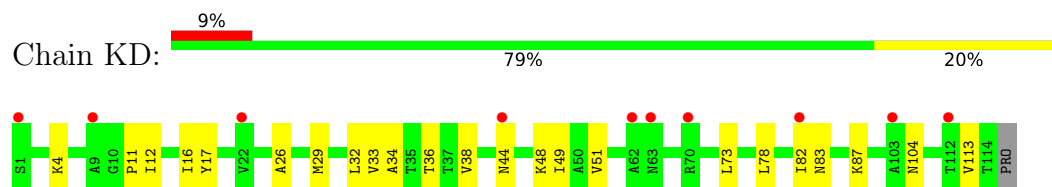
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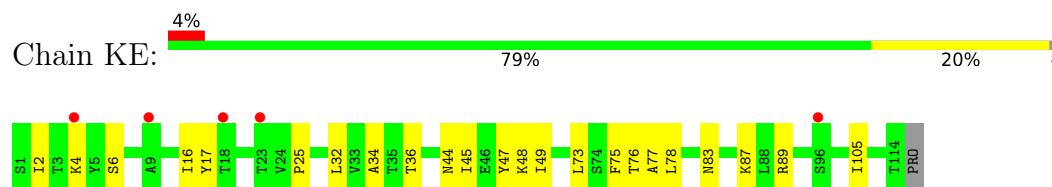
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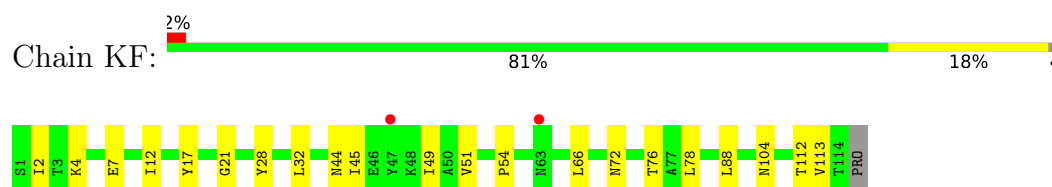
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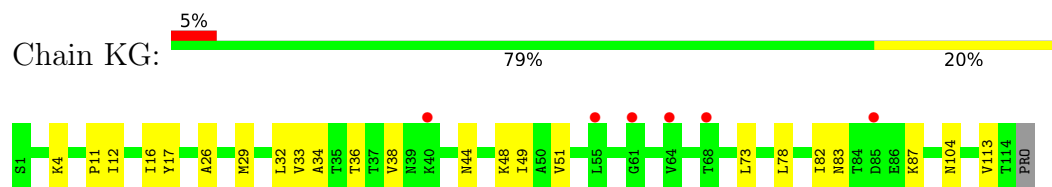
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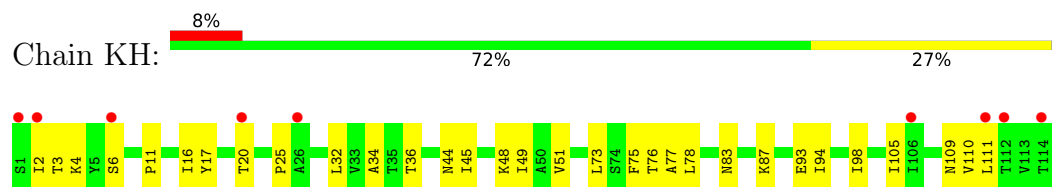
• Molecule 1: Coat protein



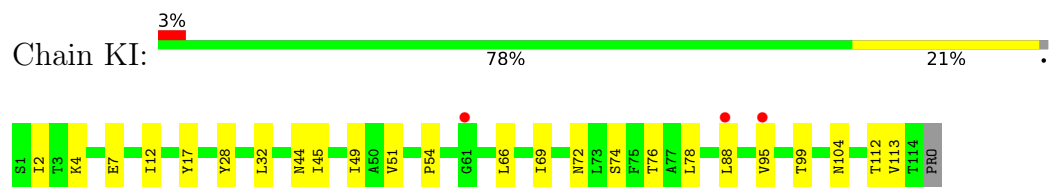
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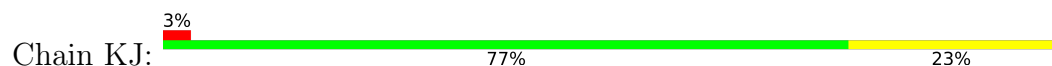
• Molecule 1: Coat protein

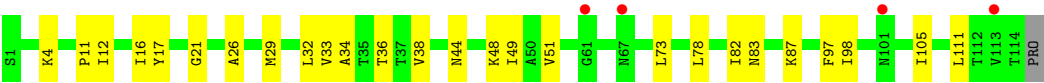


• Molecule 1: Coat protein



• Molecule 1: Coat protein





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	432.29Å 307.87Å 679.45Å 90.00° 107.15° 90.00°	Depositor
Resolution (Å)	44.26 – 3.40 44.26 – 3.40	Depositor EDS
% Data completeness (in resolution range)	50.9 (44.26-3.40) 50.9 (44.26-3.40)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 3.40Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.268 , 0.270 0.270 , 0.272	Depositor DCC
R_{free} test set	29857 reflections (2.57%)	wwPDB-VP
Wilson B-factor (Å ²)	61.0	Xtriage
Anisotropy	0.492	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 49.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.054 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	231390	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.22	0/868	0.44	0/1188
1	AB	0.24	0/868	0.46	0/1188
1	AC	0.21	0/868	0.42	0/1188
1	AD	0.22	0/868	0.44	0/1188
1	AE	0.24	0/868	0.46	0/1188
1	AF	0.22	0/868	0.42	0/1188
1	AG	0.22	0/868	0.44	0/1188
1	AH	0.24	0/868	0.46	0/1188
1	AI	0.22	0/868	0.42	0/1188
1	AJ	0.22	0/868	0.44	0/1188
1	AK	0.24	0/868	0.46	0/1188
1	AL	0.22	0/868	0.42	0/1188
1	AM	0.22	0/868	0.44	0/1188
1	AN	0.24	0/868	0.46	0/1188
1	AO	0.22	0/868	0.42	0/1188
1	AP	0.22	0/868	0.44	0/1188
1	AQ	0.24	0/868	0.46	0/1188
1	AR	0.22	0/868	0.42	0/1188
1	AS	0.22	0/868	0.44	0/1188
1	AT	0.24	0/868	0.46	0/1188
1	AU	0.22	0/868	0.42	0/1188
1	AV	0.22	0/868	0.44	0/1188
1	AW	0.24	0/868	0.46	0/1188
1	AX	0.22	0/868	0.42	0/1188
1	AY	0.22	0/868	0.44	0/1188
1	AZ	0.24	0/868	0.46	0/1188
1	BA	0.22	0/868	0.42	0/1188
1	BB	0.22	0/868	0.44	0/1188
1	BC	0.24	0/868	0.46	0/1188
1	BD	0.22	0/868	0.42	0/1188
1	BE	0.22	0/868	0.44	0/1188
1	BF	0.24	0/868	0.46	0/1188
1	BG	0.22	0/868	0.42	0/1188
1	BH	0.22	0/868	0.44	0/1188

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.24	0/868	0.46	0/1188
1	BJ	0.22	0/868	0.42	0/1188
1	BK	0.22	0/868	0.44	0/1188
1	BL	0.24	0/868	0.46	0/1188
1	BM	0.22	0/868	0.42	0/1188
1	BN	0.22	0/868	0.44	0/1188
1	BO	0.24	0/868	0.46	0/1188
1	BP	0.21	0/868	0.42	0/1188
1	BQ	0.22	0/868	0.44	0/1188
1	BR	0.24	0/868	0.46	0/1188
1	BS	0.22	0/868	0.42	0/1188
1	BT	0.22	0/868	0.44	0/1188
1	BU	0.24	0/868	0.46	0/1188
1	BV	0.22	0/868	0.42	0/1188
1	BW	0.22	0/868	0.44	0/1188
1	BX	0.24	0/868	0.46	0/1188
1	BY	0.21	0/868	0.42	0/1188
1	BZ	0.22	0/868	0.44	0/1188
1	CA	0.24	0/868	0.46	0/1188
1	CB	0.22	0/868	0.42	0/1188
1	CC	0.22	0/868	0.44	0/1188
1	CD	0.24	0/868	0.46	0/1188
1	CE	0.22	0/868	0.42	0/1188
1	CF	0.22	0/868	0.44	0/1188
1	CG	0.24	0/868	0.46	0/1188
1	CH	0.21	0/868	0.42	0/1188
1	CI	0.22	0/868	0.44	0/1188
1	CJ	0.24	0/868	0.46	0/1188
1	CK	0.22	0/868	0.42	0/1188
1	CL	0.22	0/868	0.44	0/1188
1	CM	0.24	0/868	0.46	0/1188
1	CN	0.22	0/868	0.42	0/1188
1	CO	0.22	0/868	0.44	0/1188
1	CP	0.24	0/868	0.46	0/1188
1	CQ	0.22	0/868	0.42	0/1188
1	CR	0.22	0/868	0.44	0/1188
1	CS	0.24	0/868	0.46	0/1188
1	CT	0.22	0/868	0.42	0/1188
1	CU	0.22	0/868	0.44	0/1188
1	CV	0.24	0/868	0.46	0/1188
1	CW	0.22	0/868	0.42	0/1188
1	CX	0.22	0/868	0.44	0/1188
1	CY	0.24	0/868	0.46	0/1188

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CZ	0.22	0/868	0.42	0/1188
1	DA	0.22	0/868	0.44	0/1188
1	DB	0.24	0/868	0.46	0/1188
1	DC	0.22	0/868	0.42	0/1188
1	DD	0.22	0/868	0.44	0/1188
1	DE	0.24	0/868	0.46	0/1188
1	DF	0.22	0/868	0.42	0/1188
1	DG	0.22	0/868	0.44	0/1188
1	DH	0.24	0/868	0.46	0/1188
1	DI	0.22	0/868	0.42	0/1188
1	DJ	0.22	0/868	0.44	0/1188
1	DK	0.24	0/868	0.46	0/1188
1	DL	0.22	0/868	0.42	0/1188
1	DM	0.22	0/868	0.44	0/1188
1	DN	0.24	0/868	0.46	0/1188
1	DO	0.22	0/868	0.42	0/1188
1	DP	0.22	0/868	0.44	0/1188
1	DQ	0.24	0/868	0.46	0/1188
1	DR	0.22	0/868	0.42	0/1188
1	DS	0.22	0/868	0.44	0/1188
1	DT	0.24	0/868	0.46	0/1188
1	DU	0.22	0/868	0.42	0/1188
1	DV	0.22	0/868	0.44	0/1188
1	DW	0.24	0/868	0.46	0/1188
1	DX	0.22	0/868	0.42	0/1188
1	DY	0.22	0/868	0.44	0/1188
1	DZ	0.24	0/868	0.46	0/1188
1	EA	0.22	0/868	0.42	0/1188
1	EB	0.22	0/868	0.44	0/1188
1	EC	0.24	0/868	0.46	0/1188
1	ED	0.22	0/868	0.42	0/1188
1	EE	0.22	0/868	0.44	0/1188
1	EF	0.24	0/868	0.46	0/1188
1	EG	0.22	0/868	0.42	0/1188
1	EH	0.22	0/868	0.44	0/1188
1	EI	0.24	0/868	0.46	0/1188
1	EJ	0.21	0/868	0.42	0/1188
1	EK	0.22	0/868	0.44	0/1188
1	EL	0.24	0/868	0.46	0/1188
1	EM	0.22	0/868	0.42	0/1188
1	EN	0.22	0/868	0.44	0/1188
1	EO	0.24	0/868	0.46	0/1188
1	EP	0.22	0/868	0.42	0/1188

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	EQ	0.22	0/868	0.44	0/1188
1	ER	0.24	0/868	0.46	0/1188
1	ES	0.22	0/868	0.42	0/1188
1	ET	0.22	0/868	0.44	0/1188
1	EU	0.24	0/868	0.46	0/1188
1	EV	0.21	0/868	0.42	0/1188
1	EW	0.22	0/868	0.44	0/1188
1	EX	0.24	0/868	0.46	0/1188
1	EY	0.22	0/868	0.42	0/1188
1	EZ	0.22	0/868	0.44	0/1188
1	FA	0.24	0/868	0.46	0/1188
1	FB	0.22	0/868	0.42	0/1188
1	FC	0.22	0/868	0.44	0/1188
1	FD	0.24	0/868	0.46	0/1188
1	FE	0.22	0/868	0.42	0/1188
1	FF	0.22	0/868	0.44	0/1188
1	FG	0.24	0/868	0.46	0/1188
1	FH	0.22	0/868	0.42	0/1188
1	FI	0.22	0/868	0.44	0/1188
1	FJ	0.24	0/868	0.46	0/1188
1	FK	0.22	0/868	0.42	0/1188
1	FL	0.22	0/868	0.44	0/1188
1	FM	0.24	0/868	0.46	0/1188
1	FN	0.22	0/868	0.42	0/1188
1	FO	0.22	0/868	0.44	0/1188
1	FP	0.24	0/868	0.46	0/1188
1	FQ	0.22	0/868	0.42	0/1188
1	FR	0.22	0/868	0.44	0/1188
1	FS	0.24	0/868	0.46	0/1188
1	FT	0.22	0/868	0.42	0/1188
1	FU	0.22	0/868	0.44	0/1188
1	FV	0.24	0/868	0.46	0/1188
1	FW	0.22	0/868	0.42	0/1188
1	FX	0.22	0/868	0.44	0/1188
1	FY	0.24	0/868	0.46	0/1188
1	FZ	0.22	0/868	0.42	0/1188
1	GA	0.22	0/868	0.44	0/1188
1	GB	0.24	0/868	0.46	0/1188
1	GC	0.22	0/868	0.42	0/1188
1	GD	0.22	0/868	0.44	0/1188
1	GE	0.24	0/868	0.46	0/1188
1	GF	0.22	0/868	0.42	0/1188
1	GG	0.22	0/868	0.44	0/1188

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GH	0.24	0/868	0.46	0/1188
1	GI	0.22	0/868	0.42	0/1188
1	GJ	0.22	0/868	0.44	0/1188
1	GK	0.24	0/868	0.46	0/1188
1	GL	0.21	0/868	0.42	0/1188
1	GM	0.22	0/868	0.44	0/1188
1	GN	0.24	0/868	0.46	0/1188
1	GO	0.22	0/868	0.42	0/1188
1	GP	0.22	0/868	0.44	0/1188
1	GQ	0.24	0/868	0.46	0/1188
1	GR	0.22	0/868	0.42	0/1188
1	GS	0.22	0/868	0.44	0/1188
1	GT	0.24	0/868	0.46	0/1188
1	GU	0.22	0/868	0.42	0/1188
1	GV	0.22	0/868	0.44	0/1188
1	GW	0.24	0/868	0.46	0/1188
1	GX	0.22	0/868	0.42	0/1188
1	GY	0.22	0/868	0.44	0/1188
1	GZ	0.24	0/868	0.46	0/1188
1	HA	0.22	0/868	0.42	0/1188
1	HB	0.22	0/868	0.44	0/1188
1	HC	0.24	0/868	0.46	0/1188
1	HD	0.22	0/868	0.42	0/1188
1	HE	0.22	0/868	0.44	0/1188
1	HF	0.24	0/868	0.46	0/1188
1	HG	0.22	0/868	0.42	0/1188
1	HH	0.22	0/868	0.44	0/1188
1	HI	0.24	0/868	0.46	0/1188
1	HJ	0.22	0/868	0.42	0/1188
1	HK	0.22	0/868	0.44	0/1188
1	HL	0.24	0/868	0.46	0/1188
1	HM	0.22	0/868	0.42	0/1188
1	HN	0.22	0/868	0.44	0/1188
1	HO	0.24	0/868	0.46	0/1188
1	HP	0.22	0/868	0.42	0/1188
1	HQ	0.22	0/868	0.44	0/1188
1	HR	0.24	0/868	0.46	0/1188
1	HS	0.21	0/868	0.42	0/1188
1	HT	0.22	0/868	0.44	0/1188
1	HU	0.24	0/868	0.46	0/1188
1	HV	0.22	0/868	0.42	0/1188
1	HW	0.22	0/868	0.44	0/1188
1	HX	0.24	0/868	0.46	0/1188

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	HY	0.22	0/868	0.42	0/1188
1	HZ	0.22	0/868	0.44	0/1188
1	IA	0.24	0/868	0.46	0/1188
1	IB	0.22	0/868	0.42	0/1188
1	IC	0.22	0/868	0.44	0/1188
1	ID	0.24	0/868	0.46	0/1188
1	IE	0.22	0/868	0.42	0/1188
1	IF	0.22	0/868	0.44	0/1188
1	IG	0.24	0/868	0.46	0/1188
1	IH	0.22	0/868	0.42	0/1188
1	II	0.22	0/868	0.44	0/1188
1	IJ	0.24	0/868	0.46	0/1188
1	IK	0.22	0/868	0.42	0/1188
1	IL	0.22	0/868	0.44	0/1188
1	IM	0.24	0/868	0.46	0/1188
1	IN	0.22	0/868	0.42	0/1188
1	IO	0.22	0/868	0.44	0/1188
1	IP	0.24	0/868	0.46	0/1188
1	IQ	0.22	0/868	0.42	0/1188
1	IR	0.22	0/868	0.44	0/1188
1	IS	0.24	0/868	0.46	0/1188
1	IT	0.22	0/868	0.42	0/1188
1	IU	0.22	0/868	0.44	0/1188
1	IV	0.24	0/868	0.46	0/1188
1	IW	0.22	0/868	0.42	0/1188
1	IX	0.22	0/868	0.44	0/1188
1	IY	0.24	0/868	0.46	0/1188
1	IZ	0.22	0/868	0.42	0/1188
1	JA	0.22	0/868	0.44	0/1188
1	JB	0.24	0/868	0.46	0/1188
1	JC	0.22	0/868	0.42	0/1188
1	JD	0.22	0/868	0.44	0/1188
1	JE	0.24	0/868	0.46	0/1188
1	JF	0.22	0/868	0.42	0/1188
1	JG	0.22	0/868	0.44	0/1188
1	JH	0.24	0/868	0.46	0/1188
1	JI	0.22	0/868	0.42	0/1188
1	JJ	0.22	0/868	0.44	0/1188
1	JK	0.24	0/868	0.46	0/1188
1	JL	0.22	0/868	0.42	0/1188
1	JM	0.22	0/868	0.44	0/1188
1	JN	0.24	0/868	0.46	0/1188
1	JO	0.22	0/868	0.42	0/1188

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	JP	0.22	0/868	0.44	0/1188
1	JQ	0.24	0/868	0.46	0/1188
1	JR	0.22	0/868	0.42	0/1188
1	JS	0.22	0/868	0.44	0/1188
1	JT	0.24	0/868	0.46	0/1188
1	JU	0.22	0/868	0.42	0/1188
1	JV	0.22	0/868	0.44	0/1188
1	JW	0.24	0/868	0.46	0/1188
1	JX	0.22	0/868	0.42	0/1188
1	JY	0.22	0/868	0.44	0/1188
1	JZ	0.24	0/868	0.46	0/1188
1	KA	0.22	0/868	0.42	0/1188
1	KB	0.22	0/868	0.44	0/1188
1	KC	0.24	0/868	0.46	0/1188
1	KD	0.21	0/868	0.42	0/1188
1	KE	0.22	0/868	0.44	0/1188
1	KF	0.24	0/868	0.46	0/1188
1	KG	0.22	0/868	0.42	0/1188
1	KH	0.22	0/868	0.44	0/1188
1	KI	0.24	0/868	0.46	0/1188
1	KJ	0.22	0/868	0.42	0/1188
All	All	0.23	0/234360	0.44	0/320760

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	857	0	885	21	0
1	AB	857	0	885	21	0
1	AC	857	0	885	19	0
1	AD	857	0	885	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AE	857	0	885	28	0
1	AF	857	0	885	23	0
1	AG	857	0	885	34	0
1	AH	857	0	885	19	0
1	AI	857	0	885	21	0
1	AJ	857	0	885	25	0
1	AK	857	0	885	25	0
1	AL	857	0	885	19	0
1	AM	857	0	885	34	0
1	AN	857	0	885	32	0
1	AO	857	0	885	21	0
1	AP	857	0	885	27	0
1	AQ	857	0	885	34	0
1	AR	857	0	885	22	0
1	AS	857	0	885	37	0
1	AT	857	0	885	18	0
1	AU	857	0	885	39	0
1	AV	857	0	885	34	0
1	AW	857	0	885	21	0
1	AX	857	0	885	25	0
1	AY	857	0	885	31	0
1	AZ	857	0	885	19	0
1	BA	857	0	885	22	0
1	BB	857	0	885	24	0
1	BC	857	0	885	32	0
1	BD	857	0	885	36	0
1	BE	857	0	885	24	0
1	BF	857	0	885	30	0
1	BG	857	0	885	22	0
1	BH	857	0	885	23	0
1	BI	857	0	885	18	0
1	BJ	857	0	885	20	0
1	BK	857	0	885	21	0
1	BL	857	0	885	22	0
1	BM	857	0	885	23	0
1	BN	857	0	885	22	0
1	BO	857	0	885	19	0
1	BP	857	0	885	23	0
1	BQ	857	0	885	28	0
1	BR	857	0	885	22	0
1	BS	857	0	885	23	0
1	BT	857	0	885	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BU	857	0	885	23	0
1	BV	857	0	885	20	0
1	BW	857	0	885	29	0
1	BX	857	0	885	21	0
1	BY	857	0	885	29	0
1	BZ	857	0	885	35	0
1	CA	857	0	885	32	0
1	CB	857	0	885	22	0
1	CC	857	0	885	36	0
1	CD	857	0	885	24	0
1	CE	857	0	885	18	0
1	CF	857	0	885	23	0
1	CG	857	0	885	36	0
1	CH	857	0	885	34	0
1	CI	857	0	885	26	0
1	CJ	857	0	885	27	0
1	CK	857	0	885	22	0
1	CL	857	0	885	39	0
1	CM	857	0	885	25	0
1	CN	857	0	885	26	0
1	CO	857	0	885	30	0
1	CP	857	0	885	19	0
1	CQ	857	0	885	20	0
1	CR	857	0	885	29	0
1	CS	857	0	885	18	0
1	CT	857	0	885	20	0
1	CU	857	0	885	24	0
1	CV	857	0	885	18	0
1	CW	857	0	885	20	0
1	CX	857	0	885	23	0
1	CY	857	0	885	27	0
1	CZ	857	0	885	24	0
1	DA	857	0	885	20	0
1	DB	857	0	885	20	0
1	DC	857	0	885	22	0
1	DD	857	0	885	20	0
1	DE	857	0	885	17	0
1	DF	857	0	885	24	0
1	DG	857	0	885	27	0
1	DH	857	0	885	21	0
1	DI	857	0	885	25	0
1	DJ	857	0	885	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DK	857	0	885	21	0
1	DL	857	0	885	30	0
1	DM	857	0	885	27	0
1	DN	857	0	885	26	0
1	DO	857	0	885	19	0
1	DP	857	0	885	24	0
1	DQ	857	0	885	26	0
1	DR	857	0	885	22	0
1	DS	857	0	885	21	0
1	DT	857	0	885	30	0
1	DU	857	0	885	21	0
1	DV	857	0	885	24	0
1	DW	857	0	885	18	0
1	DX	857	0	885	18	0
1	DY	857	0	885	32	0
1	DZ	857	0	885	18	0
1	EA	857	0	885	21	0
1	EB	857	0	885	36	0
1	EC	857	0	885	26	0
1	ED	857	0	885	21	0
1	EE	857	0	885	34	0
1	EF	857	0	885	32	0
1	EG	857	0	885	40	0
1	EH	857	0	885	27	0
1	EI	857	0	885	29	0
1	EJ	857	0	885	24	0
1	EK	857	0	885	27	0
1	EL	857	0	885	32	0
1	EM	857	0	885	23	0
1	EN	857	0	885	48	0
1	EO	857	0	885	25	0
1	EP	857	0	885	34	0
1	EQ	857	0	885	30	0
1	ER	857	0	885	24	0
1	ES	857	0	885	21	0
1	ET	857	0	885	31	0
1	EU	857	0	885	34	0
1	EV	857	0	885	21	0
1	EW	857	0	885	21	0
1	EX	857	0	885	19	0
1	EY	857	0	885	24	0
1	EZ	857	0	885	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	FA	857	0	885	19	0
1	FB	857	0	885	22	0
1	FC	857	0	885	25	0
1	FD	857	0	885	21	0
1	FE	857	0	885	24	0
1	FF	857	0	885	25	0
1	FG	857	0	885	26	0
1	FH	857	0	885	19	0
1	FI	857	0	885	21	0
1	FJ	857	0	885	45	0
1	FK	857	0	885	28	0
1	FL	857	0	885	23	0
1	FM	857	0	885	27	0
1	FN	857	0	885	21	0
1	FO	857	0	885	29	0
1	FP	857	0	885	20	0
1	FQ	857	0	885	18	0
1	FR	857	0	885	36	0
1	FS	857	0	885	24	0
1	FT	857	0	885	34	0
1	FU	857	0	885	37	0
1	FV	857	0	885	21	0
1	FW	857	0	885	24	0
1	FX	857	0	885	25	0
1	FY	857	0	885	29	0
1	FZ	857	0	885	25	0
1	GA	857	0	885	30	0
1	GB	857	0	885	35	0
1	GC	857	0	885	21	0
1	GD	857	0	885	22	0
1	GE	857	0	885	22	0
1	GF	857	0	885	20	0
1	GG	857	0	885	30	0
1	GH	857	0	885	25	0
1	GI	857	0	885	20	0
1	GJ	857	0	885	24	0
1	GK	857	0	885	34	0
1	GL	857	0	885	24	0
1	GM	857	0	885	21	0
1	GN	857	0	885	21	0
1	GO	857	0	885	21	0
1	GP	857	0	885	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GQ	857	0	885	18	0
1	GR	857	0	885	24	0
1	GS	857	0	885	23	0
1	GT	857	0	885	24	0
1	GU	857	0	885	24	0
1	GV	857	0	885	23	0
1	GW	857	0	885	21	0
1	GX	857	0	885	29	0
1	GY	857	0	885	39	0
1	GZ	857	0	885	19	0
1	HA	857	0	885	18	0
1	HB	857	0	885	25	0
1	HC	857	0	885	20	0
1	HD	857	0	885	13	0
1	HE	857	0	885	29	0
1	HF	857	0	885	20	0
1	HG	857	0	885	23	0
1	HH	857	0	885	24	0
1	HI	857	0	885	18	0
1	HJ	857	0	885	25	0
1	HK	857	0	885	28	0
1	HL	857	0	885	26	0
1	HM	857	0	885	15	0
1	HN	857	0	885	25	0
1	HO	857	0	885	37	0
1	HP	857	0	885	21	0
1	HQ	857	0	885	30	0
1	HR	857	0	885	23	0
1	HS	857	0	885	26	0
1	HT	857	0	885	46	0
1	HU	857	0	885	27	0
1	HV	857	0	885	31	0
1	HW	857	0	885	28	0
1	HX	857	0	885	23	0
1	HY	857	0	885	20	0
1	HZ	857	0	885	27	0
1	IA	857	0	885	19	0
1	IB	857	0	885	21	0
1	IC	857	0	885	22	0
1	ID	857	0	885	17	0
1	IE	857	0	885	24	0
1	IF	857	0	885	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	IG	857	0	885	23	0
1	IH	857	0	885	15	0
1	II	857	0	885	19	0
1	IJ	857	0	885	30	0
1	IK	857	0	885	21	0
1	IL	857	0	885	21	0
1	IM	857	0	885	44	0
1	IN	857	0	885	15	0
1	IO	857	0	885	25	0
1	IP	857	0	885	26	0
1	IQ	857	0	885	20	0
1	IR	857	0	885	22	0
1	IS	857	0	885	27	0
1	IT	857	0	885	24	0
1	IU	857	0	885	38	0
1	IV	857	0	885	21	0
1	IW	857	0	885	15	0
1	IX	857	0	885	26	0
1	IY	857	0	885	25	0
1	IZ	857	0	885	25	0
1	JA	857	0	885	34	0
1	JB	857	0	885	23	0
1	JC	857	0	885	21	0
1	JD	857	0	885	33	0
1	JE	857	0	885	34	0
1	JF	857	0	885	14	0
1	JG	857	0	885	28	0
1	JH	857	0	885	30	0
1	JI	857	0	885	16	0
1	JJ	857	0	885	22	0
1	JK	857	0	885	29	0
1	JL	857	0	885	26	0
1	JM	857	0	885	33	0
1	JN	857	0	885	31	0
1	JO	857	0	885	31	0
1	JP	857	0	885	33	0
1	JQ	857	0	885	31	0
1	JR	857	0	885	19	0
1	JS	857	0	885	23	0
1	JT	857	0	885	36	0
1	JU	857	0	885	16	0
1	JV	857	0	885	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	JW	857	0	885	18	0
1	JX	857	0	885	21	0
1	JY	857	0	885	21	0
1	JZ	857	0	885	19	0
1	KA	857	0	885	22	0
1	KB	857	0	885	26	0
1	KC	857	0	885	23	0
1	KD	857	0	885	15	0
1	KE	857	0	885	21	0
1	KF	857	0	885	18	0
1	KG	857	0	885	15	0
1	KH	857	0	885	39	0
1	KI	857	0	885	23	0
1	KJ	857	0	885	20	0
All	All	231390	0	238950	5136	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 11.

All (5136) 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:DL:95:VAL:HG13	1:GX:95:VAL:HG13	1.54	0.86
1:AU:111:LEU:HG	1:EG:11:PRO:HA	1.55	0.86
1:HJ:95:VAL:HG13	1:IZ:95:VAL:HG13	1.60	0.83
1:AX:95:VAL:HG13	1:EJ:95:VAL:HG13	1.60	0.82
1:CI:4:LYS:HE2	1:GH:112:THR:HG21	1.64	0.80
1:BD:11:PRO:HA	1:EP:111:LEU:HG	1.65	0.78
1:JD:4:LYS:HE2	1:JN:112:THR:HG21	1.64	0.78
1:EK:106:ILE:HG21	1:ER:88:LEU:HG	1.66	0.76
1:CH:73:LEU:HD12	1:FT:72:ASN:O	1.85	0.76
1:CI:71:ALA:HA	1:GH:74:SER:O	1.84	0.76
1:CN:32:LEU:HD11	1:CN:49:ILE:HG23	1.69	0.75
1:EV:32:LEU:HD11	1:EV:49:ILE:HG23	1.69	0.75
1:EA:32:LEU:HD11	1:EA:49:ILE:HG23	1.69	0.75
1:EY:32:LEU:HD11	1:EY:49:ILE:HG23	1.69	0.75
1:FT:32:LEU:HD11	1:FT:49:ILE:HG23	1.69	0.75
1:AX:32:LEU:HD11	1:AX:49:ILE:HG23	1.69	0.75
1:BS:32:LEU:HD11	1:BS:49:ILE:HG23	1.69	0.75
1:CB:32:LEU:HD11	1:CB:49:ILE:HG23	1.69	0.75
1:DI:32:LEU:HD11	1:DI:49:ILE:HG23	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IE:32:LEU:HD11	1:IE:49:ILE:HG23	1.69	0.75
1:IW:32:LEU:HD11	1:IW:49:ILE:HG23	1.69	0.75
1:BA:32:LEU:HD11	1:BA:49:ILE:HG23	1.69	0.75
1:HM:32:LEU:HD11	1:HM:49:ILE:HG23	1.69	0.75
1:KG:32:LEU:HD11	1:KG:49:ILE:HG23	1.69	0.75
1:AU:32:LEU:HD11	1:AU:49:ILE:HG23	1.69	0.75
1:BD:32:LEU:HD11	1:BD:49:ILE:HG23	1.69	0.75
1:BJ:32:LEU:HD11	1:BJ:49:ILE:HG23	1.69	0.75
1:DF:32:LEU:HD11	1:DF:49:ILE:HG23	1.69	0.75
1:IB:32:LEU:HD11	1:IB:49:ILE:HG23	1.69	0.75
1:JX:32:LEU:HD11	1:JX:49:ILE:HG23	1.69	0.75
1:AI:32:LEU:HD11	1:AI:49:ILE:HG23	1.69	0.75
1:ES:32:LEU:HD11	1:ES:49:ILE:HG23	1.69	0.75
1:JF:32:LEU:HD11	1:JF:49:ILE:HG23	1.69	0.75
1:JO:32:LEU:HD11	1:JO:49:ILE:HG23	1.69	0.75
1:DX:32:LEU:HD11	1:DX:49:ILE:HG23	1.69	0.75
1:DC:32:LEU:HD11	1:DC:49:ILE:HG23	1.69	0.74
1:FN:32:LEU:HD11	1:FN:49:ILE:HG23	1.69	0.74
1:FW:32:LEU:HD11	1:FW:49:ILE:HG23	1.69	0.74
1:HG:32:LEU:HD11	1:HG:49:ILE:HG23	1.69	0.74
1:AC:32:LEU:HD11	1:AC:49:ILE:HG23	1.69	0.74
1:BV:32:LEU:HD11	1:BV:49:ILE:HG23	1.69	0.74
1:CI:73:LEU:HA	1:GH:72:ASN:O	1.86	0.74
1:EP:32:LEU:HD11	1:EP:49:ILE:HG23	1.69	0.74
1:HP:32:LEU:HD11	1:HP:49:ILE:HG23	1.69	0.74
1:IK:32:LEU:HD11	1:IK:49:ILE:HG23	1.69	0.74
1:CT:32:LEU:HD11	1:CT:49:ILE:HG23	1.69	0.74
1:HS:32:LEU:HD11	1:HS:49:ILE:HG23	1.69	0.74
1:DO:32:LEU:HD11	1:DO:49:ILE:HG23	1.69	0.74
1:IZ:32:LEU:HD11	1:IZ:49:ILE:HG23	1.69	0.74
1:IE:95:VAL:HG13	1:KA:95:VAL:HG13	1.70	0.74
1:JC:32:LEU:HD11	1:JC:49:ILE:HG23	1.69	0.74
1:KD:32:LEU:HD11	1:KD:49:ILE:HG23	1.69	0.74
1:AO:32:LEU:HD11	1:AO:49:ILE:HG23	1.69	0.74
1:BY:32:LEU:HD11	1:BY:49:ILE:HG23	1.69	0.74
1:DI:95:VAL:HG13	1:GU:95:VAL:HG13	1.69	0.74
1:HD:32:LEU:HD11	1:HD:49:ILE:HG23	1.69	0.74
1:HJ:32:LEU:HD11	1:HJ:49:ILE:HG23	1.69	0.74
1:HV:32:LEU:HD11	1:HV:49:ILE:HG23	1.69	0.74
1:JI:32:LEU:HD11	1:JI:49:ILE:HG23	1.69	0.74
1:AL:32:LEU:HD11	1:AL:49:ILE:HG23	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:32:LEU:HD11	1:BG:49:ILE:HG23	1.69	0.74
1:CZ:32:LEU:HD11	1:CZ:49:ILE:HG23	1.69	0.74
1:DR:32:LEU:HD11	1:DR:49:ILE:HG23	1.69	0.74
1:IN:32:LEU:HD11	1:IN:49:ILE:HG23	1.69	0.74
1:FZ:32:LEU:HD11	1:FZ:49:ILE:HG23	1.69	0.74
1:IT:32:LEU:HD11	1:IT:49:ILE:HG23	1.69	0.74
1:EG:32:LEU:HD11	1:EG:49:ILE:HG23	1.69	0.74
1:GI:32:LEU:HD11	1:GI:49:ILE:HG23	1.69	0.74
1:HY:32:LEU:HD11	1:HY:49:ILE:HG23	1.69	0.74
1:DU:32:LEU:HD11	1:DU:49:ILE:HG23	1.69	0.73
1:CK:32:LEU:HD11	1:CK:49:ILE:HG23	1.69	0.73
1:ED:32:LEU:HD11	1:ED:49:ILE:HG23	1.69	0.73
1:EM:32:LEU:HD11	1:EM:49:ILE:HG23	1.69	0.73
1:HA:32:LEU:HD11	1:HA:49:ILE:HG23	1.69	0.73
1:JL:32:LEU:HD11	1:JL:49:ILE:HG23	1.69	0.73
1:FB:32:LEU:HD11	1:FB:49:ILE:HG23	1.69	0.73
1:CQ:32:LEU:HD11	1:CQ:49:ILE:HG23	1.69	0.73
1:IH:32:LEU:HD11	1:IH:49:ILE:HG23	1.69	0.73
1:IQ:32:LEU:HD11	1:IQ:49:ILE:HG23	1.69	0.73
1:JU:32:LEU:HD11	1:JU:49:ILE:HG23	1.69	0.73
1:CH:32:LEU:HD11	1:CH:49:ILE:HG23	1.69	0.73
1:FE:32:LEU:HD11	1:FE:49:ILE:HG23	1.69	0.73
1:FQ:32:LEU:HD11	1:FQ:49:ILE:HG23	1.69	0.73
1:EJ:32:LEU:HD11	1:EJ:49:ILE:HG23	1.69	0.73
1:FH:32:LEU:HD11	1:FH:49:ILE:HG23	1.69	0.73
1:GR:32:LEU:HD11	1:GR:49:ILE:HG23	1.69	0.73
1:KA:32:LEU:HD11	1:KA:49:ILE:HG23	1.69	0.73
1:AF:32:LEU:HD11	1:AF:49:ILE:HG23	1.69	0.73
1:BQ:106:ILE:HG21	1:EC:88:LEU:HG	1.68	0.73
1:CW:32:LEU:HD11	1:CW:49:ILE:HG23	1.69	0.73
1:GC:32:LEU:HD11	1:GC:49:ILE:HG23	1.69	0.73
1:GF:32:LEU:HD11	1:GF:49:ILE:HG23	1.69	0.73
1:GL:32:LEU:HD11	1:GL:49:ILE:HG23	1.69	0.73
1:FK:32:LEU:HD11	1:FK:49:ILE:HG23	1.69	0.73
1:GO:32:LEU:HD11	1:GO:49:ILE:HG23	1.69	0.73
1:GU:32:LEU:HD11	1:GU:49:ILE:HG23	1.69	0.73
1:BP:32:LEU:HD11	1:BP:49:ILE:HG23	1.69	0.73
1:AR:32:LEU:HD11	1:AR:49:ILE:HG23	1.69	0.72
1:BM:32:LEU:HD11	1:BM:49:ILE:HG23	1.69	0.72
1:CE:32:LEU:HD11	1:CE:49:ILE:HG23	1.69	0.72
1:DP:44:ASN:HB2	1:DP:78:LEU:HA	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:44:ASN:HB2	1:BE:78:LEU:HA	1.72	0.72
1:CX:44:ASN:HB2	1:CX:78:LEU:HA	1.72	0.72
1:DL:32:LEU:HD11	1:DL:49:ILE:HG23	1.69	0.72
1:EZ:44:ASN:HB2	1:EZ:78:LEU:HA	1.72	0.72
1:JV:44:ASN:HB2	1:JV:78:LEU:HA	1.72	0.72
1:AP:44:ASN:HB2	1:AP:78:LEU:HA	1.72	0.72
1:BQ:44:ASN:HB2	1:BQ:78:LEU:HA	1.72	0.72
1:GX:32:LEU:HD11	1:GX:49:ILE:HG23	1.69	0.72
1:HN:44:ASN:HB2	1:HN:78:LEU:HA	1.72	0.72
1:IR:44:ASN:HB2	1:IR:78:LEU:HA	1.72	0.72
1:KJ:32:LEU:HD11	1:KJ:49:ILE:HG23	1.69	0.72
1:AI:72:ASN:O	1:DU:73:LEU:HD12	1.89	0.72
1:BN:44:ASN:HB2	1:BN:78:LEU:HA	1.72	0.72
1:DM:44:ASN:HB2	1:DM:78:LEU:HA	1.72	0.72
1:EN:44:ASN:HB2	1:EN:78:LEU:HA	1.72	0.72
1:GG:44:ASN:HB2	1:GG:78:LEU:HA	1.72	0.72
1:GM:44:ASN:HB2	1:GM:78:LEU:HA	1.72	0.72
1:IF:44:ASN:HB2	1:IF:78:LEU:HA	1.72	0.72
1:IL:44:ASN:HB2	1:IL:78:LEU:HA	1.72	0.72
1:KB:44:ASN:HB2	1:KB:78:LEU:HA	1.72	0.72
1:BW:44:ASN:HB2	1:BW:78:LEU:HA	1.72	0.72
1:ET:44:ASN:HB2	1:ET:78:LEU:HA	1.72	0.72
1:FX:44:ASN:HB2	1:FX:78:LEU:HA	1.72	0.72
1:GD:44:ASN:HB2	1:GD:78:LEU:HA	1.72	0.72
1:GJ:44:ASN:HB2	1:GJ:78:LEU:HA	1.72	0.72
1:JR:32:LEU:HD11	1:JR:49:ILE:HG23	1.69	0.72
1:DD:44:ASN:HB2	1:DD:78:LEU:HA	1.72	0.72
1:IX:44:ASN:HB2	1:IX:78:LEU:HA	1.72	0.72
1:AD:44:ASN:HB2	1:AD:78:LEU:HA	1.72	0.72
1:EK:44:ASN:HB2	1:EK:78:LEU:HA	1.72	0.72
1:HZ:44:ASN:HB2	1:HZ:78:LEU:HA	1.72	0.72
1:DS:44:ASN:HB2	1:DS:78:LEU:HA	1.72	0.71
1:JM:44:ASN:HB2	1:JM:78:LEU:HA	1.72	0.71
1:CU:44:ASN:HB2	1:CU:78:LEU:HA	1.72	0.71
1:FI:44:ASN:HB2	1:FI:78:LEU:HA	1.72	0.71
1:FL:44:ASN:HB2	1:FL:78:LEU:HA	1.72	0.71
1:FO:44:ASN:HB2	1:FO:78:LEU:HA	1.72	0.71
1:JA:44:ASN:HB2	1:JA:78:LEU:HA	1.72	0.71
1:BZ:44:ASN:HB2	1:BZ:78:LEU:HA	1.72	0.71
1:CI:44:ASN:HB2	1:CI:78:LEU:HA	1.72	0.71
1:JG:44:ASN:HB2	1:JG:78:LEU:HA	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JS:44:ASN:HB2	1:JS:78:LEU:HA	1.72	0.71
1:IO:44:ASN:HB2	1:IO:78:LEU:HA	1.72	0.71
1:KE:44:ASN:HB2	1:KE:78:LEU:HA	1.72	0.71
1:BK:44:ASN:HB2	1:BK:78:LEU:HA	1.72	0.71
1:GS:44:ASN:HB2	1:GS:78:LEU:HA	1.72	0.71
1:HQ:44:ASN:HB2	1:HQ:78:LEU:HA	1.72	0.71
1:DF:95:VAL:HG13	1:GR:95:VAL:HG13	1.73	0.71
1:DG:44:ASN:HB2	1:DG:78:LEU:HA	1.72	0.71
1:FF:44:ASN:HB2	1:FF:78:LEU:HA	1.72	0.71
1:HK:4:LYS:HE2	1:IY:112:THR:HG21	1.72	0.71
1:HK:44:ASN:HB2	1:HK:78:LEU:HA	1.72	0.71
1:KH:44:ASN:HB2	1:KH:78:LEU:HA	1.72	0.71
1:DY:44:ASN:HB2	1:DY:78:LEU:HA	1.72	0.71
1:AJ:44:ASN:HB2	1:AJ:78:LEU:HA	1.72	0.71
1:AV:44:ASN:HB2	1:AV:78:LEU:HA	1.72	0.71
1:AY:44:ASN:HB2	1:AY:78:LEU:HA	1.72	0.71
1:CF:44:ASN:HB2	1:CF:78:LEU:HA	1.72	0.71
1:CO:44:ASN:HB2	1:CO:78:LEU:HA	1.72	0.71
1:CR:44:ASN:HB2	1:CR:78:LEU:HA	1.72	0.71
1:GV:44:ASN:HB2	1:GV:78:LEU:HA	1.72	0.71
1:HW:44:ASN:HB2	1:HW:78:LEU:HA	1.72	0.71
1:DA:44:ASN:HB2	1:DA:78:LEU:HA	1.72	0.70
1:FR:44:ASN:HB2	1:FR:78:LEU:HA	1.72	0.70
1:HH:44:ASN:HB2	1:HH:78:LEU:HA	1.72	0.70
1:IC:44:ASN:HB2	1:IC:78:LEU:HA	1.72	0.70
1:AG:44:ASN:HB2	1:AG:78:LEU:HA	1.72	0.70
1:BT:44:ASN:HB2	1:BT:78:LEU:HA	1.72	0.70
1:EW:44:ASN:HB2	1:EW:78:LEU:HA	1.72	0.70
1:EX:55:LEU:HD13	1:FI:83:ASN:HD22	1.56	0.70
1:FC:44:ASN:HB2	1:FC:78:LEU:HA	1.72	0.70
1:GY:44:ASN:HB2	1:GY:78:LEU:HA	1.72	0.70
1:HB:44:ASN:HB2	1:HB:78:LEU:HA	1.72	0.70
1:JJ:44:ASN:HB2	1:JJ:78:LEU:HA	1.72	0.70
1:JP:44:ASN:HB2	1:JP:78:LEU:HA	1.72	0.70
1:BH:44:ASN:HB2	1:BH:78:LEU:HA	1.72	0.70
1:DV:44:ASN:HB2	1:DV:78:LEU:HA	1.72	0.70
1:EB:44:ASN:HB2	1:EB:78:LEU:HA	1.72	0.70
1:BB:44:ASN:HB2	1:BB:78:LEU:HA	1.72	0.70
1:CL:44:ASN:HB2	1:CL:78:LEU:HA	1.72	0.70
1:EE:44:ASN:HB2	1:EE:78:LEU:HA	1.72	0.70
1:HE:44:ASN:HB2	1:HE:78:LEU:HA	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IU:44:ASN:HB2	1:IU:78:LEU:HA	1.72	0.70
1:JY:44:ASN:HB2	1:JY:78:LEU:HA	1.72	0.70
1:DJ:44:ASN:HB2	1:DJ:78:LEU:HA	1.72	0.70
1:HT:44:ASN:HB2	1:HT:78:LEU:HA	1.72	0.70
1:AM:44:ASN:HB2	1:AM:78:LEU:HA	1.72	0.70
1:HY:95:VAL:HG13	1:JR:95:VAL:HG13	1.74	0.70
1:JD:44:ASN:HB2	1:JD:78:LEU:HA	1.72	0.70
1:AS:44:ASN:HB2	1:AS:78:LEU:HA	1.72	0.70
1:FU:44:ASN:HB2	1:FU:78:LEU:HA	1.72	0.70
1:EH:44:ASN:HB2	1:EH:78:LEU:HA	1.72	0.70
1:EQ:44:ASN:HB2	1:EQ:78:LEU:HA	1.72	0.69
1:GP:44:ASN:HB2	1:GP:78:LEU:HA	1.72	0.69
1:CC:44:ASN:HB2	1:CC:78:LEU:HA	1.72	0.69
1:II:44:ASN:HB2	1:II:78:LEU:HA	1.72	0.69
1:CM:112:THR:HG21	1:DG:4:LYS:HE2	1.73	0.69
1:GA:44:ASN:HB2	1:GA:78:LEU:HA	1.72	0.69
1:BW:73:LEU:HD12	1:DQ:72:ASN:O	1.92	0.69
1:AA:44:ASN:HB2	1:AA:78:LEU:HA	1.72	0.69
1:AV:19:PHE:HB3	1:EF:89:ARG:NH2	2.07	0.69
1:BP:95:VAL:HG13	1:FB:95:VAL:HG13	1.75	0.69
1:IU:73:LEU:HD12	1:JE:72:ASN:O	1.92	0.69
1:AX:83:ASN:OD1	1:EJ:55:LEU:HD13	1.93	0.68
1:BQ:95:VAL:HG13	1:EC:95:VAL:HG13	1.75	0.68
1:BM:95:VAL:HG13	1:EY:95:VAL:HG13	1.76	0.68
1:AB:88:LEU:HG	1:FX:106:ILE:HG21	1.74	0.68
1:EQ:45:ILE:HG21	1:FM:108:GLY:HA3	1.76	0.68
1:BS:95:VAL:HG13	1:FE:95:VAL:HG13	1.74	0.68
1:CI:73:LEU:HD12	1:GH:72:ASN:O	1.93	0.68
1:EX:72:ASN:O	1:FI:73:LEU:HD12	1.94	0.68
1:HJ:99:THR:CG2	1:IZ:95:VAL:HG11	2.23	0.68
1:AY:73:LEU:HD12	1:EI:72:ASN:O	1.94	0.67
1:EB:106:ILE:HA	1:GB:75:PHE:HE2	1.59	0.67
1:HS:72:ASN:O	1:JL:73:LEU:HD12	1.92	0.67
1:CC:73:LEU:HD12	1:GK:72:ASN:O	1.94	0.67
1:CC:83:ASN:HD22	1:GK:55:LEU:HD13	1.60	0.67
1:EN:105:ILE:HG12	1:FJ:47:TYR:CZ	2.29	0.67
1:HI:72:ASN:O	1:JJ:73:LEU:HD12	1.95	0.67
1:ET:106:ILE:HG21	1:FG:88:LEU:HG	1.77	0.67
1:EX:112:THR:HG21	1:FI:4:LYS:HE2	1.77	0.67
1:CG:108:GLY:HA3	1:CL:45:ILE:HG21	1.75	0.67
1:EH:106:ILE:HG21	1:EO:88:LEU:HG	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EN:47:TYR:CZ	1:FJ:105:ILE:HG12	2.30	0.66
1:BS:95:VAL:HG11	1:FE:99:THR:CG2	2.25	0.66
1:CH:105:ILE:HG12	1:FT:47:TYR:CZ	2.31	0.66
1:AH:72:ASN:O	1:GD:73:LEU:HD12	1.95	0.66
1:CF:73:LEU:HD12	1:GN:72:ASN:O	1.96	0.66
1:HV:97:PHE:CG	1:JO:32:LEU:HD21	2.31	0.66
1:HT:78:LEU:HD12	1:IM:69:ILE:HG12	1.77	0.66
1:CH:98:ILE:HD11	1:FT:73:LEU:HD22	1.76	0.66
1:FA:72:ASN:O	1:FL:73:LEU:HD12	1.95	0.66
1:JD:73:LEU:HA	1:JN:72:ASN:O	1.96	0.66
1:EE:51:VAL:HG11	1:EU:90:VAL:HG13	1.77	0.66
1:AF:73:LEU:HD12	1:DR:72:ASN:O	1.96	0.65
1:AN:72:ASN:O	1:FR:73:LEU:HD12	1.95	0.65
1:AO:95:VAL:HG13	1:EA:95:VAL:HG13	1.77	0.65
1:AS:105:ILE:HG12	1:EL:47:TYR:CZ	2.30	0.65
1:IK:72:ASN:O	1:KJ:73:LEU:HD12	1.97	0.65
1:JD:89:ARG:HH22	1:JN:21:GLY:H	1.43	0.65
1:JA:73:LEU:HD12	1:JQ:72:ASN:O	1.97	0.65
1:AP:106:ILE:HG21	1:BU:88:LEU:HG	1.79	0.65
1:AN:47:TYR:CZ	1:FR:105:ILE:HG12	2.32	0.65
1:HT:51:VAL:HG11	1:IM:90:VAL:HG13	1.77	0.65
1:AN:47:TYR:CE2	1:FR:105:ILE:HG12	2.32	0.65
1:DM:73:LEU:HD12	1:GT:72:ASN:O	1.97	0.65
1:HT:73:LEU:HD12	1:IM:72:ASN:O	1.97	0.65
1:JA:106:ILE:HA	1:JQ:75:PHE:HE2	1.61	0.65
1:BS:72:ASN:O	1:FE:73:LEU:HD12	1.97	0.64
1:BD:53:TYR:CE2	1:EP:86:GLU:HG2	2.32	0.64
1:DC:73:LEU:HD12	1:GO:72:ASN:O	1.97	0.64
1:EN:45:ILE:HG21	1:FJ:108:GLY:HA3	1.79	0.64
1:HI:112:THR:HG21	1:JJ:4:LYS:HE2	1.78	0.64
1:CN:83:ASN:OD1	1:FZ:55:LEU:HD13	1.97	0.64
1:EB:73:LEU:HD12	1:GB:72:ASN:O	1.97	0.64
1:EE:73:LEU:HD12	1:EU:72:ASN:O	1.98	0.64
1:EN:109:ASN:CG	1:FJ:11:PRO:HB3	2.23	0.64
1:CC:83:ASN:ND2	1:GK:55:LEU:HD13	2.13	0.63
1:JD:71:ALA:HA	1:JN:74:SER:O	1.97	0.63
1:BQ:78:LEU:HD12	1:EC:69:ILE:HG12	1.80	0.63
1:CZ:73:LEU:HD12	1:GL:72:ASN:O	1.98	0.63
1:AD:45:ILE:HG21	1:BC:108:GLY:HA3	1.80	0.63
1:GY:105:ILE:HG12	1:HO:47:TYR:CZ	2.32	0.63
1:FP:112:THR:HG21	1:GV:4:LYS:HE2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HV:21:GLY:H	1:JO:89:ARG:HH22	1.46	0.63
1:CX:73:LEU:HD12	1:DK:72:ASN:O	1.99	0.63
1:EK:95:VAL:HG13	1:ER:95:VAL:HG13	1.81	0.63
1:HJ:95:VAL:HG11	1:IZ:99:THR:CG2	2.29	0.63
1:IU:106:ILE:HA	1:JE:75:PHE:HE2	1.63	0.63
1:AS:73:LEU:HD12	1:EL:72:ASN:O	1.97	0.63
1:IU:105:ILE:HG12	1:JE:47:TYR:CE2	2.33	0.63
1:CN:95:VAL:HG13	1:FZ:95:VAL:HG13	1.79	0.63
1:HL:108:GLY:HA3	1:JG:45:ILE:HG21	1.79	0.63
1:AM:4:LYS:HE2	1:CA:112:THR:HG21	1.81	0.62
1:CQ:72:ASN:O	1:GC:73:LEU:HD12	1.99	0.62
1:HE:45:ILE:HG21	1:HU:108:GLY:HA3	1.81	0.62
1:AE:69:ILE:HG12	1:GA:78:LEU:HD12	1.80	0.62
1:AQ:47:TYR:CZ	1:FU:105:ILE:HG12	2.34	0.62
1:AD:36:THR:HG23	1:BC:110:VAL:HB	1.81	0.62
1:AJ:73:LEU:HD12	1:BX:72:ASN:O	1.99	0.62
1:JT:72:ASN:O	1:KH:73:LEU:HD12	1.99	0.62
1:CJ:108:GLY:HA3	1:CO:45:ILE:HG21	1.81	0.62
1:BT:89:ARG:HH22	1:DN:21:GLY:H	1.44	0.62
1:EB:105:ILE:HG12	1:GB:47:TYR:CE2	2.34	0.62
1:EB:109:ASN:O	1:GB:47:TYR:HE1	1.83	0.62
1:IU:105:ILE:HG12	1:JE:47:TYR:CZ	2.35	0.62
1:DS:4:LYS:HE2	1:GQ:112:THR:HG21	1.82	0.62
1:FT:85:ASP:OD1	1:KH:20:THR:HB	1.99	0.62
1:BT:47:TYR:CZ	1:DN:105:ILE:HG12	2.35	0.62
1:EX:55:LEU:HD13	1:FI:83:ASN:ND2	2.15	0.62
1:IE:99:THR:CG2	1:KA:95:VAL:HG11	2.29	0.61
1:EE:71:ALA:HA	1:EU:74:SER:O	1.99	0.61
1:HT:73:LEU:HD13	1:IM:73:LEU:HB2	1.82	0.61
1:GZ:112:THR:HG21	1:JY:4:LYS:HE2	1.81	0.61
1:IA:112:THR:HG21	1:IC:4:LYS:HE2	1.82	0.61
1:BT:47:TYR:CE2	1:DN:105:ILE:HG12	2.35	0.61
1:AS:105:ILE:HG12	1:EL:47:TYR:CE2	2.34	0.61
1:BD:11:PRO:O	1:EP:110:VAL:HG12	2.01	0.61
1:EN:45:ILE:HD13	1:FJ:108:GLY:O	2.00	0.61
1:AX:73:LEU:HD12	1:EJ:72:ASN:O	2.00	0.61
1:AR:72:ASN:O	1:ED:73:LEU:HD12	2.01	0.61
1:AE:95:VAL:HG13	1:GA:95:VAL:HG13	1.83	0.61
1:BN:4:LYS:HE2	1:DZ:112:THR:HG21	1.83	0.61
1:HT:71:ALA:HB2	1:IM:75:PHE:HD1	1.64	0.61
1:JH:75:PHE:HD1	1:JP:71:ALA:HB2	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:89:ARG:HH22	1:BF:21:GLY:H	1.47	0.60
1:AI:95:VAL:HG13	1:DU:95:VAL:HG13	1.83	0.60
1:CG:32:LEU:HD11	1:CG:49:ILE:HG23	1.84	0.60
1:AT:32:LEU:HD11	1:AT:49:ILE:HG23	1.84	0.60
1:BO:32:LEU:HD11	1:BO:49:ILE:HG23	1.84	0.60
1:GY:112:THR:HG23	1:HO:17:TYR:OH	2.01	0.60
1:AN:32:LEU:HD11	1:AN:49:ILE:HG23	1.84	0.60
1:CV:32:LEU:HD11	1:CV:49:ILE:HG23	1.84	0.60
1:EF:32:LEU:HD11	1:EF:49:ILE:HG23	1.84	0.60
1:IY:32:LEU:HD11	1:IY:49:ILE:HG23	1.84	0.60
1:JE:32:LEU:HD11	1:JE:49:ILE:HG23	1.84	0.60
1:AK:32:LEU:HD11	1:AK:49:ILE:HG23	1.84	0.60
1:AZ:32:LEU:HD11	1:AZ:49:ILE:HG23	1.84	0.60
1:FA:32:LEU:HD11	1:FA:49:ILE:HG23	1.83	0.60
1:HR:32:LEU:HD11	1:HR:49:ILE:HG23	1.84	0.60
1:IV:32:LEU:HD11	1:IV:49:ILE:HG23	1.84	0.60
1:AC:72:ASN:O	1:DO:73:LEU:HD12	2.00	0.60
1:AH:32:LEU:HD11	1:AH:49:ILE:HG23	1.84	0.60
1:BC:32:LEU:HD11	1:BC:49:ILE:HG23	1.84	0.60
1:BJ:73:LEU:HD12	1:EV:72:ASN:O	2.01	0.60
1:DY:25:PRO:HA	1:EA:82:ILE:HG23	1.84	0.60
1:EI:32:LEU:HD11	1:EI:49:ILE:HG23	1.84	0.60
1:EX:32:LEU:HD11	1:EX:49:ILE:HG23	1.84	0.60
1:JH:32:LEU:HD11	1:JH:49:ILE:HG23	1.84	0.60
1:JQ:32:LEU:HD11	1:JQ:49:ILE:HG23	1.84	0.60
1:KC:32:LEU:HD11	1:KC:49:ILE:HG23	1.84	0.60
1:KI:32:LEU:HD11	1:KI:49:ILE:HG23	1.84	0.60
1:AO:72:ASN:O	1:EA:73:LEU:HD12	2.02	0.60
1:AS:25:PRO:HA	1:AU:82:ILE:HG23	1.84	0.60
1:BI:32:LEU:HD11	1:BI:49:ILE:HG23	1.84	0.60
1:BL:32:LEU:HD11	1:BL:49:ILE:HG23	1.84	0.60
1:BU:32:LEU:HD11	1:BU:49:ILE:HG23	1.84	0.60
1:CC:71:ALA:HB2	1:GK:75:PHE:HD1	1.66	0.60
1:CE:95:VAL:HG13	1:FQ:95:VAL:HG13	1.84	0.60
1:CS:32:LEU:HD11	1:CS:49:ILE:HG23	1.84	0.60
1:DW:32:LEU:HD11	1:DW:49:ILE:HG23	1.84	0.60
1:FC:25:PRO:HA	1:FE:82:ILE:HG23	1.84	0.60
1:FM:32:LEU:HD11	1:FM:49:ILE:HG23	1.84	0.60
1:HH:25:PRO:HA	1:HJ:82:ILE:HG23	1.84	0.60
1:HT:25:PRO:HA	1:HV:82:ILE:HG23	1.84	0.60
1:BX:32:LEU:HD11	1:BX:49:ILE:HG23	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:73:LEU:HD12	1:FQ:72:ASN:O	2.01	0.60
1:CF:25:PRO:HA	1:CH:82:ILE:HG23	1.84	0.60
1:CJ:32:LEU:HD11	1:CJ:49:ILE:HG23	1.84	0.60
1:CL:25:PRO:HA	1:CN:82:ILE:HG23	1.84	0.60
1:CM:32:LEU:HD11	1:CM:49:ILE:HG23	1.84	0.60
1:DZ:32:LEU:HD11	1:DZ:49:ILE:HG23	1.84	0.60
1:EC:32:LEU:HD11	1:EC:49:ILE:HG23	1.84	0.60
1:EN:105:ILE:HG12	1:FJ:47:TYR:CE2	2.36	0.60
1:EQ:25:PRO:HA	1:ES:82:ILE:HG23	1.84	0.60
1:FV:32:LEU:HD11	1:FV:49:ILE:HG23	1.84	0.60
1:GT:32:LEU:HD11	1:GT:49:ILE:HG23	1.84	0.60
1:GY:73:LEU:HD12	1:HO:72:ASN:O	2.02	0.60
1:HX:32:LEU:HD11	1:HX:49:ILE:HG23	1.84	0.60
1:JD:25:PRO:HA	1:JF:82:ILE:HG23	1.84	0.60
1:JG:25:PRO:HA	1:JI:82:ILE:HG23	1.84	0.60
1:JP:25:PRO:HA	1:JR:82:ILE:HG23	1.84	0.60
1:AY:25:PRO:HA	1:BA:82:ILE:HG23	1.84	0.60
1:BZ:25:PRO:HA	1:CB:82:ILE:HG23	1.84	0.60
1:DE:32:LEU:HD11	1:DE:49:ILE:HG23	1.84	0.60
1:DL:73:LEU:HD12	1:GX:72:ASN:O	2.02	0.60
1:EH:25:PRO:HA	1:EJ:82:ILE:HG23	1.84	0.60
1:EU:32:LEU:HD11	1:EU:49:ILE:HG23	1.84	0.60
1:FJ:32:LEU:HD11	1:FJ:49:ILE:HG23	1.84	0.60
1:GH:32:LEU:HD11	1:GH:49:ILE:HG23	1.84	0.60
1:GJ:25:PRO:HA	1:GL:82:ILE:HG23	1.84	0.60
1:HQ:89:ARG:HH22	1:IS:21:GLY:H	1.47	0.60
1:JB:32:LEU:HD11	1:JB:49:ILE:HG23	1.84	0.60
1:KE:25:PRO:HA	1:KG:82:ILE:HG23	1.84	0.60
1:AA:25:PRO:HA	1:AC:82:ILE:HG23	1.84	0.60
1:AD:25:PRO:HA	1:AF:82:ILE:HG23	1.84	0.60
1:AK:72:ASN:O	1:FO:73:LEU:HD12	2.01	0.60
1:BR:32:LEU:HD11	1:BR:49:ILE:HG23	1.84	0.60
1:CA:32:LEU:HD11	1:CA:49:ILE:HG23	1.84	0.60
1:DH:32:LEU:HD11	1:DH:49:ILE:HG23	1.84	0.60
1:DM:25:PRO:HA	1:DO:82:ILE:HG23	1.84	0.60
1:HO:32:LEU:HD11	1:HO:49:ILE:HG23	1.84	0.60
1:IM:32:LEU:HD11	1:IM:49:ILE:HG23	1.84	0.60
1:BE:25:PRO:HA	1:BG:82:ILE:HG23	1.84	0.59
1:CP:112:THR:HG21	1:DJ:4:LYS:HE2	1.82	0.59
1:GP:25:PRO:HA	1:GR:82:ILE:HG23	1.84	0.59
1:GW:32:LEU:HD11	1:GW:49:ILE:HG23	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IX:25:PRO:HA	1:IZ:82:ILE:HG23	1.84	0.59
1:JD:51:VAL:HG11	1:JN:90:VAL:HG13	1.84	0.59
1:JZ:32:LEU:HD11	1:JZ:49:ILE:HG23	1.84	0.59
1:AD:45:ILE:HD13	1:BC:108:GLY:O	2.02	0.59
1:HZ:25:PRO:HA	1:IB:82:ILE:HG23	1.84	0.59
1:IJ:32:LEU:HD11	1:IJ:49:ILE:HG23	1.84	0.59
1:IR:4:LYS:HE2	1:JZ:112:THR:HG21	1.82	0.59
1:IS:32:LEU:HD11	1:IS:49:ILE:HG23	1.84	0.59
1:IX:106:ILE:HG21	1:JB:88:LEU:HG	1.84	0.59
1:JK:32:LEU:HD11	1:JK:49:ILE:HG23	1.84	0.59
1:KB:25:PRO:HA	1:KD:82:ILE:HG23	1.84	0.59
1:AO:20:THR:HB	1:IF:114:THR:C	2.28	0.59
1:AU:11:PRO:HA	1:EG:111:LEU:HG	1.84	0.59
1:BD:73:LEU:HD13	1:EP:73:LEU:HD13	1.84	0.59
1:BH:25:PRO:HA	1:BJ:82:ILE:HG23	1.84	0.59
1:DB:32:LEU:HD11	1:DB:49:ILE:HG23	1.84	0.59
1:ET:25:PRO:HA	1:EV:82:ILE:HG23	1.84	0.59
1:HU:32:LEU:HD11	1:HU:49:ILE:HG23	1.84	0.59
1:JH:55:LEU:HD13	1:JP:83:ASN:HD22	1.67	0.59
1:JH:88:LEU:HG	1:JP:106:ILE:HG21	1.84	0.59
1:KF:32:LEU:HD11	1:KF:49:ILE:HG23	1.84	0.59
1:AQ:32:LEU:HD11	1:AQ:49:ILE:HG23	1.84	0.59
1:BS:106:ILE:HG21	1:FE:88:LEU:HD23	1.83	0.59
1:DJ:25:PRO:HA	1:DL:82:ILE:HG23	1.84	0.59
1:EQ:45:ILE:HD13	1:FM:108:GLY:O	2.02	0.59
1:HN:25:PRO:HA	1:HP:82:ILE:HG23	1.84	0.59
1:AM:25:PRO:HA	1:AO:82:ILE:HG23	1.84	0.59
1:AM:51:VAL:HG11	1:CA:90:VAL:HG13	1.83	0.59
1:CC:25:PRO:HA	1:CE:82:ILE:HG23	1.84	0.59
1:DA:25:PRO:HA	1:DC:82:ILE:HG23	1.84	0.59
1:EE:78:LEU:HD12	1:EU:69:ILE:HG12	1.85	0.59
1:FL:25:PRO:HA	1:FN:82:ILE:HG23	1.84	0.59
1:GA:25:PRO:HA	1:GC:82:ILE:HG23	1.84	0.59
1:GV:25:PRO:HA	1:GX:82:ILE:HG23	1.84	0.59
1:HG:72:ASN:O	1:IT:73:LEU:HD12	2.01	0.59
1:HL:32:LEU:HD11	1:HL:49:ILE:HG23	1.84	0.59
1:IC:25:PRO:HA	1:IE:82:ILE:HG23	1.84	0.59
1:IR:25:PRO:HA	1:IT:82:ILE:HG23	1.84	0.59
1:JT:32:LEU:HD11	1:JT:49:ILE:HG23	1.84	0.59
1:KH:25:PRO:HA	1:KJ:82:ILE:HG23	1.84	0.59
1:AG:47:TYR:CZ	1:BF:105:ILE:HG12	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:72:ASN:O	1:FN:73:LEU:HD12	2.02	0.59
1:EQ:45:ILE:CG2	1:FM:108:GLY:HA3	2.31	0.59
1:GB:32:LEU:HD11	1:GB:49:ILE:HG23	1.84	0.59
1:HY:72:ASN:O	1:JR:73:LEU:HD12	2.02	0.59
1:DK:32:LEU:HD11	1:DK:49:ILE:HG23	1.84	0.59
1:HV:73:LEU:HD12	1:JO:72:ASN:O	2.02	0.59
1:IA:32:LEU:HD11	1:IA:49:ILE:HG23	1.84	0.59
1:IP:32:LEU:HD11	1:IP:49:ILE:HG23	1.84	0.59
1:AG:25:PRO:HA	1:AI:82:ILE:HG23	1.84	0.59
1:AQ:72:ASN:O	1:FU:73:LEU:HD12	2.02	0.59
1:BY:72:ASN:O	1:FK:73:LEU:HD12	2.02	0.59
1:DN:32:LEU:HD11	1:DN:49:ILE:HG23	1.84	0.59
1:EO:32:LEU:HD11	1:EO:49:ILE:HG23	1.84	0.59
1:IF:25:PRO:HA	1:IH:82:ILE:HG23	1.84	0.59
1:JT:11:PRO:HB3	1:KH:109:ASN:CG	2.27	0.59
1:JY:25:PRO:HA	1:KA:82:ILE:HG23	1.84	0.59
1:AD:45:ILE:CG2	1:BC:108:GLY:HA3	2.32	0.59
1:AM:71:ALA:HB2	1:CA:75:PHE:HD1	1.66	0.59
1:AP:25:PRO:HA	1:AR:82:ILE:HG23	1.84	0.59
1:AW:32:LEU:HD11	1:AW:49:ILE:HG23	1.84	0.59
1:BF:32:LEU:HD11	1:BF:49:ILE:HG23	1.84	0.59
1:CY:108:GLY:HA3	1:GG:45:ILE:HG21	1.84	0.59
1:EB:106:ILE:HA	1:GB:75:PHE:CE2	2.37	0.59
1:EN:25:PRO:HA	1:EP:82:ILE:HG23	1.84	0.59
1:GE:32:LEU:HD11	1:GE:49:ILE:HG23	1.84	0.59
1:GZ:32:LEU:HD11	1:GZ:49:ILE:HG23	1.84	0.59
1:HC:32:LEU:HD11	1:HC:49:ILE:HG23	1.84	0.59
1:HQ:47:TYR:CE2	1:IS:105:ILE:HG12	2.38	0.59
1:ID:32:LEU:HD11	1:ID:49:ILE:HG23	1.84	0.59
1:IG:32:LEU:HD11	1:IG:49:ILE:HG23	1.84	0.59
1:AE:32:LEU:HD11	1:AE:49:ILE:HG23	1.84	0.59
1:AJ:25:PRO:HA	1:AL:82:ILE:HG23	1.84	0.59
1:AK:12:ILE:HD11	1:AK:45:ILE:HD13	1.85	0.59
1:CD:32:LEU:HD11	1:CD:49:ILE:HG23	1.84	0.59
1:CR:25:PRO:HA	1:CT:82:ILE:HG23	1.84	0.59
1:CV:72:ASN:O	1:GM:73:LEU:HD12	2.02	0.59
1:EB:105:ILE:HG12	1:GB:47:TYR:CZ	2.38	0.59
1:ER:32:LEU:HD11	1:ER:49:ILE:HG23	1.84	0.59
1:FF:25:PRO:HA	1:FH:82:ILE:HG23	1.84	0.59
1:FS:32:LEU:HD11	1:FS:49:ILE:HG23	1.84	0.59
1:HB:25:PRO:HA	1:HD:82:ILE:HG23	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HI:32:LEU:HD11	1:HI:49:ILE:HG23	1.84	0.59
1:AB:32:LEU:HD11	1:AB:49:ILE:HG23	1.84	0.58
1:AB:69:ILE:HG12	1:FX:78:LEU:HD12	1.85	0.58
1:CC:51:VAL:HG11	1:GK:90:VAL:HG13	1.83	0.58
1:CJ:12:ILE:HD11	1:CJ:45:ILE:HD13	1.85	0.58
1:DT:32:LEU:HD11	1:DT:49:ILE:HG23	1.84	0.58
1:EE:25:PRO:HA	1:EG:82:ILE:HG23	1.84	0.58
1:EE:73:LEU:HA	1:EU:72:ASN:O	2.03	0.58
1:FD:12:ILE:HD11	1:FD:45:ILE:HD13	1.85	0.58
1:FG:32:LEU:HD11	1:FG:49:ILE:HG23	1.84	0.58
1:GM:25:PRO:HA	1:GO:82:ILE:HG23	1.84	0.58
1:HE:25:PRO:HA	1:HG:82:ILE:HG23	1.84	0.58
1:HI:12:ILE:HD11	1:HI:45:ILE:HD13	1.85	0.58
1:HX:12:ILE:HD11	1:HX:45:ILE:HD13	1.85	0.58
1:IS:12:ILE:HD11	1:IS:45:ILE:HD13	1.85	0.58
1:IY:12:ILE:HD11	1:IY:45:ILE:HD13	1.85	0.58
1:JN:32:LEU:HD11	1:JN:49:ILE:HG23	1.84	0.58
1:KF:12:ILE:HD11	1:KF:45:ILE:HD13	1.85	0.58
1:AE:12:ILE:HD11	1:AE:45:ILE:HD13	1.85	0.58
1:AT:12:ILE:HD11	1:AT:45:ILE:HD13	1.85	0.58
1:BF:12:ILE:HD11	1:BF:45:ILE:HD13	1.85	0.58
1:BN:25:PRO:HA	1:BP:82:ILE:HG23	1.84	0.58
1:BW:25:PRO:HA	1:BY:82:ILE:HG23	1.84	0.58
1:CP:32:LEU:HD11	1:CP:49:ILE:HG23	1.84	0.58
1:FD:32:LEU:HD11	1:FD:49:ILE:HG23	1.84	0.58
1:FJ:12:ILE:HD11	1:FJ:45:ILE:HD13	1.85	0.58
1:FP:32:LEU:HD11	1:FP:49:ILE:HG23	1.84	0.58
1:GK:12:ILE:HD11	1:GK:45:ILE:HD13	1.85	0.58
1:HK:25:PRO:HA	1:HM:82:ILE:HG23	1.84	0.58
1:HQ:25:PRO:HA	1:HS:82:ILE:HG23	1.84	0.58
1:IG:95:VAL:HG11	1:KB:99:THR:CG2	2.33	0.58
1:IJ:12:ILE:HD11	1:IJ:45:ILE:HD13	1.85	0.58
1:IP:12:ILE:HD11	1:IP:45:ILE:HD13	1.85	0.58
1:AB:95:VAL:HG13	1:FX:95:VAL:HG13	1.84	0.58
1:AE:72:ASN:O	1:GA:73:LEU:HD12	2.04	0.58
1:BB:25:PRO:HA	1:BD:82:ILE:HG23	1.84	0.58
1:BL:12:ILE:HD11	1:BL:45:ILE:HD13	1.85	0.58
1:BQ:25:PRO:HA	1:BS:82:ILE:HG23	1.84	0.58
1:CI:25:PRO:HA	1:CK:82:ILE:HG23	1.84	0.58
1:CP:12:ILE:HD11	1:CP:45:ILE:HD13	1.85	0.58
1:CU:25:PRO:HA	1:CW:82:ILE:HG23	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DN:12:ILE:HD11	1:DN:45:ILE:HD13	1.86	0.58
1:DZ:12:ILE:HD11	1:DZ:45:ILE:HD13	1.85	0.58
1:EO:12:ILE:HD11	1:EO:45:ILE:HD13	1.85	0.58
1:FO:25:PRO:HA	1:FQ:82:ILE:HG23	1.84	0.58
1:FP:12:ILE:HD11	1:FP:45:ILE:HD13	1.85	0.58
1:GK:32:LEU:HD11	1:GK:49:ILE:HG23	1.84	0.58
1:GQ:12:ILE:HD11	1:GQ:45:ILE:HD13	1.85	0.58
1:GQ:32:LEU:HD11	1:GQ:49:ILE:HG23	1.84	0.58
1:HA:83:ASN:OD1	1:IQ:55:LEU:HD13	2.03	0.58
1:HF:32:LEU:HD11	1:HF:49:ILE:HG23	1.84	0.58
1:HW:25:PRO:HA	1:HY:82:ILE:HG23	1.84	0.58
1:IU:109:ASN:O	1:JE:47:TYR:HE1	1.87	0.58
1:JH:12:ILE:HD11	1:JH:45:ILE:HD13	1.85	0.58
1:JN:12:ILE:HD11	1:JN:45:ILE:HD13	1.85	0.58
1:JW:32:LEU:HD11	1:JW:49:ILE:HG23	1.84	0.58
1:AC:95:VAL:HG13	1:DO:95:VAL:HG13	1.84	0.58
1:BM:72:ASN:O	1:EY:73:LEU:HD12	2.03	0.58
1:CI:21:GLY:H	1:GH:89:ARG:HH22	1.51	0.58
1:CO:25:PRO:HA	1:CQ:82:ILE:HG23	1.84	0.58
1:DD:25:PRO:HA	1:DF:82:ILE:HG23	1.84	0.58
1:DP:25:PRO:HA	1:DR:82:ILE:HG23	1.84	0.58
1:DS:25:PRO:HA	1:DU:82:ILE:HG23	1.84	0.58
1:EB:25:PRO:HA	1:ED:82:ILE:HG23	1.84	0.58
1:HC:12:ILE:HD11	1:HC:45:ILE:HD13	1.85	0.58
1:IB:95:VAL:HG13	1:JX:95:VAL:HG13	1.84	0.58
1:JE:12:ILE:HD11	1:JE:45:ILE:HD13	1.85	0.58
1:JM:25:PRO:HA	1:JO:82:ILE:HG23	1.84	0.58
1:JS:25:PRO:HA	1:JU:82:ILE:HG23	1.84	0.58
1:JV:25:PRO:HA	1:JX:82:ILE:HG23	1.84	0.58
1:AN:89:ARG:HH22	1:FR:21:GLY:H	1.51	0.58
1:AQ:47:TYR:CE2	1:FU:105:ILE:HG12	2.38	0.58
1:BT:25:PRO:HA	1:BV:82:ILE:HG23	1.84	0.58
1:CI:74:SER:O	1:GH:71:ALA:HA	2.03	0.58
1:CV:12:ILE:HD11	1:CV:45:ILE:HD13	1.85	0.58
1:CX:25:PRO:HA	1:CZ:82:ILE:HG23	1.84	0.58
1:EZ:25:PRO:HA	1:FB:82:ILE:HG23	1.84	0.58
1:FR:25:PRO:HA	1:FT:82:ILE:HG23	1.84	0.58
1:GB:44:ASN:HB2	1:GB:78:LEU:HA	1.86	0.58
1:GW:44:ASN:HB2	1:GW:78:LEU:HA	1.86	0.58
1:HC:44:ASN:HB2	1:HC:78:LEU:HA	1.86	0.58
1:II:25:PRO:HA	1:IK:82:ILE:HG23	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JA:25:PRO:HA	1:JC:82:ILE:HG23	1.84	0.58
1:JK:75:PHE:HE2	1:JM:106:ILE:HA	1.69	0.58
1:AQ:44:ASN:HB2	1:AQ:78:LEU:HA	1.86	0.58
1:BR:12:ILE:HD11	1:BR:45:ILE:HD13	1.85	0.58
1:CD:44:ASN:HB2	1:CD:78:LEU:HA	1.86	0.58
1:CG:108:GLY:O	1:CL:45:ILE:HD13	2.03	0.58
1:CH:105:ILE:HA	1:FT:47:TYR:CD1	2.39	0.58
1:CU:95:VAL:HG13	1:DH:95:VAL:HG13	1.85	0.58
1:DK:44:ASN:HB2	1:DK:78:LEU:HA	1.86	0.58
1:EF:12:ILE:HD11	1:EF:45:ILE:HD13	1.85	0.58
1:EL:32:LEU:HD11	1:EL:49:ILE:HG23	1.84	0.58
1:FD:72:ASN:O	1:FF:73:LEU:HD12	2.03	0.58
1:FS:12:ILE:HD11	1:FS:45:ILE:HD13	1.85	0.58
1:FY:32:LEU:HD11	1:FY:49:ILE:HG23	1.84	0.58
1:GG:25:PRO:HA	1:GI:82:ILE:HG23	1.84	0.58
1:GN:32:LEU:HD11	1:GN:49:ILE:HG23	1.84	0.58
1:GT:12:ILE:HD11	1:GT:45:ILE:HD13	1.85	0.58
1:HO:44:ASN:HB2	1:HO:78:LEU:HA	1.86	0.58
1:JN:44:ASN:HB2	1:JN:78:LEU:HA	1.86	0.58
1:JW:12:ILE:HD11	1:JW:45:ILE:HD13	1.85	0.58
1:AK:44:ASN:HB2	1:AK:78:LEU:HA	1.86	0.58
1:AN:12:ILE:HD11	1:AN:45:ILE:HD13	1.85	0.58
1:AV:25:PRO:HA	1:AX:82:ILE:HG23	1.84	0.58
1:BQ:73:LEU:CD2	1:EC:98:ILE:HD11	2.33	0.58
1:CM:72:ASN:O	1:DG:73:LEU:HD12	2.03	0.58
1:CP:72:ASN:O	1:DJ:73:LEU:HD12	2.04	0.58
1:DV:25:PRO:HA	1:DX:82:ILE:HG23	1.84	0.58
1:EW:25:PRO:HA	1:EY:82:ILE:HG23	1.84	0.58
1:GY:25:PRO:HA	1:HA:82:ILE:HG23	1.84	0.58
1:IA:12:ILE:HD11	1:IA:45:ILE:HD13	1.85	0.58
1:IL:25:PRO:HA	1:IN:82:ILE:HG23	1.84	0.58
1:KC:44:ASN:HB2	1:KC:78:LEU:HA	1.86	0.58
1:AU:89:ARG:NH2	1:EG:19:PHE:HB3	2.19	0.58
1:BI:12:ILE:HD11	1:BI:45:ILE:HD13	1.85	0.58
1:DG:25:PRO:HA	1:DI:82:ILE:HG23	1.84	0.58
1:DZ:44:ASN:HB2	1:DZ:78:LEU:HA	1.86	0.58
1:EL:44:ASN:HB2	1:EL:78:LEU:HA	1.86	0.58
1:FM:12:ILE:HD11	1:FM:45:ILE:HD13	1.85	0.58
1:FP:21:GLY:H	1:GV:89:ARG:HH22	1.51	0.58
1:GD:25:PRO:HA	1:GF:82:ILE:HG23	1.84	0.58
1:GE:44:ASN:HB2	1:GE:78:LEU:HA	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GK:44:ASN:HB2	1:GK:78:LEU:HA	1.86	0.58
1:GQ:44:ASN:HB2	1:GQ:78:LEU:HA	1.86	0.58
1:JB:44:ASN:HB2	1:JB:78:LEU:HA	1.86	0.58
1:JT:44:ASN:HB2	1:JT:78:LEU:HA	1.86	0.58
1:AT:44:ASN:HB2	1:AT:78:LEU:HA	1.86	0.58
1:AW:12:ILE:HD11	1:AW:45:ILE:HD13	1.85	0.58
1:CG:44:ASN:HB2	1:CG:78:LEU:HA	1.86	0.58
1:CJ:44:ASN:HB2	1:CJ:78:LEU:HA	1.86	0.58
1:DE:12:ILE:HD11	1:DE:45:ILE:HD13	1.85	0.58
1:DY:73:LEU:HD12	1:FY:72:ASN:O	2.04	0.58
1:FD:44:ASN:HB2	1:FD:78:LEU:HA	1.86	0.58
1:FP:44:ASN:HB2	1:FP:78:LEU:HA	1.86	0.58
1:FY:12:ILE:HD11	1:FY:45:ILE:HD13	1.85	0.58
1:FY:44:ASN:HB2	1:FY:78:LEU:HA	1.86	0.58
1:GY:47:TYR:CZ	1:HO:105:ILE:HG12	2.39	0.58
1:GY:105:ILE:HG12	1:HO:47:TYR:CE2	2.38	0.58
1:IP:44:ASN:HB2	1:IP:78:LEU:HA	1.86	0.58
1:JH:55:LEU:HD13	1:JP:83:ASN:ND2	2.19	0.58
1:AV:45:ILE:HG21	1:EF:108:GLY:HA3	1.86	0.58
1:AV:89:ARG:HH22	1:EF:21:GLY:H	1.52	0.58
1:BB:4:LYS:HE2	1:BR:112:THR:HG21	1.84	0.58
1:BK:25:PRO:HA	1:BM:82:ILE:HG23	1.84	0.58
1:BK:32:LEU:HD11	1:BK:49:ILE:HG23	1.86	0.58
1:CS:44:ASN:HB2	1:CS:78:LEU:HA	1.86	0.58
1:CU:32:LEU:HD11	1:CU:49:ILE:HG23	1.86	0.58
1:EC:44:ASN:HB2	1:EC:78:LEU:HA	1.86	0.58
1:EL:12:ILE:HD11	1:EL:45:ILE:HD13	1.85	0.58
1:FI:25:PRO:HA	1:FK:82:ILE:HG23	1.84	0.58
1:FU:25:PRO:HA	1:FW:82:ILE:HG23	1.84	0.58
1:GM:32:LEU:HD11	1:GM:49:ILE:HG23	1.86	0.58
1:HW:32:LEU:HD11	1:HW:49:ILE:HG23	1.86	0.58
1:HX:44:ASN:HB2	1:HX:78:LEU:HA	1.86	0.58
1:ID:44:ASN:HB2	1:ID:78:LEU:HA	1.86	0.58
1:IU:25:PRO:HA	1:IW:82:ILE:HG23	1.84	0.58
1:JW:44:ASN:HB2	1:JW:78:LEU:HA	1.86	0.58
1:AE:44:ASN:HB2	1:AE:78:LEU:HA	1.86	0.57
1:CP:44:ASN:HB2	1:CP:78:LEU:HA	1.86	0.57
1:CY:32:LEU:HD11	1:CY:49:ILE:HG23	1.84	0.57
1:EN:32:LEU:HD11	1:EN:49:ILE:HG23	1.86	0.57
1:EW:32:LEU:HD11	1:EW:49:ILE:HG23	1.86	0.57
1:GS:32:LEU:HD11	1:GS:49:ILE:HG23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HC:72:ASN:O	1:JS:73:LEU:HD12	2.03	0.57
1:HF:44:ASN:HB2	1:HF:78:LEU:HA	1.86	0.57
1:HS:89:ARG:HH22	1:JL:21:GLY:H	1.52	0.57
1:IF:32:LEU:HD11	1:IF:49:ILE:HG23	1.86	0.57
1:II:32:LEU:HD11	1:II:49:ILE:HG23	1.86	0.57
1:IR:32:LEU:HD11	1:IR:49:ILE:HG23	1.86	0.57
1:JJ:25:PRO:HA	1:JL:82:ILE:HG23	1.84	0.57
1:JZ:44:ASN:HB2	1:JZ:78:LEU:HA	1.86	0.57
1:BC:44:ASN:HB2	1:BC:78:LEU:HA	1.86	0.57
1:BD:55:LEU:HD13	1:EP:83:ASN:OD1	2.03	0.57
1:CE:49:ILE:HD12	1:CE:73:LEU:HD23	1.87	0.57
1:DE:44:ASN:HB2	1:DE:78:LEU:HA	1.86	0.57
1:DG:32:LEU:HD11	1:DG:49:ILE:HG23	1.86	0.57
1:EF:44:ASN:HB2	1:EF:78:LEU:HA	1.86	0.57
1:EU:44:ASN:HB2	1:EU:78:LEU:HA	1.86	0.57
1:FC:32:LEU:HD11	1:FC:49:ILE:HG23	1.86	0.57
1:FX:25:PRO:HA	1:FZ:82:ILE:HG23	1.84	0.57
1:FZ:49:ILE:HD12	1:FZ:73:LEU:HD23	1.87	0.57
1:GN:12:ILE:HD11	1:GN:45:ILE:HD13	1.85	0.57
1:GP:32:LEU:HD11	1:GP:49:ILE:HG23	1.86	0.57
1:GS:25:PRO:HA	1:GU:82:ILE:HG23	1.84	0.57
1:HJ:99:THR:HG23	1:IZ:95:VAL:HG11	1.84	0.57
1:HO:12:ILE:HD11	1:HO:45:ILE:HD13	1.85	0.57
1:JD:74:SER:O	1:JN:71:ALA:HA	2.04	0.57
1:AA:32:LEU:HD11	1:AA:49:ILE:HG23	1.86	0.57
1:AM:78:LEU:HD12	1:CA:69:ILE:HG12	1.86	0.57
1:AN:44:ASN:HB2	1:AN:78:LEU:HA	1.86	0.57
1:BD:51:VAL:HG11	1:EP:90:VAL:HG13	1.86	0.57
1:BD:95:VAL:HG13	1:EP:95:VAL:HG13	1.85	0.57
1:BE:32:LEU:HD11	1:BE:49:ILE:HG23	1.86	0.57
1:BG:49:ILE:HD12	1:BG:73:LEU:HD23	1.87	0.57
1:BJ:49:ILE:HD12	1:BJ:73:LEU:HD23	1.87	0.57
1:BU:44:ASN:HB2	1:BU:78:LEU:HA	1.86	0.57
1:BX:12:ILE:HD11	1:BX:45:ILE:HD13	1.85	0.57
1:CA:12:ILE:HD11	1:CA:45:ILE:HD13	1.85	0.57
1:CB:49:ILE:HD12	1:CB:73:LEU:HD23	1.87	0.57
1:CY:12:ILE:HD11	1:CY:45:ILE:HD13	1.85	0.57
1:DC:49:ILE:HD12	1:DC:73:LEU:HD23	1.87	0.57
1:DQ:32:LEU:HD11	1:DQ:49:ILE:HG23	1.84	0.57
1:EK:25:PRO:HA	1:EM:82:ILE:HG23	1.84	0.57
1:EM:49:ILE:HD12	1:EM:73:LEU:HD23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EQ:32:LEU:HD11	1:EQ:49:ILE:HG23	1.86	0.57
1:FN:49:ILE:HD12	1:FN:73:LEU:HD23	1.87	0.57
1:GC:49:ILE:HD12	1:GC:73:LEU:HD23	1.87	0.57
1:GY:32:LEU:HD11	1:GY:49:ILE:HG23	1.86	0.57
1:HJ:95:VAL:HG11	1:IZ:99:THR:HG23	1.86	0.57
1:HK:32:LEU:HD11	1:HK:49:ILE:HG23	1.86	0.57
1:HL:44:ASN:HB2	1:HL:78:LEU:HA	1.86	0.57
1:IM:12:ILE:HD11	1:IM:45:ILE:HD13	1.85	0.57
1:IV:44:ASN:HB2	1:IV:78:LEU:HA	1.86	0.57
1:JF:49:ILE:HD12	1:JF:73:LEU:HD23	1.87	0.57
1:KI:12:ILE:HD11	1:KI:45:ILE:HD13	1.85	0.57
1:AG:32:LEU:HD11	1:AG:49:ILE:HG23	1.86	0.57
1:AI:49:ILE:HD12	1:AI:73:LEU:HD23	1.87	0.57
1:BB:32:LEU:HD11	1:BB:49:ILE:HG23	1.86	0.57
1:CS:12:ILE:HD11	1:CS:45:ILE:HD13	1.85	0.57
1:DK:12:ILE:HD11	1:DK:45:ILE:HD13	1.85	0.57
1:DM:32:LEU:HD11	1:DM:49:ILE:HG23	1.86	0.57
1:DV:32:LEU:HD11	1:DV:49:ILE:HG23	1.86	0.57
1:EE:32:LEU:HD11	1:EE:49:ILE:HG23	1.86	0.57
1:FA:44:ASN:HB2	1:FA:78:LEU:HA	1.86	0.57
1:FU:32:LEU:HD11	1:FU:49:ILE:HG23	1.86	0.57
1:GE:12:ILE:HD11	1:GE:45:ILE:HD13	1.85	0.57
1:GH:12:ILE:HD11	1:GH:45:ILE:HD13	1.85	0.57
1:GZ:12:ILE:HD11	1:GZ:45:ILE:HD13	1.85	0.57
1:HE:32:LEU:HD11	1:HE:49:ILE:HG23	1.86	0.57
1:IW:49:ILE:HD12	1:IW:73:LEU:HD23	1.87	0.57
1:JJ:32:LEU:HD11	1:JJ:49:ILE:HG23	1.86	0.57
1:JQ:44:ASN:HB2	1:JQ:78:LEU:HA	1.86	0.57
1:KE:32:LEU:HD11	1:KE:49:ILE:HG23	1.86	0.57
1:AD:19:PHE:HB3	1:BC:89:ARG:NH2	2.19	0.57
1:BA:49:ILE:HD12	1:BA:73:LEU:HD23	1.87	0.57
1:BD:49:ILE:HD12	1:BD:73:LEU:HD23	1.87	0.57
1:BV:49:ILE:HD12	1:BV:73:LEU:HD23	1.87	0.57
1:CV:44:ASN:HB2	1:CV:78:LEU:HA	1.86	0.57
1:DA:32:LEU:HD11	1:DA:49:ILE:HG23	1.86	0.57
1:DO:49:ILE:HD12	1:DO:73:LEU:HD23	1.87	0.57
1:EU:12:ILE:HD11	1:EU:45:ILE:HD13	1.85	0.57
1:FI:32:LEU:HD11	1:FI:49:ILE:HG23	1.86	0.57
1:FT:49:ILE:HD12	1:FT:73:LEU:HD23	1.87	0.57
1:GF:49:ILE:HD12	1:GF:73:LEU:HD23	1.87	0.57
1:HG:49:ILE:HD12	1:HG:73:LEU:HD23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HV:49:ILE:HD12	1:HV:73:LEU:HD23	1.87	0.57
1:IG:44:ASN:HB2	1:IG:78:LEU:HA	1.86	0.57
1:IJ:44:ASN:HB2	1:IJ:78:LEU:HA	1.86	0.57
1:JI:49:ILE:HD12	1:JI:73:LEU:HD23	1.87	0.57
1:JK:12:ILE:HD11	1:JK:45:ILE:HD13	1.85	0.57
1:JV:32:LEU:HD11	1:JV:49:ILE:HG23	1.86	0.57
1:AM:32:LEU:HD11	1:AM:49:ILE:HG23	1.86	0.57
1:AR:49:ILE:HD12	1:AR:73:LEU:HD23	1.87	0.57
1:AX:49:ILE:HD12	1:AX:73:LEU:HD23	1.87	0.57
1:AZ:44:ASN:HB2	1:AZ:78:LEU:HA	1.86	0.57
1:BP:49:ILE:HD12	1:BP:73:LEU:HD23	1.87	0.57
1:BR:44:ASN:HB2	1:BR:78:LEU:HA	1.86	0.57
1:BX:44:ASN:HB2	1:BX:78:LEU:HA	1.86	0.57
1:CC:32:LEU:HD11	1:CC:49:ILE:HG23	1.86	0.57
1:CN:73:LEU:HD13	1:FZ:73:LEU:HD13	1.86	0.57
1:CY:44:ASN:HB2	1:CY:78:LEU:HA	1.86	0.57
1:DM:4:LYS:HE2	1:GT:112:THR:HG21	1.86	0.57
1:DP:32:LEU:HD11	1:DP:49:ILE:HG23	1.86	0.57
1:DQ:12:ILE:HD11	1:DQ:45:ILE:HD13	1.85	0.57
1:DU:49:ILE:HD12	1:DU:73:LEU:HD23	1.87	0.57
1:EI:44:ASN:HB2	1:EI:78:LEU:HA	1.86	0.57
1:EJ:49:ILE:HD12	1:EJ:73:LEU:HD23	1.86	0.57
1:GH:44:ASN:HB2	1:GH:78:LEU:HA	1.86	0.57
1:GJ:32:LEU:HD11	1:GJ:49:ILE:HG23	1.86	0.57
1:HK:89:ARG:HH22	1:IY:21:GLY:H	1.53	0.57
1:HL:108:GLY:HA3	1:JG:45:ILE:CG2	2.35	0.57
1:HL:108:GLY:O	1:JG:45:ILE:HD13	2.05	0.57
1:IC:32:LEU:HD11	1:IC:49:ILE:HG23	1.86	0.57
1:JT:12:ILE:HD11	1:JT:45:ILE:HD13	1.85	0.57
1:JX:49:ILE:HD12	1:JX:73:LEU:HD23	1.87	0.57
1:AD:32:LEU:HD11	1:AD:49:ILE:HG23	1.86	0.57
1:AF:49:ILE:HD12	1:AF:73:LEU:HD23	1.87	0.57
1:AY:105:ILE:HG12	1:EI:47:TYR:CZ	2.39	0.57
1:BG:73:LEU:HD12	1:ES:72:ASN:O	2.04	0.57
1:BU:12:ILE:HD11	1:BU:45:ILE:HD13	1.85	0.57
1:BW:32:LEU:HD11	1:BW:49:ILE:HG23	1.86	0.57
1:CG:108:GLY:HA3	1:CL:45:ILE:CG2	2.34	0.57
1:DH:12:ILE:HD11	1:DH:45:ILE:HD13	1.85	0.57
1:EH:32:LEU:HD11	1:EH:49:ILE:HG23	1.86	0.57
1:EV:49:ILE:HD12	1:EV:73:LEU:HD23	1.87	0.57
1:EY:49:ILE:HD12	1:EY:73:LEU:HD23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FH:49:ILE:HD12	1:FH:73:LEU:HD23	1.86	0.57
1:FS:55:LEU:HD13	1:GP:83:ASN:HD22	1.70	0.57
1:GA:32:LEU:HD11	1:GA:49:ILE:HG23	1.86	0.57
1:GL:49:ILE:HD12	1:GL:73:LEU:HD23	1.87	0.57
1:HR:12:ILE:HD11	1:HR:45:ILE:HD13	1.85	0.57
1:HR:44:ASN:HB2	1:HR:78:LEU:HA	1.86	0.57
1:HW:89:ARG:HH22	1:IP:21:GLY:H	1.50	0.57
1:IG:12:ILE:HD11	1:IG:45:ILE:HD13	1.85	0.57
1:IO:25:PRO:HA	1:IQ:82:ILE:HG23	1.84	0.57
1:IZ:49:ILE:HD12	1:IZ:73:LEU:HD23	1.87	0.57
1:JR:49:ILE:HD12	1:JR:73:LEU:HD23	1.87	0.57
1:KJ:49:ILE:HD12	1:KJ:73:LEU:HD23	1.87	0.57
1:AH:12:ILE:HD11	1:AH:45:ILE:HD13	1.85	0.57
1:AH:44:ASN:HB2	1:AH:78:LEU:HA	1.86	0.57
1:AL:49:ILE:HD12	1:AL:73:LEU:HD23	1.87	0.57
1:AV:47:TYR:CZ	1:EF:105:ILE:HG12	2.39	0.57
1:BA:95:VAL:HG13	1:EM:95:VAL:HG13	1.87	0.57
1:BF:44:ASN:HB2	1:BF:78:LEU:HA	1.86	0.57
1:CA:44:ASN:HB2	1:CA:78:LEU:HA	1.86	0.57
1:CI:32:LEU:HD11	1:CI:49:ILE:HG23	1.86	0.57
1:CM:12:ILE:HD11	1:CM:45:ILE:HD13	1.85	0.57
1:CM:44:ASN:HB2	1:CM:78:LEU:HA	1.86	0.57
1:CN:49:ILE:HD12	1:CN:73:LEU:HD23	1.87	0.57
1:EC:12:ILE:HD11	1:EC:45:ILE:HD13	1.85	0.57
1:EX:44:ASN:HB2	1:EX:78:LEU:HA	1.86	0.57
1:FV:88:LEU:HG	1:GS:106:ILE:HD13	1.84	0.57
1:GN:44:ASN:HB2	1:GN:78:LEU:HA	1.86	0.57
1:GW:12:ILE:HD11	1:GW:45:ILE:HD13	1.85	0.57
1:HP:49:ILE:HD12	1:HP:73:LEU:HD23	1.87	0.57
1:IN:49:ILE:HD12	1:IN:73:LEU:HD23	1.86	0.57
1:JB:12:ILE:HD11	1:JB:45:ILE:HD13	1.85	0.57
1:JC:49:ILE:HD12	1:JC:73:LEU:HD23	1.86	0.57
1:JH:95:VAL:HG13	1:JP:95:VAL:HG13	1.86	0.57
1:JZ:12:ILE:HD11	1:JZ:45:ILE:HD13	1.85	0.57
1:AD:110:VAL:HB	1:BC:36:THR:HG23	1.87	0.57
1:AJ:32:LEU:HD11	1:AJ:49:ILE:HG23	1.87	0.57
1:AQ:12:ILE:HD11	1:AQ:45:ILE:HD13	1.85	0.57
1:BT:32:LEU:HD11	1:BT:49:ILE:HG23	1.86	0.57
1:CJ:105:ILE:HG12	1:CO:47:TYR:CZ	2.39	0.57
1:CK:49:ILE:HD12	1:CK:73:LEU:HD23	1.86	0.57
1:CN:73:LEU:HD12	1:FZ:72:ASN:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DB:44:ASN:HB2	1:DB:78:LEU:HA	1.86	0.57
1:EN:93:GLU:OE1	1:FJ:2:ILE:HG23	2.04	0.57
1:FM:44:ASN:HB2	1:FM:78:LEU:HA	1.86	0.57
1:FV:44:ASN:HB2	1:FV:78:LEU:HA	1.86	0.57
1:FW:49:ILE:HD12	1:FW:73:LEU:HD23	1.87	0.57
1:GD:32:LEU:HD11	1:GD:49:ILE:HG23	1.86	0.57
1:JM:32:LEU:HD11	1:JM:49:ILE:HG23	1.86	0.57
1:JY:32:LEU:HD11	1:JY:49:ILE:HG23	1.86	0.57
1:AL:73:LEU:HD12	1:DX:72:ASN:O	2.04	0.57
1:AO:49:ILE:HD12	1:AO:73:LEU:HD23	1.87	0.57
1:BI:44:ASN:HB2	1:BI:78:LEU:HA	1.86	0.57
1:BM:49:ILE:HD12	1:BM:73:LEU:HD23	1.87	0.57
1:BM:95:VAL:HG11	1:EY:99:THR:CG2	2.34	0.57
1:CT:73:LEU:HD12	1:GF:72:ASN:O	2.04	0.57
1:DT:12:ILE:HD11	1:DT:45:ILE:HD13	1.85	0.57
1:DW:12:ILE:HD11	1:DW:45:ILE:HD13	1.85	0.57
1:FB:49:ILE:HD12	1:FB:73:LEU:HD23	1.87	0.57
1:GB:12:ILE:HD11	1:GB:45:ILE:HD13	1.85	0.57
1:GU:49:ILE:HD12	1:GU:73:LEU:HD23	1.87	0.57
1:GZ:44:ASN:HB2	1:GZ:78:LEU:HA	1.86	0.57
1:HL:12:ILE:HD11	1:HL:45:ILE:HD13	1.85	0.57
1:IA:44:ASN:HB2	1:IA:78:LEU:HA	1.86	0.57
1:ID:12:ILE:HD11	1:ID:45:ILE:HD13	1.85	0.57
1:JG:32:LEU:HD11	1:JG:49:ILE:HG23	1.86	0.57
1:JH:44:ASN:HB2	1:JH:78:LEU:HA	1.86	0.57
1:JK:44:ASN:HB2	1:JK:78:LEU:HA	1.86	0.57
1:AV:2:ILE:HG23	1:EF:93:GLU:OE1	2.05	0.56
1:BC:12:ILE:HD11	1:BC:45:ILE:HD13	1.85	0.56
1:BO:44:ASN:HB2	1:BO:78:LEU:HA	1.86	0.56
1:CD:12:ILE:HD11	1:CD:45:ILE:HD13	1.85	0.56
1:CO:32:LEU:HD11	1:CO:49:ILE:HG23	1.87	0.56
1:CX:32:LEU:HD11	1:CX:49:ILE:HG23	1.87	0.56
1:DQ:44:ASN:HB2	1:DQ:78:LEU:HA	1.86	0.56
1:DY:32:LEU:HD11	1:DY:49:ILE:HG23	1.86	0.56
1:ET:32:LEU:HD11	1:ET:49:ILE:HG23	1.87	0.56
1:FQ:49:ILE:HD12	1:FQ:73:LEU:HD23	1.87	0.56
1:FS:44:ASN:HB2	1:FS:78:LEU:HA	1.86	0.56
1:FX:32:LEU:HD11	1:FX:49:ILE:HG23	1.86	0.56
1:GG:32:LEU:HD11	1:GG:49:ILE:HG23	1.86	0.56
1:HD:49:ILE:HD12	1:HD:73:LEU:HD23	1.87	0.56
1:HH:32:LEU:HD11	1:HH:49:ILE:HG23	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HT:81:VAL:HG21	1:IM:55:LEU:CD1	2.35	0.56
1:HU:44:ASN:HB2	1:HU:78:LEU:HA	1.86	0.56
1:JQ:12:ILE:HD11	1:JQ:45:ILE:HD13	1.85	0.56
1:KF:44:ASN:HB2	1:KF:78:LEU:HA	1.86	0.56
1:KG:49:ILE:HD12	1:KG:73:LEU:HD23	1.87	0.56
1:KH:32:LEU:HD11	1:KH:49:ILE:HG23	1.86	0.56
1:CH:49:ILE:HD12	1:CH:73:LEU:HD23	1.87	0.56
1:DB:12:ILE:HD11	1:DB:45:ILE:HD13	1.85	0.56
1:DD:32:LEU:HD11	1:DD:49:ILE:HG23	1.86	0.56
1:DH:44:ASN:HB2	1:DH:78:LEU:HA	1.86	0.56
1:EA:49:ILE:HD12	1:EA:73:LEU:HD23	1.87	0.56
1:EG:49:ILE:HD12	1:EG:73:LEU:HD23	1.87	0.56
1:EN:45:ILE:CG2	1:FJ:108:GLY:HA3	2.35	0.56
1:GI:49:ILE:HD12	1:GI:73:LEU:HD23	1.87	0.56
1:GV:32:LEU:HD11	1:GV:49:ILE:HG23	1.86	0.56
1:HA:95:VAL:HG13	1:IQ:95:VAL:HG13	1.86	0.56
1:HI:44:ASN:HB2	1:HI:78:LEU:HA	1.86	0.56
1:HQ:32:LEU:HD11	1:HQ:49:ILE:HG23	1.86	0.56
1:HQ:47:TYR:CZ	1:IS:105:ILE:HG12	2.40	0.56
1:IO:32:LEU:HD11	1:IO:49:ILE:HG23	1.86	0.56
1:JA:106:ILE:HA	1:JQ:75:PHE:CE2	2.39	0.56
1:KB:32:LEU:HD11	1:KB:49:ILE:HG23	1.86	0.56
1:AB:44:ASN:HB2	1:AB:78:LEU:HA	1.86	0.56
1:AG:47:TYR:CE2	1:BF:105:ILE:HG12	2.39	0.56
1:AP:32:LEU:HD11	1:AP:49:ILE:HG23	1.86	0.56
1:AW:44:ASN:HB2	1:AW:78:LEU:HA	1.86	0.56
1:AY:106:ILE:HA	1:EI:75:PHE:HE2	1.70	0.56
1:AZ:12:ILE:HD11	1:AZ:45:ILE:HD13	1.85	0.56
1:BD:72:ASN:O	1:EP:73:LEU:HD12	2.05	0.56
1:BO:12:ILE:HD11	1:BO:45:ILE:HD13	1.85	0.56
1:CF:32:LEU:HD11	1:CF:49:ILE:HG23	1.86	0.56
1:CQ:49:ILE:HD12	1:CQ:73:LEU:HD23	1.87	0.56
1:DI:49:ILE:HD12	1:DI:73:LEU:HD23	1.87	0.56
1:DN:44:ASN:HB2	1:DN:78:LEU:HA	1.86	0.56
1:DX:49:ILE:HD12	1:DX:73:LEU:HD23	1.87	0.56
1:EI:12:ILE:HD11	1:EI:45:ILE:HD13	1.85	0.56
1:ER:12:ILE:HD11	1:ER:45:ILE:HD13	1.85	0.56
1:ER:44:ASN:HB2	1:ER:78:LEU:HA	1.86	0.56
1:EX:12:ILE:HD11	1:EX:45:ILE:HD13	1.85	0.56
1:FA:12:ILE:HD11	1:FA:45:ILE:HD13	1.85	0.56
1:FG:44:ASN:HB2	1:FG:78:LEU:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FJ:44:ASN:HB2	1:FJ:78:LEU:HA	1.86	0.56
1:FL:32:LEU:HD11	1:FL:49:ILE:HG23	1.86	0.56
1:GT:44:ASN:HB2	1:GT:78:LEU:HA	1.86	0.56
1:HA:49:ILE:HD12	1:HA:73:LEU:HD23	1.87	0.56
1:HU:12:ILE:HD11	1:HU:45:ILE:HD13	1.85	0.56
1:IB:73:LEU:HD12	1:JX:72:ASN:O	2.05	0.56
1:IG:112:THR:HG21	1:KB:4:LYS:HE2	1.88	0.56
1:IH:49:ILE:HD12	1:IH:73:LEU:HD23	1.87	0.56
1:IS:44:ASN:HB2	1:IS:78:LEU:HA	1.86	0.56
1:IT:49:ILE:HD12	1:IT:73:LEU:HD23	1.87	0.56
1:IV:12:ILE:HD11	1:IV:45:ILE:HD13	1.85	0.56
1:JE:44:ASN:HB2	1:JE:78:LEU:HA	1.86	0.56
1:JT:47:TYR:CZ	1:KH:105:ILE:HG12	2.40	0.56
1:JU:49:ILE:HD12	1:JU:73:LEU:HD23	1.86	0.56
1:KA:49:ILE:HD12	1:KA:73:LEU:HD23	1.87	0.56
1:KC:12:ILE:HD11	1:KC:45:ILE:HD13	1.85	0.56
1:KI:44:ASN:HB2	1:KI:78:LEU:HA	1.86	0.56
1:AU:73:LEU:HD12	1:EG:72:ASN:O	2.05	0.56
1:BQ:32:LEU:HD11	1:BQ:49:ILE:HG23	1.86	0.56
1:BY:49:ILE:HD12	1:BY:73:LEU:HD23	1.87	0.56
1:DS:32:LEU:HD11	1:DS:49:ILE:HG23	1.86	0.56
1:DW:44:ASN:HB2	1:DW:78:LEU:HA	1.86	0.56
1:FF:32:LEU:HD11	1:FF:49:ILE:HG23	1.86	0.56
1:FO:32:LEU:HD11	1:FO:49:ILE:HG23	1.86	0.56
1:HM:49:ILE:HD12	1:HM:73:LEU:HD23	1.87	0.56
1:JO:49:ILE:HD12	1:JO:73:LEU:HD23	1.87	0.56
1:BS:49:ILE:HD12	1:BS:73:LEU:HD23	1.87	0.56
1:BW:94:ILE:HG13	1:DQ:49:ILE:HG21	1.87	0.56
1:BZ:32:LEU:HD11	1:BZ:49:ILE:HG23	1.86	0.56
1:CG:12:ILE:HD11	1:CG:45:ILE:HD13	1.85	0.56
1:CW:95:VAL:HG13	1:GI:95:VAL:HG13	1.86	0.56
1:EP:49:ILE:HD12	1:EP:73:LEU:HD23	1.87	0.56
1:FD:112:THR:HG21	1:FF:4:LYS:HE2	1.88	0.56
1:FV:12:ILE:HD11	1:FV:45:ILE:HD13	1.85	0.56
1:HB:32:LEU:HD11	1:HB:49:ILE:HG23	1.86	0.56
1:HJ:49:ILE:HD12	1:HJ:73:LEU:HD23	1.87	0.56
1:HT:32:LEU:HD11	1:HT:49:ILE:HG23	1.86	0.56
1:HZ:32:LEU:HD11	1:HZ:49:ILE:HG23	1.86	0.56
1:IQ:49:ILE:HD12	1:IQ:73:LEU:HD23	1.86	0.56
1:AB:12:ILE:HD11	1:AB:45:ILE:HD13	1.85	0.56
1:AC:49:ILE:HD12	1:AC:73:LEU:HD23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:21:GLY:H	1:FR:89:ARG:HH22	1.52	0.56
1:AY:32:LEU:HD11	1:AY:49:ILE:HG23	1.86	0.56
1:BH:32:LEU:HD11	1:BH:49:ILE:HG23	1.87	0.56
1:BN:32:LEU:HD11	1:BN:49:ILE:HG23	1.86	0.56
1:BY:89:ARG:HH22	1:FK:21:GLY:H	1.53	0.56
1:CG:105:ILE:HG12	1:CL:47:TYR:CZ	2.40	0.56
1:CI:89:ARG:HH22	1:GH:21:GLY:H	1.51	0.56
1:CZ:21:GLY:H	1:GL:89:ARG:HH22	1.54	0.56
1:DT:44:ASN:HB2	1:DT:78:LEU:HA	1.86	0.56
1:EN:73:LEU:HD12	1:FJ:72:ASN:O	2.04	0.56
1:EO:44:ASN:HB2	1:EO:78:LEU:HA	1.86	0.56
1:FR:32:LEU:HD11	1:FR:49:ILE:HG23	1.86	0.56
1:HE:45:ILE:CG2	1:HU:108:GLY:HA3	2.34	0.56
1:HF:12:ILE:HD11	1:HF:45:ILE:HD13	1.85	0.56
1:IE:95:VAL:HG11	1:KA:99:THR:CG2	2.35	0.56
1:IF:73:LEU:HD12	1:IJ:72:ASN:O	2.05	0.56
1:IR:4:LYS:HA	1:IR:17:TYR:HD1	1.71	0.56
1:IU:32:LEU:HD11	1:IU:49:ILE:HG23	1.86	0.56
1:JG:4:LYS:HA	1:JG:17:TYR:HD1	1.71	0.56
1:JL:49:ILE:HD12	1:JL:73:LEU:HD23	1.87	0.56
1:AD:4:LYS:HA	1:AD:17:TYR:HD1	1.71	0.56
1:AJ:4:LYS:HA	1:AJ:17:TYR:HD1	1.71	0.56
1:AS:32:LEU:HD11	1:AS:49:ILE:HG23	1.86	0.56
1:BH:73:LEU:HD12	1:BO:72:ASN:O	2.05	0.56
1:BV:72:ASN:O	1:FH:73:LEU:HD12	2.06	0.56
1:BZ:73:LEU:HD12	1:DT:72:ASN:O	2.05	0.56
1:DM:83:ASN:HD22	1:GT:55:LEU:HD13	1.70	0.56
1:DP:4:LYS:HA	1:DP:17:TYR:HD1	1.71	0.56
1:EB:4:LYS:HA	1:EB:17:TYR:HD1	1.71	0.56
1:EB:32:LEU:HD11	1:EB:49:ILE:HG23	1.86	0.56
1:ED:49:ILE:HD12	1:ED:73:LEU:HD23	1.87	0.56
1:EZ:32:LEU:HD11	1:EZ:49:ILE:HG23	1.86	0.56
1:FR:4:LYS:HA	1:FR:17:TYR:HD1	1.71	0.56
1:GJ:4:LYS:HA	1:GJ:17:TYR:HD1	1.71	0.56
1:HK:73:LEU:HA	1:IY:72:ASN:O	2.05	0.56
1:HS:49:ILE:HD12	1:HS:73:LEU:HD23	1.87	0.56
1:IE:49:ILE:HD12	1:IE:73:LEU:HD23	1.87	0.56
1:IM:44:ASN:HB2	1:IM:78:LEU:HA	1.86	0.56
1:JA:32:LEU:HD11	1:JA:49:ILE:HG23	1.86	0.56
1:JP:32:LEU:HD11	1:JP:49:ILE:HG23	1.86	0.56
1:KD:49:ILE:HD12	1:KD:73:LEU:HD23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:47:TYR:HE1	1:FR:109:ASN:O	1.88	0.56
1:AS:21:GLY:H	1:EL:89:ARG:HH22	1.54	0.56
1:BK:4:LYS:HA	1:BK:17:TYR:HD1	1.71	0.56
1:BL:44:ASN:HB2	1:BL:78:LEU:HA	1.86	0.56
1:BN:4:LYS:HA	1:BN:17:TYR:HD1	1.71	0.56
1:BQ:4:LYS:HA	1:BQ:17:TYR:HD1	1.71	0.56
1:BZ:4:LYS:HA	1:BZ:17:TYR:HD1	1.71	0.56
1:CI:4:LYS:HA	1:CI:17:TYR:HD1	1.71	0.56
1:CR:32:LEU:HD11	1:CR:49:ILE:HG23	1.86	0.56
1:CZ:49:ILE:HD12	1:CZ:73:LEU:HD23	1.87	0.56
1:DJ:32:LEU:HD11	1:DJ:49:ILE:HG23	1.86	0.56
1:DM:4:LYS:HA	1:DM:17:TYR:HD1	1.71	0.56
1:DR:49:ILE:HD12	1:DR:73:LEU:HD23	1.87	0.56
1:DY:83:ASN:HD22	1:FY:55:LEU:HD13	1.71	0.56
1:EK:32:LEU:HD11	1:EK:49:ILE:HG23	1.87	0.56
1:HY:49:ILE:HD12	1:HY:73:LEU:HD23	1.87	0.56
1:IL:4:LYS:HA	1:IL:17:TYR:HD1	1.71	0.56
1:IU:4:LYS:HA	1:IU:17:TYR:HD1	1.71	0.56
1:IX:32:LEU:HD11	1:IX:49:ILE:HG23	1.86	0.56
1:AP:4:LYS:HA	1:AP:17:TYR:HD1	1.71	0.56
1:BB:73:LEU:HD12	1:BR:72:ASN:O	2.05	0.56
1:BW:105:ILE:HG12	1:DQ:47:TYR:CZ	2.40	0.56
1:CL:32:LEU:HD11	1:CL:49:ILE:HG23	1.86	0.56
1:DD:4:LYS:HA	1:DD:17:TYR:HD1	1.71	0.56
1:DG:4:LYS:HA	1:DG:17:TYR:HD1	1.71	0.56
1:EZ:4:LYS:HA	1:EZ:17:TYR:HD1	1.71	0.56
1:FG:12:ILE:HD11	1:FG:45:ILE:HD13	1.85	0.56
1:FV:112:THR:HG21	1:GS:4:LYS:HE2	1.87	0.56
1:GO:49:ILE:HD12	1:GO:73:LEU:HD23	1.87	0.56
1:HE:45:ILE:HD13	1:HU:108:GLY:O	2.06	0.56
1:IB:49:ILE:HD12	1:IB:73:LEU:HD23	1.87	0.56
1:IF:4:LYS:HA	1:IF:17:TYR:HD1	1.71	0.56
1:JD:72:ASN:O	1:JN:73:LEU:HA	2.05	0.56
1:JS:4:LYS:HA	1:JS:17:TYR:HD1	1.71	0.56
1:JS:32:LEU:HD11	1:JS:49:ILE:HG23	1.86	0.56
1:AL:95:VAL:HG13	1:DX:95:VAL:HG13	1.88	0.56
1:AM:89:ARG:HH22	1:CA:21:GLY:H	1.54	0.56
1:AS:4:LYS:HA	1:AS:17:TYR:HD1	1.71	0.56
1:AU:49:ILE:HD12	1:AU:73:LEU:HD23	1.86	0.56
1:BE:4:LYS:HA	1:BE:17:TYR:HD1	1.71	0.56
1:DF:49:ILE:HD12	1:DF:73:LEU:HD23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EE:21:GLY:H	1:EU:89:ARG:HH22	1.53	0.56
1:EK:4:LYS:HA	1:EK:17:TYR:HD1	1.71	0.56
1:EN:4:LYS:HA	1:EN:17:TYR:HD1	1.71	0.56
1:ES:49:ILE:HD12	1:ES:73:LEU:HD23	1.87	0.56
1:FC:4:LYS:HA	1:FC:17:TYR:HD1	1.71	0.56
1:FE:49:ILE:HD12	1:FE:73:LEU:HD23	1.87	0.56
1:GR:49:ILE:HD12	1:GR:73:LEU:HD23	1.87	0.56
1:HE:4:LYS:HA	1:HE:17:TYR:HD1	1.71	0.56
1:HN:32:LEU:HD11	1:HN:49:ILE:HG23	1.86	0.56
1:HT:75:PHE:HD1	1:IM:71:ALA:HB2	1.71	0.56
1:IO:4:LYS:HA	1:IO:17:TYR:HD1	1.71	0.56
1:IY:44:ASN:HB2	1:IY:78:LEU:HA	1.86	0.56
1:JD:32:LEU:HD11	1:JD:49:ILE:HG23	1.87	0.56
1:AT:88:LEU:HG	1:EZ:106:ILE:HG21	1.88	0.55
1:AV:32:LEU:HD11	1:AV:49:ILE:HG23	1.86	0.55
1:BB:4:LYS:HA	1:BB:17:TYR:HD1	1.71	0.55
1:DJ:4:LYS:HA	1:DJ:17:TYR:HD1	1.71	0.55
1:DL:49:ILE:HD12	1:DL:73:LEU:HD23	1.86	0.55
1:DY:4:LYS:HA	1:DY:17:TYR:HD1	1.71	0.55
1:FX:4:LYS:HA	1:FX:17:TYR:HD1	1.71	0.55
1:HA:73:LEU:HD12	1:IQ:72:ASN:O	2.05	0.55
1:HH:4:LYS:HA	1:HH:17:TYR:HD1	1.71	0.55
1:IK:49:ILE:HD12	1:IK:73:LEU:HD23	1.86	0.55
1:IU:106:ILE:HA	1:JE:75:PHE:CE2	2.41	0.55
1:JD:71:ALA:HB2	1:JN:75:PHE:HD1	1.71	0.55
1:JY:4:LYS:HA	1:JY:17:TYR:HD1	1.71	0.55
1:KH:4:LYS:HA	1:KH:17:TYR:HD1	1.71	0.55
1:AN:17:TYR:OH	1:FR:112:THR:HG23	2.06	0.55
1:AN:32:LEU:HD21	1:FR:97:PHE:CG	2.41	0.55
1:BA:72:ASN:O	1:EM:73:LEU:HD12	2.06	0.55
1:BH:4:LYS:HA	1:BH:17:TYR:HD1	1.71	0.55
1:BP:72:ASN:O	1:FB:73:LEU:HD12	2.06	0.55
1:HK:4:LYS:HA	1:HK:17:TYR:HD1	1.71	0.55
1:HT:4:LYS:HA	1:HT:17:TYR:HD1	1.71	0.55
1:JM:4:LYS:HA	1:JM:17:TYR:HD1	1.71	0.55
1:AJ:83:ASN:HD22	1:BX:55:LEU:HD13	1.70	0.55
1:AY:4:LYS:HA	1:AY:17:TYR:HD1	1.71	0.55
1:CH:105:ILE:HG12	1:FT:47:TYR:CE2	2.41	0.55
1:EE:4:LYS:HA	1:EE:17:TYR:HD1	1.71	0.55
1:FI:4:LYS:HA	1:FI:17:TYR:HD1	1.71	0.55
1:HE:36:THR:HG23	1:HU:110:VAL:HB	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IX:4:LYS:HA	1:IX:17:TYR:HD1	1.71	0.55
1:JP:4:LYS:HA	1:JP:17:TYR:HD1	1.71	0.55
1:JT:49:ILE:HG21	1:KH:94:ILE:HG13	1.87	0.55
1:AM:4:LYS:HA	1:AM:17:TYR:HD1	1.71	0.55
1:AU:93:GLU:OE1	1:EG:2:ILE:HG23	2.06	0.55
1:CF:83:ASN:HD22	1:GN:55:LEU:HD13	1.70	0.55
1:CL:4:LYS:HA	1:CL:17:TYR:HD1	1.71	0.55
1:CT:49:ILE:HD12	1:CT:73:LEU:HD23	1.87	0.55
1:CW:49:ILE:HD12	1:CW:73:LEU:HD23	1.87	0.55
1:CW:72:ASN:O	1:GI:73:LEU:HD12	2.06	0.55
1:DA:4:LYS:HA	1:DA:17:TYR:HD1	1.71	0.55
1:DA:4:LYS:HE2	1:DE:112:THR:HG21	1.87	0.55
1:FK:49:ILE:HD12	1:FK:73:LEU:HD23	1.87	0.55
1:FL:4:LYS:HA	1:FL:17:TYR:HD1	1.71	0.55
1:FU:4:LYS:HA	1:FU:17:TYR:HD1	1.71	0.55
1:DI:99:THR:CG2	1:GU:95:VAL:HG11	2.36	0.55
1:HF:95:VAL:HG13	1:JV:95:VAL:HG13	1.88	0.55
1:IF:105:ILE:HG12	1:IJ:47:TYR:CZ	2.41	0.55
1:IL:32:LEU:HD11	1:IL:49:ILE:HG23	1.86	0.55
1:AP:78:LEU:HD12	1:BU:69:ILE:HG12	1.89	0.55
1:CF:4:LYS:HA	1:CF:17:TYR:HD1	1.71	0.55
1:CU:4:LYS:HA	1:CU:17:TYR:HD1	1.71	0.55
1:EH:78:LEU:HD12	1:EO:69:ILE:HG12	1.88	0.55
1:GM:4:LYS:HA	1:GM:17:TYR:HD1	1.71	0.55
1:GX:49:ILE:HD12	1:GX:73:LEU:HD23	1.87	0.55
1:II:4:LYS:HA	1:II:17:TYR:HD1	1.71	0.55
1:IL:4:LYS:HE2	1:KF:112:THR:HG21	1.87	0.55
1:KB:4:LYS:HA	1:KB:17:TYR:HD1	1.71	0.55
1:AU:98:ILE:HD11	1:EG:73:LEU:HD22	1.88	0.55
1:AW:4:LYS:HA	1:AW:17:TYR:HD1	1.72	0.55
1:CI:72:ASN:O	1:GH:73:LEU:HA	2.07	0.55
1:DV:4:LYS:HA	1:DV:17:TYR:HD1	1.71	0.55
1:EQ:47:TYR:CZ	1:FM:105:ILE:HG12	2.41	0.55
1:ET:4:LYS:HA	1:ET:17:TYR:HD1	1.71	0.55
1:HK:71:ALA:HA	1:IY:74:SER:O	2.07	0.55
1:HL:4:LYS:HA	1:HL:17:TYR:HD1	1.72	0.55
1:HQ:4:LYS:HA	1:HQ:17:TYR:HD1	1.71	0.55
1:IG:88:LEU:HG	1:KB:106:ILE:HD13	1.89	0.55
1:IJ:4:LYS:HA	1:IJ:17:TYR:HD1	1.72	0.55
1:JA:105:ILE:HG12	1:JQ:47:TYR:CE2	2.42	0.55
1:JV:4:LYS:HA	1:JV:17:TYR:HD1	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KE:4:LYS:HA	1:KE:17:TYR:HD1	1.71	0.55
1:AW:95:VAL:HG13	1:FC:95:VAL:HG13	1.89	0.55
1:BT:4:LYS:HA	1:BT:17:TYR:HD1	1.71	0.55
1:BX:4:LYS:HA	1:BX:17:TYR:HD1	1.72	0.55
1:CG:11:PRO:HB3	1:CL:109:ASN:CG	2.32	0.55
1:CP:4:LYS:HA	1:CP:17:TYR:HD1	1.72	0.55
1:DB:4:LYS:HA	1:DB:17:TYR:HD1	1.72	0.55
1:GY:4:LYS:HA	1:GY:17:TYR:HD1	1.71	0.55
1:HN:4:LYS:HA	1:HN:17:TYR:HD1	1.71	0.55
1:HQ:17:TYR:OH	1:IS:112:THR:HG22	2.07	0.55
1:HZ:4:LYS:HA	1:HZ:17:TYR:HD1	1.71	0.55
1:JB:4:LYS:HA	1:JB:17:TYR:HD1	1.72	0.55
1:JE:4:LYS:HA	1:JE:17:TYR:HD1	1.72	0.55
1:JT:4:LYS:HA	1:JT:17:TYR:HD1	1.72	0.55
1:AA:4:LYS:HA	1:AA:17:TYR:HD1	1.71	0.55
1:AH:44:ASN:ND2	1:AH:76:THR:HB	2.22	0.55
1:AW:44:ASN:ND2	1:AW:76:THR:HB	2.22	0.55
1:CC:4:LYS:HA	1:CC:17:TYR:HD1	1.71	0.55
1:CH:111:LEU:HG	1:FT:11:PRO:HA	1.88	0.55
1:CR:4:LYS:HA	1:CR:17:TYR:HD1	1.71	0.55
1:DW:4:LYS:HA	1:DW:17:TYR:HD1	1.72	0.55
1:DZ:44:ASN:ND2	1:DZ:76:THR:HB	2.22	0.55
1:EN:47:TYR:CE2	1:FJ:105:ILE:HG12	2.42	0.55
1:EU:44:ASN:ND2	1:EU:76:THR:HB	2.22	0.55
1:EW:4:LYS:HA	1:EW:17:TYR:HD1	1.71	0.55
1:EX:44:ASN:ND2	1:EX:76:THR:HB	2.22	0.55
1:FM:4:LYS:HA	1:FM:17:TYR:HD1	1.72	0.55
1:FS:88:LEU:HG	1:GP:106:ILE:HG21	1.88	0.55
1:GD:4:LYS:HA	1:GD:17:TYR:HD1	1.71	0.55
1:GE:4:LYS:HA	1:GE:17:TYR:HD1	1.72	0.55
1:GH:4:LYS:HA	1:GH:17:TYR:HD1	1.72	0.55
1:GP:4:LYS:HA	1:GP:17:TYR:HD1	1.71	0.55
1:GS:4:LYS:HA	1:GS:17:TYR:HD1	1.71	0.55
1:HB:4:LYS:HA	1:HB:17:TYR:HD1	1.71	0.55
1:HN:106:ILE:HG21	1:HR:88:LEU:HG	1.88	0.55
1:HO:4:LYS:HA	1:HO:17:TYR:HD1	1.72	0.55
1:KI:4:LYS:HA	1:KI:17:TYR:HD1	1.72	0.55
1:AN:4:LYS:HA	1:AN:17:TYR:HD1	1.72	0.55
1:AV:17:TYR:OH	1:EF:112:THR:HG22	2.07	0.55
1:AW:69:ILE:HG12	1:FC:78:LEU:HD12	1.89	0.55
1:AZ:44:ASN:ND2	1:AZ:76:THR:HB	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:4:LYS:HA	1:BC:17:TYR:HD1	1.72	0.55
1:BC:44:ASN:ND2	1:BC:76:THR:HB	2.22	0.55
1:CA:44:ASN:ND2	1:CA:76:THR:HB	2.22	0.55
1:CD:44:ASN:ND2	1:CD:76:THR:HB	2.22	0.55
1:DH:44:ASN:ND2	1:DH:76:THR:HB	2.22	0.55
1:DQ:44:ASN:ND2	1:DQ:76:THR:HB	2.22	0.55
1:EN:2:ILE:HG23	1:FJ:93:GLU:OE1	2.07	0.55
1:FF:4:LYS:HA	1:FF:17:TYR:HD1	1.71	0.55
1:FP:4:LYS:HA	1:FP:17:TYR:HD1	1.72	0.55
1:GB:44:ASN:ND2	1:GB:76:THR:HB	2.22	0.55
1:GN:4:LYS:HA	1:GN:17:TYR:HD1	1.72	0.55
1:GW:44:ASN:ND2	1:GW:76:THR:HB	2.22	0.55
1:HI:4:LYS:HA	1:HI:17:TYR:HD1	1.72	0.55
1:IP:4:LYS:HA	1:IP:17:TYR:HD1	1.72	0.55
1:AG:17:TYR:OH	1:BF:112:THR:HG22	2.07	0.54
1:AQ:44:ASN:ND2	1:AQ:76:THR:HB	2.22	0.54
1:AS:109:ASN:CG	1:EL:11:PRO:HB3	2.32	0.54
1:BI:44:ASN:ND2	1:BI:76:THR:HB	2.22	0.54
1:BW:4:LYS:HA	1:BW:17:TYR:HD1	1.71	0.54
1:CN:111:LEU:HG	1:FZ:11:PRO:HA	1.88	0.54
1:CX:4:LYS:HA	1:CX:17:TYR:HD1	1.71	0.54
1:DS:4:LYS:HA	1:DS:17:TYR:HD1	1.71	0.54
1:EQ:4:LYS:HA	1:EQ:17:TYR:HD1	1.71	0.54
1:HF:4:LYS:HA	1:HF:17:TYR:HD1	1.72	0.54
1:HH:106:ILE:HG21	1:IV:88:LEU:HG	1.87	0.54
1:HR:4:LYS:HA	1:HR:17:TYR:HD1	1.72	0.54
1:HT:94:ILE:HG13	1:IM:49:ILE:HG21	1.88	0.54
1:IV:44:ASN:ND2	1:IV:76:THR:HB	2.22	0.54
1:JK:4:LYS:HA	1:JK:17:TYR:HD1	1.72	0.54
1:JQ:44:ASN:ND2	1:JQ:76:THR:HB	2.22	0.54
1:KF:44:ASN:ND2	1:KF:76:THR:HB	2.22	0.54
1:AB:44:ASN:ND2	1:AB:76:THR:HB	2.22	0.54
1:AG:4:LYS:HA	1:AG:17:TYR:HD1	1.71	0.54
1:AM:71:ALA:HA	1:CA:74:SER:O	2.07	0.54
1:AX:99:THR:CG2	1:EJ:95:VAL:HG11	2.37	0.54
1:BL:4:LYS:HA	1:BL:17:TYR:HD1	1.72	0.54
1:BR:44:ASN:ND2	1:BR:76:THR:HB	2.22	0.54
1:CG:44:ASN:ND2	1:CG:76:THR:HB	2.22	0.54
1:DW:44:ASN:ND2	1:DW:76:THR:HB	2.22	0.54
1:DZ:4:LYS:HA	1:DZ:17:TYR:HD1	1.72	0.54
1:FA:4:LYS:HA	1:FA:17:TYR:HD1	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FD:4:LYS:HA	1:FD:17:TYR:HD1	1.72	0.54
1:FJ:4:LYS:HA	1:FJ:17:TYR:HD1	1.72	0.54
1:GA:4:LYS:HA	1:GA:17:TYR:HD1	1.71	0.54
1:JH:44:ASN:ND2	1:JH:76:THR:HB	2.22	0.54
1:JN:4:LYS:HA	1:JN:17:TYR:HD1	1.72	0.54
1:KF:4:LYS:HA	1:KF:17:TYR:HD1	1.72	0.54
1:BX:44:ASN:ND2	1:BX:76:THR:HB	2.22	0.54
1:DE:44:ASN:ND2	1:DE:76:THR:HB	2.22	0.54
1:EH:4:LYS:HA	1:EH:17:TYR:HD1	1.71	0.54
1:EO:44:ASN:ND2	1:EO:76:THR:HB	2.22	0.54
1:ER:4:LYS:HA	1:ER:17:TYR:HD1	1.72	0.54
1:ER:44:ASN:ND2	1:ER:76:THR:HB	2.22	0.54
1:FO:4:LYS:HA	1:FO:17:TYR:HD1	1.71	0.54
1:GE:44:ASN:ND2	1:GE:76:THR:HB	2.22	0.54
1:GV:4:LYS:HA	1:GV:17:TYR:HD1	1.71	0.54
1:GW:4:LYS:HA	1:GW:17:TYR:HD1	1.72	0.54
1:GZ:4:LYS:HA	1:GZ:17:TYR:HD1	1.72	0.54
1:HC:4:LYS:HA	1:HC:17:TYR:HD1	1.72	0.54
1:HX:4:LYS:HA	1:HX:17:TYR:HD1	1.72	0.54
1:IA:44:ASN:ND2	1:IA:76:THR:HB	2.22	0.54
1:ID:44:ASN:ND2	1:ID:76:THR:HB	2.23	0.54
1:JE:44:ASN:ND2	1:JE:76:THR:HB	2.22	0.54
1:JN:44:ASN:ND2	1:JN:76:THR:HB	2.22	0.54
1:JT:108:GLY:HA3	1:KH:45:ILE:HG21	1.89	0.54
1:KI:44:ASN:ND2	1:KI:76:THR:HB	2.22	0.54
1:AB:4:LYS:HA	1:AB:17:TYR:HD1	1.72	0.54
1:AH:4:LYS:HA	1:AH:17:TYR:HD1	1.72	0.54
1:AX:88:LEU:HD23	1:EJ:106:ILE:HG21	1.87	0.54
1:BI:4:LYS:HA	1:BI:17:TYR:HD1	1.72	0.54
1:BU:4:LYS:HA	1:BU:17:TYR:HD1	1.72	0.54
1:CB:95:VAL:HG13	1:FN:95:VAL:HG13	1.89	0.54
1:FV:44:ASN:ND2	1:FV:76:THR:HB	2.23	0.54
1:GH:44:ASN:ND2	1:GH:76:THR:HB	2.22	0.54
1:HO:44:ASN:ND2	1:HO:76:THR:HB	2.22	0.54
1:HR:44:ASN:ND2	1:HR:76:THR:HB	2.22	0.54
1:IS:44:ASN:ND2	1:IS:76:THR:HB	2.22	0.54
1:IY:4:LYS:HA	1:IY:17:TYR:HD1	1.72	0.54
1:JJ:4:LYS:HA	1:JJ:17:TYR:HD1	1.71	0.54
1:JK:72:ASN:O	1:JM:73:LEU:HD12	2.06	0.54
1:AE:44:ASN:ND2	1:AE:76:THR:HB	2.22	0.54
1:AM:73:LEU:HB2	1:CA:73:LEU:HD12	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:4:LYS:HA	1:AV:17:TYR:HD1	1.71	0.54
1:AY:105:ILE:HG12	1:EI:47:TYR:CE2	2.43	0.54
1:BR:4:LYS:HA	1:BR:17:TYR:HD1	1.72	0.54
1:BU:44:ASN:ND2	1:BU:76:THR:HB	2.22	0.54
1:CD:4:LYS:HA	1:CD:17:TYR:HD1	1.72	0.54
1:CS:4:LYS:HA	1:CS:17:TYR:HD1	1.72	0.54
1:DC:95:VAL:HG13	1:GO:95:VAL:HG13	1.88	0.54
1:DL:99:THR:CG2	1:GX:95:VAL:HG11	2.38	0.54
1:GQ:4:LYS:HA	1:GQ:17:TYR:HD1	1.72	0.54
1:HF:44:ASN:ND2	1:HF:76:THR:HB	2.22	0.54
1:HL:44:ASN:ND2	1:HL:76:THR:HB	2.22	0.54
1:HW:4:LYS:HA	1:HW:17:TYR:HD1	1.71	0.54
1:IG:44:ASN:ND2	1:IG:76:THR:HB	2.22	0.54
1:JA:4:LYS:HA	1:JA:17:TYR:HD1	1.71	0.54
1:JB:44:ASN:ND2	1:JB:76:THR:HB	2.22	0.54
1:JD:4:LYS:HA	1:JD:17:TYR:HD1	1.71	0.54
1:JD:67:ASN:HB3	1:JN:78:LEU:HD13	1.88	0.54
1:KC:44:ASN:ND2	1:KC:76:THR:HB	2.22	0.54
1:AT:4:LYS:HA	1:AT:17:TYR:HD1	1.72	0.54
1:CO:4:LYS:HA	1:CO:17:TYR:HD1	1.71	0.54
1:DE:4:LYS:HA	1:DE:17:TYR:HD1	1.72	0.54
1:DQ:4:LYS:HA	1:DQ:17:TYR:HD1	1.72	0.54
1:EI:44:ASN:ND2	1:EI:76:THR:HB	2.23	0.54
1:FS:44:ASN:ND2	1:FS:76:THR:HB	2.23	0.54
1:GG:4:LYS:HA	1:GG:17:TYR:HD1	1.71	0.54
1:IA:4:LYS:HA	1:IA:17:TYR:HD1	1.72	0.54
1:IJ:44:ASN:ND2	1:IJ:76:THR:HB	2.22	0.54
1:JE:60:ASP:HB3	1:JN:59:VAL:HG11	1.90	0.54
1:CY:44:ASN:ND2	1:CY:76:THR:HB	2.22	0.54
1:DB:44:ASN:ND2	1:DB:76:THR:HB	2.22	0.54
1:DK:44:ASN:ND2	1:DK:76:THR:HB	2.22	0.54
1:EF:44:ASN:ND2	1:EF:76:THR:HB	2.22	0.54
1:EN:11:PRO:HA	1:FJ:109:ASN:OD1	2.07	0.54
1:FG:44:ASN:ND2	1:FG:76:THR:HB	2.22	0.54
1:GK:44:ASN:ND2	1:GK:76:THR:HB	2.22	0.54
1:GY:2:ILE:HG23	1:HO:93:GLU:OE1	2.08	0.54
1:GY:93:GLU:OE1	1:HO:2:ILE:HG23	2.08	0.54
1:HU:4:LYS:HA	1:HU:17:TYR:HD1	1.72	0.54
1:IM:44:ASN:ND2	1:IM:76:THR:HB	2.22	0.54
1:IP:44:ASN:ND2	1:IP:76:THR:HB	2.22	0.54
1:JA:109:ASN:O	1:JQ:47:TYR:HE1	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:106:ILE:O	1:FT:77:ALA:HB1	2.07	0.54
1:CM:44:ASN:ND2	1:CM:76:THR:HB	2.22	0.54
1:CS:44:ASN:ND2	1:CS:76:THR:HB	2.22	0.54
1:CV:4:LYS:HA	1:CV:17:TYR:HD1	1.72	0.54
1:FG:4:LYS:HA	1:FG:17:TYR:HD1	1.72	0.54
1:FP:72:ASN:O	1:GV:73:LEU:HD12	2.08	0.54
1:GT:4:LYS:HA	1:GT:17:TYR:HD1	1.72	0.54
1:GZ:44:ASN:ND2	1:GZ:76:THR:HB	2.22	0.54
1:IC:4:LYS:HA	1:IC:17:TYR:HD1	1.71	0.54
1:JK:44:ASN:ND2	1:JK:76:THR:HB	2.22	0.54
1:JW:4:LYS:HA	1:JW:17:TYR:HD1	1.72	0.54
1:JW:44:ASN:ND2	1:JW:76:THR:HB	2.23	0.54
1:AD:17:TYR:OH	1:BC:112:THR:HG22	2.08	0.54
1:AK:44:ASN:ND2	1:AK:76:THR:HB	2.22	0.54
1:AS:106:ILE:HA	1:EL:75:PHE:HE2	1.73	0.54
1:AX:73:LEU:HD13	1:EJ:73:LEU:HD13	1.90	0.54
1:BF:4:LYS:HA	1:BF:17:TYR:HD1	1.72	0.54
1:DK:4:LYS:HA	1:DK:17:TYR:HD1	1.72	0.54
1:DN:44:ASN:ND2	1:DN:76:THR:HB	2.22	0.54
1:FV:4:LYS:HA	1:FV:17:TYR:HD1	1.72	0.54
1:FY:44:ASN:ND2	1:FY:76:THR:HB	2.22	0.54
1:GK:4:LYS:HA	1:GK:17:TYR:HD1	1.72	0.54
1:HV:105:ILE:HG12	1:JO:47:TYR:CZ	2.43	0.54
1:IY:44:ASN:ND2	1:IY:76:THR:HB	2.22	0.54
1:JZ:4:LYS:HA	1:JZ:17:TYR:HD1	1.72	0.54
1:AE:4:LYS:HA	1:AE:17:TYR:HD1	1.72	0.54
1:AN:44:ASN:ND2	1:AN:76:THR:HB	2.22	0.54
1:AQ:21:GLY:H	1:FU:89:ARG:HH22	1.56	0.54
1:AT:44:ASN:ND2	1:AT:76:THR:HB	2.22	0.54
1:BF:44:ASN:ND2	1:BF:76:THR:HB	2.22	0.54
1:CD:72:ASN:O	1:CR:73:LEU:HD12	2.08	0.54
1:CY:4:LYS:HA	1:CY:17:TYR:HD1	1.72	0.54
1:DN:4:LYS:HA	1:DN:17:TYR:HD1	1.72	0.54
1:DT:4:LYS:HA	1:DT:17:TYR:HD1	1.72	0.54
1:EE:71:ALA:HB2	1:EU:75:PHE:HD1	1.73	0.54
1:EN:89:ARG:NH2	1:FJ:20:THR:H	2.05	0.54
1:FJ:44:ASN:ND2	1:FJ:76:THR:HB	2.23	0.54
1:FS:4:LYS:HA	1:FS:17:TYR:HD1	1.72	0.54
1:HC:44:ASN:ND2	1:HC:76:THR:HB	2.22	0.54
1:HH:83:ASN:HD22	1:IV:55:LEU:HD13	1.73	0.54
1:HI:44:ASN:ND2	1:HI:76:THR:HB	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HU:44:ASN:ND2	1:HU:76:THR:HB	2.22	0.54
1:HX:44:ASN:ND2	1:HX:76:THR:HB	2.22	0.54
1:ID:4:LYS:HA	1:ID:17:TYR:HD1	1.72	0.54
1:IV:4:LYS:HA	1:IV:17:TYR:HD1	1.72	0.54
1:AI:73:LEU:HD22	1:DU:98:ILE:HD11	1.90	0.53
1:AQ:105:ILE:HG12	1:FU:47:TYR:CZ	2.42	0.53
1:AU:86:GLU:HG2	1:EG:53:TYR:CE2	2.43	0.53
1:BD:73:LEU:HD22	1:EP:98:ILE:HD11	1.89	0.53
1:CA:4:LYS:HA	1:CA:17:TYR:HD1	1.72	0.53
1:CF:95:VAL:HG13	1:GN:95:VAL:HG13	1.90	0.53
1:CV:44:ASN:ND2	1:CV:76:THR:HB	2.22	0.53
1:DL:73:LEU:HD13	1:GX:73:LEU:HD13	1.90	0.53
1:EN:111:LEU:HG	1:FJ:11:PRO:HA	1.90	0.53
1:EU:4:LYS:HA	1:EU:17:TYR:HD1	1.72	0.53
1:ID:72:ASN:O	1:II:73:LEU:HD12	2.08	0.53
1:JQ:4:LYS:HA	1:JQ:17:TYR:HD1	1.72	0.53
1:JT:44:ASN:ND2	1:JT:76:THR:HB	2.22	0.53
1:JW:21:GLY:H	1:KE:89:ARG:HH22	1.55	0.53
1:AZ:4:LYS:HA	1:AZ:17:TYR:HD1	1.72	0.53
1:BE:73:LEU:HD12	1:BL:72:ASN:O	2.08	0.53
1:BO:44:ASN:ND2	1:BO:76:THR:HB	2.22	0.53
1:BS:99:THR:CG2	1:FE:95:VAL:HG11	2.38	0.53
1:CC:73:LEU:HD13	1:GK:73:LEU:HB2	1.90	0.53
1:CJ:44:ASN:ND2	1:CJ:76:THR:HB	2.22	0.53
1:CM:4:LYS:HA	1:CM:17:TYR:HD1	1.72	0.53
1:FA:44:ASN:ND2	1:FA:76:THR:HB	2.22	0.53
1:GY:89:ARG:HH22	1:HO:21:GLY:H	1.55	0.53
1:KC:4:LYS:HA	1:KC:17:TYR:HD1	1.72	0.53
1:AQ:4:LYS:HA	1:AQ:17:TYR:HD1	1.72	0.53
1:BD:49:ILE:HG21	1:EP:94:ILE:HG13	1.89	0.53
1:CP:44:ASN:ND2	1:CP:76:THR:HB	2.22	0.53
1:CZ:105:ILE:HG12	1:GL:47:TYR:CZ	2.44	0.53
1:EH:4:LYS:HE2	1:EO:112:THR:HG21	1.90	0.53
1:EK:99:THR:CG2	1:ER:95:VAL:HG11	2.38	0.53
1:ET:73:LEU:CD2	1:FG:98:ILE:HD11	2.38	0.53
1:GN:44:ASN:ND2	1:GN:76:THR:HB	2.23	0.53
1:GY:97:PHE:CG	1:HO:32:LEU:HD21	2.43	0.53
1:HJ:73:LEU:HD12	1:IZ:72:ASN:O	2.08	0.53
1:HP:95:VAL:HG13	1:JC:95:VAL:HG13	1.91	0.53
1:JZ:44:ASN:ND2	1:JZ:76:THR:HB	2.23	0.53
1:AE:73:LEU:HD12	1:GA:73:LEU:HD13	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:4:LYS:HA	1:AK:17:TYR:HD1	1.72	0.53
1:AU:83:ASN:OD1	1:EG:55:LEU:HD13	2.08	0.53
1:BM:106:ILE:HG21	1:EY:88:LEU:HD23	1.91	0.53
1:BO:4:LYS:HA	1:BO:17:TYR:HD1	1.72	0.53
1:CG:4:LYS:HA	1:CG:17:TYR:HD1	1.72	0.53
1:CI:51:VAL:HG11	1:GH:90:VAL:HG13	1.91	0.53
1:EC:44:ASN:ND2	1:EC:76:THR:HB	2.22	0.53
1:EF:4:LYS:HA	1:EF:17:TYR:HD1	1.72	0.53
1:EO:4:LYS:HA	1:EO:17:TYR:HD1	1.72	0.53
1:FM:44:ASN:ND2	1:FM:76:THR:HB	2.22	0.53
1:HG:47:TYR:CZ	1:IT:105:ILE:HG12	2.44	0.53
1:IM:4:LYS:HA	1:IM:17:TYR:HD1	1.72	0.53
1:AR:83:ASN:O	1:AR:87:LYS:HG3	2.09	0.53
1:BL:44:ASN:ND2	1:BL:76:THR:HB	2.22	0.53
1:CJ:4:LYS:HA	1:CJ:17:TYR:HD1	1.72	0.53
1:CM:95:VAL:HG11	1:DG:99:THR:CG2	2.39	0.53
1:DT:44:ASN:ND2	1:DT:76:THR:HB	2.22	0.53
1:DU:83:ASN:O	1:DU:87:LYS:HG3	2.09	0.53
1:EI:4:LYS:HA	1:EI:17:TYR:HD1	1.72	0.53
1:FD:44:ASN:ND2	1:FD:76:THR:HB	2.22	0.53
1:FP:44:ASN:ND2	1:FP:76:THR:HB	2.22	0.53
1:GQ:44:ASN:ND2	1:GQ:76:THR:HB	2.22	0.53
1:GT:44:ASN:ND2	1:GT:76:THR:HB	2.23	0.53
1:HV:83:ASN:O	1:HV:87:LYS:HG3	2.09	0.53
1:JT:55:LEU:HD13	1:KH:83:ASN:HD22	1.74	0.53
1:AI:83:ASN:O	1:AI:87:LYS:HG3	2.09	0.53
1:CE:83:ASN:O	1:CE:87:LYS:HG3	2.09	0.53
1:CU:102:LYS:HG2	1:DH:88:LEU:HD23	1.91	0.53
1:DR:83:ASN:O	1:DR:87:LYS:HG3	2.09	0.53
1:EC:4:LYS:HA	1:EC:17:TYR:HD1	1.72	0.53
1:EJ:83:ASN:O	1:EJ:87:LYS:HG3	2.09	0.53
1:IE:73:LEU:HD12	1:KA:72:ASN:O	2.08	0.53
1:IS:4:LYS:HA	1:IS:17:TYR:HD1	1.72	0.53
1:JH:4:LYS:HA	1:JH:17:TYR:HD1	1.72	0.53
1:JH:72:ASN:O	1:JP:73:LEU:HD12	2.07	0.53
1:JR:83:ASN:O	1:JR:87:LYS:HG3	2.09	0.53
1:AB:75:PHE:HD1	1:FX:71:ALA:HB2	1.74	0.53
1:BJ:83:ASN:O	1:BJ:87:LYS:HG3	2.09	0.53
1:CH:21:GLY:H	1:FT:89:ARG:HH22	1.56	0.53
1:CW:83:ASN:O	1:CW:87:LYS:HG3	2.09	0.53
1:DI:95:VAL:HG11	1:GU:99:THR:CG2	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DL:83:ASN:O	1:DL:87:LYS:HG3	2.09	0.53
1:EL:4:LYS:HA	1:EL:17:TYR:HD1	1.72	0.53
1:EX:4:LYS:HA	1:EX:17:TYR:HD1	1.72	0.53
1:FB:83:ASN:O	1:FB:87:LYS:HG3	2.09	0.53
1:FS:55:LEU:HD13	1:GP:83:ASN:ND2	2.24	0.53
1:FT:83:ASN:O	1:FT:87:LYS:HG3	2.09	0.53
1:GF:83:ASN:O	1:GF:87:LYS:HG3	2.09	0.53
1:IF:47:TYR:CZ	1:IJ:105:ILE:HG12	2.44	0.53
1:IN:83:ASN:O	1:IN:87:LYS:HG3	2.09	0.53
1:JL:83:ASN:O	1:JL:87:LYS:HG3	2.09	0.53
1:KA:83:ASN:O	1:KA:87:LYS:HG3	2.09	0.53
1:KJ:83:ASN:O	1:KJ:87:LYS:HG3	2.09	0.53
1:AQ:17:TYR:OH	1:FU:112:THR:HG23	2.09	0.53
1:BM:83:ASN:O	1:BM:87:LYS:HG3	2.09	0.53
1:CQ:83:ASN:O	1:CQ:87:LYS:HG3	2.09	0.53
1:CZ:83:ASN:O	1:CZ:87:LYS:HG3	2.09	0.53
1:EM:83:ASN:O	1:EM:87:LYS:HG3	2.09	0.53
1:EV:83:ASN:O	1:EV:87:LYS:HG3	2.09	0.53
1:FY:4:LYS:HA	1:FY:17:TYR:HD1	1.72	0.53
1:GB:4:LYS:HA	1:GB:17:TYR:HD1	1.72	0.53
1:HG:90:VAL:HG13	1:IT:51:VAL:HG11	1.90	0.53
1:HP:83:ASN:O	1:HP:87:LYS:HG3	2.09	0.53
1:HW:73:LEU:HD12	1:IP:72:ASN:O	2.09	0.53
1:IE:83:ASN:O	1:IE:87:LYS:HG3	2.09	0.53
1:IG:4:LYS:HA	1:IG:17:TYR:HD1	1.72	0.53
1:KD:83:ASN:O	1:KD:87:LYS:HG3	2.09	0.53
1:AM:73:LEU:HA	1:CA:72:ASN:O	2.07	0.53
1:BA:83:ASN:O	1:BA:87:LYS:HG3	2.09	0.53
1:BV:83:ASN:O	1:BV:87:LYS:HG3	2.09	0.53
1:BY:47:TYR:CZ	1:FK:105:ILE:HG12	2.44	0.53
1:DH:4:LYS:HA	1:DH:17:TYR:HD1	1.72	0.53
1:ED:83:ASN:O	1:ED:87:LYS:HG3	2.09	0.53
1:EL:44:ASN:ND2	1:EL:76:THR:HB	2.22	0.53
1:FN:83:ASN:O	1:FN:87:LYS:HG3	2.09	0.53
1:FQ:83:ASN:O	1:FQ:87:LYS:HG3	2.09	0.53
1:GX:83:ASN:O	1:GX:87:LYS:HG3	2.09	0.53
1:HJ:83:ASN:O	1:HJ:87:LYS:HG3	2.09	0.53
1:JF:83:ASN:O	1:JF:87:LYS:HG3	2.09	0.53
1:AC:83:ASN:O	1:AC:87:LYS:HG3	2.09	0.53
1:AL:83:ASN:O	1:AL:87:LYS:HG3	2.09	0.53
1:CK:83:ASN:O	1:CK:87:LYS:HG3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DC:83:ASN:O	1:DC:87:LYS:HG3	2.09	0.53
1:EG:83:ASN:O	1:EG:87:LYS:HG3	2.09	0.53
1:FZ:83:ASN:O	1:FZ:87:LYS:HG3	2.09	0.53
1:HS:83:ASN:O	1:HS:87:LYS:HG3	2.09	0.53
1:HZ:73:LEU:HD12	1:KC:72:ASN:O	2.09	0.53
1:JU:83:ASN:O	1:JU:87:LYS:HG3	2.09	0.53
1:IB:83:ASN:O	1:IB:87:LYS:HG3	2.09	0.52
1:JC:83:ASN:O	1:JC:87:LYS:HG3	2.09	0.52
1:JH:73:LEU:HD12	1:JP:73:LEU:HD13	1.90	0.52
1:AO:83:ASN:O	1:AO:87:LYS:HG3	2.09	0.52
1:AX:83:ASN:O	1:AX:87:LYS:HG3	2.09	0.52
1:BQ:45:ILE:HG21	1:EC:108:GLY:HA3	1.91	0.52
1:CH:83:ASN:O	1:CH:87:LYS:HG3	2.09	0.52
1:CN:83:ASN:O	1:CN:87:LYS:HG3	2.09	0.52
1:DI:72:ASN:O	1:GU:73:LEU:HD12	2.09	0.52
1:DI:83:ASN:O	1:DI:87:LYS:HG3	2.09	0.52
1:GU:83:ASN:O	1:GU:87:LYS:HG3	2.09	0.52
1:HA:83:ASN:O	1:HA:87:LYS:HG3	2.09	0.52
1:IF:45:ILE:HG21	1:IJ:108:GLY:HA3	1.89	0.52
1:IG:88:LEU:HG	1:KB:106:ILE:HG21	1.91	0.52
1:IW:83:ASN:O	1:IW:87:LYS:HG3	2.09	0.52
1:JD:69:ILE:HD13	1:JN:87:LYS:HA	1.91	0.52
1:BB:71:ALA:HA	1:BR:74:SER:O	2.10	0.52
1:BD:83:ASN:O	1:BD:87:LYS:HG3	2.09	0.52
1:CB:83:ASN:O	1:CB:87:LYS:HG3	2.09	0.52
1:CJ:69:ILE:HG12	1:CO:78:LEU:HD12	1.92	0.52
1:CT:83:ASN:O	1:CT:87:LYS:HG3	2.09	0.52
1:EN:112:THR:HG23	1:FJ:17:TYR:OH	2.09	0.52
1:ES:83:ASN:O	1:ES:87:LYS:HG3	2.09	0.52
1:FW:83:ASN:O	1:FW:87:LYS:HG3	2.09	0.52
1:GI:83:ASN:O	1:GI:87:LYS:HG3	2.09	0.52
1:GO:83:ASN:O	1:GO:87:LYS:HG3	2.09	0.52
1:IH:83:ASN:O	1:IH:87:LYS:HG3	2.09	0.52
1:AG:19:PHE:HB3	1:BF:89:ARG:NH2	2.24	0.52
1:FK:83:ASN:O	1:FK:87:LYS:HG3	2.09	0.52
1:JX:83:ASN:O	1:JX:87:LYS:HG3	2.09	0.52
1:AU:94:ILE:HG13	1:EG:49:ILE:HG21	1.91	0.52
1:BK:44:ASN:HD22	1:BK:76:THR:HB	1.75	0.52
1:BZ:105:ILE:HG12	1:DT:47:TYR:CZ	2.45	0.52
1:CK:73:LEU:HD12	1:FW:72:ASN:O	2.09	0.52
1:DF:83:ASN:O	1:DF:87:LYS:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DV:44:ASN:HD22	1:DV:76:THR:HB	1.75	0.52
1:DY:105:ILE:HG12	1:FY:47:TYR:CZ	2.44	0.52
1:EA:83:ASN:O	1:EA:87:LYS:HG3	2.09	0.52
1:GD:44:ASN:HD22	1:GD:76:THR:HB	1.75	0.52
1:GM:44:ASN:HD22	1:GM:76:THR:HB	1.75	0.52
1:HE:44:ASN:HD22	1:HE:76:THR:HB	1.75	0.52
1:HH:44:ASN:HD22	1:HH:76:THR:HB	1.75	0.52
1:HQ:44:ASN:HD22	1:HQ:76:THR:HB	1.75	0.52
1:IO:4:LYS:HE2	1:KI:112:THR:HG21	1.90	0.52
1:IT:83:ASN:O	1:IT:87:LYS:HG3	2.09	0.52
1:AD:36:THR:HB	1:AD:45:ILE:HD11	1.92	0.52
1:AR:95:VAL:HG13	1:ED:95:VAL:HG13	1.92	0.52
1:AU:111:LEU:CG	1:EG:11:PRO:HA	2.36	0.52
1:BB:44:ASN:HD22	1:BB:76:THR:HB	1.75	0.52
1:BS:95:VAL:HG11	1:FE:99:THR:HG23	1.92	0.52
1:BT:17:TYR:OH	1:DN:112:THR:HG22	2.09	0.52
1:BT:36:THR:HB	1:BT:45:ILE:HD11	1.92	0.52
1:BW:44:ASN:HD22	1:BW:76:THR:HB	1.75	0.52
1:BY:83:ASN:O	1:BY:87:LYS:HG3	2.09	0.52
1:CR:44:ASN:HD22	1:CR:76:THR:HB	1.75	0.52
1:DI:73:LEU:HD12	1:GU:72:ASN:O	2.10	0.52
1:DP:95:VAL:HG13	1:GW:95:VAL:HG13	1.92	0.52
1:DX:83:ASN:O	1:DX:87:LYS:HG3	2.09	0.52
1:EP:83:ASN:O	1:EP:87:LYS:HG3	2.09	0.52
1:ER:44:ASN:HD22	1:ER:76:THR:HB	1.75	0.52
1:EY:83:ASN:O	1:EY:87:LYS:HG3	2.09	0.52
1:FH:83:ASN:O	1:FH:87:LYS:HG3	2.09	0.52
1:GV:44:ASN:HD22	1:GV:76:THR:HB	1.75	0.52
1:HK:44:ASN:HD22	1:HK:76:THR:HB	1.75	0.52
1:HT:36:THR:HB	1:HT:45:ILE:HD11	1.92	0.52
1:IO:44:ASN:HD22	1:IO:76:THR:HB	1.75	0.52
1:JA:105:ILE:HG12	1:JQ:47:TYR:CZ	2.44	0.52
1:AG:36:THR:HB	1:AG:45:ILE:HD11	1.92	0.52
1:AU:83:ASN:O	1:AU:87:LYS:HG3	2.09	0.52
1:BE:36:THR:HB	1:BE:45:ILE:HD11	1.92	0.52
1:BQ:73:LEU:HD13	1:EC:73:LEU:HD12	1.91	0.52
1:BW:83:ASN:HD22	1:DQ:55:LEU:HD13	1.74	0.52
1:CP:44:ASN:HD22	1:CP:76:THR:HB	1.75	0.52
1:DA:44:ASN:HD22	1:DA:76:THR:HB	1.75	0.52
1:FC:44:ASN:HD22	1:FC:76:THR:HB	1.75	0.52
1:FG:44:ASN:HD22	1:FG:76:THR:HB	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FV:88:LEU:HG	1:GS:106:ILE:HG21	1.91	0.52
1:GJ:36:THR:HB	1:GJ:45:ILE:HD11	1.92	0.52
1:GR:83:ASN:O	1:GR:87:LYS:HG3	2.09	0.52
1:GY:112:THR:CG2	1:HO:17:TYR:OH	2.58	0.52
1:HF:44:ASN:HD22	1:HF:76:THR:HB	1.75	0.52
1:HG:83:ASN:O	1:HG:87:LYS:HG3	2.09	0.52
1:HN:44:ASN:HD22	1:HN:76:THR:HB	1.75	0.52
1:HR:44:ASN:HD22	1:HR:76:THR:HB	1.75	0.52
1:HX:44:ASN:HD22	1:HX:76:THR:HB	1.75	0.52
1:IX:36:THR:HB	1:IX:45:ILE:HD11	1.92	0.52
1:JA:44:ASN:HD22	1:JA:76:THR:HB	1.75	0.52
1:JJ:44:ASN:HD22	1:JJ:76:THR:HB	1.75	0.52
1:JQ:44:ASN:HD22	1:JQ:76:THR:HB	1.75	0.52
1:JW:72:ASN:O	1:KE:73:LEU:HD12	2.08	0.52
1:AN:75:PHE:HE2	1:FR:106:ILE:HA	1.75	0.52
1:AV:44:ASN:HD22	1:AV:76:THR:HB	1.75	0.52
1:BE:99:THR:CG2	1:BL:95:VAL:HG11	2.39	0.52
1:BH:44:ASN:HD22	1:BH:76:THR:HB	1.75	0.52
1:BK:36:THR:HB	1:BK:45:ILE:HD11	1.92	0.52
1:BN:36:THR:HB	1:BN:45:ILE:HD11	1.92	0.52
1:BR:44:ASN:HD22	1:BR:76:THR:HB	1.75	0.52
1:CD:44:ASN:HD22	1:CD:76:THR:HB	1.75	0.52
1:CJ:108:GLY:HA3	1:CO:45:ILE:CG2	2.39	0.52
1:CN:86:GLU:HG2	1:FZ:53:TYR:CE2	2.45	0.52
1:CV:44:ASN:HD22	1:CV:76:THR:HB	1.75	0.52
1:EE:36:THR:HB	1:EE:45:ILE:HD11	1.92	0.52
1:EL:44:ASN:HD22	1:EL:76:THR:HB	1.75	0.52
1:FY:44:ASN:HD22	1:FY:76:THR:HB	1.75	0.52
1:GB:44:ASN:HD22	1:GB:76:THR:HB	1.75	0.52
1:GG:44:ASN:HD22	1:GG:76:THR:HB	1.75	0.52
1:GY:44:ASN:HD22	1:GY:76:THR:HB	1.75	0.52
1:HL:44:ASN:HD22	1:HL:76:THR:HB	1.75	0.52
1:HL:105:ILE:HG12	1:JG:47:TYR:CZ	2.44	0.52
1:HV:105:ILE:HG12	1:JO:47:TYR:CE2	2.44	0.52
1:HZ:44:ASN:HD22	1:HZ:76:THR:HB	1.75	0.52
1:IX:78:LEU:HD12	1:JB:69:ILE:HG12	1.92	0.52
1:IY:44:ASN:HD22	1:IY:76:THR:HB	1.75	0.52
1:JB:44:ASN:HD22	1:JB:76:THR:HB	1.75	0.52
1:JK:108:GLY:HA3	1:JM:45:ILE:HG21	1.91	0.52
1:JN:44:ASN:HD22	1:JN:76:THR:HB	1.75	0.52
1:JS:44:ASN:HD22	1:JS:76:THR:HB	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JW:44:ASN:HD22	1:JW:76:THR:HB	1.75	0.52
1:AM:36:THR:HB	1:AM:45:ILE:HD11	1.92	0.52
1:AV:83:ASN:HD22	1:EF:55:LEU:HD13	1.75	0.52
1:BP:83:ASN:O	1:BP:87:LYS:HG3	2.09	0.52
1:BQ:44:ASN:HD22	1:BQ:76:THR:HB	1.75	0.52
1:BT:44:ASN:HD22	1:BT:76:THR:HB	1.75	0.52
1:BW:109:ASN:CG	1:DQ:11:PRO:HB3	2.35	0.52
1:CM:44:ASN:HD22	1:CM:76:THR:HB	1.75	0.52
1:CO:44:ASN:HD22	1:CO:76:THR:HB	1.75	0.52
1:DV:89:ARG:HH22	1:GE:21:GLY:H	1.57	0.52
1:FO:44:ASN:HD22	1:FO:76:THR:HB	1.75	0.52
1:GH:44:ASN:HD22	1:GH:76:THR:HB	1.75	0.52
1:GP:44:ASN:HD22	1:GP:76:THR:HB	1.75	0.52
1:GZ:44:ASN:HD22	1:GZ:76:THR:HB	1.75	0.52
1:HV:108:GLY:C	1:JO:36:THR:HG21	2.35	0.52
1:II:44:ASN:HD22	1:II:76:THR:HB	1.75	0.52
1:IK:83:ASN:O	1:IK:87:LYS:HG3	2.09	0.52
1:IU:44:ASN:HD22	1:IU:76:THR:HB	1.75	0.52
1:JG:36:THR:HB	1:JG:45:ILE:HD11	1.92	0.52
1:KE:36:THR:HB	1:KE:45:ILE:HD11	1.92	0.52
1:KH:44:ASN:HD22	1:KH:76:THR:HB	1.75	0.52
1:BQ:36:THR:HB	1:BQ:45:ILE:HD11	1.92	0.52
1:CG:44:ASN:HD22	1:CG:76:THR:HB	1.75	0.52
1:CR:36:THR:HB	1:CR:45:ILE:HD11	1.92	0.52
1:CX:44:ASN:HD22	1:CX:76:THR:HB	1.75	0.52
1:DD:36:THR:HB	1:DD:45:ILE:HD11	1.92	0.52
1:DD:44:ASN:HD22	1:DD:76:THR:HB	1.75	0.52
1:DF:72:ASN:O	1:GR:73:LEU:HD12	2.10	0.52
1:DV:45:ILE:HG21	1:GE:108:GLY:HA3	1.92	0.52
1:DW:44:ASN:HD22	1:DW:76:THR:HB	1.75	0.52
1:EC:44:ASN:HD22	1:EC:76:THR:HB	1.75	0.52
1:EZ:36:THR:HB	1:EZ:45:ILE:HD11	1.92	0.52
1:EZ:44:ASN:HD22	1:EZ:76:THR:HB	1.75	0.52
1:FE:83:ASN:O	1:FE:87:LYS:HG3	2.09	0.52
1:FI:36:THR:HB	1:FI:45:ILE:HD11	1.92	0.52
1:FS:44:ASN:HD22	1:FS:76:THR:HB	1.75	0.52
1:GS:36:THR:HB	1:GS:45:ILE:HD11	1.92	0.52
1:GT:44:ASN:HD22	1:GT:76:THR:HB	1.75	0.52
1:HB:99:THR:CG2	1:HX:95:VAL:HG11	2.40	0.52
1:HD:83:ASN:O	1:HD:87:LYS:HG3	2.09	0.52
1:HH:95:VAL:HG13	1:IV:95:VAL:HG13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HI:55:LEU:HD13	1:JJ:83:ASN:HD22	1.74	0.52
1:HQ:36:THR:HB	1:HQ:45:ILE:HD11	1.92	0.52
1:JD:36:THR:HB	1:JD:45:ILE:HD11	1.92	0.52
1:JD:44:ASN:HD22	1:JD:76:THR:HB	1.75	0.52
1:JH:44:ASN:HD22	1:JH:76:THR:HB	1.75	0.52
1:JJ:36:THR:HB	1:JJ:45:ILE:HD11	1.92	0.52
1:JM:44:ASN:HD22	1:JM:76:THR:HB	1.75	0.52
1:AE:44:ASN:HD22	1:AE:76:THR:HB	1.75	0.51
1:AM:44:ASN:HD22	1:AM:76:THR:HB	1.75	0.51
1:CU:36:THR:HB	1:CU:45:ILE:HD11	1.92	0.51
1:DE:44:ASN:HD22	1:DE:76:THR:HB	1.75	0.51
1:DJ:44:ASN:HD22	1:DJ:76:THR:HB	1.75	0.51
1:DM:36:THR:HB	1:DM:45:ILE:HD11	1.92	0.51
1:DN:44:ASN:HD22	1:DN:76:THR:HB	1.75	0.51
1:DP:44:ASN:HD22	1:DP:76:THR:HB	1.75	0.51
1:DY:36:THR:HB	1:DY:45:ILE:HD11	1.92	0.51
1:EH:44:ASN:HD22	1:EH:76:THR:HB	1.75	0.51
1:FJ:44:ASN:HD22	1:FJ:76:THR:HB	1.75	0.51
1:FL:44:ASN:HD22	1:FL:76:THR:HB	1.75	0.51
1:GC:83:ASN:O	1:GC:87:LYS:HG3	2.09	0.51
1:HB:4:LYS:HE2	1:HX:112:THR:HG21	1.92	0.51
1:HB:36:THR:HB	1:HB:45:ILE:HD11	1.92	0.51
1:HU:44:ASN:HD22	1:HU:76:THR:HB	1.75	0.51
1:IC:44:ASN:HD22	1:IC:76:THR:HB	1.75	0.51
1:ID:44:ASN:HD22	1:ID:76:THR:HB	1.75	0.51
1:IR:36:THR:HB	1:IR:45:ILE:HD11	1.92	0.51
1:JI:83:ASN:O	1:JI:87:LYS:HG3	2.09	0.51
1:JO:83:ASN:O	1:JO:87:LYS:HG3	2.09	0.51
1:KG:83:ASN:O	1:KG:87:LYS:HG3	2.09	0.51
1:KH:36:THR:HB	1:KH:45:ILE:HD11	1.92	0.51
1:AE:88:LEU:HD23	1:GA:102:LYS:HG2	1.91	0.51
1:AJ:36:THR:HB	1:AJ:45:ILE:HD11	1.92	0.51
1:AU:47:TYR:CZ	1:EG:105:ILE:HG12	2.45	0.51
1:AY:36:THR:HB	1:AY:45:ILE:HD11	1.92	0.51
1:BG:83:ASN:O	1:BG:87:LYS:HG3	2.09	0.51
1:BM:99:THR:CG2	1:EY:95:VAL:HG11	2.40	0.51
1:CL:44:ASN:HD22	1:CL:76:THR:HB	1.75	0.51
1:EB:102:LYS:HG3	1:GB:91:LEU:HD13	1.92	0.51
1:EF:44:ASN:HD22	1:EF:76:THR:HB	1.75	0.51
1:EO:44:ASN:HD22	1:EO:76:THR:HB	1.75	0.51
1:FF:36:THR:HB	1:FF:45:ILE:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FP:44:ASN:HD22	1:FP:76:THR:HB	1.75	0.51
1:FX:36:THR:HB	1:FX:45:ILE:HD11	1.92	0.51
1:GK:44:ASN:HD22	1:GK:76:THR:HB	1.75	0.51
1:HK:36:THR:HB	1:HK:45:ILE:HD11	1.92	0.51
1:HM:83:ASN:O	1:HM:87:LYS:HG3	2.09	0.51
1:HT:90:VAL:HG13	1:IM:51:VAL:HG11	1.92	0.51
1:HY:83:ASN:O	1:HY:87:LYS:HG3	2.09	0.51
1:IB:83:ASN:OD1	1:JX:55:LEU:HD13	2.10	0.51
1:IQ:83:ASN:O	1:IQ:87:LYS:HG3	2.09	0.51
1:JH:90:VAL:HG13	1:JP:51:VAL:HG11	1.91	0.51
1:JP:36:THR:HB	1:JP:45:ILE:HD11	1.92	0.51
1:JV:36:THR:HB	1:JV:45:ILE:HD11	1.92	0.51
1:JY:36:THR:HB	1:JY:45:ILE:HD11	1.92	0.51
1:JZ:44:ASN:HD22	1:JZ:76:THR:HB	1.75	0.51
1:KB:36:THR:HB	1:KB:45:ILE:HD11	1.92	0.51
1:KB:44:ASN:HD22	1:KB:76:THR:HB	1.75	0.51
1:AA:44:ASN:HD22	1:AA:76:THR:HB	1.75	0.51
1:AF:83:ASN:O	1:AF:87:LYS:HG3	2.09	0.51
1:AG:44:ASN:HD22	1:AG:76:THR:HB	1.75	0.51
1:AS:89:ARG:HH22	1:EL:21:GLY:H	1.58	0.51
1:BC:44:ASN:HD22	1:BC:76:THR:HB	1.75	0.51
1:BH:36:THR:HB	1:BH:45:ILE:HD11	1.92	0.51
1:BS:83:ASN:O	1:BS:87:LYS:HG3	2.09	0.51
1:CJ:21:GLY:H	1:CO:89:ARG:HH22	1.57	0.51
1:EB:36:THR:HB	1:EB:45:ILE:HD11	1.92	0.51
1:EI:44:ASN:HD22	1:EI:76:THR:HB	1.75	0.51
1:FO:36:THR:HB	1:FO:45:ILE:HD11	1.92	0.51
1:FV:44:ASN:HD22	1:FV:76:THR:HB	1.75	0.51
1:GA:44:ASN:HD22	1:GA:76:THR:HB	1.75	0.51
1:GL:83:ASN:O	1:GL:87:LYS:HG3	2.09	0.51
1:GZ:72:ASN:O	1:JY:73:LEU:HD12	2.10	0.51
1:HC:44:ASN:HD22	1:HC:76:THR:HB	1.75	0.51
1:HT:44:ASN:HD22	1:HT:76:THR:HB	1.75	0.51
1:HW:44:ASN:HD22	1:HW:76:THR:HB	1.75	0.51
1:IF:109:ASN:CG	1:IJ:11:PRO:HB3	2.36	0.51
1:IJ:44:ASN:HD22	1:IJ:76:THR:HB	1.75	0.51
1:IL:44:ASN:HD22	1:IL:76:THR:HB	1.75	0.51
1:IV:44:ASN:HD22	1:IV:76:THR:HB	1.75	0.51
1:KC:44:ASN:HD22	1:KC:76:THR:HB	1.75	0.51
1:AP:4:LYS:HE2	1:BU:112:THR:HG21	1.92	0.51
1:AV:47:TYR:CE2	1:EF:105:ILE:HG12	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:36:THR:HB	1:CF:45:ILE:HD11	1.92	0.51
1:CF:44:ASN:HD22	1:CF:76:THR:HB	1.75	0.51
1:CG:49:ILE:HG21	1:CL:94:ILE:HG13	1.92	0.51
1:CI:44:ASN:HD22	1:CI:76:THR:HB	1.75	0.51
1:DS:36:THR:HB	1:DS:45:ILE:HD11	1.92	0.51
1:EH:36:THR:HB	1:EH:45:ILE:HD11	1.92	0.51
1:EK:36:THR:HB	1:EK:45:ILE:HD11	1.92	0.51
1:ET:44:ASN:HD22	1:ET:76:THR:HB	1.75	0.51
1:EU:44:ASN:HD22	1:EU:76:THR:HB	1.75	0.51
1:FR:44:ASN:HD22	1:FR:76:THR:HB	1.75	0.51
1:GY:109:ASN:CG	1:HO:11:PRO:HB3	2.35	0.51
1:HB:106:ILE:HD13	1:HX:88:LEU:HG	1.93	0.51
1:IR:44:ASN:HD22	1:IR:76:THR:HB	1.75	0.51
1:JA:110:VAL:HB	1:JQ:36:THR:HG23	1.93	0.51
1:JK:36:THR:HG23	1:JM:110:VAL:HB	1.91	0.51
1:JY:44:ASN:HD22	1:JY:76:THR:HB	1.75	0.51
1:AW:44:ASN:HD22	1:AW:76:THR:HB	1.75	0.51
1:AY:44:ASN:HD22	1:AY:76:THR:HB	1.75	0.51
1:AZ:44:ASN:HD22	1:AZ:76:THR:HB	1.75	0.51
1:CA:44:ASN:HD22	1:CA:76:THR:HB	1.75	0.51
1:CI:36:THR:HB	1:CI:45:ILE:HD11	1.92	0.51
1:CS:44:ASN:HD22	1:CS:76:THR:HB	1.75	0.51
1:DO:83:ASN:O	1:DO:87:LYS:HG3	2.09	0.51
1:EB:44:ASN:HD22	1:EB:76:THR:HB	1.75	0.51
1:EQ:36:THR:HB	1:EQ:45:ILE:HD11	1.92	0.51
1:EQ:44:ASN:HD22	1:EQ:76:THR:HB	1.75	0.51
1:FF:44:ASN:HD22	1:FF:76:THR:HB	1.75	0.51
1:FI:44:ASN:HD22	1:FI:76:THR:HB	1.75	0.51
1:GA:36:THR:HB	1:GA:45:ILE:HD11	1.92	0.51
1:GN:44:ASN:HD22	1:GN:76:THR:HB	1.75	0.51
1:GS:44:ASN:HD22	1:GS:76:THR:HB	1.75	0.51
1:IA:21:GLY:H	1:IC:89:ARG:HH22	1.59	0.51
1:IZ:83:ASN:O	1:IZ:87:LYS:HG3	2.09	0.51
1:KF:44:ASN:HD22	1:KF:76:THR:HB	1.75	0.51
1:AH:44:ASN:HD22	1:AH:76:THR:HB	1.75	0.51
1:AN:44:ASN:HD22	1:AN:76:THR:HB	1.75	0.51
1:AQ:47:TYR:HE1	1:FU:109:ASN:O	1.93	0.51
1:AT:44:ASN:HD22	1:AT:76:THR:HB	1.75	0.51
1:BN:44:ASN:HD22	1:BN:76:THR:HB	1.75	0.51
1:CC:36:THR:HB	1:CC:45:ILE:HD11	1.92	0.51
1:CG:93:GLU:OE1	1:CL:2:ILE:HG23	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DB:44:ASN:HD22	1:DB:76:THR:HB	1.75	0.51
1:DH:44:ASN:HD22	1:DH:76:THR:HB	1.75	0.51
1:DJ:36:THR:HB	1:DJ:45:ILE:HD11	1.92	0.51
1:DS:44:ASN:HD22	1:DS:76:THR:HB	1.75	0.51
1:DY:44:ASN:HD22	1:DY:76:THR:HB	1.75	0.51
1:GQ:44:ASN:HD22	1:GQ:76:THR:HB	1.75	0.51
1:IX:44:ASN:HD22	1:IX:76:THR:HB	1.75	0.51
1:JV:44:ASN:HD22	1:JV:76:THR:HB	1.75	0.51
1:AD:44:ASN:HD22	1:AD:76:THR:HB	1.75	0.51
1:AG:45:ILE:HG21	1:BF:108:GLY:HA3	1.92	0.51
1:AJ:44:ASN:HD22	1:AJ:76:THR:HB	1.75	0.51
1:AU:90:VAL:HG13	1:EG:51:VAL:HG11	1.93	0.51
1:AV:45:ILE:HD13	1:EF:108:GLY:O	2.11	0.51
1:BB:73:LEU:HA	1:BR:72:ASN:O	2.10	0.51
1:BX:44:ASN:HD22	1:BX:76:THR:HB	1.75	0.51
1:BY:47:TYR:CD1	1:FK:105:ILE:HA	2.46	0.51
1:BZ:44:ASN:HD22	1:BZ:76:THR:HB	1.75	0.51
1:CC:44:ASN:HD22	1:CC:76:THR:HB	1.75	0.51
1:CN:98:ILE:HD11	1:FZ:73:LEU:HD22	1.92	0.51
1:DG:44:ASN:HD22	1:DG:76:THR:HB	1.75	0.51
1:EN:44:ASN:HD22	1:EN:76:THR:HB	1.75	0.51
1:FL:36:THR:HB	1:FL:45:ILE:HD11	1.92	0.51
1:FR:36:THR:HB	1:FR:45:ILE:HD11	1.92	0.51
1:IE:99:THR:HG23	1:KA:95:VAL:HG11	1.92	0.51
1:IU:4:LYS:HE2	1:JE:112:THR:HG21	1.93	0.51
1:JE:44:ASN:HD22	1:JE:76:THR:HB	1.75	0.51
1:AN:112:THR:HG21	1:FR:4:LYS:HE2	1.93	0.51
1:AS:47:TYR:CZ	1:EL:105:ILE:HG12	2.46	0.51
1:AW:112:THR:HG21	1:FC:4:LYS:HE2	1.93	0.51
1:BL:44:ASN:HD22	1:BL:76:THR:HB	1.75	0.51
1:BN:16:ILE:HD12	1:BP:11:PRO:HG3	1.93	0.51
1:BZ:45:ILE:HG21	1:DT:108:GLY:HA3	1.93	0.51
1:CO:36:THR:HB	1:CO:45:ILE:HD11	1.92	0.51
1:DF:73:LEU:HD12	1:GR:72:ASN:O	2.11	0.51
1:EN:36:THR:HB	1:EN:45:ILE:HD11	1.92	0.51
1:EW:44:ASN:HD22	1:EW:76:THR:HB	1.75	0.51
1:FA:95:VAL:HG13	1:FL:95:VAL:HG13	1.92	0.51
1:GJ:44:ASN:HD22	1:GJ:76:THR:HB	1.75	0.51
1:GY:36:THR:HB	1:GY:45:ILE:HD11	1.92	0.51
1:HB:44:ASN:HD22	1:HB:76:THR:HB	1.75	0.51
1:HP:73:LEU:HD12	1:JC:72:ASN:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IL:36:THR:HB	1:IL:45:ILE:HD11	1.92	0.51
1:IO:106:ILE:HG21	1:KI:88:LEU:HG	1.92	0.51
1:JP:16:ILE:HD12	1:JR:11:PRO:HG3	1.93	0.51
1:KE:44:ASN:HD22	1:KE:76:THR:HB	1.75	0.51
1:AA:36:THR:HB	1:AA:45:ILE:HD11	1.92	0.51
1:AE:75:PHE:HD1	1:GA:71:ALA:HB2	1.75	0.51
1:BB:36:THR:HB	1:BB:45:ILE:HD11	1.92	0.51
1:BK:4:LYS:HE2	1:DW:112:THR:HG21	1.93	0.51
1:BU:44:ASN:HD22	1:BU:76:THR:HB	1.75	0.51
1:CY:105:ILE:HG12	1:GG:47:TYR:CZ	2.45	0.51
1:EN:16:ILE:HD12	1:EP:11:PRO:HG3	1.93	0.51
1:EX:44:ASN:HD22	1:EX:76:THR:HB	1.75	0.51
1:GE:44:ASN:HD22	1:GE:76:THR:HB	1.75	0.51
1:GS:16:ILE:HD12	1:GU:11:PRO:HG3	1.93	0.51
1:GY:83:ASN:HD22	1:HO:55:LEU:HD13	1.75	0.51
1:HW:16:ILE:HD12	1:HY:11:PRO:HG3	1.93	0.51
1:HZ:16:ILE:HD12	1:IB:11:PRO:HG3	1.93	0.51
1:IU:102:LYS:HG3	1:JE:91:LEU:HD13	1.92	0.51
1:JA:16:ILE:HD12	1:JC:11:PRO:HG3	1.93	0.51
1:JM:16:ILE:HD12	1:JO:11:PRO:HG3	1.93	0.51
1:JP:44:ASN:HD22	1:JP:76:THR:HB	1.75	0.51
1:JS:36:THR:HB	1:JS:45:ILE:HD11	1.92	0.51
1:AG:16:ILE:HD12	1:AI:11:PRO:HG3	1.93	0.51
1:AO:55:LEU:HD13	1:EA:83:ASN:OD1	2.11	0.51
1:BK:16:ILE:HD12	1:BM:11:PRO:HG3	1.93	0.51
1:CG:47:TYR:CZ	1:CL:105:ILE:HG12	2.46	0.51
1:CJ:89:ARG:NH2	1:CO:19:PHE:HB3	2.26	0.51
1:CL:36:THR:HB	1:CL:45:ILE:HD11	1.92	0.51
1:CX:36:THR:HB	1:CX:45:ILE:HD11	1.92	0.51
1:DD:16:ILE:HD12	1:DF:11:PRO:HG3	1.93	0.51
1:DP:36:THR:HB	1:DP:45:ILE:HD11	1.92	0.51
1:DV:36:THR:HB	1:DV:45:ILE:HD11	1.92	0.51
1:DY:112:THR:HG23	1:FY:17:TYR:OH	2.11	0.51
1:FA:44:ASN:HD22	1:FA:76:THR:HB	1.75	0.51
1:FU:44:ASN:HD22	1:FU:76:THR:HB	1.75	0.51
1:HC:112:THR:HG21	1:JS:4:LYS:HE2	1.93	0.51
1:HT:16:ILE:HD12	1:HV:11:PRO:HG3	1.93	0.51
1:HW:36:THR:HB	1:HW:45:ILE:HD11	1.92	0.51
1:HZ:36:THR:HB	1:HZ:45:ILE:HD11	1.92	0.51
1:JA:36:THR:HB	1:JA:45:ILE:HD11	1.92	0.51
1:AH:112:THR:HG21	1:GD:4:LYS:HE2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:16:ILE:HD12	1:AR:11:PRO:HG3	1.93	0.50
1:AS:36:THR:HB	1:AS:45:ILE:HD11	1.92	0.50
1:AS:44:ASN:HD22	1:AS:76:THR:HB	1.75	0.50
1:BE:44:ASN:HD22	1:BE:76:THR:HB	1.75	0.50
1:BP:73:LEU:HD12	1:FB:72:ASN:O	2.11	0.50
1:CD:108:GLY:HA3	1:CR:45:ILE:HG21	1.92	0.50
1:CE:98:ILE:HD11	1:FQ:73:LEU:HD22	1.93	0.50
1:CO:16:ILE:HD12	1:CQ:11:PRO:HG3	1.93	0.50
1:DM:44:ASN:HD22	1:DM:76:THR:HB	1.75	0.50
1:EB:16:ILE:HD12	1:ED:11:PRO:HG3	1.93	0.50
1:EW:16:ILE:HD12	1:EY:11:PRO:HG3	1.93	0.50
1:EZ:16:ILE:HD12	1:FB:11:PRO:HG3	1.93	0.50
1:FC:16:ILE:HD12	1:FE:11:PRO:HG3	1.93	0.50
1:FD:44:ASN:HD22	1:FD:76:THR:HB	1.75	0.50
1:HG:73:LEU:HD12	1:IT:72:ASN:O	2.11	0.50
1:HN:16:ILE:HD12	1:HP:11:PRO:HG3	1.93	0.50
1:HN:95:VAL:HG13	1:HR:95:VAL:HG13	1.92	0.50
1:HT:73:LEU:HD13	1:IM:73:LEU:HD12	1.92	0.50
1:IF:36:THR:HB	1:IF:45:ILE:HD11	1.92	0.50
1:IF:44:ASN:HD22	1:IF:76:THR:HB	1.75	0.50
1:IP:44:ASN:HD22	1:IP:76:THR:HB	1.75	0.50
1:JM:36:THR:HB	1:JM:45:ILE:HD11	1.92	0.50
1:JV:16:ILE:HD12	1:JX:11:PRO:HG3	1.93	0.50
1:KI:44:ASN:HD22	1:KI:76:THR:HB	1.75	0.50
1:AP:44:ASN:HD22	1:AP:76:THR:HB	1.75	0.50
1:AQ:44:ASN:HD22	1:AQ:76:THR:HB	1.75	0.50
1:BB:16:ILE:HD12	1:BD:11:PRO:HG3	1.93	0.50
1:BE:95:VAL:HG13	1:BL:95:VAL:HG13	1.92	0.50
1:BE:106:ILE:HA	1:BL:75:PHE:HE2	1.76	0.50
1:BQ:16:ILE:HD12	1:BS:11:PRO:HG3	1.93	0.50
1:BT:16:ILE:HD12	1:BV:11:PRO:HG3	1.93	0.50
1:BW:51:VAL:HG11	1:DQ:90:VAL:HG13	1.92	0.50
1:CG:72:ASN:O	1:CL:73:LEU:HD12	2.12	0.50
1:CH:112:THR:CG2	1:FT:17:TYR:OH	2.59	0.50
1:DS:16:ILE:HD12	1:DU:11:PRO:HG3	1.93	0.50
1:DV:47:TYR:CZ	1:GE:105:ILE:HG12	2.45	0.50
1:EK:44:ASN:HD22	1:EK:76:THR:HB	1.75	0.50
1:EQ:89:ARG:HH22	1:FM:21:GLY:H	1.60	0.50
1:GP:36:THR:HB	1:GP:45:ILE:HD11	1.92	0.50
1:HW:97:PHE:CG	1:IP:32:LEU:HD21	2.46	0.50
1:IG:44:ASN:HD22	1:IG:76:THR:HB	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IR:73:LEU:HD12	1:JZ:72:ASN:O	2.11	0.50
1:IU:36:THR:HB	1:IU:45:ILE:HD11	1.92	0.50
1:AV:36:THR:HB	1:AV:45:ILE:HD11	1.92	0.50
1:AV:45:ILE:CG2	1:EF:108:GLY:HA3	2.42	0.50
1:BV:32:LEU:HD13	1:BV:51:VAL:HG22	1.94	0.50
1:CL:16:ILE:HD12	1:CN:11:PRO:HG3	1.93	0.50
1:CR:16:ILE:HD12	1:CT:11:PRO:HG3	1.93	0.50
1:CU:44:ASN:HD22	1:CU:76:THR:HB	1.75	0.50
1:DL:32:LEU:HD13	1:DL:51:VAL:HG22	1.94	0.50
1:DZ:44:ASN:HD22	1:DZ:76:THR:HB	1.75	0.50
1:EN:89:ARG:HH22	1:FJ:21:GLY:H	1.58	0.50
1:ET:36:THR:HB	1:ET:45:ILE:HD11	1.92	0.50
1:EW:36:THR:HB	1:EW:45:ILE:HD11	1.92	0.50
1:FA:95:VAL:HG11	1:FL:99:THR:CG2	2.41	0.50
1:GG:16:ILE:HD12	1:GI:11:PRO:HG3	1.93	0.50
1:GG:36:THR:HB	1:GG:45:ILE:HD11	1.92	0.50
1:GM:16:ILE:HD12	1:GO:11:PRO:HG3	1.93	0.50
1:GP:16:ILE:HD12	1:GR:11:PRO:HG3	1.93	0.50
1:HF:69:ILE:HG12	1:JV:78:LEU:HD12	1.93	0.50
1:HJ:88:LEU:HD23	1:IZ:106:ILE:HG21	1.93	0.50
1:HO:44:ASN:HD22	1:HO:76:THR:HB	1.75	0.50
1:JS:16:ILE:HD12	1:JU:11:PRO:HG3	1.93	0.50
1:AK:44:ASN:HD22	1:AK:76:THR:HB	1.75	0.50
1:BW:16:ILE:HD12	1:BY:11:PRO:HG3	1.93	0.50
1:BW:36:THR:HB	1:BW:45:ILE:HD11	1.92	0.50
1:BY:77:ALA:HB1	1:FK:106:ILE:O	2.12	0.50
1:CZ:32:LEU:HD13	1:CZ:51:VAL:HG22	1.94	0.50
1:DB:21:GLY:H	1:GJ:89:ARG:HH22	1.57	0.50
1:DF:95:VAL:HG11	1:GR:99:THR:CG2	2.42	0.50
1:DI:32:LEU:HD13	1:DI:51:VAL:HG22	1.94	0.50
1:EE:4:LYS:HE2	1:EU:112:THR:HG21	1.93	0.50
1:EH:16:ILE:HD12	1:EJ:11:PRO:HG3	1.93	0.50
1:EK:78:LEU:HD12	1:ER:69:ILE:HG12	1.94	0.50
1:FF:16:ILE:HD12	1:FH:11:PRO:HG3	1.93	0.50
1:FI:16:ILE:HD12	1:FK:11:PRO:HG3	1.93	0.50
1:FO:16:ILE:HD12	1:FQ:11:PRO:HG3	1.93	0.50
1:FU:36:THR:HB	1:FU:45:ILE:HD11	1.92	0.50
1:GM:36:THR:HB	1:GM:45:ILE:HD11	1.92	0.50
1:HB:16:ILE:HD12	1:HD:11:PRO:HG3	1.93	0.50
1:HI:44:ASN:HD22	1:HI:76:THR:HB	1.75	0.50
1:HN:36:THR:HB	1:HN:45:ILE:HD11	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IA:44:ASN:HD22	1:IA:76:THR:HB	1.75	0.50
1:IC:36:THR:HB	1:IC:45:ILE:HD11	1.92	0.50
1:IK:89:ARG:HH22	1:KJ:21:GLY:H	1.58	0.50
1:IL:16:ILE:HD12	1:IN:11:PRO:HG3	1.93	0.50
1:IQ:32:LEU:HD13	1:IQ:51:VAL:HG22	1.94	0.50
1:JI:32:LEU:HD13	1:JI:51:VAL:HG22	1.94	0.50
1:JT:44:ASN:HD22	1:JT:76:THR:HB	1.75	0.50
1:AP:36:THR:HB	1:AP:45:ILE:HD11	1.92	0.50
1:AS:109:ASN:O	1:EL:47:TYR:HE1	1.95	0.50
1:BE:16:ILE:HD12	1:BG:11:PRO:HG3	1.93	0.50
1:CG:69:ILE:HG12	1:CL:78:LEU:HD12	1.94	0.50
1:CJ:108:GLY:O	1:CO:45:ILE:HD13	2.11	0.50
1:CT:32:LEU:HD13	1:CT:51:VAL:HG22	1.94	0.50
1:DG:16:ILE:HD12	1:DI:11:PRO:HG3	1.93	0.50
1:DK:44:ASN:HD22	1:DK:76:THR:HB	1.75	0.50
1:DR:32:LEU:HD13	1:DR:51:VAL:HG22	1.94	0.50
1:DS:73:LEU:HD12	1:GQ:72:ASN:O	2.11	0.50
1:EK:16:ILE:HD12	1:EM:11:PRO:HG3	1.93	0.50
1:EY:32:LEU:HD13	1:EY:51:VAL:HG22	1.94	0.50
1:FX:16:ILE:HD12	1:FZ:11:PRO:HG3	1.93	0.50
1:GV:36:THR:HB	1:GV:45:ILE:HD11	1.92	0.50
1:HG:32:LEU:HD13	1:HG:51:VAL:HG22	1.94	0.50
1:HH:83:ASN:ND2	1:IV:55:LEU:HD13	2.26	0.50
1:HL:69:ILE:HG12	1:JG:78:LEU:HD12	1.92	0.50
1:II:36:THR:HB	1:II:45:ILE:HD11	1.92	0.50
1:IM:44:ASN:HD22	1:IM:76:THR:HB	1.75	0.50
1:IU:21:GLY:H	1:JE:89:ARG:HH22	1.58	0.50
1:JG:44:ASN:HD22	1:JG:76:THR:HB	1.75	0.50
1:JK:44:ASN:HD22	1:JK:76:THR:HB	1.75	0.50
1:JY:16:ILE:HD12	1:KA:11:PRO:HG3	1.93	0.50
1:KE:16:ILE:HD12	1:KG:11:PRO:HG3	1.93	0.50
1:AB:44:ASN:HD22	1:AB:76:THR:HB	1.75	0.50
1:AI:32:LEU:HD13	1:AI:51:VAL:HG22	1.94	0.50
1:AQ:75:PHE:HE2	1:FU:106:ILE:HA	1.77	0.50
1:AY:16:ILE:HD12	1:BA:11:PRO:HG3	1.93	0.50
1:BZ:36:THR:HB	1:BZ:45:ILE:HD11	1.92	0.50
1:CH:23:THR:CG2	1:JT:85:ASP:OD2	2.59	0.50
1:CK:32:LEU:HD13	1:CK:51:VAL:HG22	1.94	0.50
1:CQ:89:ARG:HH22	1:GC:21:GLY:H	1.59	0.50
1:DA:16:ILE:HD12	1:DC:11:PRO:HG3	1.93	0.50
1:DG:36:THR:HB	1:DG:45:ILE:HD11	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FC:36:THR:HB	1:FC:45:ILE:HD11	1.92	0.50
1:GD:16:ILE:HD12	1:GF:11:PRO:HG3	1.93	0.50
1:HF:88:LEU:HG	1:JV:106:ILE:HG21	1.93	0.50
1:HJ:32:LEU:HD13	1:HJ:51:VAL:HG22	1.94	0.50
1:JD:16:ILE:HD12	1:JF:11:PRO:HG3	1.93	0.50
1:JG:16:ILE:HD12	1:JI:11:PRO:HG3	1.93	0.50
1:AF:21:GLY:H	1:DR:89:ARG:HH22	1.60	0.50
1:AL:32:LEU:HD13	1:AL:51:VAL:HG22	1.94	0.50
1:BF:44:ASN:HD22	1:BF:76:THR:HB	1.75	0.50
1:BG:32:LEU:HD13	1:BG:51:VAL:HG22	1.94	0.50
1:BO:44:ASN:HD22	1:BO:76:THR:HB	1.75	0.50
1:BZ:106:ILE:HA	1:DT:75:PHE:HE2	1.76	0.50
1:CF:83:ASN:ND2	1:GN:55:LEU:HD13	2.25	0.50
1:CX:4:LYS:HE2	1:DK:112:THR:HG21	1.94	0.50
1:CY:44:ASN:HD22	1:CY:76:THR:HB	1.75	0.50
1:DA:36:THR:HB	1:DA:45:ILE:HD11	1.92	0.50
1:EA:32:LEU:HD13	1:EA:51:VAL:HG22	1.94	0.50
1:ED:32:LEU:HD13	1:ED:51:VAL:HG22	1.94	0.50
1:EE:44:ASN:HD22	1:EE:76:THR:HB	1.75	0.50
1:GA:16:ILE:HD12	1:GC:11:PRO:HG3	1.93	0.50
1:GI:32:LEU:HD13	1:GI:51:VAL:HG22	1.94	0.50
1:GW:44:ASN:HD22	1:GW:76:THR:HB	1.75	0.50
1:GX:32:LEU:HD13	1:GX:51:VAL:HG22	1.94	0.50
1:IU:97:PHE:CG	1:JE:32:LEU:HD21	2.46	0.50
1:JK:47:TYR:CZ	1:JM:105:ILE:HG12	2.47	0.50
1:KD:32:LEU:HD13	1:KD:51:VAL:HG22	1.94	0.50
1:KH:16:ILE:HD12	1:KJ:11:PRO:HG3	1.93	0.50
1:AE:55:LEU:CD1	1:GA:81:VAL:HG21	2.42	0.50
1:AF:32:LEU:HD13	1:AF:51:VAL:HG22	1.94	0.50
1:AS:112:THR:HG23	1:EL:17:TYR:OH	2.12	0.50
1:BA:47:TYR:CZ	1:EM:105:ILE:HG12	2.46	0.50
1:CC:16:ILE:HD12	1:CE:11:PRO:HG3	1.93	0.50
1:DF:32:LEU:HD13	1:DF:51:VAL:HG22	1.94	0.50
1:DO:32:LEU:HD13	1:DO:51:VAL:HG22	1.94	0.50
1:DP:16:ILE:HD12	1:DR:11:PRO:HG3	1.93	0.50
1:ET:16:ILE:HD12	1:EV:11:PRO:HG3	1.93	0.50
1:FX:44:ASN:HD22	1:FX:76:THR:HB	1.75	0.50
1:HH:16:ILE:HD12	1:HJ:11:PRO:HG3	1.93	0.50
1:HH:36:THR:HB	1:HH:45:ILE:HD11	1.92	0.50
1:IS:44:ASN:HD22	1:IS:76:THR:HB	1.75	0.50
1:JU:32:LEU:HD13	1:JU:51:VAL:HG22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:32:LEU:HD13	1:AU:51:VAL:HG22	1.94	0.50
1:BH:16:ILE:HD12	1:BJ:11:PRO:HG3	1.93	0.50
1:BS:32:LEU:HD13	1:BS:51:VAL:HG22	1.94	0.50
1:BY:32:LEU:HD13	1:BY:51:VAL:HG22	1.94	0.50
1:CF:16:ILE:HD12	1:CH:11:PRO:HG3	1.93	0.50
1:CJ:44:ASN:HD22	1:CJ:76:THR:HB	1.75	0.50
1:DM:16:ILE:HD12	1:DO:11:PRO:HG3	1.93	0.50
1:DQ:44:ASN:HD22	1:DQ:76:THR:HB	1.75	0.50
1:EB:97:PHE:CG	1:GB:32:LEU:HD21	2.47	0.50
1:EQ:16:ILE:HD12	1:ES:11:PRO:HG3	1.93	0.50
1:FU:16:ILE:HD12	1:FW:11:PRO:HG3	1.93	0.50
1:FW:32:LEU:HD13	1:FW:51:VAL:HG22	1.94	0.50
1:GD:36:THR:HB	1:GD:45:ILE:HD11	1.92	0.50
1:GL:32:LEU:HD13	1:GL:51:VAL:HG22	1.94	0.50
1:IO:36:THR:HB	1:IO:45:ILE:HD11	1.92	0.50
1:KJ:32:LEU:HD13	1:KJ:51:VAL:HG22	1.94	0.50
1:AD:16:ILE:HD12	1:AF:11:PRO:HG3	1.93	0.49
1:AK:21:GLY:H	1:FO:89:ARG:HH22	1.59	0.49
1:AM:51:VAL:CG1	1:CA:90:VAL:HG13	2.42	0.49
1:BI:44:ASN:HD22	1:BI:76:THR:HB	1.75	0.49
1:BV:95:VAL:HG13	1:FH:95:VAL:HG13	1.94	0.49
1:CF:99:THR:CG2	1:GN:95:VAL:HG11	2.41	0.49
1:CU:16:ILE:HD12	1:CW:11:PRO:HG3	1.93	0.49
1:CX:16:ILE:HD12	1:CZ:11:PRO:HG3	1.93	0.49
1:DT:44:ASN:HD22	1:DT:76:THR:HB	1.75	0.49
1:FM:44:ASN:HD22	1:FM:76:THR:HB	1.75	0.49
1:FR:16:ILE:HD12	1:FT:11:PRO:HG3	1.93	0.49
1:FV:95:VAL:HG11	1:GS:99:THR:CG2	2.42	0.49
1:GJ:16:ILE:HD12	1:GL:11:PRO:HG3	1.93	0.49
1:HE:110:VAL:HB	1:HU:36:THR:HG23	1.94	0.49
1:HK:16:ILE:HD12	1:HM:11:PRO:HG3	1.93	0.49
1:HQ:16:ILE:HD12	1:HS:11:PRO:HG3	1.93	0.49
1:HQ:44:ASN:ND2	1:HQ:76:THR:HB	2.28	0.49
1:HS:32:LEU:HD13	1:HS:51:VAL:HG22	1.94	0.49
1:IB:32:LEU:HD13	1:IB:51:VAL:HG22	1.94	0.49
1:IF:16:ILE:HD12	1:IH:11:PRO:HG3	1.93	0.49
1:IN:32:LEU:HD13	1:IN:51:VAL:HG22	1.94	0.49
1:JJ:16:ILE:HD12	1:JL:11:PRO:HG3	1.93	0.49
1:AP:44:ASN:ND2	1:AP:76:THR:HB	2.28	0.49
1:BT:44:ASN:ND2	1:BT:76:THR:HB	2.28	0.49
1:BZ:16:ILE:HD12	1:CB:11:PRO:HG3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:44:ASN:ND2	1:CI:76:THR:HB	2.27	0.49
1:CX:44:ASN:ND2	1:CX:76:THR:HB	2.27	0.49
1:DJ:16:ILE:HD12	1:DL:11:PRO:HG3	1.93	0.49
1:FR:44:ASN:ND2	1:FR:76:THR:HB	2.28	0.49
1:GA:44:ASN:ND2	1:GA:76:THR:HB	2.28	0.49
1:GD:44:ASN:ND2	1:GD:76:THR:HB	2.28	0.49
1:HE:36:THR:HB	1:HE:45:ILE:HD11	1.92	0.49
1:HE:44:ASN:ND2	1:HE:76:THR:HB	2.28	0.49
1:HV:111:LEU:HD21	1:JO:8:SER:O	2.12	0.49
1:II:16:ILE:HD12	1:IK:11:PRO:HG3	1.93	0.49
1:IK:32:LEU:HD13	1:IK:51:VAL:HG22	1.94	0.49
1:IU:16:ILE:HD12	1:IW:11:PRO:HG3	1.93	0.49
1:IU:89:ARG:HH22	1:JE:21:GLY:H	1.60	0.49
1:IX:16:ILE:HD12	1:IZ:11:PRO:HG3	1.93	0.49
1:IX:44:ASN:ND2	1:IX:76:THR:HB	2.27	0.49
1:IX:73:LEU:CD2	1:JB:98:ILE:HD11	2.42	0.49
1:IZ:32:LEU:HD13	1:IZ:51:VAL:HG22	1.94	0.49
1:JG:44:ASN:ND2	1:JG:76:THR:HB	2.27	0.49
1:JP:44:ASN:ND2	1:JP:76:THR:HB	2.27	0.49
1:JT:110:VAL:HG12	1:KH:11:PRO:O	2.11	0.49
1:AC:32:LEU:HD13	1:AC:51:VAL:HG22	1.94	0.49
1:AM:16:ILE:HD12	1:AO:11:PRO:HG3	1.93	0.49
1:AM:44:ASN:ND2	1:AM:76:THR:HB	2.28	0.49
1:AV:16:ILE:HD12	1:AX:11:PRO:HG3	1.93	0.49
1:AY:44:ASN:ND2	1:AY:76:THR:HB	2.28	0.49
1:CG:11:PRO:HA	1:CL:111:LEU:HG	1.94	0.49
1:CH:32:LEU:HD13	1:CH:51:VAL:HG22	1.94	0.49
1:CJ:98:ILE:HD11	1:CO:73:LEU:CD2	2.42	0.49
1:CL:44:ASN:ND2	1:CL:76:THR:HB	2.28	0.49
1:EW:44:ASN:ND2	1:EW:76:THR:HB	2.27	0.49
1:FZ:32:LEU:HD13	1:FZ:51:VAL:HG22	1.94	0.49
1:GY:44:ASN:ND2	1:GY:76:THR:HB	2.28	0.49
1:HD:32:LEU:HD13	1:HD:51:VAL:HG22	1.94	0.49
1:HK:44:ASN:ND2	1:HK:76:THR:HB	2.28	0.49
1:HM:32:LEU:HD13	1:HM:51:VAL:HG22	1.94	0.49
1:HN:44:ASN:ND2	1:HN:76:THR:HB	2.28	0.49
1:IA:72:ASN:O	1:IC:73:LEU:HD12	2.12	0.49
1:IC:16:ILE:HD12	1:IE:11:PRO:HG3	1.93	0.49
1:IE:32:LEU:HD13	1:IE:51:VAL:HG22	1.94	0.49
1:IO:44:ASN:ND2	1:IO:76:THR:HB	2.28	0.49
1:JF:32:LEU:HD13	1:JF:51:VAL:HG22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JK:11:PRO:HA	1:JM:111:LEU:HG	1.94	0.49
1:AA:16:ILE:HD12	1:AC:11:PRO:HG3	1.93	0.49
1:AJ:16:ILE:HD12	1:AL:11:PRO:HG3	1.93	0.49
1:AJ:44:ASN:ND2	1:AJ:76:THR:HB	2.28	0.49
1:AR:32:LEU:HD13	1:AR:51:VAL:HG22	1.94	0.49
1:AX:32:LEU:HD13	1:AX:51:VAL:HG22	1.94	0.49
1:BB:78:LEU:HD12	1:BR:69:ILE:HG12	1.95	0.49
1:CG:11:PRO:O	1:CL:110:VAL:HG12	2.11	0.49
1:CI:16:ILE:HD12	1:CK:11:PRO:HG3	1.93	0.49
1:DA:44:ASN:ND2	1:DA:76:THR:HB	2.28	0.49
1:DC:32:LEU:HD13	1:DC:51:VAL:HG22	1.94	0.49
1:DX:32:LEU:HD13	1:DX:51:VAL:HG22	1.94	0.49
1:EN:17:TYR:OH	1:FJ:112:THR:HG22	2.12	0.49
1:FC:44:ASN:ND2	1:FC:76:THR:HB	2.27	0.49
1:FL:16:ILE:HD12	1:FN:11:PRO:HG3	1.93	0.49
1:FQ:32:LEU:HD13	1:FQ:51:VAL:HG22	1.94	0.49
1:IF:44:ASN:ND2	1:IF:76:THR:HB	2.28	0.49
1:IO:95:VAL:HG13	1:KI:95:VAL:HG13	1.94	0.49
1:IU:44:ASN:ND2	1:IU:76:THR:HB	2.27	0.49
1:JC:32:LEU:HD13	1:JC:51:VAL:HG22	1.94	0.49
1:JD:73:LEU:HB2	1:JN:73:LEU:HD12	1.94	0.49
1:KA:32:LEU:HD13	1:KA:51:VAL:HG22	1.94	0.49
1:KG:32:LEU:HD13	1:KG:51:VAL:HG22	1.94	0.49
1:AA:44:ASN:ND2	1:AA:76:THR:HB	2.28	0.49
1:AG:44:ASN:ND2	1:AG:76:THR:HB	2.28	0.49
1:AK:47:TYR:CZ	1:FO:105:ILE:HG12	2.47	0.49
1:BB:44:ASN:ND2	1:BB:76:THR:HB	2.27	0.49
1:BP:32:LEU:HD13	1:BP:51:VAL:HG22	1.94	0.49
1:BQ:44:ASN:ND2	1:BQ:76:THR:HB	2.28	0.49
1:CE:32:LEU:HD13	1:CE:51:VAL:HG22	1.94	0.49
1:EH:95:VAL:HG13	1:EO:95:VAL:HG13	1.94	0.49
1:EM:32:LEU:HD13	1:EM:51:VAL:HG22	1.94	0.49
1:ET:45:ILE:HG21	1:FG:108:GLY:HA3	1.94	0.49
1:FD:21:GLY:H	1:FF:89:ARG:HH22	1.59	0.49
1:FE:32:LEU:HD13	1:FE:51:VAL:HG22	1.94	0.49
1:FF:44:ASN:ND2	1:FF:76:THR:HB	2.28	0.49
1:FK:32:LEU:HD13	1:FK:51:VAL:HG22	1.94	0.49
1:FL:44:ASN:ND2	1:FL:76:THR:HB	2.28	0.49
1:FT:32:LEU:HD13	1:FT:51:VAL:HG22	1.94	0.49
1:GF:32:LEU:HD13	1:GF:51:VAL:HG22	1.94	0.49
1:GP:44:ASN:ND2	1:GP:76:THR:HB	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GV:16:ILE:HD12	1:GX:11:PRO:HG3	1.93	0.49
1:GY:16:ILE:HD12	1:HA:11:PRO:HG3	1.93	0.49
1:HB:44:ASN:ND2	1:HB:76:THR:HB	2.28	0.49
1:HT:44:ASN:ND2	1:HT:76:THR:HB	2.28	0.49
1:IU:112:THR:HG23	1:JE:17:TYR:OH	2.12	0.49
1:JD:51:VAL:CG1	1:JN:90:VAL:HG13	2.42	0.49
1:JY:44:ASN:ND2	1:JY:76:THR:HB	2.28	0.49
1:AC:95:VAL:HG11	1:DO:99:THR:CG2	2.43	0.49
1:AS:16:ILE:HD12	1:AU:11:PRO:HG3	1.93	0.49
1:BN:44:ASN:ND2	1:BN:76:THR:HB	2.28	0.49
1:BS:99:THR:HG23	1:FE:95:VAL:HG11	1.95	0.49
1:BW:44:ASN:ND2	1:BW:76:THR:HB	2.28	0.49
1:CY:69:ILE:HG12	1:GG:78:LEU:HD12	1.94	0.49
1:DB:105:ILE:HG12	1:GJ:47:TYR:CZ	2.47	0.49
1:DF:99:THR:CG2	1:GR:95:VAL:HG11	2.42	0.49
1:DV:16:ILE:HD12	1:DX:11:PRO:HG3	1.93	0.49
1:EQ:2:ILE:HG23	1:FM:93:GLU:OE1	2.13	0.49
1:FX:44:ASN:ND2	1:FX:76:THR:HB	2.28	0.49
1:GV:44:ASN:ND2	1:GV:76:THR:HB	2.28	0.49
1:ID:112:THR:HG21	1:II:4:LYS:HE2	1.94	0.49
1:IT:32:LEU:HD13	1:IT:51:VAL:HG22	1.94	0.49
1:JK:47:TYR:HE1	1:JM:109:ASN:O	1.95	0.49
1:AV:44:ASN:ND2	1:AV:76:THR:HB	2.28	0.49
1:BJ:32:LEU:HD13	1:BJ:51:VAL:HG22	1.94	0.49
1:CD:47:TYR:CZ	1:CR:105:ILE:HG12	2.48	0.49
1:CN:32:LEU:HD13	1:CN:51:VAL:HG22	1.94	0.49
1:CQ:32:LEU:HD13	1:CQ:51:VAL:HG22	1.94	0.49
1:CW:32:LEU:HD13	1:CW:51:VAL:HG22	1.94	0.49
1:DD:44:ASN:ND2	1:DD:76:THR:HB	2.28	0.49
1:DJ:44:ASN:ND2	1:DJ:76:THR:HB	2.28	0.49
1:DV:44:ASN:ND2	1:DV:76:THR:HB	2.27	0.49
1:EE:44:ASN:ND2	1:EE:76:THR:HB	2.28	0.49
1:EK:44:ASN:ND2	1:EK:76:THR:HB	2.28	0.49
1:EP:32:LEU:HD13	1:EP:51:VAL:HG22	1.94	0.49
1:ES:32:LEU:HD13	1:ES:51:VAL:HG22	1.94	0.49
1:FW:12:ILE:HG21	1:FW:38:VAL:HG23	1.95	0.49
1:GG:44:ASN:ND2	1:GG:76:THR:HB	2.28	0.49
1:HH:73:LEU:HD13	1:IV:73:LEU:HD12	1.95	0.49
1:HT:83:ASN:HD22	1:IM:55:LEU:HD22	1.77	0.49
1:IO:16:ILE:HD12	1:IQ:11:PRO:HG3	1.93	0.49
1:JC:12:ILE:HG21	1:JC:38:VAL:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:44:ASN:ND2	1:AD:76:THR:HB	2.27	0.49
1:BP:95:VAL:HG11	1:FB:99:THR:CG2	2.42	0.49
1:CB:32:LEU:HD13	1:CB:51:VAL:HG22	1.94	0.49
1:CR:44:ASN:ND2	1:CR:76:THR:HB	2.28	0.49
1:DF:12:ILE:HG21	1:DF:38:VAL:HG23	1.95	0.49
1:DI:12:ILE:HG21	1:DI:38:VAL:HG23	1.95	0.49
1:DY:16:ILE:HD12	1:EA:11:PRO:HG3	1.93	0.49
1:EE:16:ILE:HD12	1:EG:11:PRO:HG3	1.93	0.49
1:EE:73:LEU:HD13	1:EU:73:LEU:HB2	1.93	0.49
1:EH:44:ASN:ND2	1:EH:76:THR:HB	2.28	0.49
1:EQ:44:ASN:ND2	1:EQ:76:THR:HB	2.28	0.49
1:EV:32:LEU:HD13	1:EV:51:VAL:HG22	1.94	0.49
1:FN:32:LEU:HD13	1:FN:51:VAL:HG22	1.94	0.49
1:FO:44:ASN:ND2	1:FO:76:THR:HB	2.28	0.49
1:FU:44:ASN:ND2	1:FU:76:THR:HB	2.28	0.49
1:GC:32:LEU:HD13	1:GC:51:VAL:HG22	1.94	0.49
1:GR:12:ILE:HG21	1:GR:38:VAL:HG23	1.95	0.49
1:GS:44:ASN:ND2	1:GS:76:THR:HB	2.28	0.49
1:HJ:12:ILE:HG21	1:HJ:38:VAL:HG23	1.95	0.49
1:HV:97:PHE:CD1	1:JO:32:LEU:HD21	2.47	0.49
1:II:44:ASN:ND2	1:II:76:THR:HB	2.28	0.49
1:IL:44:ASN:ND2	1:IL:76:THR:HB	2.27	0.49
1:JJ:44:ASN:ND2	1:JJ:76:THR:HB	2.28	0.49
1:JX:32:LEU:HD13	1:JX:51:VAL:HG22	1.94	0.49
1:KE:44:ASN:ND2	1:KE:76:THR:HB	2.28	0.49
1:AC:12:ILE:HG21	1:AC:38:VAL:HG23	1.95	0.49
1:AD:83:ASN:HD22	1:BC:55:LEU:HD13	1.77	0.49
1:AL:12:ILE:HG21	1:AL:38:VAL:HG23	1.95	0.49
1:AO:32:LEU:HD13	1:AO:51:VAL:HG22	1.94	0.49
1:AW:88:LEU:HD23	1:FC:102:LYS:HG2	1.93	0.49
1:BS:12:ILE:HG21	1:BS:38:VAL:HG23	1.95	0.49
1:BZ:44:ASN:ND2	1:BZ:76:THR:HB	2.28	0.49
1:CB:12:ILE:HG21	1:CB:38:VAL:HG23	1.95	0.49
1:CC:44:ASN:ND2	1:CC:76:THR:HB	2.28	0.49
1:CK:12:ILE:HG21	1:CK:38:VAL:HG23	1.95	0.49
1:CT:12:ILE:HG21	1:CT:38:VAL:HG23	1.95	0.49
1:DG:44:ASN:ND2	1:DG:76:THR:HB	2.28	0.49
1:DS:44:ASN:ND2	1:DS:76:THR:HB	2.28	0.49
1:DV:47:TYR:CE2	1:GE:105:ILE:HG12	2.48	0.49
1:DX:12:ILE:HG21	1:DX:38:VAL:HG23	1.95	0.49
1:EB:112:THR:HG23	1:GB:17:TYR:OH	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ED:12:ILE:HG21	1:ED:38:VAL:HG23	1.95	0.49
1:FE:12:ILE:HG21	1:FE:38:VAL:HG23	1.95	0.49
1:GR:32:LEU:HD13	1:GR:51:VAL:HG22	1.94	0.49
1:HA:32:LEU:HD13	1:HA:51:VAL:HG22	1.94	0.49
1:HG:12:ILE:HG21	1:HG:38:VAL:HG23	1.95	0.49
1:HS:12:ILE:HG21	1:HS:38:VAL:HG23	1.95	0.49
1:HZ:44:ASN:ND2	1:HZ:76:THR:HB	2.28	0.49
1:HZ:45:ILE:HG21	1:KC:108:GLY:HA3	1.94	0.49
1:IC:44:ASN:ND2	1:IC:76:THR:HB	2.27	0.49
1:IR:44:ASN:ND2	1:IR:76:THR:HB	2.28	0.49
1:JD:44:ASN:ND2	1:JD:76:THR:HB	2.28	0.49
1:JT:55:LEU:HD13	1:KH:83:ASN:ND2	2.28	0.49
1:KH:44:ASN:ND2	1:KH:76:THR:HB	2.28	0.49
1:AQ:11:PRO:HB3	1:FU:109:ASN:CG	2.37	0.49
1:AQ:32:LEU:HD21	1:FU:97:PHE:CG	2.48	0.49
1:AS:44:ASN:ND2	1:AS:76:THR:HB	2.28	0.49
1:AY:21:GLY:H	1:EI:89:ARG:HH22	1.61	0.49
1:BD:32:LEU:HD13	1:BD:51:VAL:HG22	1.94	0.49
1:BQ:102:LYS:HG2	1:EC:88:LEU:HD23	1.95	0.49
1:CU:44:ASN:ND2	1:CU:76:THR:HB	2.28	0.49
1:DY:44:ASN:ND2	1:DY:76:THR:HB	2.28	0.49
1:DY:105:ILE:HG12	1:FY:47:TYR:CE2	2.48	0.49
1:EN:112:THR:CG2	1:FJ:17:TYR:OH	2.61	0.49
1:HA:12:ILE:HG21	1:HA:38:VAL:HG23	1.95	0.49
1:HY:32:LEU:HD13	1:HY:51:VAL:HG22	1.94	0.49
1:IE:12:ILE:HG21	1:IE:38:VAL:HG23	1.95	0.49
1:JL:32:LEU:HD13	1:JL:51:VAL:HG22	1.94	0.49
1:JM:44:ASN:ND2	1:JM:76:THR:HB	2.28	0.49
1:JS:44:ASN:ND2	1:JS:76:THR:HB	2.28	0.49
1:JV:44:ASN:ND2	1:JV:76:THR:HB	2.28	0.49
1:KB:16:ILE:HD12	1:KD:11:PRO:HG3	1.93	0.49
1:KB:44:ASN:ND2	1:KB:76:THR:HB	2.28	0.49
1:AJ:4:LYS:HE2	1:BX:112:THR:HG21	1.95	0.48
1:AN:104:ASN:ND2	1:AN:113:VAL:HB	2.29	0.48
1:BA:32:LEU:HD13	1:BA:51:VAL:HG22	1.94	0.48
1:BG:12:ILE:HG21	1:BG:38:VAL:HG23	1.95	0.48
1:BH:44:ASN:ND2	1:BH:76:THR:HB	2.28	0.48
1:CN:12:ILE:HG21	1:CN:38:VAL:HG23	1.95	0.48
1:CO:44:ASN:ND2	1:CO:76:THR:HB	2.28	0.48
1:CQ:106:ILE:HG21	1:GC:88:LEU:HD23	1.93	0.48
1:DL:88:LEU:CD2	1:GX:102:LYS:HG2	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DM:44:ASN:ND2	1:DM:76:THR:HB	2.28	0.48
1:DM:83:ASN:ND2	1:GT:55:LEU:HD13	2.28	0.48
1:DO:12:ILE:HG21	1:DO:38:VAL:HG23	1.95	0.48
1:EA:12:ILE:HG21	1:EA:38:VAL:HG23	1.95	0.48
1:EP:12:ILE:HG21	1:EP:38:VAL:HG23	1.95	0.48
1:EQ:36:THR:HG23	1:FM:110:VAL:HB	1.95	0.48
1:EY:12:ILE:HG21	1:EY:38:VAL:HG23	1.95	0.48
1:EZ:44:ASN:ND2	1:EZ:76:THR:HB	2.28	0.48
1:HE:16:ILE:HD12	1:HG:11:PRO:HG3	1.93	0.48
1:HH:44:ASN:ND2	1:HH:76:THR:HB	2.27	0.48
1:HL:36:THR:HG23	1:JG:110:VAL:HB	1.95	0.48
1:HP:32:LEU:HD13	1:HP:51:VAL:HG22	1.94	0.48
1:IW:12:ILE:HG21	1:IW:38:VAL:HG23	1.95	0.48
1:JI:12:ILE:HG21	1:JI:38:VAL:HG23	1.95	0.48
1:JT:11:PRO:O	1:KH:110:VAL:HG12	2.13	0.48
1:AD:110:VAL:HG12	1:BC:11:PRO:O	2.13	0.48
1:AU:12:ILE:HG21	1:AU:38:VAL:HG23	1.95	0.48
1:BA:12:ILE:HG21	1:BA:38:VAL:HG23	1.95	0.48
1:BE:44:ASN:ND2	1:BE:76:THR:HB	2.28	0.48
1:BT:109:ASN:O	1:DN:47:TYR:HE1	1.95	0.48
1:CF:44:ASN:ND2	1:CF:76:THR:HB	2.28	0.48
1:CG:20:THR:H	1:CL:89:ARG:NH2	2.11	0.48
1:EB:89:ARG:HH22	1:GB:21:GLY:H	1.61	0.48
1:EJ:32:LEU:HD13	1:EJ:51:VAL:HG22	1.94	0.48
1:ES:12:ILE:HG21	1:ES:38:VAL:HG23	1.95	0.48
1:EV:12:ILE:HG21	1:EV:38:VAL:HG23	1.95	0.48
1:GF:12:ILE:HG21	1:GF:38:VAL:HG23	1.95	0.48
1:GJ:44:ASN:ND2	1:GJ:76:THR:HB	2.28	0.48
1:IB:12:ILE:HG21	1:IB:38:VAL:HG23	1.95	0.48
1:IK:73:LEU:HD22	1:KJ:98:ILE:HD11	1.95	0.48
1:IM:104:ASN:ND2	1:IM:113:VAL:HB	2.29	0.48
1:IR:89:ARG:HH22	1:JZ:21:GLY:H	1.60	0.48
1:IW:32:LEU:HD13	1:IW:51:VAL:HG22	1.94	0.48
1:AH:55:LEU:HD13	1:GD:83:ASN:HD22	1.79	0.48
1:AO:12:ILE:HG21	1:AO:38:VAL:HG23	1.95	0.48
1:AX:98:ILE:HD11	1:EJ:73:LEU:HD22	1.95	0.48
1:BK:44:ASN:ND2	1:BK:76:THR:HB	2.28	0.48
1:CH:97:PHE:CG	1:FT:32:LEU:HD21	2.48	0.48
1:CY:108:GLY:HA3	1:GG:45:ILE:CG2	2.42	0.48
1:EG:32:LEU:HD13	1:EG:51:VAL:HG22	1.94	0.48
1:EN:109:ASN:ND2	1:FJ:11:PRO:HB3	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:32:LEU:HD13	1:FB:51:VAL:HG22	1.94	0.48
1:FI:44:ASN:ND2	1:FI:76:THR:HB	2.28	0.48
1:GU:12:ILE:HG21	1:GU:38:VAL:HG23	1.95	0.48
1:HI:104:ASN:ND2	1:HI:113:VAL:HB	2.29	0.48
1:HL:104:ASN:ND2	1:HL:113:VAL:HB	2.29	0.48
1:HW:44:ASN:ND2	1:HW:76:THR:HB	2.27	0.48
1:IQ:12:ILE:HG21	1:IQ:38:VAL:HG23	1.95	0.48
1:IV:104:ASN:ND2	1:IV:113:VAL:HB	2.29	0.48
1:IZ:12:ILE:HG21	1:IZ:38:VAL:HG23	1.95	0.48
1:KD:12:ILE:HG21	1:KD:38:VAL:HG23	1.95	0.48
1:AB:104:ASN:ND2	1:AB:113:VAL:HB	2.29	0.48
1:AN:32:LEU:HD21	1:FR:97:PHE:CD1	2.48	0.48
1:AP:95:VAL:HG13	1:BU:95:VAL:HG13	1.94	0.48
1:AR:12:ILE:HG21	1:AR:38:VAL:HG23	1.95	0.48
1:AX:12:ILE:HG21	1:AX:38:VAL:HG23	1.95	0.48
1:BI:104:ASN:ND2	1:BI:113:VAL:HB	2.29	0.48
1:BL:104:ASN:ND2	1:BL:113:VAL:HB	2.29	0.48
1:BY:47:TYR:CE2	1:FK:105:ILE:HG12	2.47	0.48
1:DM:106:ILE:HA	1:GT:75:PHE:HE2	1.79	0.48
1:DW:104:ASN:ND2	1:DW:113:VAL:HB	2.29	0.48
1:EB:44:ASN:ND2	1:EB:76:THR:HB	2.28	0.48
1:EB:110:VAL:HB	1:GB:36:THR:HG23	1.95	0.48
1:EF:104:ASN:ND2	1:EF:113:VAL:HB	2.29	0.48
1:EN:94:ILE:HG13	1:FJ:49:ILE:HG21	1.94	0.48
1:FA:104:ASN:ND2	1:FA:113:VAL:HB	2.29	0.48
1:FD:104:ASN:ND2	1:FD:113:VAL:HB	2.29	0.48
1:GU:32:LEU:HD13	1:GU:51:VAL:HG22	1.94	0.48
1:HM:12:ILE:HG21	1:HM:38:VAL:HG23	1.95	0.48
1:JO:32:LEU:HD13	1:JO:51:VAL:HG22	1.94	0.48
1:KG:12:ILE:HG21	1:KG:38:VAL:HG23	1.95	0.48
1:AG:73:LEU:CD2	1:BF:98:ILE:HD11	2.44	0.48
1:AK:104:ASN:ND2	1:AK:113:VAL:HB	2.29	0.48
1:AT:104:ASN:ND2	1:AT:113:VAL:HB	2.29	0.48
1:BR:104:ASN:ND2	1:BR:113:VAL:HB	2.29	0.48
1:CD:104:ASN:ND2	1:CD:113:VAL:HB	2.29	0.48
1:CG:104:ASN:ND2	1:CG:113:VAL:HB	2.29	0.48
1:CJ:105:ILE:HG12	1:CO:47:TYR:CE2	2.48	0.48
1:CV:21:GLY:H	1:GM:89:ARG:HH22	1.60	0.48
1:DE:104:ASN:ND2	1:DE:113:VAL:HB	2.29	0.48
1:EG:12:ILE:HG21	1:EG:38:VAL:HG23	1.95	0.48
1:EK:106:ILE:HD13	1:ER:88:LEU:HG	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EN:44:ASN:ND2	1:EN:76:THR:HB	2.28	0.48
1:EN:106:ILE:HA	1:FJ:75:PHE:HE2	1.77	0.48
1:FA:112:THR:HG21	1:FL:4:LYS:HE2	1.95	0.48
1:GH:104:ASN:ND2	1:GH:113:VAL:HB	2.29	0.48
1:GO:12:ILE:HG21	1:GO:38:VAL:HG23	1.95	0.48
1:GO:32:LEU:HD13	1:GO:51:VAL:HG22	1.94	0.48
1:GX:12:ILE:HG21	1:GX:38:VAL:HG23	1.95	0.48
1:HN:99:THR:CG2	1:HR:95:VAL:HG11	2.44	0.48
1:HP:72:ASN:O	1:JC:73:LEU:HD12	2.13	0.48
1:HW:83:ASN:HD22	1:IP:55:LEU:HD13	1.79	0.48
1:IE:95:VAL:HG11	1:KA:99:THR:HG23	1.94	0.48
1:JA:44:ASN:ND2	1:JA:76:THR:HB	2.28	0.48
1:JK:104:ASN:ND2	1:JK:113:VAL:HB	2.29	0.48
1:JL:12:ILE:HG21	1:JL:38:VAL:HG23	1.95	0.48
1:JR:32:LEU:HD13	1:JR:51:VAL:HG22	1.94	0.48
1:JW:105:ILE:HG12	1:KE:47:TYR:CZ	2.49	0.48
1:JZ:104:ASN:ND2	1:JZ:113:VAL:HB	2.29	0.48
1:KF:104:ASN:ND2	1:KF:113:VAL:HB	2.29	0.48
1:AZ:104:ASN:ND2	1:AZ:113:VAL:HB	2.29	0.48
1:BD:53:TYR:CE2	1:EP:86:GLU:CG	2.97	0.48
1:BO:104:ASN:ND2	1:BO:113:VAL:HB	2.29	0.48
1:CM:104:ASN:ND2	1:CM:113:VAL:HB	2.29	0.48
1:EI:104:ASN:ND2	1:EI:113:VAL:HB	2.29	0.48
1:FG:104:ASN:ND2	1:FG:113:VAL:HB	2.29	0.48
1:FT:12:ILE:HG21	1:FT:38:VAL:HG23	1.95	0.48
1:GL:12:ILE:HG21	1:GL:38:VAL:HG23	1.95	0.48
1:GZ:88:LEU:HG	1:JY:106:ILE:HD13	1.95	0.48
1:HF:95:VAL:HG11	1:JV:99:THR:CG2	2.44	0.48
1:HN:4:LYS:HE2	1:HR:112:THR:HG21	1.93	0.48
1:IG:95:VAL:HG11	1:KB:99:THR:HG22	1.95	0.48
1:IH:12:ILE:HG21	1:IH:38:VAL:HG23	1.95	0.48
1:IH:32:LEU:HD13	1:IH:51:VAL:HG22	1.94	0.48
1:JB:104:ASN:ND2	1:JB:113:VAL:HB	2.29	0.48
1:JR:12:ILE:HG21	1:JR:38:VAL:HG23	1.95	0.48
1:JT:104:ASN:ND2	1:JT:113:VAL:HB	2.29	0.48
1:JX:12:ILE:HG21	1:JX:38:VAL:HG23	1.95	0.48
1:KA:12:ILE:HG21	1:KA:38:VAL:HG23	1.95	0.48
1:AF:12:ILE:HG21	1:AF:38:VAL:HG23	1.95	0.48
1:AO:73:LEU:HD22	1:EA:98:ILE:HD11	1.96	0.48
1:BM:12:ILE:HG21	1:BM:38:VAL:HG23	1.95	0.48
1:CC:32:LEU:CD1	1:CC:49:ILE:HG23	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DB:104:ASN:ND2	1:DB:113:VAL:HB	2.29	0.48
1:DH:104:ASN:ND2	1:DH:113:VAL:HB	2.29	0.48
1:DP:4:LYS:HE2	1:GW:112:THR:HG21	1.96	0.48
1:DT:104:ASN:ND2	1:DT:113:VAL:HB	2.29	0.48
1:FM:104:ASN:ND2	1:FM:113:VAL:HB	2.29	0.48
1:GM:44:ASN:ND2	1:GM:76:THR:HB	2.28	0.48
1:HT:73:LEU:HB2	1:IM:73:LEU:HD12	1.95	0.48
1:HV:32:LEU:HD13	1:HV:51:VAL:HG22	1.94	0.48
1:IA:104:ASN:ND2	1:IA:113:VAL:HB	2.29	0.48
1:IR:16:ILE:HD12	1:IT:11:PRO:HG3	1.93	0.48
1:IX:95:VAL:HG13	1:JB:95:VAL:HG13	1.96	0.48
1:JH:104:ASN:ND2	1:JH:113:VAL:HB	2.29	0.48
1:JW:104:ASN:ND2	1:JW:113:VAL:HB	2.29	0.48
1:AU:89:ARG:NH2	1:EG:20:THR:H	2.12	0.48
1:AU:105:ILE:HG12	1:EG:47:TYR:CZ	2.48	0.48
1:AW:104:ASN:ND2	1:AW:113:VAL:HB	2.29	0.48
1:BC:104:ASN:ND2	1:BC:113:VAL:HB	2.29	0.48
1:BD:20:THR:H	1:EP:89:ARG:HH22	1.62	0.48
1:BH:32:LEU:CD1	1:BH:49:ILE:HG23	2.44	0.48
1:BM:32:LEU:HD13	1:BM:51:VAL:HG22	1.94	0.48
1:BN:106:ILE:HG21	1:DZ:88:LEU:HG	1.96	0.48
1:BW:32:LEU:CD1	1:BW:49:ILE:HG23	2.44	0.48
1:BY:12:ILE:HG21	1:BY:38:VAL:HG23	1.95	0.48
1:CN:110:VAL:HG12	1:FZ:11:PRO:O	2.13	0.48
1:CP:104:ASN:ND2	1:CP:113:VAL:HB	2.29	0.48
1:DA:32:LEU:CD1	1:DA:49:ILE:HG23	2.44	0.48
1:DP:44:ASN:ND2	1:DP:76:THR:HB	2.28	0.48
1:EC:104:ASN:ND2	1:EC:113:VAL:HB	2.29	0.48
1:ER:104:ASN:ND2	1:ER:113:VAL:HB	2.29	0.48
1:ET:44:ASN:ND2	1:ET:76:THR:HB	2.28	0.48
1:EU:104:ASN:ND2	1:EU:113:VAL:HB	2.29	0.48
1:FL:32:LEU:CD1	1:FL:49:ILE:HG23	2.44	0.48
1:GB:104:ASN:ND2	1:GB:113:VAL:HB	2.29	0.48
1:GQ:104:ASN:ND2	1:GQ:113:VAL:HB	2.29	0.48
1:GS:32:LEU:CD1	1:GS:49:ILE:HG23	2.44	0.48
1:HI:21:GLY:H	1:JJ:89:ARG:HH22	1.62	0.48
1:HU:104:ASN:ND2	1:HU:113:VAL:HB	2.29	0.48
1:HX:104:ASN:ND2	1:HX:113:VAL:HB	2.29	0.48
1:JA:32:LEU:CD1	1:JA:49:ILE:HG23	2.44	0.48
1:JE:104:ASN:ND2	1:JE:113:VAL:HB	2.29	0.48
1:JP:32:LEU:CD1	1:JP:49:ILE:HG23	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JS:32:LEU:CD1	1:JS:49:ILE:HG23	2.44	0.48
1:JU:12:ILE:HG21	1:JU:38:VAL:HG23	1.95	0.48
1:AE:88:LEU:HG	1:GA:106:ILE:HG21	1.95	0.48
1:AH:104:ASN:ND2	1:AH:113:VAL:HB	2.29	0.48
1:AM:106:ILE:HG21	1:CA:88:LEU:HG	1.96	0.48
1:BB:32:LEU:CD1	1:BB:49:ILE:HG23	2.44	0.48
1:BK:32:LEU:CD1	1:BK:49:ILE:HG23	2.44	0.48
1:BP:106:ILE:HG21	1:FB:88:LEU:HD23	1.95	0.48
1:DJ:32:LEU:CD1	1:DJ:49:ILE:HG23	2.44	0.48
1:EN:109:ASN:CG	1:FJ:11:PRO:CB	2.87	0.48
1:EO:104:ASN:ND2	1:EO:113:VAL:HB	2.29	0.48
1:FF:32:LEU:CD1	1:FF:49:ILE:HG23	2.44	0.48
1:FJ:104:ASN:ND2	1:FJ:113:VAL:HB	2.29	0.48
1:GZ:104:ASN:ND2	1:GZ:113:VAL:HB	2.29	0.48
1:HB:32:LEU:CD1	1:HB:49:ILE:HG23	2.44	0.48
1:HC:69:ILE:HG12	1:JS:78:LEU:HD12	1.95	0.48
1:HO:104:ASN:ND2	1:HO:113:VAL:HB	2.29	0.48
1:HT:32:LEU:CD1	1:HT:49:ILE:HG23	2.44	0.48
1:IF:2:ILE:HG23	1:IJ:93:GLU:OE1	2.13	0.48
1:IG:95:VAL:HG13	1:KB:95:VAL:HG13	1.95	0.48
1:IU:32:LEU:CD1	1:IU:49:ILE:HG23	2.44	0.48
1:IY:104:ASN:ND2	1:IY:113:VAL:HB	2.29	0.48
1:JA:98:ILE:CD1	1:JQ:73:LEU:HD13	2.44	0.48
1:JK:47:TYR:CE2	1:JM:105:ILE:HG12	2.48	0.48
1:JY:32:LEU:CD1	1:JY:49:ILE:HG23	2.44	0.48
1:KH:32:LEU:CD1	1:KH:49:ILE:HG23	2.44	0.48
1:KJ:12:ILE:HG21	1:KJ:38:VAL:HG23	1.95	0.48
1:AE:104:ASN:ND2	1:AE:113:VAL:HB	2.29	0.48
1:AP:32:LEU:CD1	1:AP:49:ILE:HG23	2.44	0.48
1:BJ:21:GLY:H	1:EV:89:ARG:HH22	1.62	0.48
1:BJ:95:VAL:HG13	1:EV:95:VAL:HG13	1.95	0.48
1:BT:32:LEU:CD1	1:BT:49:ILE:HG23	2.44	0.48
1:CI:4:LYS:CE	1:GH:112:THR:HG21	2.39	0.48
1:CK:95:VAL:HG13	1:FW:95:VAL:HG13	1.95	0.48
1:CO:32:LEU:CD1	1:CO:49:ILE:HG23	2.44	0.48
1:CU:73:LEU:HD12	1:DH:72:ASN:O	2.14	0.48
1:CW:12:ILE:HG21	1:CW:38:VAL:HG23	1.95	0.48
1:CZ:12:ILE:HG21	1:CZ:38:VAL:HG23	1.95	0.48
1:DR:12:ILE:HG21	1:DR:38:VAL:HG23	1.95	0.48
1:DS:32:LEU:CD1	1:DS:49:ILE:HG23	2.44	0.48
1:EQ:19:PHE:HB3	1:FM:89:ARG:NH2	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ET:32:LEU:CD1	1:ET:49:ILE:HG23	2.44	0.48
1:FO:32:LEU:CD1	1:FO:49:ILE:HG23	2.44	0.48
1:FV:104:ASN:ND2	1:FV:113:VAL:HB	2.29	0.48
1:GK:104:ASN:ND2	1:GK:113:VAL:HB	2.29	0.48
1:GP:32:LEU:CD1	1:GP:49:ILE:HG23	2.44	0.48
1:GT:104:ASN:ND2	1:GT:113:VAL:HB	2.29	0.48
1:GV:32:LEU:CD1	1:GV:49:ILE:HG23	2.44	0.48
1:HP:12:ILE:HG21	1:HP:38:VAL:HG23	1.95	0.48
1:HZ:32:LEU:CD1	1:HZ:49:ILE:HG23	2.44	0.48
1:HZ:89:ARG:HH22	1:KC:21:GLY:H	1.62	0.48
1:IC:32:LEU:CD1	1:IC:49:ILE:HG23	2.44	0.48
1:IF:89:ARG:HH22	1:IJ:21:GLY:H	1.61	0.48
1:JM:32:LEU:CD1	1:JM:49:ILE:HG23	2.44	0.48
1:JO:12:ILE:HG21	1:JO:38:VAL:HG23	1.95	0.48
1:JT:11:PRO:HA	1:KH:111:LEU:HG	1.95	0.48
1:KC:104:ASN:ND2	1:KC:113:VAL:HB	2.29	0.48
1:AA:73:LEU:HD12	1:BI:72:ASN:O	2.14	0.47
1:AU:73:LEU:HD13	1:EG:73:LEU:HD13	1.96	0.47
1:BD:12:ILE:HG21	1:BD:38:VAL:HG23	1.95	0.47
1:BN:32:LEU:CD1	1:BN:49:ILE:HG23	2.44	0.47
1:BP:12:ILE:HG21	1:BP:38:VAL:HG23	1.95	0.47
1:BY:32:LEU:HD21	1:FK:97:PHE:CG	2.49	0.47
1:CH:12:ILE:HG21	1:CH:38:VAL:HG23	1.95	0.47
1:CM:75:PHE:HE2	1:DG:106:ILE:HA	1.79	0.47
1:CU:99:THR:CG2	1:DH:95:VAL:HG11	2.44	0.47
1:DK:104:ASN:ND2	1:DK:113:VAL:HB	2.29	0.47
1:DN:104:ASN:ND2	1:DN:113:VAL:HB	2.29	0.47
1:DU:32:LEU:HD13	1:DU:51:VAL:HG22	1.94	0.47
1:DZ:104:ASN:ND2	1:DZ:113:VAL:HB	2.29	0.47
1:EE:74:SER:N	1:EU:72:ASN:O	2.42	0.47
1:EX:104:ASN:ND2	1:EX:113:VAL:HB	2.29	0.47
1:EZ:32:LEU:CD1	1:EZ:49:ILE:HG23	2.44	0.47
1:FC:32:LEU:CD1	1:FC:49:ILE:HG23	2.44	0.47
1:FN:12:ILE:HG21	1:FN:38:VAL:HG23	1.95	0.47
1:FS:104:ASN:ND2	1:FS:113:VAL:HB	2.29	0.47
1:FX:32:LEU:CD1	1:FX:49:ILE:HG23	2.44	0.47
1:GI:12:ILE:HG21	1:GI:38:VAL:HG23	1.95	0.47
1:HC:104:ASN:ND2	1:HC:113:VAL:HB	2.29	0.47
1:HE:32:LEU:CD1	1:HE:49:ILE:HG23	2.44	0.47
1:HN:73:LEU:HD12	1:HR:72:ASN:O	2.14	0.47
1:HV:12:ILE:HG21	1:HV:38:VAL:HG23	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IF:94:ILE:HG13	1:IJ:49:ILE:HG21	1.95	0.47
1:IK:12:ILE:HG21	1:IK:38:VAL:HG23	1.95	0.47
1:JD:47:TYR:CZ	1:JN:105:ILE:HG12	2.48	0.47
1:JK:75:PHE:CE2	1:JM:106:ILE:HA	2.49	0.47
1:JK:108:GLY:O	1:JM:45:ILE:HD13	2.14	0.47
1:JV:32:LEU:CD1	1:JV:49:ILE:HG23	2.44	0.47
1:AG:32:LEU:CD1	1:AG:49:ILE:HG23	2.44	0.47
1:BV:12:ILE:HG21	1:BV:38:VAL:HG23	1.95	0.47
1:BY:95:VAL:HG13	1:FK:95:VAL:HG13	1.97	0.47
1:BZ:110:VAL:HB	1:DT:36:THR:HG23	1.95	0.47
1:CJ:104:ASN:ND2	1:CJ:113:VAL:HB	2.29	0.47
1:CS:104:ASN:ND2	1:CS:113:VAL:HB	2.29	0.47
1:CY:104:ASN:ND2	1:CY:113:VAL:HB	2.29	0.47
1:DL:12:ILE:HG21	1:DL:38:VAL:HG23	1.95	0.47
1:EH:106:ILE:HD13	1:EO:88:LEU:HG	1.96	0.47
1:FH:32:LEU:HD13	1:FH:51:VAL:HG22	1.94	0.47
1:FK:12:ILE:HG21	1:FK:38:VAL:HG23	1.95	0.47
1:FP:104:ASN:ND2	1:FP:113:VAL:HB	2.29	0.47
1:GC:12:ILE:HG21	1:GC:38:VAL:HG23	1.95	0.47
1:HH:78:LEU:HD12	1:IV:69:ILE:HG12	1.96	0.47
1:HR:104:ASN:ND2	1:HR:113:VAL:HB	2.29	0.47
1:IT:12:ILE:HG21	1:IT:38:VAL:HG23	1.95	0.47
1:JQ:104:ASN:ND2	1:JQ:113:VAL:HB	2.29	0.47
1:AE:90:VAL:HG13	1:GA:51:VAL:HG11	1.95	0.47
1:AK:47:TYR:CE2	1:FO:105:ILE:HG12	2.49	0.47
1:AN:60:ASP:HB3	1:CA:59:VAL:HG11	1.95	0.47
1:AV:73:LEU:CD2	1:EF:98:ILE:HD11	2.44	0.47
1:BE:32:LEU:CD1	1:BE:49:ILE:HG23	2.44	0.47
1:BH:106:ILE:HA	1:BO:75:PHE:HE2	1.79	0.47
1:BZ:105:ILE:HG12	1:DT:47:TYR:CE2	2.49	0.47
1:CE:12:ILE:HG21	1:CE:38:VAL:HG23	1.95	0.47
1:CL:32:LEU:CD1	1:CL:49:ILE:HG23	2.44	0.47
1:CR:32:LEU:CD1	1:CR:49:ILE:HG23	2.44	0.47
1:CS:95:VAL:HG13	1:DD:95:VAL:HG13	1.96	0.47
1:DM:32:LEU:CD1	1:DM:49:ILE:HG23	2.44	0.47
1:EB:32:LEU:CD1	1:EB:49:ILE:HG23	2.44	0.47
1:EJ:12:ILE:HG21	1:EJ:38:VAL:HG23	1.95	0.47
1:EK:32:LEU:CD1	1:EK:49:ILE:HG23	2.44	0.47
1:ET:36:THR:HG23	1:FG:110:VAL:HB	1.96	0.47
1:ET:78:LEU:HD12	1:FG:69:ILE:HG12	1.96	0.47
1:EW:32:LEU:CD1	1:EW:49:ILE:HG23	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FH:12:ILE:HG21	1:FH:38:VAL:HG23	1.95	0.47
1:GY:45:ILE:HG21	1:HO:108:GLY:HA3	1.95	0.47
1:HH:32:LEU:CD1	1:HH:49:ILE:HG23	2.44	0.47
1:HV:105:ILE:HA	1:JO:47:TYR:CD1	2.49	0.47
1:HZ:105:ILE:HG12	1:KC:47:TYR:CZ	2.49	0.47
1:ID:104:ASN:ND2	1:ID:113:VAL:HB	2.29	0.47
1:IL:32:LEU:CD1	1:IL:49:ILE:HG23	2.44	0.47
1:JD:32:LEU:CD1	1:JD:49:ILE:HG23	2.44	0.47
1:AE:73:LEU:HB2	1:GA:73:LEU:HD13	1.95	0.47
1:AK:47:TYR:HE1	1:FO:109:ASN:O	1.97	0.47
1:AY:32:LEU:CD1	1:AY:49:ILE:HG23	2.44	0.47
1:AY:109:ASN:O	1:EI:47:TYR:HE1	1.98	0.47
1:BJ:12:ILE:HG21	1:BJ:38:VAL:HG23	1.95	0.47
1:CQ:12:ILE:HG21	1:CQ:38:VAL:HG23	1.95	0.47
1:CV:55:LEU:HD13	1:GM:83:ASN:HD22	1.78	0.47
1:CV:104:ASN:ND2	1:CV:113:VAL:HB	2.29	0.47
1:CX:32:LEU:CD1	1:CX:49:ILE:HG23	2.44	0.47
1:DP:32:LEU:CD1	1:DP:49:ILE:HG23	2.44	0.47
1:EB:98:ILE:CD1	1:GB:73:LEU:HD13	2.44	0.47
1:FB:12:ILE:HG21	1:FB:38:VAL:HG23	1.95	0.47
1:FI:32:LEU:CD1	1:FI:49:ILE:HG23	2.44	0.47
1:GN:104:ASN:ND2	1:GN:113:VAL:HB	2.29	0.47
1:HF:104:ASN:ND2	1:HF:113:VAL:HB	2.29	0.47
1:HK:32:LEU:CD1	1:HK:49:ILE:HG23	2.44	0.47
1:HT:21:GLY:H	1:IM:89:ARG:HH22	1.62	0.47
1:HW:47:TYR:CZ	1:IP:105:ILE:HG12	2.49	0.47
1:HY:12:ILE:HG21	1:HY:38:VAL:HG23	1.95	0.47
1:IO:78:LEU:HD12	1:KI:69:ILE:HG12	1.95	0.47
1:IO:99:THR:CG2	1:KI:95:VAL:HG11	2.44	0.47
1:IP:104:ASN:ND2	1:IP:113:VAL:HB	2.29	0.47
1:JJ:32:LEU:CD1	1:JJ:49:ILE:HG23	2.44	0.47
1:JK:108:GLY:HA3	1:JM:45:ILE:CG2	2.44	0.47
1:KB:32:LEU:CD1	1:KB:49:ILE:HG23	2.44	0.47
1:KE:32:LEU:CD1	1:KE:49:ILE:HG23	2.44	0.47
1:AN:91:LEU:HD13	1:FR:102:LYS:HG3	1.97	0.47
1:BK:83:ASN:HD22	1:DW:55:LEU:HD13	1.79	0.47
1:BQ:73:LEU:HD22	1:EC:98:ILE:HD11	1.96	0.47
1:BW:21:GLY:H	1:DQ:89:ARG:HH22	1.62	0.47
1:BZ:32:LEU:CD1	1:BZ:49:ILE:HG23	2.44	0.47
1:CG:36:THR:HG23	1:CL:110:VAL:HB	1.95	0.47
1:CJ:93:GLU:OE1	1:CO:2:ILE:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DI:106:ILE:HG21	1:GU:88:LEU:HD23	1.96	0.47
1:EB:97:PHE:CD1	1:GB:32:LEU:HD21	2.50	0.47
1:EN:32:LEU:CD1	1:EN:49:ILE:HG23	2.44	0.47
1:GY:32:LEU:CD1	1:GY:49:ILE:HG23	2.44	0.47
1:HB:95:VAL:HG13	1:HX:95:VAL:HG13	1.96	0.47
1:HD:12:ILE:HG21	1:HD:38:VAL:HG23	1.95	0.47
1:HT:74:SER:N	1:IM:72:ASN:O	2.36	0.47
1:IF:32:LEU:CD1	1:IF:49:ILE:HG23	2.44	0.47
1:IG:104:ASN:ND2	1:IG:113:VAL:HB	2.29	0.47
1:IN:12:ILE:HG21	1:IN:38:VAL:HG23	1.95	0.47
1:JA:111:LEU:HG	1:JQ:11:PRO:HA	1.95	0.47
1:KI:104:ASN:ND2	1:KI:113:VAL:HB	2.29	0.47
1:AI:12:ILE:HG21	1:AI:38:VAL:HG23	1.95	0.47
1:AQ:89:ARG:HH22	1:FU:21:GLY:H	1.62	0.47
1:CF:102:LYS:HG2	1:GN:88:LEU:HD23	1.96	0.47
1:DG:32:LEU:CD1	1:DG:49:ILE:HG23	2.44	0.47
1:FS:72:ASN:O	1:GP:73:LEU:HD12	2.14	0.47
1:FY:104:ASN:ND2	1:FY:113:VAL:HB	2.29	0.47
1:GD:32:LEU:CD1	1:GD:49:ILE:HG23	2.44	0.47
1:GY:47:TYR:CE2	1:HO:105:ILE:HG12	2.49	0.47
1:HE:95:VAL:HG13	1:HU:95:VAL:HG13	1.97	0.47
1:HW:32:LEU:CD1	1:HW:49:ILE:HG23	2.44	0.47
1:HW:112:THR:HG23	1:IP:17:TYR:OH	2.14	0.47
1:IS:104:ASN:ND2	1:IS:113:VAL:HB	2.29	0.47
1:JG:32:LEU:CD1	1:JG:49:ILE:HG23	2.44	0.47
1:AD:32:LEU:CD1	1:AD:49:ILE:HG23	2.44	0.47
1:AD:47:TYR:CZ	1:BC:105:ILE:HG12	2.49	0.47
1:AK:75:PHE:HE2	1:FO:106:ILE:HA	1.80	0.47
1:AM:32:LEU:CD1	1:AM:49:ILE:HG23	2.44	0.47
1:AN:72:ASN:O	1:FR:73:LEU:HA	2.15	0.47
1:AQ:108:GLY:HA3	1:FU:45:ILE:HG21	1.97	0.47
1:AV:32:LEU:CD1	1:AV:49:ILE:HG23	2.44	0.47
1:BD:69:ILE:HG12	1:EP:78:LEU:HD12	1.96	0.47
1:BW:83:ASN:ND2	1:DQ:55:LEU:HD13	2.29	0.47
1:BX:104:ASN:ND2	1:BX:113:VAL:HB	2.29	0.47
1:CF:32:LEU:CD1	1:CF:49:ILE:HG23	2.44	0.47
1:CI:32:LEU:CD1	1:CI:49:ILE:HG23	2.44	0.47
1:CM:75:PHE:CE2	1:DG:106:ILE:HA	2.49	0.47
1:CP:55:LEU:HD13	1:DJ:83:ASN:HD22	1.80	0.47
1:CU:32:LEU:CD1	1:CU:49:ILE:HG23	2.44	0.47
1:DA:73:LEU:HD12	1:DE:72:ASN:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DB:108:GLY:HA3	1:GJ:45:ILE:HG21	1.95	0.47
1:DC:12:ILE:HG21	1:DC:38:VAL:HG23	1.95	0.47
1:DL:69:ILE:HG12	1:GX:78:LEU:HD12	1.97	0.47
1:DU:12:ILE:HG21	1:DU:38:VAL:HG23	1.95	0.47
1:DY:97:PHE:CG	1:FY:32:LEU:HD21	2.50	0.47
1:EE:89:ARG:HH22	1:EU:21:GLY:H	1.62	0.47
1:EK:71:ALA:HB2	1:ER:75:PHE:HD1	1.80	0.47
1:EL:104:ASN:ND2	1:EL:113:VAL:HB	2.29	0.47
1:EN:109:ASN:OD1	1:FJ:11:PRO:HA	2.14	0.47
1:EQ:47:TYR:CE2	1:FM:105:ILE:HG12	2.49	0.47
1:ET:95:VAL:HG13	1:FG:95:VAL:HG13	1.95	0.47
1:FQ:12:ILE:HG21	1:FQ:38:VAL:HG23	1.95	0.47
1:FR:32:LEU:CD1	1:FR:49:ILE:HG23	2.44	0.47
1:FU:32:LEU:CD1	1:FU:49:ILE:HG23	2.44	0.47
1:GA:32:LEU:CD1	1:GA:49:ILE:HG23	2.44	0.47
1:GE:104:ASN:ND2	1:GE:113:VAL:HB	2.29	0.47
1:GG:32:LEU:CD1	1:GG:49:ILE:HG23	2.44	0.47
1:GJ:32:LEU:CD1	1:GJ:49:ILE:HG23	2.44	0.47
1:HQ:32:LEU:CD1	1:HQ:49:ILE:HG23	2.44	0.47
1:HZ:47:TYR:CZ	1:KC:105:ILE:HG12	2.49	0.47
1:IJ:104:ASN:ND2	1:IJ:113:VAL:HB	2.29	0.47
1:IX:32:LEU:CD1	1:IX:49:ILE:HG23	2.44	0.47
1:DQ:104:ASN:ND2	1:DQ:113:VAL:HB	2.29	0.47
1:FP:72:ASN:O	1:GV:73:LEU:HA	2.15	0.47
1:FZ:12:ILE:HG21	1:FZ:38:VAL:HG23	1.95	0.47
1:HW:4:LYS:HE2	1:IP:112:THR:HG21	1.97	0.47
1:JF:12:ILE:HG21	1:JF:38:VAL:HG23	1.95	0.47
1:AQ:104:ASN:ND2	1:AQ:113:VAL:HB	2.29	0.47
1:AR:51:VAL:HG11	1:ED:90:VAL:HG13	1.96	0.47
1:AU:2:ILE:HG23	1:EG:93:GLU:OE1	2.15	0.47
1:BN:106:ILE:HD13	1:DZ:88:LEU:HG	1.96	0.47
1:BQ:32:LEU:CD1	1:BQ:49:ILE:HG23	2.44	0.47
1:BT:45:ILE:HG21	1:DN:108:GLY:HA3	1.96	0.47
1:CH:102:LYS:HG3	1:FT:91:LEU:CD1	2.45	0.47
1:CS:88:LEU:HG	1:DD:106:ILE:HG21	1.96	0.47
1:CY:21:GLY:H	1:GG:89:ARG:HH22	1.61	0.47
1:DL:83:ASN:OD1	1:GX:55:LEU:HD13	2.15	0.47
1:EM:12:ILE:HG21	1:EM:38:VAL:HG23	1.95	0.47
1:EQ:32:LEU:CD1	1:EQ:49:ILE:HG23	2.44	0.47
1:IU:98:ILE:CD1	1:JE:73:LEU:HD13	2.44	0.47
1:JN:104:ASN:ND2	1:JN:113:VAL:HB	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:32:LEU:CD1	1:AA:49:ILE:HG23	2.44	0.47
1:AS:45:ILE:HG21	1:EL:108:GLY:HA3	1.97	0.47
1:AZ:4:LYS:HD3	1:AZ:7:GLU:OE2	2.16	0.47
1:BF:104:ASN:ND2	1:BF:113:VAL:HB	2.29	0.47
1:BU:104:ASN:ND2	1:BU:113:VAL:HB	2.29	0.47
1:CC:72:ASN:HB3	1:GK:74:SER:OG	2.15	0.47
1:DI:99:THR:HG23	1:GU:95:VAL:HG11	1.96	0.47
1:DV:32:LEU:CD1	1:DV:49:ILE:HG23	2.44	0.47
1:FA:88:LEU:HD23	1:FL:102:LYS:HG2	1.97	0.47
1:GW:104:ASN:ND2	1:GW:113:VAL:HB	2.29	0.47
1:HH:73:LEU:HD12	1:IV:72:ASN:O	2.14	0.47
1:HM:4:LYS:HA	1:HM:17:TYR:HD1	1.81	0.47
1:HW:105:ILE:HG12	1:IP:47:TYR:CZ	2.50	0.47
1:IF:51:VAL:HG11	1:IJ:90:VAL:HG13	1.97	0.47
1:AS:32:LEU:CD1	1:AS:49:ILE:HG23	2.44	0.46
1:AS:105:ILE:HG23	1:EL:47:TYR:CG	2.51	0.46
1:BS:106:ILE:HD13	1:FE:88:LEU:HD21	1.96	0.46
1:BT:45:ILE:HD13	1:DN:108:GLY:O	2.15	0.46
1:CD:105:ILE:HG12	1:CR:47:TYR:CZ	2.50	0.46
1:CZ:4:LYS:HA	1:CZ:17:TYR:HD1	1.80	0.46
1:DF:4:LYS:HA	1:DF:17:TYR:HD1	1.81	0.46
1:EB:111:LEU:HG	1:GB:11:PRO:HA	1.97	0.46
1:EY:4:LYS:HA	1:EY:17:TYR:HD1	1.81	0.46
1:FW:4:LYS:HA	1:FW:17:TYR:HD1	1.81	0.46
1:GZ:4:LYS:HD3	1:GZ:7:GLU:OE2	2.16	0.46
1:HB:73:LEU:HD12	1:HX:72:ASN:O	2.15	0.46
1:HN:32:LEU:CD1	1:HN:49:ILE:HG23	2.44	0.46
1:HR:4:LYS:HD3	1:HR:7:GLU:OE2	2.16	0.46
1:HS:4:LYS:HA	1:HS:17:TYR:HD1	1.81	0.46
1:IZ:4:LYS:HA	1:IZ:17:TYR:HD1	1.80	0.46
1:KA:4:LYS:HA	1:KA:17:TYR:HD1	1.81	0.46
1:AH:4:LYS:HD3	1:AH:7:GLU:OE2	2.16	0.46
1:AI:95:VAL:HG11	1:DU:99:THR:CG2	2.46	0.46
1:AJ:32:LEU:CD1	1:AJ:49:ILE:HG23	2.44	0.46
1:AX:4:LYS:HA	1:AX:17:TYR:HD1	1.81	0.46
1:BT:105:ILE:HG12	1:DN:47:TYR:CZ	2.50	0.46
1:CI:105:ILE:HG12	1:GH:47:TYR:CZ	2.51	0.46
1:CM:4:LYS:HD3	1:CM:7:GLU:OE2	2.16	0.46
1:CP:4:LYS:HD3	1:CP:7:GLU:OE2	2.16	0.46
1:CQ:4:LYS:HA	1:CQ:17:TYR:HD1	1.80	0.46
1:CV:4:LYS:HD3	1:CV:7:GLU:OE2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DD:32:LEU:CD1	1:DD:49:ILE:HG23	2.44	0.46
1:DE:4:LYS:HD3	1:DE:7:GLU:OE2	2.16	0.46
1:DO:4:LYS:HA	1:DO:17:TYR:HD1	1.81	0.46
1:DR:4:LYS:HA	1:DR:17:TYR:HD1	1.81	0.46
1:DW:4:LYS:HD3	1:DW:7:GLU:OE2	2.16	0.46
1:EA:4:LYS:HA	1:EA:17:TYR:HD1	1.80	0.46
1:FS:4:LYS:HD3	1:FS:7:GLU:OE2	2.15	0.46
1:FS:69:ILE:HG12	1:GP:78:LEU:HD12	1.96	0.46
1:GC:4:LYS:HA	1:GC:17:TYR:HD1	1.81	0.46
1:GI:4:LYS:HA	1:GI:17:TYR:HD1	1.81	0.46
1:GW:4:LYS:HD3	1:GW:7:GLU:OE2	2.16	0.46
1:HJ:4:LYS:HA	1:HJ:17:TYR:HD1	1.81	0.46
1:HU:4:LYS:HD3	1:HU:7:GLU:OE2	2.16	0.46
1:IU:97:PHE:CD1	1:JE:32:LEU:HD21	2.51	0.46
1:JD:21:GLY:H	1:JN:89:ARG:HH22	1.63	0.46
1:JK:4:LYS:HD3	1:JK:7:GLU:OE2	2.16	0.46
1:JX:4:LYS:HA	1:JX:17:TYR:HD1	1.80	0.46
1:BA:4:LYS:HA	1:BA:17:TYR:HD1	1.81	0.46
1:BG:4:LYS:HA	1:BG:17:TYR:HD1	1.80	0.46
1:BG:72:ASN:O	1:ES:73:LEU:HD12	2.15	0.46
1:BI:4:LYS:HD3	1:BI:7:GLU:OE2	2.15	0.46
1:BP:4:LYS:HA	1:BP:17:TYR:HD1	1.81	0.46
1:BX:4:LYS:HD3	1:BX:7:GLU:OE2	2.16	0.46
1:CA:4:LYS:HD3	1:CA:7:GLU:OE2	2.16	0.46
1:CY:4:LYS:HD3	1:CY:7:GLU:OE2	2.16	0.46
1:DC:21:GLY:H	1:GO:89:ARG:HH22	1.61	0.46
1:DH:4:LYS:HD3	1:DH:7:GLU:OE2	2.16	0.46
1:DQ:4:LYS:HD3	1:DQ:7:GLU:OE2	2.16	0.46
1:EH:71:ALA:HB2	1:EO:75:PHE:HD1	1.81	0.46
1:EL:4:LYS:HD3	1:EL:7:GLU:OE2	2.16	0.46
1:ES:4:LYS:HA	1:ES:17:TYR:HD1	1.80	0.46
1:FB:4:LYS:HA	1:FB:17:TYR:HD1	1.81	0.46
1:FS:75:PHE:HD1	1:GP:71:ALA:HB2	1.79	0.46
1:FT:4:LYS:HA	1:FT:17:TYR:HD1	1.81	0.46
1:HD:4:LYS:HA	1:HD:17:TYR:HD1	1.80	0.46
1:HF:4:LYS:HD3	1:HF:7:GLU:OE2	2.16	0.46
1:IE:4:LYS:HA	1:IE:17:TYR:HD1	1.80	0.46
1:IN:4:LYS:HA	1:IN:17:TYR:HD1	1.81	0.46
1:IO:32:LEU:CD1	1:IO:49:ILE:HG23	2.44	0.46
1:IO:106:ILE:HD13	1:KI:88:LEU:HG	1.95	0.46
1:JQ:4:LYS:HD3	1:JQ:7:GLU:OE2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JT:4:LYS:HD3	1:JT:7:GLU:OE2	2.16	0.46
1:AD:11:PRO:O	1:BC:110:VAL:HG12	2.16	0.46
1:AD:73:LEU:CD2	1:BC:98:ILE:HD11	2.45	0.46
1:AN:4:LYS:HD3	1:AN:7:GLU:OE2	2.16	0.46
1:AQ:4:LYS:HD3	1:AQ:7:GLU:OE2	2.16	0.46
1:AR:73:LEU:HD22	1:ED:98:ILE:HD11	1.97	0.46
1:BE:4:LYS:HE2	1:BL:112:THR:HG21	1.97	0.46
1:BJ:4:LYS:HA	1:BJ:17:TYR:HD1	1.81	0.46
1:BM:4:LYS:HA	1:BM:17:TYR:HD1	1.81	0.46
1:CC:75:PHE:HD1	1:GK:71:ALA:HB2	1.80	0.46
1:DL:88:LEU:HD23	1:GX:106:ILE:HG21	1.97	0.46
1:DY:32:LEU:CD1	1:DY:49:ILE:HG23	2.44	0.46
1:DZ:4:LYS:HD3	1:DZ:7:GLU:OE2	2.16	0.46
1:EE:32:LEU:CD1	1:EE:49:ILE:HG23	2.44	0.46
1:EP:4:LYS:HA	1:EP:17:TYR:HD1	1.80	0.46
1:EQ:73:LEU:CD2	1:FM:98:ILE:HD11	2.45	0.46
1:FE:4:LYS:HA	1:FE:17:TYR:HD1	1.81	0.46
1:FM:4:LYS:HD3	1:FM:7:GLU:OE2	2.16	0.46
1:HC:4:LYS:HD3	1:HC:7:GLU:OE2	2.16	0.46
1:HQ:45:ILE:HG21	1:IS:108:GLY:HA3	1.96	0.46
1:HS:72:ASN:O	1:JL:73:LEU:HA	2.15	0.46
1:IE:88:LEU:HD23	1:KA:106:ILE:HG21	1.96	0.46
1:IR:32:LEU:CD1	1:IR:49:ILE:HG23	2.44	0.46
1:JC:4:LYS:HA	1:JC:17:TYR:HD1	1.80	0.46
1:JE:4:LYS:HD3	1:JE:7:GLU:OE2	2.16	0.46
1:JH:4:LYS:HD3	1:JH:7:GLU:OE2	2.16	0.46
1:JL:4:LYS:HA	1:JL:17:TYR:HD1	1.81	0.46
1:JN:4:LYS:HA	1:JN:17:TYR:CD1	2.51	0.46
1:AL:98:ILE:HD11	1:DX:73:LEU:HD22	1.97	0.46
1:BD:4:LYS:HA	1:BD:17:TYR:HD1	1.81	0.46
1:BF:4:LYS:HD3	1:BF:7:GLU:OE2	2.16	0.46
1:BL:4:LYS:HA	1:BL:17:TYR:CD1	2.51	0.46
1:BL:4:LYS:HD3	1:BL:7:GLU:OE2	2.16	0.46
1:CW:4:LYS:HA	1:CW:17:TYR:HD1	1.80	0.46
1:DK:4:LYS:HD3	1:DK:7:GLU:OE2	2.16	0.46
1:EG:4:LYS:HA	1:EG:17:TYR:HD1	1.81	0.46
1:EI:4:LYS:HD3	1:EI:7:GLU:OE2	2.16	0.46
1:GZ:95:VAL:HG11	1:JY:99:THR:CG2	2.46	0.46
1:HB:110:VAL:HA	1:HX:47:TYR:CE1	2.51	0.46
1:IA:4:LYS:HD3	1:IA:7:GLU:OE2	2.16	0.46
1:II:32:LEU:CD1	1:II:49:ILE:HG23	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IJ:4:LYS:HD3	1:IJ:7:GLU:OE2	2.16	0.46
1:IK:4:LYS:HA	1:IK:17:TYR:HD1	1.80	0.46
1:IV:4:LYS:HD3	1:IV:7:GLU:OE2	2.16	0.46
1:IW:4:LYS:HA	1:IW:17:TYR:HD1	1.80	0.46
1:JD:78:LEU:HD12	1:JN:69:ILE:HG12	1.98	0.46
1:JZ:4:LYS:HD3	1:JZ:7:GLU:OE2	2.16	0.46
1:KD:4:LYS:HA	1:KD:17:TYR:HD1	1.81	0.46
1:AB:4:LYS:HD3	1:AB:7:GLU:OE2	2.16	0.46
1:AH:4:LYS:HA	1:AH:17:TYR:CD1	2.51	0.46
1:AM:67:ASN:HB3	1:CA:78:LEU:HD13	1.98	0.46
1:AP:71:ALA:HB2	1:BU:75:PHE:HD1	1.80	0.46
1:BO:4:LYS:HA	1:BO:17:TYR:CD1	2.51	0.46
1:BU:4:LYS:HD3	1:BU:7:GLU:OE2	2.16	0.46
1:CB:73:LEU:HD22	1:FN:98:ILE:HD11	1.98	0.46
1:CG:4:LYS:HD3	1:CG:7:GLU:OE2	2.16	0.46
1:CN:4:LYS:HA	1:CN:17:TYR:HD1	1.80	0.46
1:CX:106:ILE:HA	1:DK:75:PHE:HE2	1.80	0.46
1:DC:4:LYS:HA	1:DC:17:TYR:HD1	1.80	0.46
1:EH:32:LEU:CD1	1:EH:49:ILE:HG23	2.44	0.46
1:EN:109:ASN:O	1:FJ:47:TYR:HE1	1.98	0.46
1:EO:4:LYS:HA	1:EO:17:TYR:CD1	2.51	0.46
1:EQ:78:LEU:HD12	1:FM:69:ILE:HG12	1.97	0.46
1:FK:4:LYS:HA	1:FK:17:TYR:HD1	1.80	0.46
1:FN:4:LYS:HA	1:FN:17:TYR:HD1	1.81	0.46
1:FY:4:LYS:HD3	1:FY:7:GLU:OE2	2.16	0.46
1:GR:4:LYS:HA	1:GR:17:TYR:HD1	1.81	0.46
1:GY:109:ASN:O	1:HO:47:TYR:HE1	1.97	0.46
1:HN:78:LEU:HD12	1:HR:69:ILE:HG12	1.97	0.46
1:HS:47:TYR:CZ	1:JL:105:ILE:HG12	2.51	0.46
1:ID:4:LYS:HD3	1:ID:7:GLU:OE2	2.16	0.46
1:IP:4:LYS:HD3	1:IP:7:GLU:OE2	2.15	0.46
1:JA:4:LYS:HE2	1:JQ:112:THR:HG21	1.97	0.46
1:AV:36:THR:HG23	1:EF:110:VAL:HB	1.96	0.46
1:BK:73:LEU:HD12	1:DW:72:ASN:O	2.16	0.46
1:BO:4:LYS:HD3	1:BO:7:GLU:OE2	2.16	0.46
1:BR:4:LYS:HD3	1:BR:7:GLU:OE2	2.16	0.46
1:CA:104:ASN:ND2	1:CA:113:VAL:HB	2.29	0.46
1:CN:90:VAL:HG13	1:FZ:51:VAL:HG11	1.97	0.46
1:CY:108:GLY:O	1:GG:45:ILE:HD13	2.15	0.46
1:DQ:4:LYS:HA	1:DQ:17:TYR:CD1	2.51	0.46
1:ER:4:LYS:HA	1:ER:17:TYR:CD1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EU:4:LYS:HD3	1:EU:7:GLU:OE2	2.15	0.46
1:EX:4:LYS:HA	1:EX:17:TYR:CD1	2.51	0.46
1:FJ:4:LYS:HA	1:FJ:17:TYR:CD1	2.51	0.46
1:FJ:4:LYS:HD3	1:FJ:7:GLU:OE2	2.16	0.46
1:FQ:4:LYS:HA	1:FQ:17:TYR:HD1	1.80	0.46
1:GH:4:LYS:HD3	1:GH:7:GLU:OE2	2.15	0.46
1:GM:32:LEU:CD1	1:GM:49:ILE:HG23	2.44	0.46
1:HG:89:ARG:HH22	1:IT:21:GLY:H	1.63	0.46
1:HP:105:ILE:HG12	1:JC:47:TYR:CZ	2.50	0.46
1:IB:4:LYS:HA	1:IB:17:TYR:HD1	1.80	0.46
1:IG:4:LYS:HD3	1:IG:7:GLU:OE2	2.15	0.46
1:IH:4:LYS:HA	1:IH:17:TYR:HD1	1.80	0.46
1:IQ:4:LYS:HA	1:IQ:17:TYR:HD1	1.80	0.46
1:JW:55:LEU:HD13	1:KE:83:ASN:HD22	1.81	0.46
1:JZ:4:LYS:HA	1:JZ:17:TYR:CD1	2.51	0.46
1:KC:4:LYS:HD3	1:KC:7:GLU:OE2	2.16	0.46
1:KF:4:LYS:HA	1:KF:17:TYR:CD1	2.51	0.46
1:KI:4:LYS:HD3	1:KI:7:GLU:OE2	2.16	0.46
1:AF:4:LYS:HA	1:AF:17:TYR:HD1	1.80	0.46
1:AJ:51:VAL:HG11	1:BX:90:VAL:HG13	1.98	0.46
1:BD:36:THR:HG23	1:EP:110:VAL:HB	1.97	0.46
1:BP:99:THR:CG2	1:FB:95:VAL:HG11	2.45	0.46
1:BV:4:LYS:HA	1:BV:17:TYR:HD1	1.81	0.46
1:BY:4:LYS:HA	1:BY:17:TYR:HD1	1.80	0.46
1:CC:95:VAL:HG13	1:GK:95:VAL:HG13	1.98	0.46
1:CD:4:LYS:HD3	1:CD:7:GLU:OE2	2.15	0.46
1:CZ:72:ASN:O	1:GL:73:LEU:HD12	2.15	0.46
1:DV:45:ILE:CG2	1:GE:108:GLY:HA3	2.46	0.46
1:DY:89:ARG:HH22	1:FY:21:GLY:H	1.64	0.46
1:EB:21:GLY:H	1:GB:89:ARG:HH22	1.63	0.46
1:EF:4:LYS:HD3	1:EF:7:GLU:OE2	2.16	0.46
1:ET:69:ILE:CG2	1:FG:90:VAL:HG21	2.46	0.46
1:ET:73:LEU:HD22	1:FG:98:ILE:HD11	1.98	0.46
1:FH:4:LYS:HA	1:FH:17:TYR:HD1	1.80	0.46
1:FV:4:LYS:HD3	1:FV:7:GLU:OE2	2.16	0.46
1:FZ:4:LYS:HA	1:FZ:17:TYR:HD1	1.81	0.46
1:GB:4:LYS:HD3	1:GB:7:GLU:OE2	2.16	0.46
1:GO:4:LYS:HA	1:GO:17:TYR:HD1	1.80	0.46
1:GT:4:LYS:HD3	1:GT:7:GLU:OE2	2.16	0.46
1:HO:4:LYS:HD3	1:HO:7:GLU:OE2	2.16	0.46
1:HT:87:LYS:HG2	1:IM:69:ILE:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IB:98:ILE:HD11	1:JX:73:LEU:HD22	1.97	0.46
1:IT:4:LYS:HA	1:IT:17:TYR:HD1	1.80	0.46
1:JH:69:ILE:HG12	1:JP:78:LEU:HD12	1.97	0.46
1:JR:4:LYS:HA	1:JR:17:TYR:HD1	1.81	0.46
1:JW:4:LYS:HD3	1:JW:7:GLU:OE2	2.16	0.46
1:AV:19:PHE:CZ	1:EF:93:GLU:HG3	2.51	0.46
1:CM:72:ASN:O	1:DG:73:LEU:HA	2.16	0.46
1:CW:106:ILE:HG21	1:GI:88:LEU:HD23	1.98	0.46
1:DP:99:THR:CG2	1:GW:95:VAL:HG11	2.45	0.46
1:DT:4:LYS:HA	1:DT:17:TYR:CD1	2.51	0.46
1:DX:4:LYS:HA	1:DX:17:TYR:HD1	1.81	0.46
1:ER:4:LYS:HD3	1:ER:7:GLU:OE2	2.16	0.46
1:FG:4:LYS:HA	1:FG:17:TYR:CD1	2.51	0.46
1:FM:4:LYS:HA	1:FM:17:TYR:CD1	2.51	0.46
1:GK:4:LYS:HD3	1:GK:7:GLU:OE2	2.16	0.46
1:GU:4:LYS:HA	1:GU:17:TYR:HD1	1.80	0.46
1:HL:4:LYS:HD3	1:HL:7:GLU:OE2	2.16	0.46
1:IJ:4:LYS:HA	1:IJ:17:TYR:CD1	2.51	0.46
1:IS:4:LYS:HD3	1:IS:7:GLU:OE2	2.16	0.46
1:JF:4:LYS:HA	1:JF:17:TYR:HD1	1.80	0.46
1:JU:4:LYS:HA	1:JU:17:TYR:HD1	1.81	0.46
1:AB:4:LYS:HA	1:AB:17:TYR:CD1	2.51	0.46
1:AI:4:LYS:HA	1:AI:17:TYR:HD1	1.80	0.46
1:AM:72:ASN:O	1:CA:73:LEU:HA	2.16	0.46
1:AM:74:SER:O	1:CA:71:ALA:HA	2.16	0.46
1:BE:106:ILE:HA	1:BL:75:PHE:CE2	2.51	0.46
1:BG:95:VAL:HG13	1:ES:95:VAL:HG13	1.98	0.46
1:BQ:91:LEU:HD23	1:EC:102:LYS:HG3	1.97	0.46
1:BU:4:LYS:HA	1:BU:17:TYR:CD1	2.51	0.46
1:BY:21:GLY:H	1:FK:89:ARG:HH22	1.65	0.46
1:CG:2:ILE:HG23	1:CL:93:GLU:OE1	2.15	0.46
1:CQ:95:VAL:HG13	1:GC:95:VAL:HG13	1.98	0.46
1:CT:95:VAL:HG13	1:GF:95:VAL:HG13	1.98	0.46
1:CV:4:LYS:HA	1:CV:17:TYR:CD1	2.51	0.46
1:EO:4:LYS:HD3	1:EO:7:GLU:OE2	2.16	0.46
1:FP:4:LYS:HA	1:FP:17:TYR:CD1	2.51	0.46
1:FS:73:LEU:HD12	1:GP:73:LEU:HD13	1.98	0.46
1:GL:4:LYS:HA	1:GL:17:TYR:HD1	1.81	0.46
1:HA:98:ILE:HD11	1:IQ:73:LEU:HD22	1.97	0.46
1:HG:4:LYS:HA	1:HG:17:TYR:HD1	1.81	0.46
1:HI:4:LYS:HD3	1:HI:7:GLU:OE2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HT:83:ASN:ND2	1:IM:55:LEU:HD13	2.30	0.46
1:HX:4:LYS:HD3	1:HX:7:GLU:OE2	2.16	0.46
1:JA:102:LYS:HG3	1:JQ:91:LEU:HD13	1.97	0.46
1:JI:4:LYS:HA	1:JI:17:TYR:HD1	1.80	0.46
1:JT:73:LEU:HD12	1:KH:73:LEU:HD13	1.97	0.46
1:KG:4:LYS:HA	1:KG:17:TYR:HD1	1.80	0.46
1:AM:47:TYR:CZ	1:CA:105:ILE:HG12	2.52	0.45
1:AS:97:PHE:CG	1:EL:32:LEU:HD21	2.51	0.45
1:AY:109:ASN:CG	1:EI:11:PRO:HB3	2.41	0.45
1:AZ:4:LYS:HA	1:AZ:17:TYR:CD1	2.51	0.45
1:BT:105:ILE:HG12	1:DN:47:TYR:CE2	2.51	0.45
1:BZ:109:ASN:CG	1:DT:11:PRO:HB3	2.41	0.45
1:CB:47:TYR:CZ	1:FN:105:ILE:HG12	2.52	0.45
1:CC:73:LEU:HD13	1:GK:73:LEU:HD12	1.97	0.45
1:CH:4:LYS:HA	1:CH:17:TYR:HD1	1.80	0.45
1:CT:72:ASN:O	1:GF:73:LEU:HD12	2.16	0.45
1:CV:47:TYR:CZ	1:GM:105:ILE:HG12	2.52	0.45
1:DE:4:LYS:HA	1:DE:17:TYR:CD1	2.51	0.45
1:DN:4:LYS:HD3	1:DN:7:GLU:OE2	2.16	0.45
1:EM:4:LYS:HA	1:EM:17:TYR:HD1	1.80	0.45
1:EN:78:LEU:HD12	1:FJ:69:ILE:HG12	1.98	0.45
1:FA:4:LYS:HD3	1:FA:7:GLU:OE2	2.16	0.45
1:FP:4:LYS:HD3	1:FP:7:GLU:OE2	2.16	0.45
1:GQ:4:LYS:HD3	1:GQ:7:GLU:OE2	2.16	0.45
1:GY:17:TYR:OH	1:HO:112:THR:HG22	2.16	0.45
1:HV:4:LYS:HA	1:HV:17:TYR:HD1	1.80	0.45
1:HW:109:ASN:O	1:IP:47:TYR:HE1	2.00	0.45
1:IR:73:LEU:HA	1:JZ:72:ASN:O	2.17	0.45
1:JB:4:LYS:HA	1:JB:17:TYR:CD1	2.51	0.45
1:JB:4:LYS:HD3	1:JB:7:GLU:OE2	2.16	0.45
1:AC:4:LYS:HA	1:AC:17:TYR:HD1	1.80	0.45
1:AC:106:ILE:HG21	1:DO:88:LEU:HD23	1.98	0.45
1:AE:4:LYS:HD3	1:AE:7:GLU:OE2	2.16	0.45
1:AU:89:ARG:HH22	1:EG:20:THR:N	2.14	0.45
1:AW:4:LYS:HD3	1:AW:7:GLU:OE2	2.16	0.45
1:BZ:111:LEU:HG	1:DT:11:PRO:HA	1.99	0.45
1:CJ:60:ASP:HB3	1:GH:59:VAL:HG11	1.99	0.45
1:CK:4:LYS:HA	1:CK:17:TYR:HD1	1.81	0.45
1:DI:4:LYS:HA	1:DI:17:TYR:HD1	1.80	0.45
1:FA:69:ILE:HG12	1:FL:78:LEU:HD12	1.97	0.45
1:FD:72:ASN:O	1:FF:73:LEU:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FG:4:LYS:HD3	1:FG:7:GLU:OE2	2.16	0.45
1:GE:4:LYS:HA	1:GE:17:TYR:CD1	2.51	0.45
1:GE:4:LYS:HD3	1:GE:7:GLU:OE2	2.16	0.45
1:HV:105:ILE:HA	1:JO:47:TYR:CE1	2.51	0.45
1:IM:4:LYS:HD3	1:IM:7:GLU:OE2	2.16	0.45
1:JT:47:TYR:CE2	1:KH:105:ILE:HG12	2.52	0.45
1:AJ:83:ASN:ND2	1:BX:55:LEU:HD13	2.30	0.45
1:AL:4:LYS:HA	1:AL:17:TYR:HD1	1.81	0.45
1:AU:4:LYS:HA	1:AU:17:TYR:HD1	1.80	0.45
1:AW:72:ASN:O	1:FC:73:LEU:HD12	2.15	0.45
1:BH:4:LYS:HE2	1:BO:112:THR:HG21	1.96	0.45
1:BR:4:LYS:HA	1:BR:17:TYR:CD1	2.51	0.45
1:BS:4:LYS:HA	1:BS:17:TYR:HD1	1.81	0.45
1:BZ:109:ASN:O	1:DT:47:TYR:HE1	2.00	0.45
1:DU:4:LYS:HA	1:DU:17:TYR:HD1	1.80	0.45
1:EJ:4:LYS:HA	1:EJ:17:TYR:HD1	1.80	0.45
1:EX:4:LYS:HD3	1:EX:7:GLU:OE2	2.16	0.45
1:FS:4:LYS:HA	1:FS:17:TYR:CD1	2.51	0.45
1:GZ:4:LYS:HA	1:GZ:17:TYR:CD1	2.51	0.45
1:HC:4:LYS:HA	1:HC:17:TYR:CD1	2.51	0.45
1:HF:4:LYS:HA	1:HF:17:TYR:CD1	2.51	0.45
1:HK:74:SER:O	1:IY:71:ALA:HA	2.16	0.45
1:HT:55:LEU:HD13	1:IM:81:VAL:HG21	1.99	0.45
1:JN:4:LYS:HD3	1:JN:7:GLU:OE2	2.16	0.45
1:AK:4:LYS:HD3	1:AK:7:GLU:OE2	2.15	0.45
1:AT:4:LYS:HD3	1:AT:7:GLU:OE2	2.16	0.45
1:AZ:88:LEU:HG	1:EW:106:ILE:HG21	1.98	0.45
1:BA:89:ARG:HH22	1:EM:21:GLY:H	1.64	0.45
1:BC:4:LYS:HD3	1:BC:7:GLU:OE2	2.16	0.45
1:BD:20:THR:H	1:EP:89:ARG:NH2	2.14	0.45
1:BD:88:LEU:CD2	1:EP:102:LYS:HG2	2.47	0.45
1:BF:4:LYS:HA	1:BF:17:TYR:CD1	2.51	0.45
1:BI:4:LYS:HA	1:BI:17:TYR:CD1	2.51	0.45
1:BT:47:TYR:HE1	1:DN:109:ASN:O	1.99	0.45
1:CE:4:LYS:HA	1:CE:17:TYR:HD1	1.80	0.45
1:CY:4:LYS:HA	1:CY:17:TYR:CD1	2.51	0.45
1:CY:98:ILE:HD11	1:GG:73:LEU:CD2	2.47	0.45
1:DC:98:ILE:HD11	1:GO:73:LEU:HD22	1.96	0.45
1:DI:88:LEU:HD23	1:GU:106:ILE:HG21	1.99	0.45
1:DL:98:ILE:HD11	1:GX:73:LEU:HD22	1.98	0.45
1:DT:4:LYS:HD3	1:DT:7:GLU:OE2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DY:109:ASN:O	1:FY:47:TYR:HE1	1.99	0.45
1:HA:4:LYS:HA	1:HA:17:TYR:HD1	1.81	0.45
1:IL:89:ARG:HH22	1:KF:21:GLY:H	1.64	0.45
1:JO:4:LYS:HA	1:JO:17:TYR:HD1	1.81	0.45
1:AG:45:ILE:CG2	1:BF:108:GLY:HA3	2.46	0.45
1:AK:4:LYS:HA	1:AK:17:TYR:CD1	2.51	0.45
1:AO:34:ALA:HA	1:AO:48:LYS:O	2.17	0.45
1:AS:106:ILE:O	1:EL:77:ALA:HB1	2.17	0.45
1:AY:98:ILE:CD1	1:EI:73:LEU:HD13	2.47	0.45
1:BA:34:ALA:HA	1:BA:48:LYS:O	2.17	0.45
1:BV:73:LEU:HD12	1:FH:72:ASN:O	2.16	0.45
1:CM:95:VAL:HG11	1:DG:99:THR:HG22	1.97	0.45
1:CS:4:LYS:HD3	1:CS:7:GLU:OE2	2.16	0.45
1:CT:4:LYS:HA	1:CT:17:TYR:HD1	1.81	0.45
1:CZ:89:ARG:HH22	1:GL:21:GLY:H	1.64	0.45
1:DF:34:ALA:HA	1:DF:48:LYS:O	2.17	0.45
1:DL:4:LYS:HA	1:DL:17:TYR:HD1	1.80	0.45
1:DW:4:LYS:HA	1:DW:17:TYR:CD1	2.51	0.45
1:EC:4:LYS:HD3	1:EC:7:GLU:OE2	2.16	0.45
1:EE:55:LEU:HD13	1:EU:81:VAL:HG21	1.98	0.45
1:EG:34:ALA:HA	1:EG:48:LYS:O	2.17	0.45
1:EJ:34:ALA:HA	1:EJ:48:LYS:O	2.17	0.45
1:FV:55:LEU:HD13	1:GS:83:ASN:HD22	1.81	0.45
1:FY:4:LYS:HA	1:FY:17:TYR:CD1	2.51	0.45
1:GN:4:LYS:HD3	1:GN:7:GLU:OE2	2.16	0.45
1:HD:34:ALA:HA	1:HD:48:LYS:O	2.17	0.45
1:HO:4:LYS:HA	1:HO:17:TYR:CD1	2.51	0.45
1:HQ:47:TYR:HE1	1:IS:109:ASN:O	1.99	0.45
1:HU:60:ASP:HB3	1:IM:59:VAL:HG11	1.98	0.45
1:HV:34:ALA:HA	1:HV:48:LYS:O	2.17	0.45
1:ID:4:LYS:HA	1:ID:17:TYR:CD1	2.51	0.45
1:IY:4:LYS:HD3	1:IY:7:GLU:OE2	2.16	0.45
1:JT:110:VAL:HB	1:KH:36:THR:HG23	1.98	0.45
1:JW:47:TYR:CZ	1:KE:105:ILE:HG12	2.51	0.45
1:JX:34:ALA:HA	1:JX:48:LYS:O	2.17	0.45
1:KJ:4:LYS:HA	1:KJ:17:TYR:HD1	1.81	0.45
1:AB:73:LEU:HD12	1:FX:73:LEU:HB2	1.99	0.45
1:AO:4:LYS:HA	1:AO:17:TYR:HD1	1.80	0.45
1:AQ:4:LYS:HA	1:AQ:17:TYR:CD1	2.51	0.45
1:BD:51:VAL:CG1	1:EP:90:VAL:HG13	2.45	0.45
1:BD:55:LEU:CD1	1:EP:81:VAL:HG21	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:97:PHE:CG	1:DN:32:LEU:HD21	2.52	0.45
1:BW:73:LEU:HD13	1:DQ:73:LEU:HB2	1.98	0.45
1:CG:110:VAL:HB	1:CL:36:THR:HG23	1.98	0.45
1:CH:34:ALA:HA	1:CH:48:LYS:O	2.17	0.45
1:DC:105:ILE:HG12	1:GO:47:TYR:CZ	2.52	0.45
1:DN:4:LYS:HA	1:DN:17:TYR:CD1	2.51	0.45
1:DZ:4:LYS:HA	1:DZ:17:TYR:CD1	2.51	0.45
1:ED:4:LYS:HA	1:ED:17:TYR:HD1	1.81	0.45
1:EI:4:LYS:HA	1:EI:17:TYR:CD1	2.51	0.45
1:GO:34:ALA:HA	1:GO:48:LYS:O	2.17	0.45
1:HG:34:ALA:HA	1:HG:48:LYS:O	2.17	0.45
1:HK:73:LEU:HD12	1:IY:72:ASN:O	2.15	0.45
1:HL:4:LYS:HA	1:HL:17:TYR:CD1	2.51	0.45
1:HP:4:LYS:HA	1:HP:17:TYR:HD1	1.81	0.45
1:HR:4:LYS:HA	1:HR:17:TYR:CD1	2.51	0.45
1:ID:95:VAL:HG13	1:II:95:VAL:HG13	1.98	0.45
1:IZ:34:ALA:HA	1:IZ:48:LYS:O	2.17	0.45
1:JR:34:ALA:HA	1:JR:48:LYS:O	2.17	0.45
1:AC:34:ALA:HA	1:AC:48:LYS:O	2.17	0.45
1:AI:89:ARG:HH22	1:DU:21:GLY:H	1.65	0.45
1:AN:75:PHE:CE2	1:FR:106:ILE:HA	2.50	0.45
1:AT:4:LYS:HA	1:AT:17:TYR:CD1	2.51	0.45
1:AV:19:PHE:CE1	1:EF:93:GLU:HG3	2.52	0.45
1:CD:4:LYS:HA	1:CD:17:TYR:CD1	2.51	0.45
1:CE:34:ALA:HA	1:CE:48:LYS:O	2.17	0.45
1:CH:112:THR:HG22	1:FT:17:TYR:OH	2.16	0.45
1:CJ:4:LYS:HA	1:CJ:17:TYR:CD1	2.51	0.45
1:CK:34:ALA:HA	1:CK:48:LYS:O	2.17	0.45
1:CM:4:LYS:HA	1:CM:17:TYR:CD1	2.51	0.45
1:CN:94:ILE:HG13	1:FZ:49:ILE:HG21	1.98	0.45
1:DB:105:ILE:HG12	1:GJ:47:TYR:CE2	2.51	0.45
1:FD:4:LYS:HD3	1:FD:7:GLU:OE2	2.16	0.45
1:FN:34:ALA:HA	1:FN:48:LYS:O	2.17	0.45
1:GX:4:LYS:HA	1:GX:17:TYR:HD1	1.81	0.45
1:HL:105:ILE:HG12	1:JG:47:TYR:CE2	2.52	0.45
1:HL:110:VAL:HB	1:JG:36:THR:HG23	1.98	0.45
1:HT:51:VAL:CG1	1:IM:90:VAL:HG13	2.46	0.45
1:IO:71:ALA:HA	1:KI:74:SER:O	2.16	0.45
1:IP:4:LYS:HA	1:IP:17:TYR:CD1	2.51	0.45
1:IU:102:LYS:HG3	1:JE:91:LEU:CD1	2.46	0.45
1:JH:4:LYS:HA	1:JH:17:TYR:CD1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:34:ALA:HA	1:AF:48:LYS:O	2.17	0.45
1:AQ:105:ILE:HG12	1:FU:47:TYR:CE2	2.52	0.45
1:AY:106:ILE:HA	1:EI:75:PHE:CE2	2.50	0.45
1:BA:73:LEU:HD12	1:EM:72:ASN:O	2.17	0.45
1:BE:102:LYS:HG2	1:BL:88:LEU:HD23	1.98	0.45
1:CS:72:ASN:O	1:DD:73:LEU:HD12	2.16	0.45
1:DH:4:LYS:HA	1:DH:17:TYR:CD1	2.51	0.45
1:DJ:75:PHE:HZ	1:DJ:87:LYS:HB3	1.82	0.45
1:DL:34:ALA:HA	1:DL:48:LYS:O	2.17	0.45
1:DP:78:LEU:HD12	1:GW:69:ILE:HG12	1.98	0.45
1:DV:45:ILE:HD13	1:GE:108:GLY:O	2.17	0.45
1:EU:4:LYS:HA	1:EU:17:TYR:CD1	2.51	0.45
1:EY:34:ALA:HA	1:EY:48:LYS:O	2.17	0.45
1:FD:89:ARG:HH22	1:FF:21:GLY:H	1.64	0.45
1:GU:34:ALA:HA	1:GU:48:LYS:O	2.17	0.45
1:HT:83:ASN:HD22	1:IM:55:LEU:HD13	1.82	0.45
1:HX:4:LYS:HA	1:HX:17:TYR:CD1	2.51	0.45
1:HY:4:LYS:HA	1:HY:17:TYR:HD1	1.80	0.45
1:IF:83:ASN:HD22	1:IJ:55:LEU:HD13	1.81	0.45
1:IF:93:GLU:OE1	1:IJ:2:ILE:HG23	2.16	0.45
1:IH:34:ALA:HA	1:IH:48:LYS:O	2.17	0.45
1:JF:34:ALA:HA	1:JF:48:LYS:O	2.17	0.45
1:JL:34:ALA:HA	1:JL:48:LYS:O	2.17	0.45
1:KF:4:LYS:HD3	1:KF:7:GLU:OE2	2.16	0.45
1:AD:75:PHE:HZ	1:AD:87:LYS:HB3	1.82	0.45
1:AE:55:LEU:HD13	1:GA:83:ASN:ND2	2.32	0.45
1:AR:34:ALA:HA	1:AR:48:LYS:O	2.17	0.45
1:BX:4:LYS:HA	1:BX:17:TYR:CD1	2.51	0.45
1:CB:34:ALA:HA	1:CB:48:LYS:O	2.17	0.45
1:CJ:4:LYS:HD3	1:CJ:7:GLU:OE2	2.16	0.45
1:CM:91:LEU:HD12	1:DG:106:ILE:HG23	1.98	0.45
1:CQ:73:LEU:HD12	1:GC:72:ASN:O	2.17	0.45
1:CW:34:ALA:HA	1:CW:48:LYS:O	2.17	0.45
1:DR:34:ALA:HA	1:DR:48:LYS:O	2.17	0.45
1:ED:34:ALA:HA	1:ED:48:LYS:O	2.17	0.45
1:EM:34:ALA:HA	1:EM:48:LYS:O	2.17	0.45
1:EN:21:GLY:H	1:FJ:89:ARG:HH22	1.63	0.45
1:EQ:17:TYR:OH	1:FM:112:THR:HG22	2.17	0.45
1:FS:95:VAL:HG13	1:GP:95:VAL:HG13	1.98	0.45
1:GD:75:PHE:HZ	1:GD:87:LYS:HB3	1.82	0.45
1:HP:21:GLY:H	1:JC:89:ARG:HH22	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HU:4:LYS:HA	1:HU:17:TYR:CD1	2.51	0.45
1:IT:34:ALA:HA	1:IT:48:LYS:O	2.17	0.45
1:IW:34:ALA:HA	1:IW:48:LYS:O	2.17	0.45
1:JC:34:ALA:HA	1:JC:48:LYS:O	2.17	0.45
1:JE:4:LYS:HA	1:JE:17:TYR:CD1	2.51	0.45
1:JK:110:VAL:HB	1:JM:36:THR:HG23	1.98	0.45
1:JQ:4:LYS:HA	1:JQ:17:TYR:CD1	2.51	0.45
1:JW:4:LYS:HA	1:JW:17:TYR:CD1	2.51	0.45
1:AF:12:ILE:HA	1:AF:36:THR:OG1	2.17	0.45
1:AW:95:VAL:HG11	1:FC:99:THR:CG2	2.47	0.45
1:BY:34:ALA:HA	1:BY:48:LYS:O	2.17	0.45
1:CD:21:GLY:H	1:CR:89:ARG:HH22	1.65	0.45
1:CI:75:PHE:HZ	1:CI:87:LYS:HB3	1.82	0.45
1:CK:12:ILE:HA	1:CK:36:THR:OG1	2.18	0.45
1:CZ:12:ILE:HA	1:CZ:36:THR:OG1	2.17	0.45
1:DI:12:ILE:HA	1:DI:36:THR:OG1	2.18	0.45
1:DO:12:ILE:HA	1:DO:36:THR:OG1	2.18	0.45
1:DY:83:ASN:ND2	1:FY:55:LEU:HD13	2.32	0.45
1:EB:4:LYS:HE2	1:GB:112:THR:HG21	1.99	0.45
1:EB:102:LYS:HG3	1:GB:91:LEU:CD1	2.46	0.45
1:EF:4:LYS:HA	1:EF:17:TYR:CD1	2.51	0.45
1:FE:34:ALA:HA	1:FE:48:LYS:O	2.17	0.45
1:FV:4:LYS:HA	1:FV:17:TYR:CD1	2.51	0.45
1:GF:34:ALA:HA	1:GF:48:LYS:O	2.17	0.45
1:GI:34:ALA:HA	1:GI:48:LYS:O	2.17	0.45
1:GL:34:ALA:HA	1:GL:48:LYS:O	2.17	0.45
1:HC:90:VAL:HG13	1:JS:51:VAL:HG11	1.99	0.45
1:IE:72:ASN:O	1:KA:73:LEU:HD12	2.17	0.45
1:IK:34:ALA:HA	1:IK:48:LYS:O	2.17	0.45
1:IO:75:PHE:HZ	1:IO:87:LYS:HB3	1.82	0.45
1:IT:12:ILE:HA	1:IT:36:THR:OG1	2.17	0.45
1:IV:4:LYS:HA	1:IV:17:TYR:CD1	2.51	0.45
1:IY:4:LYS:HA	1:IY:17:TYR:CD1	2.51	0.45
1:JA:89:ARG:HH22	1:JQ:21:GLY:H	1.65	0.45
1:JD:75:PHE:HZ	1:JD:87:LYS:HB3	1.82	0.45
1:JP:75:PHE:HZ	1:JP:87:LYS:HB3	1.82	0.45
1:JV:75:PHE:HZ	1:JV:87:LYS:HB3	1.82	0.45
1:KA:12:ILE:HA	1:KA:36:THR:OG1	2.18	0.45
1:AG:45:ILE:HD13	1:BF:108:GLY:O	2.16	0.44
1:AI:106:ILE:HG21	1:DU:88:LEU:HD23	1.98	0.44
1:AJ:75:PHE:HZ	1:AJ:87:LYS:HB3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:47:TYR:CG	1:FR:105:ILE:HG23	2.52	0.44
1:AR:4:LYS:HA	1:AR:17:TYR:HD1	1.80	0.44
1:BB:51:VAL:HG11	1:BR:90:VAL:HG13	1.99	0.44
1:BM:12:ILE:HA	1:BM:36:THR:OG1	2.18	0.44
1:BM:34:ALA:HA	1:BM:48:LYS:O	2.17	0.44
1:BP:34:ALA:HA	1:BP:48:LYS:O	2.17	0.44
1:BQ:36:THR:HG23	1:EC:110:VAL:HB	1.99	0.44
1:BQ:75:PHE:HZ	1:BQ:87:LYS:HB3	1.82	0.44
1:BS:34:ALA:HA	1:BS:48:LYS:O	2.17	0.44
1:CC:75:PHE:HZ	1:CC:87:LYS:HB3	1.82	0.44
1:CQ:34:ALA:HA	1:CQ:48:LYS:O	2.17	0.44
1:CX:75:PHE:HZ	1:CX:87:LYS:HB3	1.82	0.44
1:DB:4:LYS:HD3	1:DB:7:GLU:OE2	2.16	0.44
1:DC:12:ILE:HA	1:DC:36:THR:OG1	2.17	0.44
1:DL:91:LEU:HD11	1:GX:105:ILE:CG2	2.47	0.44
1:DS:75:PHE:HZ	1:DS:87:LYS:HB3	1.82	0.44
1:DU:34:ALA:HA	1:DU:48:LYS:O	2.17	0.44
1:DX:34:ALA:HA	1:DX:48:LYS:O	2.17	0.44
1:EB:75:PHE:HZ	1:EB:87:LYS:HB3	1.82	0.44
1:EL:4:LYS:HA	1:EL:17:TYR:CD1	2.51	0.44
1:EP:12:ILE:HA	1:EP:36:THR:OG1	2.17	0.44
1:FC:75:PHE:HZ	1:FC:87:LYS:HB3	1.82	0.44
1:FE:12:ILE:HA	1:FE:36:THR:OG1	2.18	0.44
1:FT:34:ALA:HA	1:FT:48:LYS:O	2.17	0.44
1:GM:75:PHE:HZ	1:GM:87:LYS:HB3	1.82	0.44
1:GT:4:LYS:HA	1:GT:17:TYR:CD1	2.51	0.44
1:GU:12:ILE:HA	1:GU:36:THR:OG1	2.18	0.44
1:GZ:55:LEU:HD13	1:JY:83:ASN:HD22	1.83	0.44
1:HA:12:ILE:HA	1:HA:36:THR:OG1	2.17	0.44
1:HS:73:LEU:HD22	1:JL:98:ILE:HD11	1.99	0.44
1:HW:97:PHE:CD1	1:IP:32:LEU:HD21	2.52	0.44
1:IX:75:PHE:HZ	1:IX:87:LYS:HB3	1.82	0.44
1:JA:75:PHE:HZ	1:JA:87:LYS:HB3	1.82	0.44
1:JK:4:LYS:HA	1:JK:17:TYR:CD1	2.51	0.44
1:JT:36:THR:HG23	1:KH:110:VAL:HB	1.98	0.44
1:JX:12:ILE:HA	1:JX:36:THR:OG1	2.17	0.44
1:KA:34:ALA:HA	1:KA:48:LYS:O	2.17	0.44
1:KD:34:ALA:HA	1:KD:48:LYS:O	2.17	0.44
1:AC:12:ILE:HA	1:AC:36:THR:OG1	2.18	0.44
1:AP:75:PHE:HZ	1:AP:87:LYS:HB3	1.82	0.44
1:AR:12:ILE:HA	1:AR:36:THR:OG1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:75:PHE:HZ	1:AS:87:LYS:HB3	1.82	0.44
1:AX:34:ALA:HA	1:AX:48:LYS:O	2.17	0.44
1:BH:78:LEU:HD12	1:BO:69:ILE:HG12	1.99	0.44
1:BI:28:TYR:O	1:BI:54:PRO:HG2	2.18	0.44
1:BK:89:ARG:HH22	1:DW:21:GLY:H	1.65	0.44
1:BT:45:ILE:CG2	1:DN:108:GLY:HA3	2.48	0.44
1:BZ:45:ILE:HD13	1:DT:108:GLY:O	2.18	0.44
1:CH:51:VAL:HG11	1:FT:90:VAL:HG13	1.99	0.44
1:CN:12:ILE:HA	1:CN:36:THR:OG1	2.18	0.44
1:CT:12:ILE:HA	1:CT:36:THR:OG1	2.18	0.44
1:DB:4:LYS:HA	1:DB:17:TYR:CD1	2.51	0.44
1:DV:75:PHE:HZ	1:DV:87:LYS:HB3	1.82	0.44
1:ED:12:ILE:HA	1:ED:36:THR:OG1	2.18	0.44
1:EP:34:ALA:HA	1:EP:48:LYS:O	2.17	0.44
1:EQ:75:PHE:HZ	1:EQ:87:LYS:HB3	1.82	0.44
1:FF:75:PHE:HZ	1:FF:87:LYS:HB3	1.82	0.44
1:FK:12:ILE:HA	1:FK:36:THR:OG1	2.18	0.44
1:FX:75:PHE:HZ	1:FX:87:LYS:HB3	1.82	0.44
1:GB:4:LYS:HA	1:GB:17:TYR:CD1	2.51	0.44
1:GH:4:LYS:HA	1:GH:17:TYR:CD1	2.51	0.44
1:GS:75:PHE:HZ	1:GS:87:LYS:HB3	1.82	0.44
1:HE:75:PHE:HZ	1:HE:87:LYS:HB3	1.82	0.44
1:HV:73:LEU:HA	1:JO:72:ASN:O	2.18	0.44
1:JT:73:LEU:HD13	1:KH:98:ILE:HD11	1.99	0.44
1:AI:34:ALA:HA	1:AI:48:LYS:O	2.17	0.44
1:AM:75:PHE:HZ	1:AM:87:LYS:HB3	1.82	0.44
1:AY:89:ARG:HH22	1:EI:21:GLY:H	1.64	0.44
1:BA:90:VAL:HG13	1:EM:51:VAL:HG11	1.98	0.44
1:BH:75:PHE:HZ	1:BH:87:LYS:HB3	1.82	0.44
1:BP:12:ILE:HA	1:BP:36:THR:OG1	2.18	0.44
1:CA:28:TYR:O	1:CA:54:PRO:HG2	2.18	0.44
1:CB:4:LYS:HA	1:CB:17:TYR:HD1	1.80	0.44
1:CL:75:PHE:HZ	1:CL:87:LYS:HB3	1.82	0.44
1:CT:34:ALA:HA	1:CT:48:LYS:O	2.17	0.44
1:DS:106:ILE:HD13	1:GQ:88:LEU:HG	1.99	0.44
1:DX:12:ILE:HA	1:DX:36:THR:OG1	2.18	0.44
1:EU:28:TYR:O	1:EU:54:PRO:HG2	2.18	0.44
1:EV:4:LYS:HA	1:EV:17:TYR:HD1	1.81	0.44
1:FJ:28:TYR:O	1:FJ:54:PRO:HG2	2.18	0.44
1:GA:75:PHE:HZ	1:GA:87:LYS:HB3	1.83	0.44
1:GR:34:ALA:HA	1:GR:48:LYS:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HA:34:ALA:HA	1:HA:48:LYS:O	2.17	0.44
1:HG:12:ILE:HA	1:HG:36:THR:OG1	2.18	0.44
1:HJ:34:ALA:HA	1:HJ:48:LYS:O	2.17	0.44
1:HK:75:PHE:HZ	1:HK:87:LYS:HB3	1.82	0.44
1:HK:78:LEU:HD12	1:IY:69:ILE:HG12	2.00	0.44
1:HX:28:TYR:O	1:HX:54:PRO:HG2	2.18	0.44
1:IN:34:ALA:HA	1:IN:48:LYS:O	2.17	0.44
1:JT:4:LYS:HA	1:JT:17:TYR:CD1	2.51	0.44
1:AB:28:TYR:O	1:AB:54:PRO:HG2	2.18	0.44
1:AE:28:TYR:O	1:AE:54:PRO:HG2	2.18	0.44
1:AE:55:LEU:HD13	1:GA:83:ASN:HD22	1.83	0.44
1:AF:83:ASN:OD1	1:DR:55:LEU:HD13	2.17	0.44
1:AG:75:PHE:HZ	1:AG:87:LYS:HB3	1.82	0.44
1:AK:112:THR:HG21	1:FO:4:LYS:HE2	1.99	0.44
1:AR:73:LEU:HD12	1:ED:72:ASN:O	2.18	0.44
1:AV:75:PHE:HZ	1:AV:87:LYS:HB3	1.82	0.44
1:AX:12:ILE:HA	1:AX:36:THR:OG1	2.17	0.44
1:BG:12:ILE:HA	1:BG:36:THR:OG1	2.18	0.44
1:BG:34:ALA:HA	1:BG:48:LYS:O	2.17	0.44
1:BK:75:PHE:HZ	1:BK:87:LYS:HB3	1.82	0.44
1:BS:12:ILE:HA	1:BS:36:THR:OG1	2.17	0.44
1:BV:34:ALA:HA	1:BV:48:LYS:O	2.17	0.44
1:BW:78:LEU:HD12	1:DQ:69:ILE:HG12	2.00	0.44
1:BY:12:ILE:HA	1:BY:36:THR:OG1	2.17	0.44
1:CF:75:PHE:HZ	1:CF:87:LYS:HB3	1.82	0.44
1:CR:75:PHE:HZ	1:CR:87:LYS:HB3	1.82	0.44
1:CV:28:TYR:O	1:CV:54:PRO:HG2	2.18	0.44
1:CW:73:LEU:HD12	1:GI:72:ASN:O	2.17	0.44
1:CZ:34:ALA:HA	1:CZ:48:LYS:O	2.17	0.44
1:CZ:97:PHE:CG	1:GL:32:LEU:HD21	2.51	0.44
1:DF:12:ILE:HA	1:DF:36:THR:OG1	2.17	0.44
1:DO:34:ALA:HA	1:DO:48:LYS:O	2.17	0.44
1:DW:28:TYR:O	1:DW:54:PRO:HG2	2.18	0.44
1:EN:110:VAL:HB	1:FJ:36:THR:HG23	1.99	0.44
1:ES:12:ILE:HA	1:ES:36:THR:OG1	2.18	0.44
1:EV:34:ALA:HA	1:EV:48:LYS:O	2.17	0.44
1:EZ:75:PHE:HZ	1:EZ:87:LYS:HB3	1.82	0.44
1:FB:12:ILE:HA	1:FB:36:THR:OG1	2.17	0.44
1:FG:28:TYR:O	1:FG:54:PRO:HG2	2.18	0.44
1:FH:34:ALA:HA	1:FH:48:LYS:O	2.17	0.44
1:FQ:34:ALA:HA	1:FQ:48:LYS:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FV:95:VAL:HG11	1:GS:99:THR:HG22	1.99	0.44
1:GF:4:LYS:HA	1:GF:17:TYR:HD1	1.81	0.44
1:GK:28:TYR:O	1:GK:54:PRO:HG2	2.18	0.44
1:GX:12:ILE:HA	1:GX:36:THR:OG1	2.17	0.44
1:HE:73:LEU:CD2	1:HU:98:ILE:HD11	2.47	0.44
1:HL:11:PRO:O	1:JG:110:VAL:HG12	2.15	0.44
1:HT:72:ASN:HB3	1:IM:74:SER:OG	2.16	0.44
1:IB:34:ALA:HA	1:IB:48:LYS:O	2.17	0.44
1:IG:28:TYR:O	1:IG:54:PRO:HG2	2.18	0.44
1:IH:12:ILE:HA	1:IH:36:THR:OG1	2.18	0.44
1:IL:75:PHE:HZ	1:IL:87:LYS:HB3	1.83	0.44
1:IS:4:LYS:HA	1:IS:17:TYR:CD1	2.51	0.44
1:JC:12:ILE:HA	1:JC:36:THR:OG1	2.18	0.44
1:JT:90:VAL:HG13	1:KH:51:VAL:HG11	2.00	0.44
1:JU:34:ALA:HA	1:JU:48:LYS:O	2.17	0.44
1:AE:4:LYS:HA	1:AE:17:TYR:CD1	2.51	0.44
1:AF:98:ILE:HD11	1:DR:73:LEU:HD22	2.00	0.44
1:AK:28:TYR:O	1:AK:54:PRO:HG2	2.18	0.44
1:AN:4:LYS:HA	1:AN:17:TYR:CD1	2.51	0.44
1:AN:105:ILE:HG12	1:FR:47:TYR:CZ	2.53	0.44
1:AO:44:ASN:HB2	1:AO:78:LEU:HA	2.00	0.44
1:BC:4:LYS:HA	1:BC:17:TYR:CD1	2.51	0.44
1:BD:34:ALA:HA	1:BD:48:LYS:O	2.17	0.44
1:BM:73:LEU:HD12	1:EY:72:ASN:O	2.17	0.44
1:BT:75:PHE:HZ	1:BT:87:LYS:HB3	1.82	0.44
1:BZ:45:ILE:CG2	1:DT:108:GLY:HA3	2.47	0.44
1:CG:4:LYS:HA	1:CG:17:TYR:CD1	2.51	0.44
1:CK:36:THR:HG23	1:FW:110:VAL:HB	1.98	0.44
1:CU:78:LEU:HD12	1:DH:69:ILE:HG12	2.00	0.44
1:DB:28:TYR:O	1:DB:54:PRO:HG2	2.18	0.44
1:DI:34:ALA:HA	1:DI:48:LYS:O	2.17	0.44
1:DK:4:LYS:HA	1:DK:17:TYR:CD1	2.51	0.44
1:DK:28:TYR:O	1:DK:54:PRO:HG2	2.18	0.44
1:DL:12:ILE:HA	1:DL:36:THR:OG1	2.17	0.44
1:EH:75:PHE:HZ	1:EH:87:LYS:HB3	1.82	0.44
1:EL:28:TYR:O	1:EL:54:PRO:HG2	2.18	0.44
1:EO:28:TYR:O	1:EO:54:PRO:HG2	2.18	0.44
1:EV:12:ILE:HA	1:EV:36:THR:OG1	2.17	0.44
1:FK:34:ALA:HA	1:FK:48:LYS:O	2.17	0.44
1:FO:75:PHE:HZ	1:FO:87:LYS:HB3	1.82	0.44
1:GI:12:ILE:HA	1:GI:36:THR:OG1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GX:34:ALA:HA	1:GX:48:LYS:O	2.17	0.44
1:HJ:44:ASN:HB2	1:HJ:78:LEU:HA	2.00	0.44
1:HM:12:ILE:HA	1:HM:36:THR:OG1	2.17	0.44
1:HN:75:PHE:HZ	1:HN:87:LYS:HB3	1.82	0.44
1:HY:12:ILE:HA	1:HY:36:THR:OG1	2.17	0.44
1:ID:69:ILE:HG12	1:II:78:LEU:HD12	1.99	0.44
1:IF:75:PHE:HZ	1:IF:87:LYS:HB3	1.82	0.44
1:IF:78:LEU:HD12	1:IJ:69:ILE:HG12	2.00	0.44
1:II:75:PHE:HZ	1:II:87:LYS:HB3	1.82	0.44
1:IQ:34:ALA:HA	1:IQ:48:LYS:O	2.17	0.44
1:IV:28:TYR:O	1:IV:54:PRO:HG2	2.18	0.44
1:IY:28:TYR:O	1:IY:54:PRO:HG2	2.18	0.44
1:JI:34:ALA:HA	1:JI:48:LYS:O	2.17	0.44
1:JJ:75:PHE:HZ	1:JJ:87:LYS:HB3	1.82	0.44
1:JK:11:PRO:HB3	1:JM:109:ASN:CG	2.43	0.44
1:JM:75:PHE:HZ	1:JM:87:LYS:HB3	1.82	0.44
1:JN:28:TYR:O	1:JN:54:PRO:HG2	2.18	0.44
1:JS:75:PHE:HZ	1:JS:87:LYS:HB3	1.82	0.44
1:JT:28:TYR:O	1:JT:54:PRO:HG2	2.18	0.44
1:KI:28:TYR:O	1:KI:54:PRO:HG2	2.18	0.44
1:KJ:34:ALA:HA	1:KJ:48:LYS:O	2.17	0.44
1:AE:71:ALA:HB2	1:GA:75:PHE:HD1	1.83	0.44
1:AY:75:PHE:HZ	1:AY:87:LYS:HB3	1.82	0.44
1:BX:28:TYR:O	1:BX:54:PRO:HG2	2.18	0.44
1:CB:89:ARG:HH22	1:FN:21:GLY:H	1.65	0.44
1:CJ:28:TYR:O	1:CJ:54:PRO:HG2	2.18	0.44
1:CV:32:LEU:CD1	1:CV:49:ILE:HG23	2.48	0.44
1:DB:108:GLY:HA3	1:GJ:45:ILE:CG2	2.48	0.44
1:DE:28:TYR:O	1:DE:54:PRO:HG2	2.18	0.44
1:DP:75:PHE:HZ	1:DP:87:LYS:HB3	1.82	0.44
1:DT:32:LEU:CD1	1:DT:49:ILE:HG23	2.48	0.44
1:DX:44:ASN:HB2	1:DX:78:LEU:HA	2.00	0.44
1:EA:12:ILE:HA	1:EA:36:THR:OG1	2.18	0.44
1:EC:28:TYR:O	1:EC:54:PRO:HG2	2.18	0.44
1:EE:81:VAL:HG21	1:EU:55:LEU:CD1	2.47	0.44
1:EG:12:ILE:HA	1:EG:36:THR:OG1	2.18	0.44
1:EM:12:ILE:HA	1:EM:36:THR:OG1	2.18	0.44
1:EN:97:PHE:CG	1:FJ:32:LEU:HD21	2.52	0.44
1:EY:12:ILE:HA	1:EY:36:THR:OG1	2.17	0.44
1:FB:34:ALA:HA	1:FB:48:LYS:O	2.17	0.44
1:FG:32:LEU:CD1	1:FG:49:ILE:HG23	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FR:75:PHE:HZ	1:FR:87:LYS:HB3	1.82	0.44
1:FY:28:TYR:O	1:FY:54:PRO:HG2	2.18	0.44
1:GF:44:ASN:HB2	1:GF:78:LEU:HA	2.00	0.44
1:GX:44:ASN:HB2	1:GX:78:LEU:HA	2.00	0.44
1:GY:75:PHE:HZ	1:GY:87:LYS:HB3	1.82	0.44
1:GY:97:PHE:CD1	1:HO:32:LEU:HD21	2.53	0.44
1:HA:88:LEU:HD23	1:IQ:106:ILE:HG21	2.00	0.44
1:HQ:73:LEU:CD2	1:IS:98:ILE:HD11	2.48	0.44
1:HS:73:LEU:HA	1:JL:72:ASN:O	2.18	0.44
1:HT:95:VAL:HG13	1:IM:95:VAL:HG13	1.98	0.44
1:HY:44:ASN:HB2	1:HY:78:LEU:HA	2.00	0.44
1:IA:4:LYS:HA	1:IA:17:TYR:CD1	2.51	0.44
1:IJ:28:TYR:O	1:IJ:54:PRO:HG2	2.18	0.44
1:IK:12:ILE:HA	1:IK:36:THR:OG1	2.18	0.44
1:IU:75:PHE:HZ	1:IU:87:LYS:HB3	1.82	0.44
1:JL:12:ILE:HA	1:JL:36:THR:OG1	2.17	0.44
1:JO:12:ILE:HA	1:JO:36:THR:OG1	2.17	0.44
1:JY:75:PHE:HZ	1:JY:87:LYS:HB3	1.82	0.44
1:KE:75:PHE:HZ	1:KE:87:LYS:HB3	1.82	0.44
1:AA:78:LEU:HD12	1:BI:69:ILE:HG12	1.99	0.44
1:AL:12:ILE:HA	1:AL:36:THR:OG1	2.18	0.44
1:AW:32:LEU:CD1	1:AW:49:ILE:HG23	2.48	0.44
1:AX:91:LEU:HD11	1:EJ:105:ILE:CG2	2.48	0.44
1:BD:12:ILE:HA	1:BD:36:THR:OG1	2.17	0.44
1:BO:28:TYR:O	1:BO:54:PRO:HG2	2.18	0.44
1:BY:72:ASN:O	1:FK:73:LEU:HA	2.18	0.44
1:BY:73:LEU:HD22	1:FK:98:ILE:HD11	1.99	0.44
1:CJ:112:THR:HG22	1:CO:17:TYR:OH	2.17	0.44
1:CO:75:PHE:HZ	1:CO:87:LYS:HB3	1.82	0.44
1:DB:32:LEU:CD1	1:DB:49:ILE:HG23	2.48	0.44
1:DI:95:VAL:HG11	1:GU:99:THR:HG23	1.98	0.44
1:EA:34:ALA:HA	1:EA:48:LYS:O	2.17	0.44
1:EG:44:ASN:HB2	1:EG:78:LEU:HA	2.00	0.44
1:EH:67:ASN:HB3	1:EO:78:LEU:HD13	1.99	0.44
1:FE:44:ASN:HB2	1:FE:78:LEU:HA	2.00	0.44
1:FL:75:PHE:HZ	1:FL:87:LYS:HB3	1.82	0.44
1:FP:28:TYR:O	1:FP:54:PRO:HG2	2.18	0.44
1:FT:44:ASN:HB2	1:FT:78:LEU:HA	2.00	0.44
1:FW:44:ASN:HB2	1:FW:78:LEU:HA	2.00	0.44
1:FY:32:LEU:CD1	1:FY:49:ILE:HG23	2.48	0.44
1:GK:4:LYS:HA	1:GK:17:TYR:CD1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GW:28:TYR:O	1:GW:54:PRO:HG2	2.18	0.44
1:HE:110:VAL:HG12	1:HU:11:PRO:O	2.18	0.44
1:HF:112:THR:HG21	1:JV:4:LYS:HE2	2.00	0.44
1:HL:32:LEU:CD1	1:HL:49:ILE:HG23	2.48	0.44
1:HM:34:ALA:HA	1:HM:48:LYS:O	2.17	0.44
1:HO:32:LEU:CD1	1:HO:49:ILE:HG23	2.48	0.44
1:HQ:71:ALA:HB3	1:IS:94:ILE:HD11	2.00	0.44
1:HS:12:ILE:HA	1:HS:36:THR:OG1	2.17	0.44
1:HT:73:LEU:HA	1:IM:73:LEU:HA	1.99	0.44
1:HY:73:LEU:HD22	1:JR:98:ILE:HD11	2.00	0.44
1:IA:28:TYR:O	1:IA:54:PRO:HG2	2.18	0.44
1:JB:28:TYR:O	1:JB:54:PRO:HG2	2.18	0.44
1:KI:4:LYS:HA	1:KI:17:TYR:CD1	2.51	0.44
1:AN:28:TYR:O	1:AN:54:PRO:HG2	2.18	0.44
1:AX:44:ASN:HB2	1:AX:78:LEU:HA	2.00	0.44
1:BA:12:ILE:HA	1:BA:36:THR:OG1	2.17	0.44
1:BC:28:TYR:O	1:BC:54:PRO:HG2	2.18	0.44
1:BC:32:LEU:CD1	1:BC:49:ILE:HG23	2.48	0.44
1:BF:28:TYR:O	1:BF:54:PRO:HG2	2.18	0.44
1:BJ:44:ASN:HB2	1:BJ:78:LEU:HA	2.00	0.44
1:BN:89:ARG:HH22	1:DZ:21:GLY:H	1.64	0.44
1:BU:28:TYR:O	1:BU:54:PRO:HG2	2.18	0.44
1:CB:12:ILE:HA	1:CB:36:THR:OG1	2.17	0.44
1:CH:12:ILE:HA	1:CH:36:THR:OG1	2.18	0.44
1:CM:28:TYR:O	1:CM:54:PRO:HG2	2.18	0.44
1:CN:34:ALA:HA	1:CN:48:LYS:O	2.17	0.44
1:CU:75:PHE:HZ	1:CU:87:LYS:HB3	1.82	0.44
1:CV:112:THR:HG21	1:GM:4:LYS:HE2	2.00	0.44
1:DL:99:THR:HG23	1:GX:95:VAL:HG11	2.00	0.44
1:DN:28:TYR:O	1:DN:54:PRO:HG2	2.18	0.44
1:EI:32:LEU:CD1	1:EI:49:ILE:HG23	2.48	0.44
1:EJ:26:ALA:HA	1:EJ:29:MET:HB2	2.00	0.44
1:EK:75:PHE:HZ	1:EK:87:LYS:HB3	1.82	0.44
1:ES:34:ALA:HA	1:ES:48:LYS:O	2.17	0.44
1:EX:32:LEU:CD1	1:EX:49:ILE:HG23	2.48	0.44
1:FZ:12:ILE:HA	1:FZ:36:THR:OG1	2.18	0.44
1:GF:12:ILE:HA	1:GF:36:THR:OG1	2.18	0.44
1:GJ:75:PHE:HZ	1:GJ:87:LYS:HB3	1.82	0.44
1:GT:28:TYR:O	1:GT:54:PRO:HG2	2.18	0.44
1:GV:75:PHE:HZ	1:GV:87:LYS:HB3	1.82	0.44
1:HP:12:ILE:HA	1:HP:36:THR:OG1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HU:32:LEU:CD1	1:HU:49:ILE:HG23	2.48	0.44
1:HV:12:ILE:HA	1:HV:36:THR:OG1	2.18	0.44
1:HV:71:ALA:HA	1:JO:74:SER:O	2.18	0.44
1:HY:34:ALA:HA	1:HY:48:LYS:O	2.17	0.44
1:HZ:75:PHE:HZ	1:HZ:87:LYS:HB3	1.82	0.44
1:IB:44:ASN:HB2	1:IB:78:LEU:HA	2.00	0.44
1:IF:105:ILE:HG12	1:IJ:47:TYR:CE2	2.53	0.44
1:IG:32:LEU:CD1	1:IG:49:ILE:HG23	2.48	0.44
1:IP:28:TYR:O	1:IP:54:PRO:HG2	2.18	0.44
1:JC:44:ASN:HB2	1:JC:78:LEU:HA	2.00	0.44
1:KG:34:ALA:HA	1:KG:48:LYS:O	2.17	0.44
1:AD:2:ILE:HG23	1:BC:93:GLU:OE1	2.18	0.44
1:AH:95:VAL:HG13	1:GD:95:VAL:HG13	2.00	0.44
1:AR:44:ASN:HB2	1:AR:78:LEU:HA	2.00	0.44
1:AU:12:ILE:HA	1:AU:36:THR:OG1	2.18	0.44
1:AU:34:ALA:HA	1:AU:48:LYS:O	2.17	0.44
1:AU:44:ASN:HB2	1:AU:78:LEU:HA	2.00	0.44
1:AZ:28:TYR:O	1:AZ:54:PRO:HG2	2.18	0.44
1:BP:88:LEU:HD23	1:FB:106:ILE:HG21	1.98	0.44
1:BT:112:THR:HG23	1:DN:17:TYR:OH	2.18	0.44
1:CC:78:LEU:HD12	1:GK:69:ILE:HG12	1.99	0.44
1:CQ:44:ASN:HB2	1:CQ:78:LEU:HA	2.00	0.44
1:CS:112:THR:HG21	1:DD:4:LYS:HE2	1.99	0.44
1:DH:32:LEU:CD1	1:DH:49:ILE:HG23	2.48	0.44
1:DK:32:LEU:CD1	1:DK:49:ILE:HG23	2.48	0.44
1:DQ:28:TYR:O	1:DQ:54:PRO:HG2	2.18	0.44
1:ED:44:ASN:HB2	1:ED:78:LEU:HA	2.00	0.44
1:EE:74:SER:O	1:EU:71:ALA:HA	2.18	0.44
1:EE:75:PHE:HZ	1:EE:87:LYS:HB3	1.82	0.44
1:EN:105:ILE:HG23	1:FJ:47:TYR:CG	2.53	0.44
1:EP:44:ASN:HB2	1:EP:78:LEU:HA	2.00	0.44
1:EW:75:PHE:HZ	1:EW:87:LYS:HB3	1.82	0.44
1:FD:28:TYR:O	1:FD:54:PRO:HG2	2.18	0.44
1:FN:44:ASN:HB2	1:FN:78:LEU:HA	2.00	0.44
1:FQ:44:ASN:HB2	1:FQ:78:LEU:HA	2.00	0.44
1:FV:28:TYR:O	1:FV:54:PRO:HG2	2.18	0.44
1:FW:34:ALA:HA	1:FW:48:LYS:O	2.17	0.44
1:GB:32:LEU:CD1	1:GB:49:ILE:HG23	2.48	0.44
1:GO:12:ILE:HA	1:GO:36:THR:OG1	2.17	0.44
1:GQ:32:LEU:CD1	1:GQ:49:ILE:HG23	2.48	0.44
1:HA:44:ASN:HB2	1:HA:78:LEU:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HC:55:LEU:HD13	1:JS:83:ASN:HD22	1.83	0.44
1:HF:72:ASN:O	1:JV:73:LEU:HD12	2.18	0.44
1:HP:34:ALA:HA	1:HP:48:LYS:O	2.17	0.44
1:HW:75:PHE:HZ	1:HW:87:LYS:HB3	1.82	0.44
1:IK:44:ASN:HB2	1:IK:78:LEU:HA	2.00	0.44
1:JF:44:ASN:HB2	1:JF:78:LEU:HA	2.00	0.44
1:JZ:28:TYR:O	1:JZ:54:PRO:HG2	2.18	0.44
1:KC:4:LYS:HA	1:KC:17:TYR:CD1	2.51	0.44
1:KD:12:ILE:HA	1:KD:36:THR:OG1	2.17	0.44
1:KJ:44:ASN:HB2	1:KJ:78:LEU:HA	2.00	0.44
1:AC:44:ASN:HB2	1:AC:78:LEU:HA	2.00	0.43
1:AD:36:THR:CG2	1:BC:110:VAL:HB	2.47	0.43
1:AG:73:LEU:HD22	1:BF:98:ILE:HD11	2.00	0.43
1:AJ:99:THR:CG2	1:BX:95:VAL:HG11	2.48	0.43
1:AZ:32:LEU:CD1	1:AZ:49:ILE:HG23	2.48	0.43
1:BG:26:ALA:HA	1:BG:29:MET:HB2	2.00	0.43
1:BJ:26:ALA:HA	1:BJ:29:MET:HB2	2.00	0.43
1:BJ:34:ALA:HA	1:BJ:48:LYS:O	2.17	0.43
1:BK:106:ILE:HG21	1:DW:88:LEU:HG	2.00	0.43
1:BL:28:TYR:O	1:BL:54:PRO:HG2	2.18	0.43
1:BM:26:ALA:HA	1:BM:29:MET:HB2	2.00	0.43
1:CD:108:GLY:HA3	1:CR:45:ILE:CG2	2.48	0.43
1:CG:32:LEU:CD1	1:CG:49:ILE:HG23	2.48	0.43
1:CH:26:ALA:HA	1:CH:29:MET:HB2	2.01	0.43
1:CH:111:LEU:HD21	1:FT:8:SER:O	2.17	0.43
1:CN:44:ASN:HB2	1:CN:78:LEU:HA	2.00	0.43
1:CS:32:LEU:CD1	1:CS:49:ILE:HG23	2.48	0.43
1:CT:44:ASN:HB2	1:CT:78:LEU:HA	2.00	0.43
1:DC:44:ASN:HB2	1:DC:78:LEU:HA	2.00	0.43
1:DL:44:ASN:HB2	1:DL:78:LEU:HA	2.00	0.43
1:DU:44:ASN:HB2	1:DU:78:LEU:HA	2.00	0.43
1:EG:26:ALA:HA	1:EG:29:MET:HB2	2.00	0.43
1:EM:26:ALA:HA	1:EM:29:MET:HB2	2.00	0.43
1:EN:51:VAL:HG11	1:FJ:90:VAL:HG13	2.00	0.43
1:ES:44:ASN:HB2	1:ES:78:LEU:HA	2.00	0.43
1:FN:26:ALA:HA	1:FN:29:MET:HB2	2.00	0.43
1:FU:75:PHE:HZ	1:FU:87:LYS:HB3	1.82	0.43
1:FW:12:ILE:HA	1:FW:36:THR:OG1	2.17	0.43
1:FZ:26:ALA:HA	1:FZ:29:MET:HB2	2.00	0.43
1:FZ:34:ALA:HA	1:FZ:48:LYS:O	2.17	0.43
1:GB:28:TYR:O	1:GB:54:PRO:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GC:34:ALA:HA	1:GC:48:LYS:O	2.17	0.43
1:GR:44:ASN:HB2	1:GR:78:LEU:HA	2.00	0.43
1:HD:12:ILE:HA	1:HD:36:THR:OG1	2.18	0.43
1:HG:44:ASN:HB2	1:HG:78:LEU:HA	2.00	0.43
1:HO:28:TYR:O	1:HO:54:PRO:HG2	2.18	0.43
1:ID:32:LEU:CD1	1:ID:49:ILE:HG23	2.48	0.43
1:IN:12:ILE:HA	1:IN:36:THR:OG1	2.17	0.43
1:JI:12:ILE:HA	1:JI:36:THR:OG1	2.17	0.43
1:JK:32:LEU:CD1	1:JK:49:ILE:HG23	2.48	0.43
1:JW:28:TYR:O	1:JW:54:PRO:HG2	2.18	0.43
1:KC:28:TYR:O	1:KC:54:PRO:HG2	2.18	0.43
1:KG:12:ILE:HA	1:KG:36:THR:OG1	2.17	0.43
1:KG:26:ALA:HA	1:KG:29:MET:HB2	2.00	0.43
1:KJ:12:ILE:HA	1:KJ:36:THR:OG1	2.18	0.43
1:AB:90:VAL:HG13	1:FX:51:VAL:HG11	2.01	0.43
1:AK:32:LEU:HD21	1:FO:97:PHE:CG	2.54	0.43
1:AL:44:ASN:HB2	1:AL:78:LEU:HA	2.00	0.43
1:AO:26:ALA:HA	1:AO:29:MET:HB2	2.01	0.43
1:BA:44:ASN:HB2	1:BA:78:LEU:HA	2.00	0.43
1:BG:98:ILE:HD11	1:ES:73:LEU:HD22	2.00	0.43
1:BM:44:ASN:HB2	1:BM:78:LEU:HA	2.00	0.43
1:BM:99:THR:HG23	1:EY:95:VAL:HG11	2.00	0.43
1:BP:55:LEU:HD13	1:FB:83:ASN:OD1	2.18	0.43
1:BQ:11:PRO:O	1:EC:110:VAL:HG12	2.17	0.43
1:BR:28:TYR:O	1:BR:54:PRO:HG2	2.18	0.43
1:DD:75:PHE:HZ	1:DD:87:LYS:HB3	1.82	0.43
1:DH:28:TYR:O	1:DH:54:PRO:HG2	2.18	0.43
1:DM:75:PHE:HZ	1:DM:87:LYS:HB3	1.82	0.43
1:DR:12:ILE:HA	1:DR:36:THR:OG1	2.17	0.43
1:DY:75:PHE:HZ	1:DY:87:LYS:HB3	1.82	0.43
1:EC:4:LYS:HA	1:EC:17:TYR:CD1	2.51	0.43
1:FA:32:LEU:CD1	1:FA:49:ILE:HG23	2.48	0.43
1:FD:74:SER:O	1:FF:71:ALA:HA	2.17	0.43
1:FM:32:LEU:CD1	1:FM:49:ILE:HG23	2.48	0.43
1:FS:28:TYR:O	1:FS:54:PRO:HG2	2.18	0.43
1:GH:28:TYR:O	1:GH:54:PRO:HG2	2.18	0.43
1:GW:4:LYS:HA	1:GW:17:TYR:CD1	2.51	0.43
1:HC:28:TYR:O	1:HC:54:PRO:HG2	2.18	0.43
1:HQ:45:ILE:CG2	1:IS:108:GLY:HA3	2.48	0.43
1:HR:28:TYR:O	1:HR:54:PRO:HG2	2.18	0.43
1:HW:105:ILE:HG12	1:IP:47:TYR:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IB:26:ALA:HA	1:IB:29:MET:HB2	2.00	0.43
1:IE:34:ALA:HA	1:IE:48:LYS:O	2.17	0.43
1:IF:45:ILE:CG2	1:IJ:108:GLY:HA3	2.48	0.43
1:IK:47:TYR:CZ	1:KJ:105:ILE:HG12	2.52	0.43
1:IL:106:ILE:HD13	1:KF:88:LEU:HG	2.00	0.43
1:IW:12:ILE:HA	1:IW:36:THR:OG1	2.17	0.43
1:IW:44:ASN:HB2	1:IW:78:LEU:HA	2.00	0.43
1:IX:71:ALA:HB2	1:JB:75:PHE:HD1	1.83	0.43
1:IZ:12:ILE:HA	1:IZ:36:THR:OG1	2.18	0.43
1:JC:26:ALA:HA	1:JC:29:MET:HB2	2.00	0.43
1:JK:73:LEU:HD13	1:JM:98:ILE:HD11	2.00	0.43
1:JO:34:ALA:HA	1:JO:48:LYS:O	2.17	0.43
1:KD:26:ALA:HA	1:KD:29:MET:HB2	2.00	0.43
1:AA:75:PHE:HZ	1:AA:87:LYS:HB3	1.82	0.43
1:AO:12:ILE:HA	1:AO:36:THR:OG1	2.17	0.43
1:AS:106:ILE:HA	1:EL:75:PHE:CE2	2.52	0.43
1:AW:28:TYR:O	1:AW:54:PRO:HG2	2.18	0.43
1:BJ:12:ILE:HA	1:BJ:36:THR:OG1	2.18	0.43
1:BS:44:ASN:HB2	1:BS:78:LEU:HA	2.00	0.43
1:CD:28:TYR:O	1:CD:54:PRO:HG2	2.18	0.43
1:CD:108:GLY:O	1:CR:45:ILE:HD13	2.18	0.43
1:CE:12:ILE:HA	1:CE:36:THR:OG1	2.17	0.43
1:CG:109:ASN:OD1	1:CL:11:PRO:HA	2.18	0.43
1:CZ:98:ILE:HD11	1:GL:73:LEU:HD22	2.00	0.43
1:DF:44:ASN:HB2	1:DF:78:LEU:HA	2.00	0.43
1:DG:75:PHE:HZ	1:DG:87:LYS:HB3	1.82	0.43
1:DU:26:ALA:HA	1:DU:29:MET:HB2	2.00	0.43
1:EH:95:VAL:HG11	1:EO:99:THR:CG2	2.49	0.43
1:ER:32:LEU:CD1	1:ER:49:ILE:HG23	2.48	0.43
1:ET:19:PHE:HB3	1:FG:89:ARG:NH2	2.33	0.43
1:FB:44:ASN:HB2	1:FB:78:LEU:HA	2.00	0.43
1:FH:44:ASN:HB2	1:FH:78:LEU:HA	2.00	0.43
1:GG:75:PHE:HZ	1:GG:87:LYS:HB3	1.82	0.43
1:GQ:28:TYR:O	1:GQ:54:PRO:HG2	2.18	0.43
1:GT:32:LEU:CD1	1:GT:49:ILE:HG23	2.48	0.43
1:GU:26:ALA:HA	1:GU:29:MET:HB2	2.00	0.43
1:GU:44:ASN:HB2	1:GU:78:LEU:HA	2.00	0.43
1:HE:47:TYR:CZ	1:HU:105:ILE:HG12	2.53	0.43
1:HM:26:ALA:HA	1:HM:29:MET:HB2	2.00	0.43
1:HS:95:VAL:HG13	1:JL:95:VAL:HG13	2.00	0.43
1:JF:12:ILE:HA	1:JF:36:THR:OG1	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:2:ILE:HG23	1:BF:93:GLU:OE1	2.18	0.43
1:BJ:98:ILE:HD11	1:EV:73:LEU:HD22	2.01	0.43
1:BP:44:ASN:HB2	1:BP:78:LEU:HA	2.00	0.43
1:BZ:47:TYR:CZ	1:DT:105:ILE:HG12	2.53	0.43
1:CA:4:LYS:HA	1:CA:17:TYR:CD1	2.51	0.43
1:CA:32:LEU:CD1	1:CA:49:ILE:HG23	2.48	0.43
1:CW:12:ILE:HA	1:CW:36:THR:OG1	2.18	0.43
1:CX:83:ASN:HD22	1:DK:55:LEU:HD13	1.82	0.43
1:DA:75:PHE:HZ	1:DA:87:LYS:HB3	1.82	0.43
1:DC:34:ALA:HA	1:DC:48:LYS:O	2.17	0.43
1:DQ:32:LEU:CD1	1:DQ:49:ILE:HG23	2.48	0.43
1:DU:12:ILE:HA	1:DU:36:THR:OG1	2.18	0.43
1:DZ:28:TYR:O	1:DZ:54:PRO:HG2	2.18	0.43
1:EA:44:ASN:HB2	1:EA:78:LEU:HA	2.00	0.43
1:EJ:12:ILE:HA	1:EJ:36:THR:OG1	2.18	0.43
1:ET:73:LEU:HD13	1:FG:73:LEU:HD12	2.01	0.43
1:EU:32:LEU:CD1	1:EU:49:ILE:HG23	2.48	0.43
1:FA:4:LYS:HA	1:FA:17:TYR:CD1	2.51	0.43
1:FH:26:ALA:HA	1:FH:29:MET:HB2	2.00	0.43
1:FN:12:ILE:HA	1:FN:36:THR:OG1	2.17	0.43
1:FT:12:ILE:HA	1:FT:36:THR:OG1	2.18	0.43
1:GN:28:TYR:O	1:GN:54:PRO:HG2	2.18	0.43
1:GN:32:LEU:CD1	1:GN:49:ILE:HG23	2.48	0.43
1:GZ:28:TYR:O	1:GZ:54:PRO:HG2	2.18	0.43
1:HH:102:LYS:HG2	1:IV:88:LEU:HD23	2.01	0.43
1:HP:44:ASN:HB2	1:HP:78:LEU:HA	2.00	0.43
1:HS:34:ALA:HA	1:HS:48:LYS:O	2.17	0.43
1:HU:28:TYR:O	1:HU:54:PRO:HG2	2.18	0.43
1:IC:75:PHE:HZ	1:IC:87:LYS:HB3	1.82	0.43
1:ID:28:TYR:O	1:ID:54:PRO:HG2	2.18	0.43
1:IF:45:ILE:HD13	1:IJ:108:GLY:O	2.19	0.43
1:IN:26:ALA:HA	1:IN:29:MET:HB2	2.00	0.43
1:IO:73:LEU:HA	1:KI:72:ASN:O	2.18	0.43
1:IP:32:LEU:CD1	1:IP:49:ILE:HG23	2.48	0.43
1:IQ:12:ILE:HA	1:IQ:36:THR:OG1	2.17	0.43
1:IS:28:TYR:O	1:IS:54:PRO:HG2	2.18	0.43
1:IW:26:ALA:HA	1:IW:29:MET:HB2	2.00	0.43
1:JF:26:ALA:HA	1:JF:29:MET:HB2	2.00	0.43
1:JG:75:PHE:HZ	1:JG:87:LYS:HB3	1.82	0.43
1:JI:44:ASN:HB2	1:JI:78:LEU:HA	2.00	0.43
1:JX:26:ALA:HA	1:JX:29:MET:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KI:32:LEU:HD13	1:KI:51:VAL:HG22	2.01	0.43
1:AB:98:ILE:HD11	1:FX:73:LEU:CD2	2.48	0.43
1:AD:47:TYR:CE2	1:BC:105:ILE:HG12	2.54	0.43
1:AF:26:ALA:HA	1:AF:29:MET:HB2	2.00	0.43
1:AQ:28:TYR:O	1:AQ:54:PRO:HG2	2.18	0.43
1:AQ:32:LEU:CD1	1:AQ:49:ILE:HG23	2.48	0.43
1:AQ:32:LEU:HD13	1:AQ:51:VAL:HG22	2.01	0.43
1:AT:112:THR:HG21	1:EZ:4:LYS:HE2	2.01	0.43
1:AU:26:ALA:HA	1:AU:29:MET:HB2	2.00	0.43
1:BD:44:ASN:HB2	1:BD:78:LEU:HA	2.00	0.43
1:BN:75:PHE:HZ	1:BN:87:LYS:HB3	1.82	0.43
1:BU:32:LEU:HD13	1:BU:51:VAL:HG22	2.01	0.43
1:CF:73:LEU:HD13	1:GN:73:LEU:HD12	2.00	0.43
1:CK:98:ILE:HD11	1:FW:73:LEU:HD22	1.99	0.43
1:CP:28:TYR:O	1:CP:54:PRO:HG2	2.18	0.43
1:CQ:12:ILE:HA	1:CQ:36:THR:OG1	2.17	0.43
1:CU:45:ILE:HG23	1:CU:77:ALA:HB3	2.01	0.43
1:DO:26:ALA:HA	1:DO:29:MET:HB2	2.00	0.43
1:EH:73:LEU:CD2	1:EO:98:ILE:HD11	2.48	0.43
1:EK:73:LEU:HD13	1:ER:73:LEU:HD12	1.99	0.43
1:EP:26:ALA:HA	1:EP:29:MET:HB2	2.00	0.43
1:ER:28:TYR:O	1:ER:54:PRO:HG2	2.18	0.43
1:EX:28:TYR:O	1:EX:54:PRO:HG2	2.18	0.43
1:FD:32:LEU:CD1	1:FD:49:ILE:HG23	2.48	0.43
1:FE:26:ALA:HA	1:FE:29:MET:HB2	2.00	0.43
1:FK:44:ASN:HB2	1:FK:78:LEU:HA	2.00	0.43
1:GC:12:ILE:HA	1:GC:36:THR:OG1	2.17	0.43
1:GL:26:ALA:HA	1:GL:29:MET:HB2	2.00	0.43
1:GR:26:ALA:HA	1:GR:29:MET:HB2	2.00	0.43
1:GZ:32:LEU:HD13	1:GZ:51:VAL:HG22	2.01	0.43
1:HF:32:LEU:CD1	1:HF:49:ILE:HG23	2.48	0.43
1:HV:26:ALA:HA	1:HV:29:MET:HB2	2.00	0.43
1:HV:44:ASN:HB2	1:HV:78:LEU:HA	2.00	0.43
1:IE:12:ILE:HA	1:IE:36:THR:OG1	2.18	0.43
1:JR:12:ILE:HA	1:JR:36:THR:OG1	2.18	0.43
1:JT:32:LEU:CD1	1:JT:49:ILE:HG23	2.48	0.43
1:KA:26:ALA:HA	1:KA:29:MET:HB2	2.01	0.43
1:AG:106:ILE:HG21	1:BF:88:LEU:HG	2.01	0.43
1:AL:26:ALA:HA	1:AL:29:MET:HB2	2.00	0.43
1:AL:34:ALA:HA	1:AL:48:LYS:O	2.17	0.43
1:AN:32:LEU:CD1	1:AN:49:ILE:HG23	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:73:LEU:HD13	1:EA:73:LEU:HD13	2.00	0.43
1:AS:102:LYS:HG3	1:EL:91:LEU:HD13	1.99	0.43
1:AT:28:TYR:O	1:AT:54:PRO:HG2	2.18	0.43
1:AU:19:PHE:HB3	1:EG:89:ARG:NH2	2.34	0.43
1:BE:75:PHE:HZ	1:BE:87:LYS:HB3	1.82	0.43
1:BF:32:LEU:HD13	1:BF:51:VAL:HG22	2.01	0.43
1:BH:34:ALA:HA	1:BH:48:LYS:O	2.19	0.43
1:BL:32:LEU:CD1	1:BL:49:ILE:HG23	2.48	0.43
1:BO:32:LEU:HD13	1:BO:51:VAL:HG22	2.01	0.43
1:CD:32:LEU:CD1	1:CD:49:ILE:HG23	2.48	0.43
1:CD:75:PHE:HE2	1:CR:106:ILE:HA	1.83	0.43
1:CG:28:TYR:O	1:CG:54:PRO:HG2	2.18	0.43
1:CK:44:ASN:HB2	1:CK:78:LEU:HA	2.00	0.43
1:CS:4:LYS:HA	1:CS:17:TYR:CD1	2.51	0.43
1:CU:106:ILE:HA	1:DH:75:PHE:HE2	1.84	0.43
1:CY:28:TYR:O	1:CY:54:PRO:HG2	2.18	0.43
1:DF:106:ILE:HG21	1:GR:88:LEU:HD23	2.00	0.43
1:DK:32:LEU:HD13	1:DK:51:VAL:HG22	2.01	0.43
1:EA:26:ALA:HA	1:EA:29:MET:HB2	2.01	0.43
1:EF:28:TYR:O	1:EF:54:PRO:HG2	2.18	0.43
1:EI:28:TYR:O	1:EI:54:PRO:HG2	2.18	0.43
1:EV:26:ALA:HA	1:EV:29:MET:HB2	2.00	0.43
1:FA:28:TYR:O	1:FA:54:PRO:HG2	2.18	0.43
1:FA:32:LEU:HD13	1:FA:51:VAL:HG22	2.01	0.43
1:GE:28:TYR:O	1:GE:54:PRO:HG2	2.18	0.43
1:GE:32:LEU:HD13	1:GE:51:VAL:HG22	2.01	0.43
1:GI:44:ASN:HB2	1:GI:78:LEU:HA	2.00	0.43
1:GO:26:ALA:HA	1:GO:29:MET:HB2	2.00	0.43
1:GR:12:ILE:HA	1:GR:36:THR:OG1	2.17	0.43
1:GW:32:LEU:HD13	1:GW:51:VAL:HG22	2.01	0.43
1:GY:45:ILE:HD13	1:HO:108:GLY:O	2.18	0.43
1:HI:28:TYR:O	1:HI:54:PRO:HG2	2.18	0.43
1:HJ:12:ILE:HA	1:HJ:36:THR:OG1	2.17	0.43
1:IM:32:LEU:HD13	1:IM:51:VAL:HG22	2.01	0.43
1:IT:44:ASN:HB2	1:IT:78:LEU:HA	2.00	0.43
1:IX:45:ILE:HG21	1:JB:108:GLY:HA3	2.01	0.43
1:JE:32:LEU:CD1	1:JE:49:ILE:HG23	2.48	0.43
1:JE:32:LEU:HD13	1:JE:51:VAL:HG22	2.01	0.43
1:JH:28:TYR:O	1:JH:54:PRO:HG2	2.18	0.43
1:JH:32:LEU:CD1	1:JH:49:ILE:HG23	2.48	0.43
1:JK:73:LEU:HD13	1:JM:98:ILE:CD1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JU:12:ILE:HA	1:JU:36:THR:OG1	2.18	0.43
1:KG:44:ASN:HB2	1:KG:78:LEU:HA	2.00	0.43
1:AC:73:LEU:HD22	1:DO:98:ILE:HD11	2.00	0.43
1:AG:34:ALA:HA	1:AG:48:LYS:O	2.19	0.43
1:AG:45:ILE:HG23	1:AG:77:ALA:HB3	2.01	0.43
1:AG:69:ILE:CG2	1:BF:90:VAL:HG21	2.49	0.43
1:AH:32:LEU:HD13	1:AH:51:VAL:HG22	2.01	0.43
1:AW:4:LYS:HA	1:AW:17:TYR:CD1	2.51	0.43
1:BB:75:PHE:HZ	1:BB:87:LYS:HB3	1.82	0.43
1:BT:45:ILE:HG23	1:BT:77:ALA:HB3	2.01	0.43
1:BY:44:ASN:HB2	1:BY:78:LEU:HA	2.00	0.43
1:CF:34:ALA:HA	1:CF:48:LYS:O	2.19	0.43
1:CJ:88:LEU:HG	1:CO:106:ILE:HG21	2.01	0.43
1:CN:26:ALA:HA	1:CN:29:MET:HB2	2.00	0.43
1:CT:98:ILE:HD11	1:GF:73:LEU:HD22	2.00	0.43
1:DH:32:LEU:HD13	1:DH:51:VAL:HG22	2.01	0.43
1:DM:110:VAL:HB	1:GT:36:THR:HG23	1.99	0.43
1:DT:28:TYR:O	1:DT:54:PRO:HG2	2.18	0.43
1:EU:32:LEU:HD13	1:EU:51:VAL:HG22	2.01	0.43
1:EX:32:LEU:HD13	1:EX:51:VAL:HG22	2.01	0.43
1:FI:75:PHE:HZ	1:FI:87:LYS:HB3	1.83	0.43
1:FM:28:TYR:O	1:FM:54:PRO:HG2	2.18	0.43
1:GF:26:ALA:HA	1:GF:29:MET:HB2	2.01	0.43
1:GK:32:LEU:CD1	1:GK:49:ILE:HG23	2.48	0.43
1:GL:12:ILE:HA	1:GL:36:THR:OG1	2.18	0.43
1:HB:110:VAL:HA	1:HX:47:TYR:HE1	1.84	0.43
1:HE:78:LEU:HD12	1:HU:69:ILE:HG12	2.00	0.43
1:HF:28:TYR:O	1:HF:54:PRO:HG2	2.18	0.43
1:HF:32:LEU:HD13	1:HF:51:VAL:HG22	2.01	0.43
1:HQ:45:ILE:HD13	1:IS:108:GLY:O	2.18	0.43
1:HT:34:ALA:HA	1:HT:48:LYS:O	2.19	0.43
1:IA:72:ASN:O	1:IC:73:LEU:HA	2.18	0.43
1:IB:12:ILE:HA	1:IB:36:THR:OG1	2.17	0.43
1:ID:32:LEU:HD13	1:ID:51:VAL:HG22	2.01	0.43
1:IL:34:ALA:HA	1:IL:48:LYS:O	2.19	0.43
1:IM:4:LYS:HA	1:IM:17:TYR:CD1	2.51	0.43
1:IM:28:TYR:O	1:IM:54:PRO:HG2	2.18	0.43
1:IT:26:ALA:HA	1:IT:29:MET:HB2	2.00	0.43
1:IX:45:ILE:HG23	1:IX:77:ALA:HB3	2.01	0.43
1:JA:102:LYS:HG3	1:JQ:91:LEU:CD1	2.49	0.43
1:JD:34:ALA:HA	1:JD:48:LYS:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JM:34:ALA:HA	1:JM:48:LYS:O	2.19	0.43
1:JS:34:ALA:HA	1:JS:48:LYS:O	2.19	0.43
1:JT:108:GLY:HA3	1:KH:45:ILE:CG2	2.48	0.43
1:JX:44:ASN:HB2	1:JX:78:LEU:HA	2.00	0.43
1:JZ:32:LEU:HD13	1:JZ:51:VAL:HG22	2.01	0.43
1:KB:34:ALA:HA	1:KB:48:LYS:O	2.19	0.43
1:KF:28:TYR:O	1:KF:54:PRO:HG2	2.18	0.43
1:KJ:26:ALA:HA	1:KJ:29:MET:HB2	2.00	0.43
1:AD:34:ALA:HA	1:AD:48:LYS:O	2.19	0.43
1:AD:45:ILE:HG23	1:AD:77:ALA:HB3	2.01	0.43
1:AE:32:LEU:CD1	1:AE:49:ILE:HG23	2.48	0.43
1:AF:44:ASN:HB2	1:AF:78:LEU:HA	2.00	0.43
1:AQ:2:ILE:HG23	1:FU:93:GLU:OE1	2.18	0.43
1:AY:34:ALA:HA	1:AY:48:LYS:O	2.19	0.43
1:BB:34:ALA:HA	1:BB:48:LYS:O	2.19	0.43
1:BV:12:ILE:HA	1:BV:36:THR:OG1	2.17	0.43
1:BW:45:ILE:HG23	1:BW:77:ALA:HB3	2.01	0.43
1:CA:32:LEU:HD13	1:CA:51:VAL:HG22	2.01	0.43
1:CB:26:ALA:HA	1:CB:29:MET:HB2	2.01	0.43
1:CG:105:ILE:HG12	1:CL:47:TYR:CE2	2.54	0.43
1:CH:95:VAL:HG13	1:FT:95:VAL:HG13	2.00	0.43
1:CS:28:TYR:O	1:CS:54:PRO:HG2	2.18	0.43
1:CW:44:ASN:HB2	1:CW:78:LEU:HA	2.00	0.43
1:DA:34:ALA:HA	1:DA:48:LYS:O	2.19	0.43
1:DM:110:VAL:HG12	1:GT:11:PRO:O	2.18	0.43
1:DS:34:ALA:HA	1:DS:48:LYS:O	2.19	0.43
1:EB:45:ILE:HG23	1:EB:77:ALA:HB3	2.01	0.43
1:EC:32:LEU:CD1	1:EC:49:ILE:HG23	2.48	0.43
1:ET:75:PHE:HZ	1:ET:87:LYS:HB3	1.82	0.43
1:EV:44:ASN:HB2	1:EV:78:LEU:HA	2.00	0.43
1:FH:12:ILE:HA	1:FH:36:THR:OG1	2.17	0.43
1:FO:34:ALA:HA	1:FO:48:LYS:O	2.19	0.43
1:GG:45:ILE:HG23	1:GG:77:ALA:HB3	2.01	0.43
1:GJ:45:ILE:HG23	1:GJ:77:ALA:HB3	2.01	0.43
1:GK:32:LEU:HD13	1:GK:51:VAL:HG22	2.01	0.43
1:GY:51:VAL:HG11	1:HO:90:VAL:HG13	2.00	0.43
1:HB:75:PHE:HZ	1:HB:87:LYS:HB3	1.82	0.43
1:HD:44:ASN:HB2	1:HD:78:LEU:HA	2.00	0.43
1:HH:45:ILE:HG23	1:HH:77:ALA:HB3	2.01	0.43
1:HL:28:TYR:O	1:HL:54:PRO:HG2	2.18	0.43
1:HN:106:ILE:HD13	1:HR:88:LEU:HG	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HP:26:ALA:HA	1:HP:29:MET:HB2	2.00	0.43
1:HQ:34:ALA:HA	1:HQ:48:LYS:O	2.19	0.43
1:HT:90:VAL:HG13	1:IM:51:VAL:CG1	2.48	0.43
1:HW:45:ILE:HG23	1:HW:77:ALA:HB3	2.01	0.43
1:HZ:34:ALA:HA	1:HZ:48:LYS:O	2.19	0.43
1:IC:34:ALA:HA	1:IC:48:LYS:O	2.19	0.43
1:IH:26:ALA:HA	1:IH:29:MET:HB2	2.00	0.43
1:II:45:ILE:HG23	1:II:77:ALA:HB3	2.01	0.43
1:IJ:32:LEU:CD1	1:IJ:49:ILE:HG23	2.48	0.43
1:IL:73:LEU:HD12	1:KF:72:ASN:O	2.19	0.43
1:IO:95:VAL:HG11	1:KI:99:THR:CG2	2.49	0.43
1:JA:45:ILE:HG23	1:JA:77:ALA:HB3	2.01	0.43
1:JG:45:ILE:HG23	1:JG:77:ALA:HB3	2.01	0.43
1:JH:73:LEU:HB2	1:JP:73:LEU:HD13	2.00	0.43
1:JT:73:LEU:HD13	1:KH:98:ILE:CD1	2.48	0.43
1:JY:45:ILE:HG23	1:JY:77:ALA:HB3	2.01	0.43
1:KC:32:LEU:CD1	1:KC:49:ILE:HG23	2.48	0.43
1:KH:45:ILE:HG23	1:KH:77:ALA:HB3	2.01	0.43
1:AE:32:LEU:HD13	1:AE:51:VAL:HG22	2.01	0.43
1:AE:59:VAL:HG11	1:GB:60:ASP:HB3	2.00	0.43
1:AN:74:SER:O	1:FR:71:ALA:HA	2.18	0.43
1:AQ:108:GLY:O	1:FU:45:ILE:HD13	2.19	0.43
1:AU:110:VAL:HB	1:EG:36:THR:HG23	2.00	0.43
1:BI:32:LEU:HD13	1:BI:51:VAL:HG22	2.01	0.43
1:BZ:34:ALA:HA	1:BZ:48:LYS:O	2.19	0.43
1:CC:34:ALA:HA	1:CC:48:LYS:O	2.19	0.43
1:CH:108:GLY:HA3	1:FT:45:ILE:HB	2.01	0.43
1:CK:26:ALA:HA	1:CK:29:MET:HB2	2.00	0.43
1:CM:47:TYR:HE1	1:DG:109:ASN:O	2.02	0.43
1:CW:95:VAL:HG11	1:GI:99:THR:CG2	2.48	0.43
1:CX:34:ALA:HA	1:CX:48:LYS:O	2.19	0.43
1:CZ:51:VAL:HG11	1:GL:90:VAL:HG13	2.01	0.43
1:DD:34:ALA:HA	1:DD:48:LYS:O	2.19	0.43
1:DI:44:ASN:HB2	1:DI:78:LEU:HA	2.00	0.43
1:DV:17:TYR:OH	1:GE:112:THR:HG22	2.19	0.43
1:DX:26:ALA:HA	1:DX:29:MET:HB2	2.00	0.43
1:EF:32:LEU:CD1	1:EF:49:ILE:HG23	2.48	0.43
1:EK:95:VAL:HG11	1:ER:99:THR:HG23	2.01	0.43
1:ES:26:ALA:HA	1:ES:29:MET:HB2	2.00	0.43
1:ET:45:ILE:HG23	1:ET:77:ALA:HB3	2.01	0.43
1:EY:44:ASN:HB2	1:EY:78:LEU:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FI:45:ILE:HG23	1:FI:77:ALA:HB3	2.01	0.43
1:FL:34:ALA:HA	1:FL:48:LYS:O	2.19	0.43
1:FP:32:LEU:HD13	1:FP:51:VAL:HG22	2.01	0.43
1:FQ:12:ILE:HA	1:FQ:36:THR:OG1	2.18	0.43
1:FV:32:LEU:HD13	1:FV:51:VAL:HG22	2.01	0.43
1:FV:32:LEU:CD1	1:FV:49:ILE:HG23	2.48	0.43
1:FX:34:ALA:HA	1:FX:48:LYS:O	2.19	0.43
1:GB:32:LEU:HD13	1:GB:51:VAL:HG22	2.01	0.43
1:GL:44:ASN:HB2	1:GL:78:LEU:HA	2.00	0.43
1:GM:45:ILE:HG23	1:GM:77:ALA:HB3	2.01	0.43
1:HC:95:VAL:HG13	1:JS:95:VAL:HG13	2.00	0.43
1:HE:45:ILE:HG23	1:HE:77:ALA:HB3	2.01	0.43
1:HQ:45:ILE:HG23	1:HQ:77:ALA:HB3	2.01	0.43
1:HQ:75:PHE:HZ	1:HQ:87:LYS:HB3	1.82	0.43
1:HS:26:ALA:HA	1:HS:29:MET:HB2	2.00	0.43
1:HS:44:ASN:HB2	1:HS:78:LEU:HA	2.00	0.43
1:HT:75:PHE:HZ	1:HT:87:LYS:HB3	1.82	0.43
1:IG:4:LYS:HA	1:IG:17:TYR:CD1	2.51	0.43
1:IU:45:ILE:HG23	1:IU:77:ALA:HB3	2.01	0.43
1:IX:34:ALA:HA	1:IX:48:LYS:O	2.19	0.43
1:JE:28:TYR:O	1:JE:54:PRO:HG2	2.18	0.43
1:JM:45:ILE:HG23	1:JM:77:ALA:HB3	2.01	0.43
1:JV:34:ALA:HA	1:JV:48:LYS:O	2.19	0.43
1:KB:75:PHE:HZ	1:KB:87:LYS:HB3	1.83	0.43
1:AP:106:ILE:HD13	1:BU:88:LEU:HG	2.01	0.43
1:AQ:17:TYR:OH	1:FU:112:THR:CG2	2.67	0.43
1:AY:45:ILE:HG23	1:AY:77:ALA:HB3	2.01	0.43
1:AY:102:LYS:HG3	1:EI:91:LEU:HD13	2.00	0.43
1:BD:26:ALA:HA	1:BD:29:MET:HB2	2.00	0.43
1:BN:34:ALA:HA	1:BN:48:LYS:O	2.19	0.43
1:BZ:45:ILE:HG23	1:BZ:77:ALA:HB3	2.01	0.43
1:CD:32:LEU:HD13	1:CD:51:VAL:HG22	2.01	0.43
1:CF:44:ASN:OD1	1:CF:44:ASN:C	2.62	0.43
1:CG:73:LEU:HD12	1:CL:73:LEU:HD13	1.99	0.43
1:CM:88:LEU:HG	1:DG:106:ILE:HD13	1.99	0.43
1:CQ:26:ALA:HA	1:CQ:29:MET:HB2	2.00	0.43
1:CR:45:ILE:HG23	1:CR:77:ALA:HB3	2.01	0.43
1:CT:83:ASN:OD1	1:GF:55:LEU:HD13	2.18	0.43
1:DL:88:LEU:HD22	1:GX:102:LYS:HG2	2.01	0.43
1:DL:95:VAL:HG11	1:GX:99:THR:HG23	2.01	0.43
1:DN:32:LEU:HD13	1:DN:51:VAL:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:34:ALA:HA	1:DP:48:LYS:O	2.19	0.43
1:DV:34:ALA:HA	1:DV:48:LYS:O	2.19	0.43
1:DW:32:LEU:CD1	1:DW:49:ILE:HG23	2.48	0.43
1:EI:32:LEU:HD13	1:EI:51:VAL:HG22	2.01	0.43
1:EK:34:ALA:HA	1:EK:48:LYS:O	2.19	0.43
1:EZ:34:ALA:HA	1:EZ:48:LYS:O	2.19	0.43
1:FD:4:LYS:HA	1:FD:17:TYR:CD1	2.51	0.43
1:GD:34:ALA:HA	1:GD:48:LYS:O	2.19	0.43
1:GN:32:LEU:HD13	1:GN:51:VAL:HG22	2.01	0.43
1:GQ:4:LYS:HA	1:GQ:17:TYR:CD1	2.51	0.43
1:GS:45:ILE:HG23	1:GS:77:ALA:HB3	2.01	0.43
1:HH:34:ALA:HA	1:HH:48:LYS:O	2.19	0.43
1:HM:44:ASN:HB2	1:HM:78:LEU:HA	2.00	0.43
1:HR:32:LEU:HD13	1:HR:51:VAL:HG22	2.01	0.43
1:HT:71:ALA:HB2	1:IM:75:PHE:CD1	2.50	0.43
1:HV:112:THR:CG2	1:JO:17:TYR:OH	2.66	0.43
1:IH:44:ASN:HB2	1:IH:78:LEU:HA	2.00	0.43
1:IJ:32:LEU:HD13	1:IJ:51:VAL:HG22	2.01	0.43
1:IZ:44:ASN:HB2	1:IZ:78:LEU:HA	2.00	0.43
1:JB:32:LEU:CD1	1:JB:49:ILE:HG23	2.48	0.43
1:JB:32:LEU:HD13	1:JB:51:VAL:HG22	2.01	0.43
1:JL:26:ALA:HA	1:JL:29:MET:HB2	2.01	0.43
1:JQ:32:LEU:HD13	1:JQ:51:VAL:HG22	2.01	0.43
1:JW:32:LEU:CD1	1:JW:49:ILE:HG23	2.48	0.43
1:KE:45:ILE:HG23	1:KE:77:ALA:HB3	2.01	0.43
1:AI:44:ASN:HB2	1:AI:78:LEU:HA	2.00	0.42
1:AV:83:ASN:ND2	1:EF:55:LEU:HD13	2.34	0.42
1:BG:44:ASN:HB2	1:BG:78:LEU:HA	2.00	0.42
1:BL:32:LEU:HD13	1:BL:51:VAL:HG22	2.01	0.42
1:BO:32:LEU:CD1	1:BO:49:ILE:HG23	2.48	0.42
1:BP:26:ALA:HA	1:BP:29:MET:HB2	2.00	0.42
1:BX:32:LEU:CD1	1:BX:49:ILE:HG23	2.48	0.42
1:CI:2:ILE:HD13	1:CI:32:LEU:HD23	2.01	0.42
1:CY:93:GLU:OE1	1:GG:2:ILE:HG23	2.17	0.42
1:DA:44:ASN:OD1	1:DA:44:ASN:C	2.62	0.42
1:DM:34:ALA:HA	1:DM:48:LYS:O	2.19	0.42
1:DM:98:ILE:CD1	1:GT:73:LEU:HD13	2.49	0.42
1:DY:97:PHE:CD1	1:FY:32:LEU:HD21	2.54	0.42
1:ED:26:ALA:HA	1:ED:29:MET:HB2	2.00	0.42
1:EL:32:LEU:HD13	1:EL:51:VAL:HG22	2.01	0.42
1:EN:45:ILE:HG23	1:EN:77:ALA:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EX:95:VAL:HG11	1:FI:99:THR:CG2	2.49	0.42
1:FM:32:LEU:HD13	1:FM:51:VAL:HG22	2.01	0.42
1:FP:74:SER:O	1:GV:71:ALA:HA	2.19	0.42
1:FS:32:LEU:CD1	1:FS:49:ILE:HG23	2.48	0.42
1:GT:32:LEU:HD13	1:GT:51:VAL:HG22	2.01	0.42
1:GY:94:ILE:HG13	1:HO:49:ILE:HG21	2.01	0.42
1:HB:34:ALA:HA	1:HB:48:LYS:O	2.19	0.42
1:HC:32:LEU:HD13	1:HC:51:VAL:HG22	2.01	0.42
1:HH:75:PHE:HZ	1:HH:87:LYS:HB3	1.82	0.42
1:HK:44:ASN:OD1	1:HK:44:ASN:C	2.62	0.42
1:HO:32:LEU:HD13	1:HO:51:VAL:HG22	2.01	0.42
1:HS:106:ILE:HG21	1:JL:88:LEU:HD23	2.00	0.42
1:HV:72:ASN:O	1:JO:73:LEU:HA	2.18	0.42
1:IF:45:ILE:HG23	1:IF:77:ALA:HB3	2.01	0.42
1:IQ:44:ASN:HB2	1:IQ:78:LEU:HA	2.00	0.42
1:IR:75:PHE:HZ	1:IR:87:LYS:HB3	1.82	0.42
1:IU:34:ALA:HA	1:IU:48:LYS:O	2.19	0.42
1:JA:97:PHE:CG	1:JQ:32:LEU:HD21	2.54	0.42
1:JH:32:LEU:HD13	1:JH:51:VAL:HG22	2.01	0.42
1:JI:26:ALA:HA	1:JI:29:MET:HB2	2.00	0.42
1:JP:34:ALA:HA	1:JP:48:LYS:O	2.19	0.42
1:JP:44:ASN:OD1	1:JP:44:ASN:C	2.62	0.42
1:JQ:28:TYR:O	1:JQ:54:PRO:HG2	2.18	0.42
1:JR:44:ASN:HB2	1:JR:78:LEU:HA	2.00	0.42
1:JT:2:ILE:HG23	1:KH:93:GLU:OE1	2.19	0.42
1:JY:44:ASN:OD1	1:JY:44:ASN:C	2.62	0.42
1:KH:75:PHE:HZ	1:KH:87:LYS:HB3	1.82	0.42
1:AC:26:ALA:HA	1:AC:29:MET:HB2	2.00	0.42
1:AD:2:ILE:HD13	1:AD:32:LEU:HD23	2.01	0.42
1:AF:88:LEU:HD23	1:DR:106:ILE:HG21	2.01	0.42
1:AG:44:ASN:OD1	1:AG:44:ASN:C	2.62	0.42
1:AI:12:ILE:HA	1:AI:36:THR:OG1	2.17	0.42
1:AN:32:LEU:HD13	1:AN:51:VAL:HG22	2.01	0.42
1:AP:34:ALA:HA	1:AP:48:LYS:O	2.19	0.42
1:BA:26:ALA:HA	1:BA:29:MET:HB2	2.00	0.42
1:BC:32:LEU:HD13	1:BC:51:VAL:HG22	2.01	0.42
1:BG:51:VAL:HG11	1:ES:90:VAL:HG13	2.01	0.42
1:BZ:75:PHE:HZ	1:BZ:87:LYS:HB3	1.83	0.42
1:CD:47:TYR:CE2	1:CR:105:ILE:HG12	2.54	0.42
1:CR:34:ALA:HA	1:CR:48:LYS:O	2.19	0.42
1:CY:89:ARG:NH2	1:GG:19:PHE:HB3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DB:32:LEU:HD13	1:DB:51:VAL:HG22	2.01	0.42
1:DG:2:ILE:HD13	1:DG:32:LEU:HD23	2.02	0.42
1:DI:26:ALA:HA	1:DI:29:MET:HB2	2.00	0.42
1:DP:45:ILE:HG23	1:DP:77:ALA:HB3	2.01	0.42
1:DW:32:LEU:HD13	1:DW:51:VAL:HG22	2.01	0.42
1:EE:2:ILE:HD13	1:EE:32:LEU:HD23	2.01	0.42
1:EH:34:ALA:HA	1:EH:48:LYS:O	2.19	0.42
1:EK:95:VAL:HG11	1:ER:99:THR:CG2	2.49	0.42
1:EW:2:ILE:HD13	1:EW:32:LEU:HD23	2.01	0.42
1:EW:44:ASN:OD1	1:EW:44:ASN:C	2.62	0.42
1:FQ:26:ALA:HA	1:FQ:29:MET:HB2	2.00	0.42
1:FV:90:VAL:HG21	1:GS:69:ILE:CG2	2.49	0.42
1:FW:26:ALA:HA	1:FW:29:MET:HB2	2.00	0.42
1:GM:34:ALA:HA	1:GM:48:LYS:O	2.19	0.42
1:GO:44:ASN:HB2	1:GO:78:LEU:HA	2.00	0.42
1:GY:34:ALA:HA	1:GY:48:LYS:O	2.19	0.42
1:HD:26:ALA:HA	1:HD:29:MET:HB2	2.00	0.42
1:HJ:26:ALA:HA	1:HJ:29:MET:HB2	2.00	0.42
1:HK:51:VAL:HG11	1:IY:90:VAL:HG13	2.00	0.42
1:HS:21:GLY:H	1:JL:89:ARG:HH22	1.67	0.42
1:HT:44:ASN:C	1:HT:44:ASN:OD1	2.62	0.42
1:HT:69:ILE:HG12	1:IM:78:LEU:HD12	2.01	0.42
1:IE:26:ALA:HA	1:IE:29:MET:HB2	2.00	0.42
1:II:34:ALA:HA	1:II:48:LYS:O	2.19	0.42
1:IO:44:ASN:OD1	1:IO:44:ASN:C	2.62	0.42
1:IP:32:LEU:HD13	1:IP:51:VAL:HG22	2.01	0.42
1:IV:32:LEU:HD13	1:IV:51:VAL:HG22	2.01	0.42
1:JG:34:ALA:HA	1:JG:48:LYS:O	2.19	0.42
1:JP:45:ILE:HG23	1:JP:77:ALA:HB3	2.01	0.42
1:JQ:32:LEU:CD1	1:JQ:49:ILE:HG23	2.48	0.42
1:JU:26:ALA:HA	1:JU:29:MET:HB2	2.00	0.42
1:KA:44:ASN:HB2	1:KA:78:LEU:HA	2.00	0.42
1:KE:34:ALA:HA	1:KE:48:LYS:O	2.19	0.42
1:KH:34:ALA:HA	1:KH:48:LYS:O	2.19	0.42
1:AD:73:LEU:HD13	1:BC:73:LEU:HD12	2.01	0.42
1:AH:28:TYR:O	1:AH:54:PRO:HG2	2.18	0.42
1:AK:32:LEU:HD13	1:AK:51:VAL:HG22	2.01	0.42
1:AM:34:ALA:HA	1:AM:48:LYS:O	2.19	0.42
1:AR:26:ALA:HA	1:AR:29:MET:HB2	2.00	0.42
1:AU:72:ASN:O	1:EG:73:LEU:HD12	2.19	0.42
1:AV:32:LEU:HD21	1:EF:97:PHE:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:95:VAL:HG13	1:BO:95:VAL:HG13	2.01	0.42
1:BK:44:ASN:OD1	1:BK:44:ASN:C	2.62	0.42
1:BK:45:ILE:HG23	1:BK:77:ALA:HB3	2.01	0.42
1:BQ:45:ILE:HG23	1:BQ:77:ALA:HB3	2.01	0.42
1:BV:44:ASN:HB2	1:BV:78:LEU:HA	2.00	0.42
1:CC:2:ILE:HD13	1:CC:32:LEU:HD23	2.02	0.42
1:CD:36:THR:HG23	1:CR:110:VAL:HB	2.01	0.42
1:CJ:32:LEU:CD1	1:CJ:49:ILE:HG23	2.48	0.42
1:CO:34:ALA:HA	1:CO:48:LYS:O	2.19	0.42
1:CZ:73:LEU:HA	1:GL:72:ASN:O	2.20	0.42
1:DG:45:ILE:HG23	1:DG:77:ALA:HB3	2.01	0.42
1:DJ:34:ALA:HA	1:DJ:48:LYS:O	2.19	0.42
1:DJ:45:ILE:HG23	1:DJ:77:ALA:HB3	2.01	0.42
1:DL:95:VAL:HG11	1:GX:99:THR:CG2	2.49	0.42
1:DR:44:ASN:HB2	1:DR:78:LEU:HA	2.00	0.42
1:DY:34:ALA:HA	1:DY:48:LYS:O	2.19	0.42
1:DY:44:ASN:OD1	1:DY:44:ASN:C	2.62	0.42
1:DZ:32:LEU:CD1	1:DZ:49:ILE:HG23	2.48	0.42
1:EB:34:ALA:HA	1:EB:48:LYS:O	2.19	0.42
1:EF:32:LEU:HD13	1:EF:51:VAL:HG22	2.01	0.42
1:EH:2:ILE:HD13	1:EH:32:LEU:HD23	2.02	0.42
1:EK:45:ILE:HG23	1:EK:77:ALA:HB3	2.01	0.42
1:EL:32:LEU:CD1	1:EL:49:ILE:HG23	2.48	0.42
1:EN:75:PHE:HZ	1:EN:87:LYS:HB3	1.82	0.42
1:EQ:34:ALA:HA	1:EQ:48:LYS:O	2.19	0.42
1:FK:26:ALA:HA	1:FK:29:MET:HB2	2.00	0.42
1:FL:45:ILE:HG23	1:FL:77:ALA:HB3	2.01	0.42
1:FU:34:ALA:HA	1:FU:48:LYS:O	2.19	0.42
1:GA:2:ILE:HD13	1:GA:32:LEU:HD23	2.01	0.42
1:GJ:2:ILE:HD13	1:GJ:32:LEU:HD23	2.02	0.42
1:GJ:34:ALA:HA	1:GJ:48:LYS:O	2.19	0.42
1:GJ:44:ASN:OD1	1:GJ:44:ASN:C	2.62	0.42
1:GN:4:LYS:HA	1:GN:17:TYR:CD1	2.51	0.42
1:GP:75:PHE:HZ	1:GP:87:LYS:HB3	1.82	0.42
1:GV:45:ILE:HG23	1:GV:77:ALA:HB3	2.01	0.42
1:HG:26:ALA:HA	1:HG:29:MET:HB2	2.00	0.42
1:HI:55:LEU:HD13	1:JJ:83:ASN:ND2	2.34	0.42
1:IA:32:LEU:CD1	1:IA:49:ILE:HG23	2.48	0.42
1:IE:44:ASN:HB2	1:IE:78:LEU:HA	2.00	0.42
1:IU:105:ILE:HG23	1:JE:47:TYR:CG	2.55	0.42
1:IU:109:ASN:CG	1:JE:11:PRO:HB3	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IV:32:LEU:CD1	1:IV:49:ILE:HG23	2.48	0.42
1:IZ:26:ALA:HA	1:IZ:29:MET:HB2	2.00	0.42
1:JG:2:ILE:HD13	1:JG:32:LEU:HD23	2.01	0.42
1:JH:95:VAL:HG11	1:JP:99:THR:CG2	2.49	0.42
1:JJ:45:ILE:HG23	1:JJ:77:ALA:HB3	2.01	0.42
1:JK:28:TYR:O	1:JK:54:PRO:HG2	2.18	0.42
1:JY:34:ALA:HA	1:JY:48:LYS:O	2.19	0.42
1:AA:45:ILE:HG23	1:AA:77:ALA:HB3	2.01	0.42
1:AA:89:ARG:HH22	1:BI:21:GLY:H	1.66	0.42
1:AD:44:ASN:OD1	1:AD:44:ASN:C	2.62	0.42
1:AJ:2:ILE:HD13	1:AJ:32:LEU:HD23	2.02	0.42
1:AS:44:ASN:OD1	1:AS:44:ASN:C	2.62	0.42
1:BE:45:ILE:HG23	1:BE:77:ALA:HB3	2.01	0.42
1:CB:44:ASN:HB2	1:CB:78:LEU:HA	2.00	0.42
1:CC:4:LYS:HE2	1:GK:112:THR:HG21	2.01	0.42
1:CC:94:ILE:HG13	1:GK:49:ILE:HG21	2.01	0.42
1:CC:106:ILE:HG21	1:GK:88:LEU:HG	2.01	0.42
1:CL:34:ALA:HA	1:CL:48:LYS:O	2.19	0.42
1:CP:32:LEU:CD1	1:CP:49:ILE:HG23	2.48	0.42
1:CP:32:LEU:HD13	1:CP:51:VAL:HG22	2.01	0.42
1:CR:44:ASN:OD1	1:CR:44:ASN:C	2.62	0.42
1:CU:110:VAL:HA	1:DH:47:TYR:CE1	2.54	0.42
1:CW:26:ALA:HA	1:CW:29:MET:HB2	2.00	0.42
1:CX:98:ILE:CD1	1:DK:73:LEU:HD13	2.50	0.42
1:DM:45:ILE:HG23	1:DM:77:ALA:HB3	2.01	0.42
1:DY:36:THR:HG23	1:FY:110:VAL:HB	2.00	0.42
1:EJ:44:ASN:HB2	1:EJ:78:LEU:HA	2.00	0.42
1:EO:32:LEU:HD13	1:EO:51:VAL:HG22	2.01	0.42
1:ET:34:ALA:HA	1:ET:48:LYS:O	2.19	0.42
1:FB:26:ALA:HA	1:FB:29:MET:HB2	2.01	0.42
1:FC:34:ALA:HA	1:FC:48:LYS:O	2.19	0.42
1:FC:44:ASN:OD1	1:FC:44:ASN:C	2.62	0.42
1:FC:45:ILE:HG23	1:FC:77:ALA:HB3	2.01	0.42
1:FU:2:ILE:HD13	1:FU:32:LEU:HD23	2.01	0.42
1:FX:44:ASN:OD1	1:FX:44:ASN:C	2.62	0.42
1:GP:44:ASN:OD1	1:GP:44:ASN:C	2.62	0.42
1:HA:26:ALA:HA	1:HA:29:MET:HB2	2.00	0.42
1:HI:32:LEU:CD1	1:HI:49:ILE:HG23	2.48	0.42
1:HT:55:LEU:CD1	1:IM:81:VAL:HG21	2.49	0.42
1:HU:32:LEU:HD13	1:HU:51:VAL:HG22	2.01	0.42
1:IG:32:LEU:HD13	1:IG:51:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IG:72:ASN:O	1:KB:73:LEU:HD12	2.18	0.42
1:IN:44:ASN:HB2	1:IN:78:LEU:HA	2.00	0.42
1:JA:2:ILE:HD13	1:JA:32:LEU:HD23	2.01	0.42
1:JG:44:ASN:OD1	1:JG:44:ASN:C	2.62	0.42
1:JL:44:ASN:HB2	1:JL:78:LEU:HA	2.00	0.42
1:JV:45:ILE:HG23	1:JV:77:ALA:HB3	2.01	0.42
1:JY:2:ILE:HD13	1:JY:32:LEU:HD23	2.02	0.42
1:AA:2:ILE:HD13	1:AA:32:LEU:HD23	2.02	0.42
1:AA:34:ALA:HA	1:AA:48:LYS:O	2.19	0.42
1:AA:95:VAL:HG13	1:BI:95:VAL:HG13	2.02	0.42
1:AB:32:LEU:HD13	1:AB:51:VAL:HG22	2.01	0.42
1:AK:32:LEU:CD1	1:AK:49:ILE:HG23	2.48	0.42
1:AS:51:VAL:HG11	1:EL:90:VAL:HG13	2.01	0.42
1:AV:45:ILE:HG23	1:AV:77:ALA:HB3	2.01	0.42
1:AZ:112:THR:HG21	1:EW:4:LYS:HE2	2.01	0.42
1:BQ:2:ILE:HD13	1:BQ:32:LEU:HD23	2.01	0.42
1:BV:89:ARG:HH22	1:FH:21:GLY:H	1.67	0.42
1:BY:26:ALA:HA	1:BY:29:MET:HB2	2.00	0.42
1:BZ:36:THR:HG23	1:DT:110:VAL:HB	2.01	0.42
1:CC:44:ASN:OD1	1:CC:44:ASN:C	2.62	0.42
1:CE:26:ALA:HA	1:CE:29:MET:HB2	2.00	0.42
1:CO:45:ILE:HG23	1:CO:77:ALA:HB3	2.01	0.42
1:CP:4:LYS:HA	1:CP:17:TYR:CD1	2.51	0.42
1:CT:26:ALA:HA	1:CT:29:MET:HB2	2.00	0.42
1:CV:32:LEU:HD13	1:CV:51:VAL:HG22	2.01	0.42
1:CX:45:ILE:HG23	1:CX:77:ALA:HB3	2.01	0.42
1:DG:44:ASN:OD1	1:DG:44:ASN:C	2.62	0.42
1:DJ:44:ASN:OD1	1:DJ:44:ASN:C	2.63	0.42
1:DO:44:ASN:HB2	1:DO:78:LEU:HA	2.00	0.42
1:DV:2:ILE:HD13	1:DV:32:LEU:HD23	2.02	0.42
1:DY:45:ILE:HG23	1:DY:77:ALA:HB3	2.01	0.42
1:EB:47:TYR:CZ	1:GB:105:ILE:HG12	2.54	0.42
1:EQ:2:ILE:HD13	1:EQ:32:LEU:HD23	2.02	0.42
1:FR:45:ILE:HG23	1:FR:77:ALA:HB3	2.01	0.42
1:GA:34:ALA:HA	1:GA:48:LYS:O	2.19	0.42
1:GC:26:ALA:HA	1:GC:29:MET:HB2	2.00	0.42
1:GD:44:ASN:C	1:GD:44:ASN:OD1	2.62	0.42
1:GH:32:LEU:HD13	1:GH:51:VAL:HG22	2.01	0.42
1:GI:26:ALA:HA	1:GI:29:MET:HB2	2.00	0.42
1:GV:34:ALA:HA	1:GV:48:LYS:O	2.19	0.42
1:HC:32:LEU:CD1	1:HC:49:ILE:HG23	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HI:4:LYS:HA	1:HI:17:TYR:CD1	2.51	0.42
1:HK:72:ASN:O	1:IY:73:LEU:HA	2.19	0.42
1:HM:16:ILE:HG23	1:HM:33:VAL:HG22	2.02	0.42
1:HR:32:LEU:CD1	1:HR:49:ILE:HG23	2.48	0.42
1:HT:69:ILE:HD13	1:IM:87:LYS:HG2	2.01	0.42
1:HV:89:ARG:HH22	1:JO:21:GLY:H	1.66	0.42
1:HW:44:ASN:OD1	1:HW:44:ASN:C	2.62	0.42
1:HW:47:TYR:CE2	1:IP:105:ILE:HG12	2.54	0.42
1:IU:44:ASN:OD1	1:IU:44:ASN:C	2.62	0.42
1:JD:44:ASN:OD1	1:JD:44:ASN:C	2.62	0.42
1:JN:32:LEU:CD1	1:JN:49:ILE:HG23	2.48	0.42
1:JR:26:ALA:HA	1:JR:29:MET:HB2	2.01	0.42
1:JS:44:ASN:OD1	1:JS:44:ASN:C	2.62	0.42
1:JT:32:LEU:HD13	1:JT:51:VAL:HG22	2.01	0.42
1:JU:44:ASN:HB2	1:JU:78:LEU:HA	2.00	0.42
1:KB:45:ILE:HG23	1:KB:77:ALA:HB3	2.01	0.42
1:AM:2:ILE:HD13	1:AM:32:LEU:HD23	2.02	0.42
1:AU:16:ILE:HG23	1:AU:33:VAL:HG22	2.02	0.42
1:AU:86:GLU:CG	1:EG:53:TYR:CE2	3.02	0.42
1:AX:99:THR:HG23	1:EJ:95:VAL:HG11	2.00	0.42
1:BG:105:ILE:HG12	1:ES:47:TYR:CZ	2.54	0.42
1:BN:45:ILE:HG23	1:BN:77:ALA:HB3	2.01	0.42
1:BQ:34:ALA:HA	1:BQ:48:LYS:O	2.19	0.42
1:BU:32:LEU:CD1	1:BU:49:ILE:HG23	2.48	0.42
1:BW:34:ALA:HA	1:BW:48:LYS:O	2.19	0.42
1:BW:75:PHE:HZ	1:BW:87:LYS:HB3	1.82	0.42
1:CC:83:ASN:HD22	1:GK:55:LEU:CD1	2.30	0.42
1:CG:32:LEU:HD13	1:CG:51:VAL:HG22	2.01	0.42
1:CI:34:ALA:HA	1:CI:48:LYS:O	2.19	0.42
1:CL:45:ILE:HG23	1:CL:77:ALA:HB3	2.01	0.42
1:CY:32:LEU:CD1	1:CY:49:ILE:HG23	2.48	0.42
1:DB:108:GLY:O	1:GJ:45:ILE:HD13	2.19	0.42
1:DC:26:ALA:HA	1:DC:29:MET:HB2	2.01	0.42
1:DD:45:ILE:HG23	1:DD:77:ALA:HB3	2.01	0.42
1:DF:26:ALA:HA	1:DF:29:MET:HB2	2.00	0.42
1:DY:47:TYR:CZ	1:FY:105:ILE:HG12	2.55	0.42
1:EB:2:ILE:HD13	1:EB:32:LEU:HD23	2.02	0.42
1:EM:44:ASN:HB2	1:EM:78:LEU:HA	2.00	0.42
1:EW:45:ILE:HG23	1:EW:77:ALA:HB3	2.01	0.42
1:FD:32:LEU:HD13	1:FD:51:VAL:HG22	2.01	0.42
1:FL:44:ASN:OD1	1:FL:44:ASN:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GI:16:ILE:HG23	1:GI:33:VAL:HG22	2.02	0.42
1:GS:44:ASN:OD1	1:GS:44:ASN:C	2.62	0.42
1:GY:21:GLY:H	1:HO:89:ARG:HH22	1.67	0.42
1:HE:2:ILE:HD13	1:HE:32:LEU:HD23	2.01	0.42
1:HG:51:VAL:HG11	1:IT:90:VAL:HG13	2.01	0.42
1:HL:95:VAL:HG13	1:JG:95:VAL:HG13	2.02	0.42
1:IF:34:ALA:HA	1:IF:48:LYS:O	2.19	0.42
1:IU:106:ILE:O	1:JE:77:ALA:HB1	2.20	0.42
1:JA:44:ASN:OD1	1:JA:44:ASN:C	2.62	0.42
1:JJ:44:ASN:OD1	1:JJ:44:ASN:C	2.62	0.42
1:KF:32:LEU:CD1	1:KF:49:ILE:HG23	2.48	0.42
1:KI:32:LEU:CD1	1:KI:49:ILE:HG23	2.48	0.42
1:AH:2:ILE:HD13	1:AH:32:LEU:HD23	2.02	0.42
1:AJ:88:LEU:CD2	1:BX:106:ILE:HG13	2.50	0.42
1:AS:45:ILE:HG23	1:AS:77:ALA:HB3	2.01	0.42
1:AX:26:ALA:HA	1:AX:29:MET:HB2	2.01	0.42
1:AY:44:ASN:OD1	1:AY:44:ASN:C	2.62	0.42
1:BB:44:ASN:OD1	1:BB:44:ASN:C	2.62	0.42
1:BE:44:ASN:OD1	1:BE:44:ASN:C	2.62	0.42
1:BG:16:ILE:HG23	1:BG:33:VAL:HG22	2.02	0.42
1:BX:32:LEU:HD13	1:BX:51:VAL:HG22	2.01	0.42
1:CF:45:ILE:HG23	1:CF:77:ALA:HB3	2.01	0.42
1:CH:44:ASN:HB2	1:CH:78:LEU:HA	2.00	0.42
1:CJ:32:LEU:HD13	1:CJ:51:VAL:HG22	2.01	0.42
1:CR:2:ILE:HD13	1:CR:32:LEU:HD23	2.02	0.42
1:CU:44:ASN:C	1:CU:44:ASN:OD1	2.62	0.42
1:CY:73:LEU:HD12	1:GG:73:LEU:HD13	2.02	0.42
1:CZ:44:ASN:HB2	1:CZ:78:LEU:HA	2.00	0.42
1:DF:16:ILE:HG23	1:DF:33:VAL:HG22	2.02	0.42
1:DG:34:ALA:HA	1:DG:48:LYS:O	2.19	0.42
1:DO:16:ILE:HG23	1:DO:33:VAL:HG22	2.02	0.42
1:EE:75:PHE:HD1	1:EU:71:ALA:HB2	1.84	0.42
1:EY:26:ALA:HA	1:EY:29:MET:HB2	2.00	0.42
1:FD:47:TYR:CZ	1:FF:105:ILE:HG12	2.55	0.42
1:FJ:32:LEU:CD1	1:FJ:49:ILE:HG23	2.48	0.42
1:FK:16:ILE:HG23	1:FK:33:VAL:HG22	2.02	0.42
1:FR:2:ILE:HD13	1:FR:32:LEU:HD23	2.01	0.42
1:FS:32:LEU:HD13	1:FS:51:VAL:HG22	2.01	0.42
1:FX:45:ILE:HG23	1:FX:77:ALA:HB3	2.01	0.42
1:FY:32:LEU:HD13	1:FY:51:VAL:HG22	2.01	0.42
1:FZ:44:ASN:HB2	1:FZ:78:LEU:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GG:34:ALA:HA	1:GG:48:LYS:O	2.19	0.42
1:GQ:32:LEU:HD13	1:GQ:51:VAL:HG22	2.01	0.42
1:GW:32:LEU:CD1	1:GW:49:ILE:HG23	2.48	0.42
1:HE:34:ALA:HA	1:HE:48:LYS:O	2.19	0.42
1:HN:34:ALA:HA	1:HN:48:LYS:O	2.19	0.42
1:IC:2:ILE:HD13	1:IC:32:LEU:HD23	2.02	0.42
1:IC:44:ASN:OD1	1:IC:44:ASN:C	2.62	0.42
1:IF:44:ASN:C	1:IF:44:ASN:OD1	2.62	0.42
1:IF:112:THR:HG23	1:IJ:17:TYR:OH	2.20	0.42
1:II:2:ILE:HD13	1:II:32:LEU:HD23	2.02	0.42
1:II:44:ASN:OD1	1:II:44:ASN:C	2.62	0.42
1:IL:44:ASN:OD1	1:IL:44:ASN:C	2.62	0.42
1:IO:34:ALA:HA	1:IO:48:LYS:O	2.19	0.42
1:IQ:16:ILE:HG23	1:IQ:33:VAL:HG22	2.02	0.42
1:IT:16:ILE:HG23	1:IT:33:VAL:HG22	2.02	0.42
1:IX:2:ILE:HD13	1:IX:32:LEU:HD23	2.02	0.42
1:IY:32:LEU:CD1	1:IY:49:ILE:HG23	2.48	0.42
1:IZ:16:ILE:HG23	1:IZ:33:VAL:HG22	2.02	0.42
1:JJ:2:ILE:HD13	1:JJ:32:LEU:HD23	2.01	0.42
1:JJ:34:ALA:HA	1:JJ:48:LYS:O	2.19	0.42
1:JN:32:LEU:HD13	1:JN:51:VAL:HG22	2.01	0.42
1:JO:44:ASN:HB2	1:JO:78:LEU:HA	2.00	0.42
1:KA:16:ILE:HG23	1:KA:33:VAL:HG22	2.02	0.42
1:KB:44:ASN:OD1	1:KB:44:ASN:C	2.62	0.42
1:KE:44:ASN:OD1	1:KE:44:ASN:C	2.62	0.42
1:AH:32:LEU:CD1	1:AH:49:ILE:HG23	2.48	0.42
1:AI:26:ALA:HA	1:AI:29:MET:HB2	2.00	0.42
1:AK:55:LEU:HD13	1:FO:83:ASN:HD22	1.85	0.42
1:AR:11:PRO:HA	1:ED:111:LEU:HG	2.02	0.42
1:AS:34:ALA:HA	1:AS:48:LYS:O	2.19	0.42
1:AT:2:ILE:HD13	1:AT:32:LEU:HD23	2.02	0.42
1:AT:32:LEU:CD1	1:AT:49:ILE:HG23	2.48	0.42
1:AU:108:GLY:HA3	1:EG:45:ILE:HB	2.02	0.42
1:AW:32:LEU:HD13	1:AW:51:VAL:HG22	2.01	0.42
1:AZ:32:LEU:HD13	1:AZ:51:VAL:HG22	2.01	0.42
1:BD:16:ILE:HG23	1:BD:33:VAL:HG22	2.02	0.42
1:BF:32:LEU:CD1	1:BF:49:ILE:HG23	2.48	0.42
1:BG:21:GLY:H	1:ES:89:ARG:HH22	1.68	0.42
1:BL:2:ILE:HD13	1:BL:32:LEU:HD23	2.02	0.42
1:BS:26:ALA:HA	1:BS:29:MET:HB2	2.00	0.42
1:BU:2:ILE:HD13	1:BU:32:LEU:HD23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:44:ASN:C	1:BW:44:ASN:OD1	2.62	0.42
1:BW:73:LEU:HD13	1:DQ:73:LEU:HD12	2.01	0.42
1:BY:16:ILE:HG23	1:BY:33:VAL:HG22	2.02	0.42
1:CE:44:ASN:HB2	1:CE:78:LEU:HA	2.00	0.42
1:CF:2:ILE:HD13	1:CF:32:LEU:HD23	2.02	0.42
1:CK:72:ASN:O	1:FW:73:LEU:HD12	2.20	0.42
1:DI:32:LEU:CD1	1:DI:49:ILE:HG23	2.46	0.42
1:DP:106:ILE:HD13	1:GW:88:LEU:HG	2.01	0.42
1:DR:16:ILE:HG23	1:DR:33:VAL:HG22	2.02	0.42
1:EB:106:ILE:O	1:GB:77:ALA:HB1	2.20	0.42
1:EH:45:ILE:HG23	1:EH:77:ALA:HB3	2.01	0.42
1:ER:32:LEU:HD13	1:ER:51:VAL:HG22	2.01	0.42
1:ET:2:ILE:HD13	1:ET:32:LEU:HD23	2.02	0.42
1:ET:45:ILE:CG2	1:FG:108:GLY:HA3	2.50	0.42
1:FD:2:ILE:HD13	1:FD:32:LEU:HD23	2.02	0.42
1:FG:32:LEU:HD13	1:FG:51:VAL:HG22	2.01	0.42
1:FO:45:ILE:HG23	1:FO:77:ALA:HB3	2.01	0.42
1:FP:32:LEU:CD1	1:FP:49:ILE:HG23	2.48	0.42
1:FS:90:VAL:HG13	1:GP:51:VAL:HG11	2.00	0.42
1:FX:2:ILE:HD13	1:FX:32:LEU:HD23	2.01	0.42
1:GA:45:ILE:HG23	1:GA:77:ALA:HB3	2.01	0.42
1:GD:2:ILE:HD13	1:GD:32:LEU:HD23	2.01	0.42
1:GM:2:ILE:HD13	1:GM:32:LEU:HD23	2.02	0.42
1:GP:34:ALA:HA	1:GP:48:LYS:O	2.19	0.42
1:GP:45:ILE:HG23	1:GP:77:ALA:HB3	2.01	0.42
1:GU:16:ILE:HG23	1:GU:33:VAL:HG22	2.02	0.42
1:HG:73:LEU:HD22	1:IT:98:ILE:HD11	2.00	0.42
1:HK:2:ILE:HD13	1:HK:32:LEU:HD23	2.01	0.42
1:HT:69:ILE:HG12	1:IM:78:LEU:CD1	2.50	0.42
1:HW:34:ALA:HA	1:HW:48:LYS:O	2.19	0.42
1:HZ:45:ILE:HD13	1:KC:108:GLY:O	2.20	0.42
1:HZ:45:ILE:HG23	1:HZ:77:ALA:HB3	2.01	0.42
1:IF:2:ILE:HD13	1:IF:32:LEU:HD23	2.02	0.42
1:IK:16:ILE:HG23	1:IK:33:VAL:HG22	2.02	0.42
1:IM:32:LEU:CD1	1:IM:49:ILE:HG23	2.48	0.42
1:IO:2:ILE:HD13	1:IO:32:LEU:HD23	2.02	0.42
1:IO:45:ILE:HG23	1:IO:77:ALA:HB3	2.01	0.42
1:IR:34:ALA:HA	1:IR:48:LYS:O	2.19	0.42
1:IS:32:LEU:CD1	1:IS:49:ILE:HG23	2.48	0.42
1:JA:34:ALA:HA	1:JA:48:LYS:O	2.19	0.42
1:JD:2:ILE:HD13	1:JD:32:LEU:HD23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JO:26:ALA:HA	1:JO:29:MET:HB2	2.00	0.42
1:AF:16:ILE:HG23	1:AF:33:VAL:HG22	2.02	0.42
1:AJ:34:ALA:HA	1:AJ:48:LYS:O	2.19	0.42
1:AS:6:SER:OG	1:AU:11:PRO:HB3	2.20	0.42
1:AT:32:LEU:HD13	1:AT:51:VAL:HG22	2.01	0.42
1:BC:2:ILE:HD13	1:BC:32:LEU:HD23	2.02	0.42
1:BF:2:ILE:HD13	1:BF:32:LEU:HD23	2.02	0.42
1:BH:45:ILE:HG23	1:BH:77:ALA:HB3	2.01	0.42
1:BJ:16:ILE:HG23	1:BJ:33:VAL:HG22	2.02	0.42
1:BK:34:ALA:HA	1:BK:48:LYS:O	2.19	0.42
1:BM:95:VAL:HG11	1:EY:99:THR:HG23	1.99	0.42
1:BR:2:ILE:HD13	1:BR:32:LEU:HD23	2.02	0.42
1:BS:16:ILE:HG23	1:BS:33:VAL:HG22	2.02	0.42
1:BT:6:SER:OG	1:BV:11:PRO:HB3	2.20	0.42
1:BV:26:ALA:HA	1:BV:29:MET:HB2	2.01	0.42
1:CH:16:ILE:HG23	1:CH:33:VAL:HG22	2.02	0.42
1:CM:32:LEU:HD13	1:CM:51:VAL:HG22	2.01	0.42
1:CX:95:VAL:HG13	1:DK:95:VAL:HG13	2.02	0.42
1:CZ:16:ILE:HG23	1:CZ:33:VAL:HG22	2.02	0.42
1:DD:44:ASN:C	1:DD:44:ASN:OD1	2.62	0.42
1:DE:2:ILE:HD13	1:DE:32:LEU:HD23	2.02	0.42
1:DE:32:LEU:HD13	1:DE:51:VAL:HG22	2.01	0.42
1:DL:26:ALA:HA	1:DL:29:MET:HB2	2.00	0.42
1:DN:2:ILE:HD13	1:DN:32:LEU:HD23	2.02	0.42
1:DS:44:ASN:OD1	1:DS:44:ASN:C	2.62	0.42
1:DU:16:ILE:HG23	1:DU:33:VAL:HG22	2.02	0.42
1:DZ:2:ILE:HD13	1:DZ:32:LEU:HD23	2.02	0.42
1:DZ:32:LEU:HD13	1:DZ:51:VAL:HG22	2.01	0.42
1:EC:32:LEU:HD13	1:EC:51:VAL:HG22	2.01	0.42
1:EM:32:LEU:CD1	1:EM:49:ILE:HG23	2.46	0.42
1:EN:110:VAL:HG11	1:FJ:13:GLY:C	2.44	0.42
1:EQ:45:ILE:HG23	1:EQ:77:ALA:HB3	2.01	0.42
1:ET:47:TYR:CZ	1:FG:105:ILE:HG12	2.55	0.42
1:EU:2:ILE:HD13	1:EU:32:LEU:HD23	2.02	0.42
1:EV:16:ILE:HG23	1:EV:33:VAL:HG22	2.02	0.42
1:FA:2:ILE:HD13	1:FA:32:LEU:HD23	2.02	0.42
1:FE:16:ILE:HG23	1:FE:33:VAL:HG22	2.02	0.42
1:FF:34:ALA:HA	1:FF:48:LYS:O	2.19	0.42
1:FN:16:ILE:HG23	1:FN:33:VAL:HG22	2.02	0.42
1:FO:6:SER:OG	1:FQ:11:PRO:HB3	2.20	0.42
1:FU:44:ASN:OD1	1:FU:44:ASN:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GP:2:ILE:HD13	1:GP:32:LEU:HD23	2.02	0.42
1:GQ:2:ILE:HD13	1:GQ:32:LEU:HD23	2.02	0.42
1:GY:45:ILE:HG23	1:GY:77:ALA:HB3	2.01	0.42
1:HE:44:ASN:OD1	1:HE:44:ASN:C	2.62	0.42
1:HG:16:ILE:HG23	1:HG:33:VAL:HG22	2.02	0.42
1:HL:2:ILE:HD13	1:HL:32:LEU:HD23	2.02	0.42
1:HN:44:ASN:OD1	1:HN:44:ASN:C	2.63	0.42
1:HP:51:VAL:HG11	1:JC:90:VAL:HG13	2.00	0.42
1:HQ:19:PHE:HB3	1:IS:89:ARG:NH2	2.34	0.42
1:HR:2:ILE:HD13	1:HR:32:LEU:HD23	2.02	0.42
1:HS:74:SER:O	1:JL:71:ALA:HA	2.19	0.42
1:HT:45:ILE:HG23	1:HT:77:ALA:HB3	2.01	0.42
1:HY:26:ALA:HA	1:HY:29:MET:HB2	2.00	0.42
1:HZ:44:ASN:OD1	1:HZ:44:ASN:C	2.62	0.42
1:IC:45:ILE:HG23	1:IC:77:ALA:HB3	2.01	0.42
1:IQ:26:ALA:HA	1:IQ:29:MET:HB2	2.00	0.42
1:IS:32:LEU:HD13	1:IS:51:VAL:HG22	2.01	0.42
1:JM:2:ILE:HD13	1:JM:32:LEU:HD23	2.02	0.42
1:JZ:32:LEU:CD1	1:JZ:49:ILE:HG23	2.48	0.42
1:KC:32:LEU:HD13	1:KC:51:VAL:HG22	2.01	0.42
1:AF:72:ASN:O	1:DR:73:LEU:HD12	2.19	0.42
1:AP:6:SER:OG	1:AR:11:PRO:HB3	2.20	0.42
1:AV:6:SER:OG	1:AX:11:PRO:HB3	2.20	0.42
1:BD:20:THR:N	1:EP:89:ARG:HH22	2.17	0.42
1:BM:16:ILE:HG23	1:BM:33:VAL:HG22	2.02	0.42
1:BO:2:ILE:HD13	1:BO:32:LEU:HD23	2.02	0.42
1:BQ:44:ASN:OD1	1:BQ:44:ASN:C	2.62	0.42
1:CB:16:ILE:HG23	1:CB:33:VAL:HG22	2.02	0.42
1:CD:69:ILE:HG12	1:CR:78:LEU:HD12	2.02	0.42
1:CF:6:SER:OG	1:CH:11:PRO:HB3	2.20	0.42
1:CG:21:GLY:H	1:CL:89:ARG:HH22	1.68	0.42
1:CI:6:SER:OG	1:CK:11:PRO:HB3	2.20	0.42
1:CU:34:ALA:HA	1:CU:48:LYS:O	2.19	0.42
1:CZ:26:ALA:HA	1:CZ:29:MET:HB2	2.00	0.42
1:DC:16:ILE:HG23	1:DC:33:VAL:HG22	2.02	0.42
1:DD:2:ILE:HD13	1:DD:32:LEU:HD23	2.01	0.42
1:DR:26:ALA:HA	1:DR:29:MET:HB2	2.00	0.42
1:EB:44:ASN:OD1	1:EB:44:ASN:C	2.62	0.42
1:EH:6:SER:OG	1:EJ:11:PRO:HB3	2.20	0.42
1:EH:73:LEU:HB2	1:EO:73:LEU:HD12	2.01	0.42
1:EK:2:ILE:HD13	1:EK:32:LEU:HD23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EN:34:ALA:HA	1:EN:48:LYS:O	2.19	0.42
1:ET:44:ASN:OD1	1:ET:44:ASN:C	2.62	0.42
1:EW:34:ALA:HA	1:EW:48:LYS:O	2.19	0.42
1:EZ:2:ILE:HD13	1:EZ:32:LEU:HD23	2.02	0.42
1:FR:6:SER:OG	1:FT:11:PRO:HB3	2.20	0.42
1:FR:34:ALA:HA	1:FR:48:LYS:O	2.19	0.42
1:FR:44:ASN:OD1	1:FR:44:ASN:C	2.62	0.42
1:FT:26:ALA:HA	1:FT:29:MET:HB2	2.00	0.42
1:GH:32:LEU:CD1	1:GH:49:ILE:HG23	2.48	0.42
1:GL:16:ILE:HG23	1:GL:33:VAL:HG22	2.02	0.42
1:GS:6:SER:OG	1:GU:11:PRO:HB3	2.20	0.42
1:GT:2:ILE:HD13	1:GT:32:LEU:HD23	2.02	0.42
1:GZ:32:LEU:CD1	1:GZ:49:ILE:HG23	2.48	0.42
1:HB:2:ILE:HD13	1:HB:32:LEU:HD23	2.02	0.42
1:HC:2:ILE:HD13	1:HC:32:LEU:HD23	2.02	0.42
1:HI:2:ILE:HD13	1:HI:32:LEU:HD23	2.02	0.42
1:HJ:16:ILE:HG23	1:HJ:33:VAL:HG22	2.02	0.42
1:HK:34:ALA:HA	1:HK:48:LYS:O	2.19	0.42
1:HQ:69:ILE:CG2	1:IS:90:VAL:HG21	2.48	0.42
1:HZ:45:ILE:CG2	1:KC:108:GLY:HA3	2.50	0.42
1:HZ:105:ILE:HG12	1:KC:47:TYR:CE2	2.55	0.42
1:IA:32:LEU:HD13	1:IA:51:VAL:HG22	2.01	0.42
1:IK:26:ALA:HA	1:IK:29:MET:HB2	2.00	0.42
1:IR:44:ASN:OD1	1:IR:44:ASN:C	2.62	0.42
1:IR:45:ILE:HG23	1:IR:77:ALA:HB3	2.01	0.42
1:IY:32:LEU:HD13	1:IY:51:VAL:HG22	2.01	0.42
1:JF:16:ILE:HG23	1:JF:33:VAL:HG22	2.02	0.42
1:JK:32:LEU:HD13	1:JK:51:VAL:HG22	2.01	0.42
1:JX:16:ILE:HG23	1:JX:33:VAL:HG22	2.02	0.42
1:KH:44:ASN:OD1	1:KH:44:ASN:C	2.62	0.42
1:AE:49:ILE:HG21	1:GA:94:ILE:HG13	2.02	0.41
1:AJ:6:SER:OG	1:AL:11:PRO:HB3	2.20	0.41
1:AJ:44:ASN:OD1	1:AJ:44:ASN:C	2.62	0.41
1:AP:2:ILE:HD13	1:AP:32:LEU:HD23	2.01	0.41
1:AP:44:ASN:C	1:AP:44:ASN:OD1	2.62	0.41
1:AQ:2:ILE:HD13	1:AQ:32:LEU:HD23	2.02	0.41
1:AS:94:ILE:HG13	1:EL:49:ILE:HG21	2.02	0.41
1:AU:90:VAL:HG13	1:EG:51:VAL:CG1	2.50	0.41
1:AV:34:ALA:HA	1:AV:48:LYS:O	2.19	0.41
1:AW:88:LEU:HG	1:FC:106:ILE:HG21	2.02	0.41
1:AZ:21:GLY:H	1:EW:89:ARG:HH22	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:55:LEU:HD13	1:EW:83:ASN:HD22	1.85	0.41
1:BA:73:LEU:HD22	1:EM:98:ILE:HD11	2.01	0.41
1:BB:6:SER:OG	1:BD:11:PRO:HB3	2.20	0.41
1:BI:32:LEU:CD1	1:BI:49:ILE:HG23	2.48	0.41
1:BK:2:ILE:HD13	1:BK:32:LEU:HD23	2.01	0.41
1:BQ:45:ILE:CG2	1:EC:108:GLY:HA3	2.49	0.41
1:BR:32:LEU:CD1	1:BR:49:ILE:HG23	2.48	0.41
1:BT:34:ALA:HA	1:BT:48:LYS:O	2.19	0.41
1:BZ:2:ILE:HD13	1:BZ:32:LEU:HD23	2.02	0.41
1:BZ:6:SER:OG	1:CB:11:PRO:HB3	2.20	0.41
1:CK:97:PHE:CG	1:FW:32:LEU:HD21	2.55	0.41
1:CP:95:VAL:HG11	1:DJ:99:THR:CG2	2.50	0.41
1:CS:32:LEU:HD13	1:CS:51:VAL:HG22	2.01	0.41
1:CW:16:ILE:HG23	1:CW:33:VAL:HG22	2.02	0.41
1:CX:44:ASN:OD1	1:CX:44:ASN:C	2.62	0.41
1:DA:45:ILE:HG23	1:DA:77:ALA:HB3	2.01	0.41
1:DC:32:LEU:CD1	1:DC:49:ILE:HG23	2.46	0.41
1:DG:6:SER:OG	1:DI:11:PRO:HB3	2.20	0.41
1:DQ:2:ILE:HD13	1:DQ:32:LEU:HD23	2.02	0.41
1:DS:89:ARG:HH22	1:GQ:21:GLY:H	1.66	0.41
1:DT:32:LEU:HD13	1:DT:51:VAL:HG22	2.01	0.41
1:DW:2:ILE:HD13	1:DW:32:LEU:HD23	2.02	0.41
1:DY:2:ILE:HD13	1:DY:32:LEU:HD23	2.01	0.41
1:EE:44:ASN:OD1	1:EE:44:ASN:C	2.62	0.41
1:EE:45:ILE:HG23	1:EE:77:ALA:HB3	2.01	0.41
1:EH:44:ASN:OD1	1:EH:44:ASN:C	2.62	0.41
1:EJ:16:ILE:HG23	1:EJ:33:VAL:HG22	2.02	0.41
1:EK:6:SER:OG	1:EM:11:PRO:HB3	2.20	0.41
1:EK:44:ASN:C	1:EK:44:ASN:OD1	2.62	0.41
1:EN:44:ASN:OD1	1:EN:44:ASN:C	2.62	0.41
1:EQ:44:ASN:C	1:EQ:44:ASN:OD1	2.62	0.41
1:FB:16:ILE:HG23	1:FB:33:VAL:HG22	2.02	0.41
1:FG:2:ILE:HD13	1:FG:32:LEU:HD23	2.02	0.41
1:FI:44:ASN:OD1	1:FI:44:ASN:C	2.62	0.41
1:FJ:32:LEU:HD13	1:FJ:51:VAL:HG22	2.01	0.41
1:FV:2:ILE:HD13	1:FV:32:LEU:HD23	2.02	0.41
1:FX:6:SER:OG	1:FZ:11:PRO:HB3	2.20	0.41
1:GA:6:SER:OG	1:GC:11:PRO:HB3	2.20	0.41
1:GC:44:ASN:HB2	1:GC:78:LEU:HA	2.00	0.41
1:GE:2:ILE:HD13	1:GE:32:LEU:HD23	2.02	0.41
1:GR:16:ILE:HG23	1:GR:33:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HJ:72:ASN:O	1:IZ:73:LEU:HD12	2.19	0.41
1:HK:6:SER:OG	1:HM:11:PRO:HB3	2.20	0.41
1:HQ:73:LEU:HD22	1:IS:98:ILE:HD11	2.02	0.41
1:HT:73:LEU:CD1	1:IM:73:LEU:HB2	2.50	0.41
1:IL:45:ILE:HG23	1:IL:77:ALA:HB3	2.01	0.41
1:IR:78:LEU:HD12	1:JZ:69:ILE:HG12	2.01	0.41
1:IX:44:ASN:OD1	1:IX:44:ASN:C	2.62	0.41
1:IY:2:ILE:HD13	1:IY:32:LEU:HD23	2.02	0.41
1:JA:6:SER:OG	1:JC:11:PRO:HB3	2.20	0.41
1:JV:6:SER:OG	1:JX:11:PRO:HB3	2.20	0.41
1:JV:44:ASN:OD1	1:JV:44:ASN:C	2.62	0.41
1:KD:44:ASN:HB2	1:KD:78:LEU:HA	2.00	0.41
1:AA:6:SER:OG	1:AC:11:PRO:HB3	2.20	0.41
1:AJ:45:ILE:HG23	1:AJ:77:ALA:HB3	2.01	0.41
1:AK:2:ILE:HD13	1:AK:32:LEU:HD23	2.02	0.41
1:AM:81:VAL:HG21	1:CA:55:LEU:CD1	2.50	0.41
1:AP:73:LEU:HB2	1:BU:73:LEU:HD12	2.01	0.41
1:AV:2:ILE:HD13	1:AV:32:LEU:HD23	2.01	0.41
1:AZ:72:ASN:O	1:EW:73:LEU:HD12	2.21	0.41
1:BB:45:ILE:HG23	1:BB:77:ALA:HB3	2.01	0.41
1:BJ:72:ASN:O	1:EV:73:LEU:HD12	2.19	0.41
1:BP:16:ILE:HG23	1:BP:33:VAL:HG22	2.02	0.41
1:BR:32:LEU:HD13	1:BR:51:VAL:HG22	2.01	0.41
1:CA:2:ILE:HD13	1:CA:32:LEU:HD23	2.02	0.41
1:CC:69:ILE:HD13	1:GK:87:LYS:HG2	2.02	0.41
1:CK:16:ILE:HG23	1:CK:33:VAL:HG22	2.02	0.41
1:CP:21:GLY:H	1:DJ:89:ARG:HH22	1.68	0.41
1:CW:32:LEU:CD1	1:CW:49:ILE:HG23	2.46	0.41
1:CY:32:LEU:HD13	1:CY:51:VAL:HG22	2.01	0.41
1:CY:110:VAL:HB	1:GG:36:THR:HG23	2.01	0.41
1:DB:2:ILE:HD13	1:DB:32:LEU:HD23	2.02	0.41
1:DK:2:ILE:HD13	1:DK:32:LEU:HD23	2.02	0.41
1:DQ:32:LEU:HD13	1:DQ:51:VAL:HG22	2.01	0.41
1:DS:6:SER:OG	1:DU:11:PRO:HB3	2.20	0.41
1:DT:2:ILE:HD13	1:DT:32:LEU:HD23	2.02	0.41
1:EF:2:ILE:HD13	1:EF:32:LEU:HD23	2.02	0.41
1:EN:2:ILE:HD13	1:EN:32:LEU:HD23	2.02	0.41
1:EN:6:SER:OG	1:EP:11:PRO:HB3	2.20	0.41
1:ET:6:SER:OG	1:EV:11:PRO:HB3	2.20	0.41
1:EZ:6:SER:OG	1:FB:11:PRO:HB3	2.20	0.41
1:EZ:44:ASN:C	1:EZ:44:ASN:OD1	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FC:2:ILE:HD13	1:FC:32:LEU:HD23	2.02	0.41
1:FF:2:ILE:HD13	1:FF:32:LEU:HD23	2.02	0.41
1:FP:2:ILE:HD13	1:FP:32:LEU:HD23	2.02	0.41
1:FV:88:LEU:CG	1:GS:106:ILE:HD13	2.50	0.41
1:FW:32:LEU:CD1	1:FW:49:ILE:HG23	2.46	0.41
1:GD:6:SER:OG	1:GF:11:PRO:HB3	2.20	0.41
1:GM:6:SER:OG	1:GO:11:PRO:HB3	2.20	0.41
1:GS:2:ILE:HD13	1:GS:32:LEU:HD23	2.02	0.41
1:GS:34:ALA:HA	1:GS:48:LYS:O	2.19	0.41
1:GY:44:ASN:OD1	1:GY:44:ASN:C	2.62	0.41
1:HH:44:ASN:OD1	1:HH:44:ASN:C	2.62	0.41
1:HN:6:SER:OG	1:HP:11:PRO:HB3	2.20	0.41
1:HW:2:ILE:HD13	1:HW:32:LEU:HD23	2.01	0.41
1:IF:89:ARG:NH2	1:IJ:20:THR:H	2.18	0.41
1:IH:16:ILE:HG23	1:IH:33:VAL:HG22	2.02	0.41
1:IL:2:ILE:HD13	1:IL:32:LEU:HD23	2.02	0.41
1:IM:2:ILE:HD13	1:IM:32:LEU:HD23	2.02	0.41
1:IS:2:ILE:HD13	1:IS:32:LEU:HD23	2.02	0.41
1:IU:6:SER:OG	1:IW:11:PRO:HB3	2.20	0.41
1:IV:2:ILE:HD13	1:IV:32:LEU:HD23	2.02	0.41
1:IX:89:ARG:HH22	1:JB:21:GLY:H	1.66	0.41
1:JA:98:ILE:HD11	1:JQ:73:LEU:HD13	2.01	0.41
1:JC:16:ILE:HG23	1:JC:33:VAL:HG22	2.02	0.41
1:JD:74:SER:N	1:JN:72:ASN:O	2.46	0.41
1:JK:2:ILE:HD13	1:JK:32:LEU:HD23	2.02	0.41
1:JM:6:SER:OG	1:JO:11:PRO:HB3	2.20	0.41
1:JS:6:SER:OG	1:JU:11:PRO:HB3	2.20	0.41
1:JV:2:ILE:HD13	1:JV:32:LEU:HD23	2.01	0.41
1:KE:6:SER:OG	1:KG:11:PRO:HB3	2.20	0.41
1:KF:2:ILE:HD13	1:KF:32:LEU:HD23	2.02	0.41
1:AH:95:VAL:HG11	1:GD:99:THR:CG2	2.49	0.41
1:AI:16:ILE:HG23	1:AI:33:VAL:HG22	2.02	0.41
1:AM:44:ASN:OD1	1:AM:44:ASN:C	2.62	0.41
1:AN:2:ILE:HD13	1:AN:32:LEU:HD23	2.02	0.41
1:AP:45:ILE:HG23	1:AP:77:ALA:HB3	2.01	0.41
1:AQ:32:LEU:HD21	1:FU:97:PHE:CD1	2.56	0.41
1:AT:21:GLY:H	1:EZ:89:ARG:HH22	1.67	0.41
1:AU:73:LEU:HD22	1:EG:98:ILE:HD11	2.02	0.41
1:AY:2:ILE:HD13	1:AY:32:LEU:HD23	2.02	0.41
1:BD:53:TYR:CZ	1:EP:86:GLU:CG	3.04	0.41
1:BS:106:ILE:HD13	1:FE:88:LEU:CD2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:44:ASN:OD1	1:BT:44:ASN:C	2.62	0.41
1:CE:16:ILE:HG23	1:CE:33:VAL:HG22	2.02	0.41
1:CJ:2:ILE:HD13	1:CJ:32:LEU:HD23	2.02	0.41
1:CL:2:ILE:HD13	1:CL:32:LEU:HD23	2.01	0.41
1:CS:2:ILE:HD13	1:CS:32:LEU:HD23	2.02	0.41
1:DE:32:LEU:CD1	1:DE:49:ILE:HG23	2.48	0.41
1:DF:88:LEU:HD23	1:GR:106:ILE:HG21	2.01	0.41
1:DM:2:ILE:HD13	1:DM:32:LEU:HD23	2.01	0.41
1:DM:6:SER:OG	1:DO:11:PRO:HB3	2.20	0.41
1:DS:2:ILE:HD13	1:DS:32:LEU:HD23	2.02	0.41
1:DV:44:ASN:OD1	1:DV:44:ASN:C	2.62	0.41
1:EA:16:ILE:HG23	1:EA:33:VAL:HG22	2.02	0.41
1:EE:73:LEU:HB2	1:EU:73:LEU:HD12	2.01	0.41
1:EG:16:ILE:HG23	1:EG:33:VAL:HG22	2.02	0.41
1:FF:44:ASN:OD1	1:FF:44:ASN:C	2.62	0.41
1:FH:16:ILE:HG23	1:FH:33:VAL:HG22	2.02	0.41
1:GD:45:ILE:HG23	1:GD:77:ALA:HB3	2.01	0.41
1:GH:2:ILE:HD13	1:GH:32:LEU:HD23	2.02	0.41
1:GJ:6:SER:OG	1:GL:11:PRO:HB3	2.20	0.41
1:HB:44:ASN:OD1	1:HB:44:ASN:C	2.62	0.41
1:HH:2:ILE:HD13	1:HH:32:LEU:HD23	2.01	0.41
1:HK:47:TYR:CZ	1:IY:105:ILE:HG12	2.55	0.41
1:HL:72:ASN:O	1:JG:73:LEU:HD12	2.20	0.41
1:HM:32:LEU:CD1	1:HM:49:ILE:HG23	2.46	0.41
1:HN:2:ILE:HD13	1:HN:32:LEU:HD23	2.01	0.41
1:HO:2:ILE:HD13	1:HO:32:LEU:HD23	2.02	0.41
1:HP:16:ILE:HG23	1:HP:33:VAL:HG22	2.02	0.41
1:HQ:44:ASN:C	1:HQ:44:ASN:OD1	2.62	0.41
1:HX:32:LEU:CD1	1:HX:49:ILE:HG23	2.48	0.41
1:HY:95:VAL:HG11	1:JR:99:THR:CG2	2.51	0.41
1:IA:2:ILE:HD13	1:IA:32:LEU:HD23	2.02	0.41
1:IB:88:LEU:HD23	1:JX:106:ILE:HG21	2.02	0.41
1:IK:11:PRO:HA	1:KJ:111:LEU:HG	2.01	0.41
1:IK:32:LEU:HD21	1:KJ:97:PHE:CG	2.56	0.41
1:IN:16:ILE:HG23	1:IN:33:VAL:HG22	2.02	0.41
1:IO:6:SER:OG	1:IQ:11:PRO:HB3	2.20	0.41
1:JA:21:GLY:H	1:JQ:89:ARG:HH22	1.68	0.41
1:JE:2:ILE:HD13	1:JE:32:LEU:HD23	2.02	0.41
1:JH:2:ILE:HD13	1:JH:32:LEU:HD23	2.02	0.41
1:JM:44:ASN:C	1:JM:44:ASN:OD1	2.62	0.41
1:JN:2:ILE:HD13	1:JN:32:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JP:2:ILE:HD13	1:JP:32:LEU:HD23	2.01	0.41
1:JW:32:LEU:HD13	1:JW:51:VAL:HG22	2.01	0.41
1:KB:6:SER:OG	1:KD:11:PRO:HB3	2.20	0.41
1:KF:32:LEU:HD13	1:KF:51:VAL:HG22	2.01	0.41
1:AA:44:ASN:C	1:AA:44:ASN:OD1	2.62	0.41
1:AD:6:SER:OG	1:AF:11:PRO:HB3	2.20	0.41
1:AJ:95:VAL:HG13	1:BX:95:VAL:HG13	2.03	0.41
1:AO:16:ILE:HG23	1:AO:33:VAL:HG22	2.02	0.41
1:AW:88:LEU:HG	1:FC:106:ILE:HD13	2.02	0.41
1:BB:2:ILE:HD13	1:BB:32:LEU:HD23	2.02	0.41
1:BN:73:LEU:HD12	1:DZ:72:ASN:O	2.20	0.41
1:BV:16:ILE:HG23	1:BV:33:VAL:HG22	2.02	0.41
1:BZ:44:ASN:OD1	1:BZ:44:ASN:C	2.62	0.41
1:CC:45:ILE:HG23	1:CC:77:ALA:HB3	2.01	0.41
1:CY:2:ILE:HD13	1:CY:32:LEU:HD23	2.02	0.41
1:DP:44:ASN:C	1:DP:44:ASN:OD1	2.62	0.41
1:DQ:44:ASN:CB	1:DQ:78:LEU:HA	2.51	0.41
1:EC:2:ILE:HD13	1:EC:32:LEU:HD23	2.02	0.41
1:EG:32:LEU:CD1	1:EG:49:ILE:HG23	2.46	0.41
1:EN:111:LEU:HD11	1:FJ:10:GLY:C	2.45	0.41
1:EZ:45:ILE:HG23	1:EZ:77:ALA:HB3	2.01	0.41
1:FL:2:ILE:HD13	1:FL:32:LEU:HD23	2.01	0.41
1:FS:2:ILE:HD13	1:FS:32:LEU:HD23	2.02	0.41
1:FU:6:SER:OG	1:FW:11:PRO:HB3	2.20	0.41
1:FW:16:ILE:HG23	1:FW:33:VAL:HG22	2.02	0.41
1:GV:44:ASN:OD1	1:GV:44:ASN:C	2.62	0.41
1:HK:21:GLY:H	1:IY:89:ARG:HH22	1.69	0.41
1:HS:16:ILE:HG23	1:HS:33:VAL:HG22	2.02	0.41
1:HX:32:LEU:HD13	1:HX:51:VAL:HG22	2.01	0.41
1:IA:44:ASN:CB	1:IA:78:LEU:HA	2.51	0.41
1:IR:2:ILE:HD13	1:IR:32:LEU:HD23	2.02	0.41
1:IX:6:SER:OG	1:IZ:11:PRO:HB3	2.20	0.41
1:JT:11:PRO:HB3	1:KH:109:ASN:OD1	2.19	0.41
1:AG:6:SER:OG	1:AI:11:PRO:HB3	2.20	0.41
1:AG:71:ALA:HB3	1:BF:94:ILE:HD11	2.03	0.41
1:AQ:75:PHE:CE2	1:FU:106:ILE:HA	2.55	0.41
1:AT:95:VAL:HG13	1:EZ:95:VAL:HG13	2.02	0.41
1:AW:2:ILE:HD13	1:AW:32:LEU:HD23	2.02	0.41
1:BE:34:ALA:HA	1:BE:48:LYS:O	2.19	0.41
1:BW:6:SER:OG	1:BY:11:PRO:HB3	2.20	0.41
1:BW:105:ILE:HG12	1:DQ:47:TYR:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:2:ILE:HD13	1:BX:32:LEU:HD23	2.02	0.41
1:CM:44:ASN:CB	1:CM:78:LEU:HA	2.51	0.41
1:CO:44:ASN:OD1	1:CO:44:ASN:C	2.62	0.41
1:CP:2:ILE:HD13	1:CP:32:LEU:HD23	2.02	0.41
1:CT:32:LEU:CD1	1:CT:49:ILE:HG23	2.46	0.41
1:DH:2:ILE:HD13	1:DH:32:LEU:HD23	2.02	0.41
1:DV:45:ILE:HG23	1:DV:77:ALA:HB3	2.01	0.41
1:DV:78:LEU:HD12	1:GE:69:ILE:HG12	2.02	0.41
1:EC:44:ASN:CB	1:EC:78:LEU:HA	2.51	0.41
1:EE:90:VAL:HG13	1:EU:51:VAL:HG11	2.03	0.41
1:EF:60:ASP:HB3	1:EU:59:VAL:HG11	2.01	0.41
1:EP:16:ILE:HG23	1:EP:33:VAL:HG22	2.02	0.41
1:FF:6:SER:OG	1:FH:11:PRO:HB3	2.20	0.41
1:FF:45:ILE:HG23	1:FF:77:ALA:HB3	2.01	0.41
1:FI:6:SER:OG	1:FK:11:PRO:HB3	2.20	0.41
1:FM:2:ILE:HD13	1:FM:32:LEU:HD23	2.02	0.41
1:FU:45:ILE:HG23	1:FU:77:ALA:HB3	2.01	0.41
1:GC:16:ILE:HG23	1:GC:33:VAL:HG22	2.02	0.41
1:GG:44:ASN:C	1:GG:44:ASN:OD1	2.62	0.41
1:GK:44:ASN:CB	1:GK:78:LEU:HA	2.51	0.41
1:GT:44:ASN:CB	1:GT:78:LEU:HA	2.51	0.41
1:GV:2:ILE:HD13	1:GV:32:LEU:HD23	2.01	0.41
1:HB:45:ILE:HG23	1:HB:77:ALA:HB3	2.01	0.41
1:HE:6:SER:OG	1:HG:11:PRO:HB3	2.20	0.41
1:HN:45:ILE:HG23	1:HN:77:ALA:HB3	2.01	0.41
1:HV:16:ILE:HG23	1:HV:33:VAL:HG22	2.02	0.41
1:HY:16:ILE:HG23	1:HY:33:VAL:HG22	2.02	0.41
1:IB:16:ILE:HG23	1:IB:33:VAL:HG22	2.02	0.41
1:IE:32:LEU:CD1	1:IE:49:ILE:HG23	2.46	0.41
1:JB:44:ASN:CB	1:JB:78:LEU:HA	2.51	0.41
1:JH:73:LEU:HD12	1:JP:73:LEU:HB2	2.02	0.41
1:JO:16:ILE:HG23	1:JO:33:VAL:HG22	2.02	0.41
1:KF:44:ASN:CB	1:KF:78:LEU:HA	2.51	0.41
1:KI:2:ILE:HD13	1:KI:32:LEU:HD23	2.02	0.41
1:AL:16:ILE:HG23	1:AL:33:VAL:HG22	2.02	0.41
1:AM:45:ILE:HG23	1:AM:77:ALA:HB3	2.01	0.41
1:AM:76:THR:HG23	1:CA:70:ARG:O	2.20	0.41
1:BB:95:VAL:HG13	1:BR:95:VAL:HG13	2.02	0.41
1:CI:45:ILE:HG23	1:CI:77:ALA:HB3	2.01	0.41
1:CS:44:ASN:CB	1:CS:78:LEU:HA	2.51	0.41
1:CU:2:ILE:HD13	1:CU:32:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:105:ILE:HG12	1:GG:47:TYR:CE2	2.56	0.41
1:DA:6:SER:OG	1:DC:11:PRO:HB3	2.20	0.41
1:DJ:2:ILE:HD13	1:DJ:32:LEU:HD23	2.02	0.41
1:DM:44:ASN:OD1	1:DM:44:ASN:C	2.62	0.41
1:EE:34:ALA:HA	1:EE:48:LYS:O	2.19	0.41
1:EI:2:ILE:HD13	1:EI:32:LEU:HD23	2.02	0.41
1:EL:2:ILE:HD13	1:EL:32:LEU:HD23	2.02	0.41
1:EQ:6:SER:OG	1:ES:11:PRO:HB3	2.20	0.41
1:EY:16:ILE:HG23	1:EY:33:VAL:HG22	2.02	0.41
1:FI:34:ALA:HA	1:FI:48:LYS:O	2.19	0.41
1:FZ:16:ILE:HG23	1:FZ:33:VAL:HG22	2.02	0.41
1:GM:44:ASN:OD1	1:GM:44:ASN:C	2.62	0.41
1:GY:2:ILE:HD13	1:GY:32:LEU:HD23	2.02	0.41
1:HI:32:LEU:HD13	1:HI:51:VAL:HG22	2.01	0.41
1:HS:32:LEU:HD21	1:JL:97:PHE:CG	2.55	0.41
1:HT:6:SER:OG	1:HV:11:PRO:HB3	2.20	0.41
1:IA:74:SER:O	1:IC:71:ALA:HA	2.20	0.41
1:IF:6:SER:OG	1:IH:11:PRO:HB3	2.20	0.41
1:IJ:2:ILE:HD13	1:IJ:32:LEU:HD23	2.02	0.41
1:IR:6:SER:OG	1:IT:11:PRO:HB3	2.20	0.41
1:JK:105:ILE:HG12	1:JM:47:TYR:CZ	2.55	0.41
1:JR:16:ILE:HG23	1:JR:33:VAL:HG22	2.02	0.41
1:JZ:44:ASN:CB	1:JZ:78:LEU:HA	2.51	0.41
1:AD:83:ASN:ND2	1:BC:55:LEU:HD13	2.34	0.41
1:AD:106:ILE:HG21	1:BC:88:LEU:HG	2.02	0.41
1:AF:89:ARG:HH22	1:DR:21:GLY:H	1.69	0.41
1:AV:19:PHE:CE2	1:EF:89:ARG:HG3	2.56	0.41
1:AZ:44:ASN:CB	1:AZ:78:LEU:HA	2.51	0.41
1:BA:16:ILE:HG23	1:BA:33:VAL:HG22	2.02	0.41
1:BE:2:ILE:HD13	1:BE:32:LEU:HD23	2.01	0.41
1:BH:6:SER:OG	1:BJ:11:PRO:HB3	2.20	0.41
1:BY:36:THR:HG21	1:FK:108:GLY:C	2.45	0.41
1:BY:73:LEU:HA	1:FK:72:ASN:O	2.20	0.41
1:CD:11:PRO:HB3	1:CR:109:ASN:CG	2.46	0.41
1:CI:44:ASN:OD1	1:CI:44:ASN:C	2.62	0.41
1:CK:11:PRO:HA	1:FW:111:LEU:HG	2.03	0.41
1:CM:21:GLY:H	1:DG:89:ARG:HH22	1.69	0.41
1:CM:32:LEU:CD1	1:CM:49:ILE:HG23	2.48	0.41
1:CO:2:ILE:HD13	1:CO:32:LEU:HD23	2.02	0.41
1:CT:16:ILE:HG23	1:CT:33:VAL:HG22	2.02	0.41
1:CX:98:ILE:HD11	1:DK:73:LEU:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:44:ASN:CB	1:CY:78:LEU:HA	2.51	0.41
1:DJ:6:SER:OG	1:DL:11:PRO:HB3	2.20	0.41
1:DL:32:LEU:CD1	1:DL:49:ILE:HG23	2.46	0.41
1:DN:44:ASN:CB	1:DN:78:LEU:HA	2.51	0.41
1:DY:110:VAL:HB	1:FY:36:THR:HG23	2.02	0.41
1:EB:109:ASN:CG	1:GB:11:PRO:HB3	2.45	0.41
1:EM:104:ASN:OD1	1:EM:113:VAL:HB	2.21	0.41
1:EV:104:ASN:OD1	1:EV:113:VAL:HB	2.21	0.41
1:EX:2:ILE:HD13	1:EX:32:LEU:HD23	2.02	0.41
1:FC:6:SER:OG	1:FE:11:PRO:HB3	2.20	0.41
1:FO:44:ASN:OD1	1:FO:44:ASN:C	2.62	0.41
1:FQ:104:ASN:OD1	1:FQ:113:VAL:HB	2.21	0.41
1:GP:6:SER:OG	1:GR:11:PRO:HB3	2.20	0.41
1:GZ:2:ILE:HD13	1:GZ:32:LEU:HD23	2.02	0.41
1:HH:6:SER:OG	1:HJ:11:PRO:HB3	2.20	0.41
1:HK:45:ILE:HG23	1:HK:77:ALA:HB3	2.01	0.41
1:HL:32:LEU:HD13	1:HL:51:VAL:HG22	2.01	0.41
1:HO:44:ASN:CB	1:HO:78:LEU:HA	2.51	0.41
1:HQ:6:SER:OG	1:HS:11:PRO:HB3	2.20	0.41
1:HR:44:ASN:CB	1:HR:78:LEU:HA	2.51	0.41
1:HS:104:ASN:OD1	1:HS:113:VAL:HB	2.21	0.41
1:HZ:110:VAL:HB	1:KC:36:THR:HG23	2.02	0.41
1:IG:74:SER:O	1:KB:71:ALA:HA	2.20	0.41
1:IL:6:SER:OG	1:IN:11:PRO:HB3	2.20	0.41
1:IY:44:ASN:CB	1:IY:78:LEU:HA	2.51	0.41
1:JJ:6:SER:OG	1:JL:11:PRO:HB3	2.20	0.41
1:JL:16:ILE:HG23	1:JL:33:VAL:HG22	2.02	0.41
1:JS:45:ILE:HG23	1:JS:77:ALA:HB3	2.01	0.41
1:JZ:2:ILE:HD13	1:JZ:32:LEU:HD23	2.02	0.41
1:AD:110:VAL:HA	1:BC:47:TYR:CE1	2.56	0.41
1:AG:47:TYR:HE1	1:BF:109:ASN:O	2.04	0.41
1:AG:69:ILE:HD13	1:BF:87:LYS:HA	2.03	0.41
1:AI:104:ASN:OD1	1:AI:113:VAL:HB	2.21	0.41
1:AL:104:ASN:OD1	1:AL:113:VAL:HB	2.21	0.41
1:AR:89:ARG:HH22	1:ED:21:GLY:H	1.66	0.41
1:AS:98:ILE:CD1	1:EL:73:LEU:HD13	2.51	0.41
1:AV:44:ASN:OD1	1:AV:44:ASN:C	2.62	0.41
1:AV:53:TYR:CE2	1:EF:86:GLU:CG	3.04	0.41
1:AY:4:LYS:HE2	1:EI:112:THR:HG21	2.02	0.41
1:BL:44:ASN:CB	1:BL:78:LEU:HA	2.51	0.41
1:BN:2:ILE:HD13	1:BN:32:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:44:ASN:OD1	1:BN:44:ASN:C	2.62	0.41
1:BT:2:ILE:HD13	1:BT:32:LEU:HD23	2.02	0.41
1:BV:104:ASN:OD1	1:BV:113:VAL:HB	2.21	0.41
1:CA:44:ASN:CB	1:CA:78:LEU:HA	2.51	0.41
1:CC:21:GLY:H	1:GK:89:ARG:HH22	1.68	0.41
1:CH:109:ASN:HA	1:FT:11:PRO:O	2.20	0.41
1:CJ:110:VAL:HB	1:CO:36:THR:HG23	2.02	0.41
1:CL:44:ASN:OD1	1:CL:44:ASN:C	2.62	0.41
1:CU:6:SER:OG	1:CW:11:PRO:HB3	2.20	0.41
1:DA:89:ARG:HH22	1:DE:21:GLY:H	1.66	0.41
1:DC:51:VAL:HG11	1:GO:90:VAL:HG13	2.02	0.41
1:DC:104:ASN:OD1	1:DC:113:VAL:HB	2.21	0.41
1:DX:16:ILE:HG23	1:DX:33:VAL:HG22	2.02	0.41
1:EA:32:LEU:CD1	1:EA:49:ILE:HG23	2.46	0.41
1:EA:104:ASN:OD1	1:EA:113:VAL:HB	2.21	0.41
1:EB:6:SER:OG	1:ED:11:PRO:HB3	2.20	0.41
1:EH:99:THR:CG2	1:EO:95:VAL:HG11	2.51	0.41
1:EO:2:ILE:HD13	1:EO:32:LEU:HD23	2.02	0.41
1:EV:32:LEU:CD1	1:EV:49:ILE:HG23	2.46	0.41
1:FN:104:ASN:OD1	1:FN:113:VAL:HB	2.21	0.41
1:FT:104:ASN:OD1	1:FT:113:VAL:HB	2.21	0.41
1:GA:44:ASN:C	1:GA:44:ASN:OD1	2.62	0.41
1:GF:104:ASN:OD1	1:GF:113:VAL:HB	2.21	0.41
1:GG:6:SER:OG	1:GI:11:PRO:HB3	2.20	0.41
1:GO:16:ILE:HG23	1:GO:33:VAL:HG22	2.02	0.41
1:GU:104:ASN:OD1	1:GU:113:VAL:HB	2.21	0.41
1:GV:4:LYS:HG2	1:GV:17:TYR:CE1	2.56	0.41
1:HB:4:LYS:HG2	1:HB:17:TYR:CE1	2.56	0.41
1:HF:2:ILE:HD13	1:HF:32:LEU:HD23	2.02	0.41
1:HF:44:ASN:CB	1:HF:78:LEU:HA	2.51	0.41
1:HJ:91:LEU:HD11	1:IZ:105:ILE:CG2	2.51	0.41
1:HP:104:ASN:OD1	1:HP:113:VAL:HB	2.21	0.41
1:HV:88:LEU:HD23	1:JO:106:ILE:HG21	2.03	0.41
1:HW:6:SER:OG	1:HY:11:PRO:HB3	2.20	0.41
1:HZ:6:SER:OG	1:IB:11:PRO:HB3	2.20	0.41
1:IE:16:ILE:HG23	1:IE:33:VAL:HG22	2.02	0.41
1:IE:104:ASN:OD1	1:IE:113:VAL:HB	2.21	0.41
1:IS:44:ASN:CB	1:IS:78:LEU:HA	2.51	0.41
1:IU:2:ILE:HD13	1:IU:32:LEU:HD23	2.02	0.41
1:JD:45:ILE:HG23	1:JD:77:ALA:HB3	2.01	0.41
1:JH:74:SER:OG	1:JP:72:ASN:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JI:16:ILE:HG23	1:JI:33:VAL:HG22	2.02	0.41
1:JU:16:ILE:HG23	1:JU:33:VAL:HG22	2.02	0.41
1:JX:104:ASN:OD1	1:JX:113:VAL:HB	2.21	0.41
1:KC:2:ILE:HD13	1:KC:32:LEU:HD23	2.02	0.41
1:KD:16:ILE:HG23	1:KD:33:VAL:HG22	2.02	0.41
1:KD:104:ASN:OD1	1:KD:113:VAL:HB	2.21	0.41
1:KE:2:ILE:HD13	1:KE:32:LEU:HD23	2.01	0.41
1:AG:4:LYS:HG2	1:AG:17:TYR:CE1	2.56	0.41
1:AH:55:LEU:HD13	1:GD:83:ASN:ND2	2.36	0.41
1:AK:105:ILE:HG12	1:FO:47:TYR:CZ	2.56	0.41
1:AM:21:GLY:H	1:CA:89:ARG:HH22	1.67	0.41
1:AO:104:ASN:OD1	1:AO:113:VAL:HB	2.21	0.41
1:AR:104:ASN:OD1	1:AR:113:VAL:HB	2.21	0.41
1:AS:2:ILE:HD13	1:AS:32:LEU:HD23	2.02	0.41
1:AU:104:ASN:OD1	1:AU:113:VAL:HB	2.21	0.41
1:AX:102:LYS:HG2	1:EJ:88:LEU:CD2	2.51	0.41
1:AY:4:LYS:HG2	1:AY:17:TYR:CE1	2.56	0.41
1:AY:6:SER:OG	1:BA:11:PRO:HB3	2.20	0.41
1:AZ:2:ILE:HD13	1:AZ:32:LEU:HD23	2.02	0.41
1:BE:110:VAL:HA	1:BL:47:TYR:CE1	2.56	0.41
1:BG:104:ASN:OD1	1:BG:113:VAL:HB	2.21	0.41
1:BH:2:ILE:HD13	1:BH:32:LEU:HD23	2.02	0.41
1:BH:44:ASN:OD1	1:BH:44:ASN:C	2.62	0.41
1:BH:106:ILE:HA	1:BO:75:PHE:CE2	2.56	0.41
1:BP:104:ASN:OD1	1:BP:113:VAL:HB	2.21	0.41
1:BV:73:LEU:HD22	1:FH:98:ILE:HD11	2.02	0.41
1:BW:2:ILE:HD13	1:BW:32:LEU:HD23	2.02	0.41
1:BZ:4:LYS:HG2	1:BZ:17:TYR:CE1	2.56	0.41
1:BZ:89:ARG:HH22	1:DT:21:GLY:H	1.68	0.41
1:CC:74:SER:N	1:GK:72:ASN:O	2.42	0.41
1:CG:2:ILE:HD13	1:CG:32:LEU:HD23	2.02	0.41
1:CH:104:ASN:OD1	1:CH:113:VAL:HB	2.21	0.41
1:CL:3:THR:OG1	1:CL:20:THR:HG22	2.21	0.41
1:CL:4:LYS:HG2	1:CL:17:TYR:CE1	2.56	0.41
1:CN:104:ASN:OD1	1:CN:113:VAL:HB	2.21	0.41
1:CO:6:SER:OG	1:CQ:11:PRO:HB3	2.20	0.41
1:CQ:104:ASN:OD1	1:CQ:113:VAL:HB	2.21	0.41
1:CR:4:LYS:HG2	1:CR:17:TYR:CE1	2.56	0.41
1:CR:6:SER:OG	1:CT:11:PRO:HB3	2.20	0.41
1:DA:2:ILE:HD13	1:DA:32:LEU:HD23	2.01	0.41
1:DJ:4:LYS:HG2	1:DJ:17:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DL:102:LYS:HG2	1:GX:88:LEU:CD2	2.50	0.41
1:DM:3:THR:OG1	1:DM:20:THR:HG22	2.21	0.41
1:DM:106:ILE:HA	1:GT:75:PHE:CE2	2.56	0.41
1:DS:45:ILE:HG23	1:DS:77:ALA:HB3	2.01	0.41
1:DV:3:THR:OG1	1:DV:20:THR:HG22	2.21	0.41
1:DY:6:SER:OG	1:EA:11:PRO:HB3	2.20	0.41
1:DY:45:ILE:HG21	1:FY:108:GLY:HA3	2.02	0.41
1:ED:16:ILE:HG23	1:ED:33:VAL:HG22	2.02	0.41
1:EI:44:ASN:CB	1:EI:78:LEU:HA	2.51	0.41
1:EK:83:ASN:HD22	1:ER:55:LEU:HD13	1.85	0.41
1:EQ:4:LYS:HG2	1:EQ:17:TYR:CE1	2.56	0.41
1:ER:44:ASN:CB	1:ER:78:LEU:HA	2.51	0.41
1:ET:4:LYS:HG2	1:ET:17:TYR:CE1	2.56	0.41
1:EW:4:LYS:HG2	1:EW:17:TYR:CE1	2.56	0.41
1:EY:104:ASN:OD1	1:EY:113:VAL:HB	2.21	0.41
1:FC:3:THR:OG1	1:FC:20:THR:HG22	2.21	0.41
1:FI:2:ILE:HD13	1:FI:32:LEU:HD23	2.02	0.41
1:FI:4:LYS:HG2	1:FI:17:TYR:CE1	2.56	0.41
1:FJ:2:ILE:HD13	1:FJ:32:LEU:HD23	2.02	0.41
1:FS:112:THR:HG21	1:GP:4:LYS:HE2	2.01	0.41
1:FU:3:THR:OG1	1:FU:20:THR:HG22	2.21	0.41
1:FY:2:ILE:HD13	1:FY:32:LEU:HD23	2.02	0.41
1:GA:3:THR:OG1	1:GA:20:THR:HG22	2.21	0.41
1:GG:2:ILE:HD13	1:GG:32:LEU:HD23	2.02	0.41
1:GJ:3:THR:OG1	1:GJ:20:THR:HG22	2.21	0.41
1:GK:2:ILE:HD13	1:GK:32:LEU:HD23	2.02	0.41
1:GN:44:ASN:CB	1:GN:78:LEU:HA	2.51	0.41
1:GR:32:LEU:CD1	1:GR:49:ILE:HG23	2.46	0.41
1:GW:2:ILE:HD13	1:GW:32:LEU:HD23	2.02	0.41
1:GX:26:ALA:HA	1:GX:29:MET:HB2	2.01	0.41
1:HE:4:LYS:HG2	1:HE:17:TYR:CE1	2.56	0.41
1:HE:11:PRO:O	1:HU:110:VAL:HG12	2.20	0.41
1:HE:73:LEU:HD13	1:HU:73:LEU:HD12	2.02	0.41
1:HJ:32:LEU:CD1	1:HJ:49:ILE:HG23	2.46	0.41
1:HQ:2:ILE:HD13	1:HQ:32:LEU:HD23	2.02	0.41
1:HQ:3:THR:OG1	1:HQ:20:THR:HG22	2.21	0.41
1:HX:44:ASN:CB	1:HX:78:LEU:HA	2.51	0.41
1:HY:104:ASN:OD1	1:HY:113:VAL:HB	2.21	0.41
1:HY:106:ILE:HG21	1:JR:88:LEU:HD23	2.03	0.41
1:HZ:2:ILE:HD13	1:HZ:32:LEU:HD23	2.02	0.41
1:HZ:4:LYS:HG2	1:HZ:17:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IB:104:ASN:OD1	1:IB:113:VAL:HB	2.21	0.41
1:IG:69:ILE:HG12	1:KB:78:LEU:HD12	2.02	0.41
1:IH:104:ASN:OD1	1:IH:113:VAL:HB	2.21	0.41
1:IR:3:THR:OG1	1:IR:20:THR:HG22	2.21	0.41
1:IU:3:THR:OG1	1:IU:20:THR:HG22	2.21	0.41
1:IU:111:LEU:HG	1:JE:11:PRO:HA	2.03	0.41
1:IW:16:ILE:HG23	1:IW:33:VAL:HG22	2.02	0.41
1:IZ:104:ASN:OD1	1:IZ:113:VAL:HB	2.21	0.41
1:JA:4:LYS:HG2	1:JA:17:TYR:CE1	2.56	0.41
1:JA:97:PHE:CD1	1:JQ:32:LEU:HD21	2.56	0.41
1:JD:4:LYS:HG2	1:JD:17:TYR:CE1	2.56	0.41
1:JD:51:VAL:HG21	1:JN:94:ILE:CG1	2.50	0.41
1:JF:104:ASN:OD1	1:JF:113:VAL:HB	2.21	0.41
1:JI:32:LEU:CD1	1:JI:49:ILE:HG23	2.46	0.41
1:JL:104:ASN:OD1	1:JL:113:VAL:HB	2.21	0.41
1:JS:3:THR:OG1	1:JS:20:THR:HG22	2.21	0.41
1:JS:4:LYS:HG2	1:JS:17:TYR:CE1	2.56	0.41
1:JU:104:ASN:OD1	1:JU:113:VAL:HB	2.21	0.41
1:JV:3:THR:OG1	1:JV:20:THR:HG22	2.21	0.41
1:KB:2:ILE:HD13	1:KB:32:LEU:HD23	2.01	0.41
1:KB:4:LYS:HG2	1:KB:17:TYR:CE1	2.56	0.41
1:AA:4:LYS:HG2	1:AA:17:TYR:CE1	2.56	0.41
1:AJ:4:LYS:HG2	1:AJ:17:TYR:CE1	2.56	0.41
1:AP:51:VAL:HG11	1:BU:90:VAL:HG13	2.03	0.41
1:AQ:36:THR:HG23	1:FU:110:VAL:HB	2.03	0.41
1:AX:16:ILE:HG23	1:AX:33:VAL:HG22	2.02	0.41
1:AX:86:GLU:OE1	1:AX:86:GLU:N	2.53	0.41
1:BE:4:LYS:HG2	1:BE:17:TYR:CE1	2.56	0.41
1:BF:44:ASN:CB	1:BF:78:LEU:HA	2.51	0.41
1:CB:32:LEU:CD1	1:CB:49:ILE:HG23	2.46	0.41
1:CB:104:ASN:OD1	1:CB:113:VAL:HB	2.21	0.41
1:CC:55:LEU:CD1	1:GK:81:VAL:HG21	2.51	0.41
1:CC:71:ALA:HA	1:GK:74:SER:O	2.21	0.41
1:CG:44:ASN:CB	1:CG:78:LEU:HA	2.51	0.41
1:CG:112:THR:HG22	1:CL:17:TYR:OH	2.21	0.41
1:CO:4:LYS:HG2	1:CO:17:TYR:CE1	2.56	0.41
1:CQ:16:ILE:HG23	1:CQ:33:VAL:HG22	2.02	0.41
1:CU:4:LYS:HG2	1:CU:17:TYR:CE1	2.56	0.41
1:DD:6:SER:OG	1:DF:11:PRO:HB3	2.20	0.41
1:DI:16:ILE:HG23	1:DI:33:VAL:HG22	2.02	0.41
1:DM:4:LYS:HG2	1:DM:17:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:2:ILE:HD13	1:DP:32:LEU:HD23	2.02	0.41
1:DP:3:THR:OG1	1:DP:20:THR:HG22	2.21	0.41
1:DY:4:LYS:HG2	1:DY:17:TYR:CE1	2.56	0.41
1:EG:104:ASN:OD1	1:EG:113:VAL:HB	2.21	0.41
1:EQ:3:THR:OG1	1:EQ:20:THR:HG22	2.21	0.41
1:ET:89:ARG:HH22	1:FG:21:GLY:H	1.68	0.41
1:EW:6:SER:OG	1:EY:11:PRO:HB3	2.20	0.41
1:EX:44:ASN:CB	1:EX:78:LEU:HA	2.51	0.41
1:FC:4:LYS:HG2	1:FC:17:TYR:CE1	2.56	0.41
1:FE:32:LEU:CD1	1:FE:49:ILE:HG23	2.46	0.41
1:FM:44:ASN:CB	1:FM:78:LEU:HA	2.51	0.41
1:FP:90:VAL:HG13	1:GV:51:VAL:HG11	2.03	0.41
1:FQ:16:ILE:HG23	1:FQ:33:VAL:HG22	2.02	0.41
1:GC:86:GLU:OE1	1:GC:86:GLU:N	2.53	0.41
1:GC:104:ASN:OD1	1:GC:113:VAL:HB	2.21	0.41
1:GY:83:ASN:ND2	1:HO:55:LEU:HD13	2.36	0.41
1:HG:21:GLY:H	1:IT:89:ARG:HH22	1.69	0.41
1:HG:55:LEU:HD13	1:IT:83:ASN:OD1	2.21	0.41
1:HL:112:THR:HG22	1:JG:17:TYR:OH	2.20	0.41
1:HN:83:ASN:HD22	1:HR:55:LEU:HD13	1.86	0.41
1:HU:44:ASN:CB	1:HU:78:LEU:HA	2.51	0.41
1:HV:104:ASN:OD1	1:HV:113:VAL:HB	2.21	0.41
1:HW:3:THR:OG1	1:HW:20:THR:HG22	2.21	0.41
1:HX:2:ILE:HD13	1:HX:32:LEU:HD23	2.02	0.41
1:IQ:104:ASN:OD1	1:IQ:113:VAL:HB	2.21	0.41
1:JB:2:ILE:HD13	1:JB:32:LEU:HD23	2.02	0.41
1:JM:4:LYS:HG2	1:JM:17:TYR:CE1	2.56	0.41
1:JP:6:SER:OG	1:JR:11:PRO:HB3	2.20	0.41
1:KG:16:ILE:HG23	1:KG:33:VAL:HG22	2.02	0.41
1:KH:2:ILE:HD13	1:KH:32:LEU:HD23	2.02	0.41
1:AA:51:VAL:HG11	1:BI:90:VAL:HG13	2.03	0.40
1:AB:2:ILE:HD13	1:AB:32:LEU:HD23	2.02	0.40
1:AB:73:LEU:HD12	1:FX:73:LEU:HD13	2.02	0.40
1:AE:2:ILE:HD13	1:AE:32:LEU:HD23	2.02	0.40
1:AF:95:VAL:HG13	1:DR:95:VAL:HG13	2.02	0.40
1:AG:2:ILE:HD13	1:AG:32:LEU:HD23	2.02	0.40
1:AK:89:ARG:HH22	1:FO:21:GLY:H	1.67	0.40
1:AN:11:PRO:HB3	1:FR:109:ASN:CG	2.46	0.40
1:AQ:108:GLY:HA3	1:FU:45:ILE:CG2	2.51	0.40
1:AY:94:ILE:HG13	1:EI:49:ILE:HG21	2.02	0.40
1:BB:89:ARG:HH22	1:BR:21:GLY:H	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:6:SER:OG	1:BG:11:PRO:HB3	2.20	0.40
1:BI:2:ILE:HD13	1:BI:32:LEU:HD23	2.02	0.40
1:BN:6:SER:OG	1:BP:11:PRO:HB3	2.20	0.40
1:BR:44:ASN:CB	1:BR:78:LEU:HA	2.51	0.40
1:BT:3:THR:OG1	1:BT:20:THR:HG22	2.21	0.40
1:BZ:3:THR:OG1	1:BZ:20:THR:HG22	2.21	0.40
1:BZ:94:ILE:HG13	1:DT:49:ILE:HG21	2.02	0.40
1:CB:73:LEU:HD12	1:FN:72:ASN:O	2.21	0.40
1:CC:6:SER:OG	1:CE:11:PRO:HB3	2.20	0.40
1:CG:11:PRO:HB3	1:CL:109:ASN:OD1	2.21	0.40
1:CH:69:ILE:HG12	1:FT:78:LEU:HD12	2.03	0.40
1:CN:16:ILE:HG23	1:CN:33:VAL:HG22	2.02	0.40
1:CR:3:THR:OG1	1:CR:20:THR:HG22	2.21	0.40
1:CU:110:VAL:HA	1:DH:47:TYR:HE1	1.85	0.40
1:CX:6:SER:OG	1:CZ:11:PRO:HB3	2.20	0.40
1:DB:72:ASN:O	1:GJ:73:LEU:HD12	2.21	0.40
1:DF:99:THR:HG23	1:GR:95:VAL:HG11	2.03	0.40
1:DL:16:ILE:HG23	1:DL:33:VAL:HG22	2.02	0.40
1:DP:73:LEU:HD12	1:GW:72:ASN:O	2.20	0.40
1:DY:2:ILE:HG23	1:FY:93:GLU:OE1	2.22	0.40
1:EB:98:ILE:HD11	1:GB:73:LEU:HD13	2.04	0.40
1:EE:105:ILE:HG12	1:EU:47:TYR:CZ	2.55	0.40
1:EK:4:LYS:HG2	1:EK:17:TYR:CE1	2.56	0.40
1:EO:44:ASN:CB	1:EO:78:LEU:HA	2.51	0.40
1:ET:3:THR:OG1	1:ET:20:THR:HG22	2.21	0.40
1:FT:16:ILE:HG23	1:FT:33:VAL:HG22	2.02	0.40
1:GG:4:LYS:HG2	1:GG:17:TYR:CE1	2.56	0.40
1:GO:104:ASN:OD1	1:GO:113:VAL:HB	2.21	0.40
1:GV:6:SER:OG	1:GX:11:PRO:HB3	2.20	0.40
1:GY:3:THR:OG1	1:GY:20:THR:HG22	2.21	0.40
1:GY:89:ARG:NH2	1:HO:20:THR:H	2.18	0.40
1:GZ:21:GLY:H	1:JY:89:ARG:HH22	1.69	0.40
1:HB:3:THR:OG1	1:HB:20:THR:HG22	2.21	0.40
1:HB:102:LYS:HG2	1:HX:88:LEU:HD23	2.01	0.40
1:HJ:104:ASN:OD1	1:HJ:113:VAL:HB	2.21	0.40
1:HK:4:LYS:HG2	1:HK:17:TYR:CE1	2.56	0.40
1:HL:21:GLY:H	1:JG:89:ARG:HH22	1.67	0.40
1:HN:4:LYS:HG2	1:HN:17:TYR:CE1	2.56	0.40
1:HU:2:ILE:HD13	1:HU:32:LEU:HD23	2.02	0.40
1:HZ:3:THR:OG1	1:HZ:20:THR:HG22	2.21	0.40
1:IC:3:THR:OG1	1:IC:20:THR:HG22	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IW:104:ASN:OD1	1:IW:113:VAL:HB	2.21	0.40
1:JG:6:SER:OG	1:JI:11:PRO:HB3	2.20	0.40
1:JH:75:PHE:CD1	1:JP:71:ALA:HB2	2.52	0.40
1:JI:104:ASN:OD1	1:JI:113:VAL:HB	2.21	0.40
1:JQ:2:ILE:HD13	1:JQ:32:LEU:HD23	2.02	0.40
1:KG:104:ASN:OD1	1:KG:113:VAL:HB	2.21	0.40
1:KJ:16:ILE:HG23	1:KJ:33:VAL:HG22	2.02	0.40
1:AC:16:ILE:HG23	1:AC:33:VAL:HG22	2.02	0.40
1:AD:3:THR:OG1	1:AD:20:THR:HG22	2.21	0.40
1:AG:3:THR:OG1	1:AG:20:THR:HG22	2.21	0.40
1:AJ:3:THR:OG1	1:AJ:20:THR:HG22	2.21	0.40
1:AK:17:TYR:OH	1:FO:112:THR:HG23	2.21	0.40
1:AS:4:LYS:HG2	1:AS:17:TYR:CE1	2.56	0.40
1:AS:30:PRO:HB3	1:AS:53:TYR:HA	2.04	0.40
1:AT:44:ASN:CB	1:AT:78:LEU:HA	2.51	0.40
1:BD:32:LEU:CD1	1:BD:49:ILE:HG23	2.46	0.40
1:BH:30:PRO:HB3	1:BH:53:TYR:HA	2.04	0.40
1:BN:4:LYS:HG2	1:BN:17:TYR:CE1	2.56	0.40
1:BT:4:LYS:HG2	1:BT:17:TYR:CE1	2.56	0.40
1:BW:4:LYS:HG2	1:BW:17:TYR:CE1	2.56	0.40
1:BZ:98:ILE:CD1	1:DT:73:LEU:HD13	2.50	0.40
1:CE:104:ASN:OD1	1:CE:113:VAL:HB	2.21	0.40
1:CK:32:LEU:CD1	1:CK:49:ILE:HG23	2.46	0.40
1:CM:2:ILE:HD13	1:CM:32:LEU:HD23	2.02	0.40
1:CO:3:THR:OG1	1:CO:20:THR:HG22	2.21	0.40
1:CP:44:ASN:CB	1:CP:78:LEU:HA	2.51	0.40
1:CV:2:ILE:HD13	1:CV:32:LEU:HD23	2.02	0.40
1:CX:4:LYS:HG2	1:CX:17:TYR:CE1	2.56	0.40
1:DK:44:ASN:CB	1:DK:78:LEU:HA	2.51	0.40
1:DM:98:ILE:HD11	1:GT:73:LEU:HD13	2.03	0.40
1:DU:104:ASN:OD1	1:DU:113:VAL:HB	2.21	0.40
1:DY:3:THR:OG1	1:DY:20:THR:HG22	2.21	0.40
1:EE:51:VAL:CG1	1:EU:90:VAL:HG13	2.50	0.40
1:EM:16:ILE:HG23	1:EM:33:VAL:HG22	2.02	0.40
1:EQ:11:PRO:O	1:FM:110:VAL:HG12	2.20	0.40
1:ER:2:ILE:HD13	1:ER:32:LEU:HD23	2.02	0.40
1:FD:44:ASN:CB	1:FD:78:LEU:HA	2.51	0.40
1:FF:3:THR:OG1	1:FF:20:THR:HG22	2.21	0.40
1:FF:4:LYS:HG2	1:FF:17:TYR:CE1	2.56	0.40
1:FL:6:SER:OG	1:FN:11:PRO:HB3	2.20	0.40
1:FO:3:THR:OG1	1:FO:20:THR:HG22	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FP:105:ILE:HG12	1:GV:47:TYR:CZ	2.56	0.40
1:FR:4:LYS:HG2	1:FR:17:TYR:CE1	2.56	0.40
1:FX:4:LYS:HG2	1:FX:17:TYR:CE1	2.56	0.40
1:FY:44:ASN:CB	1:FY:78:LEU:HA	2.51	0.40
1:GQ:44:ASN:CB	1:GQ:78:LEU:HA	2.51	0.40
1:GW:44:ASN:CB	1:GW:78:LEU:HA	2.51	0.40
1:GY:4:LYS:HG2	1:GY:17:TYR:CE1	2.56	0.40
1:HC:44:ASN:CB	1:HC:78:LEU:HA	2.51	0.40
1:HK:3:THR:OG1	1:HK:20:THR:HG22	2.21	0.40
1:HQ:4:LYS:HG2	1:HQ:17:TYR:CE1	2.56	0.40
1:HT:2:ILE:HD13	1:HT:32:LEU:HD23	2.02	0.40
1:HT:30:PRO:HB3	1:HT:53:TYR:HA	2.04	0.40
1:IX:3:THR:OG1	1:IX:20:THR:HG22	2.21	0.40
1:JC:104:ASN:OD1	1:JC:113:VAL:HB	2.21	0.40
1:JH:106:ILE:HG13	1:JP:88:LEU:CD2	2.52	0.40
1:JO:104:ASN:OD1	1:JO:113:VAL:HB	2.21	0.40
1:JP:4:LYS:HG2	1:JP:17:TYR:CE1	2.56	0.40
1:JY:6:SER:OG	1:KA:11:PRO:HB3	2.20	0.40
1:AB:32:LEU:CD1	1:AB:49:ILE:HG23	2.48	0.40
1:AD:4:LYS:HG2	1:AD:17:TYR:CE1	2.56	0.40
1:AG:30:PRO:HB3	1:AG:53:TYR:HA	2.04	0.40
1:AL:72:ASN:O	1:DX:73:LEU:HD12	2.21	0.40
1:AM:4:LYS:HG2	1:AM:17:TYR:CE1	2.56	0.40
1:AP:4:LYS:HG2	1:AP:17:TYR:CE1	2.56	0.40
1:AS:3:THR:OG1	1:AS:20:THR:HG22	2.21	0.40
1:AV:4:LYS:HG2	1:AV:17:TYR:CE1	2.56	0.40
1:BA:104:ASN:OD1	1:BA:113:VAL:HB	2.21	0.40
1:BD:104:ASN:OD1	1:BD:113:VAL:HB	2.21	0.40
1:BJ:104:ASN:OD1	1:BJ:113:VAL:HB	2.21	0.40
1:BU:44:ASN:CB	1:BU:78:LEU:HA	2.51	0.40
1:BZ:112:THR:HG23	1:DT:17:TYR:OH	2.22	0.40
1:CF:3:THR:OG1	1:CF:20:THR:HG22	2.21	0.40
1:CX:2:ILE:HD13	1:CX:32:LEU:HD23	2.02	0.40
1:DD:4:LYS:HG2	1:DD:17:TYR:CE1	2.56	0.40
1:DG:3:THR:OG1	1:DG:20:THR:HG22	2.21	0.40
1:DP:6:SER:OG	1:DR:11:PRO:HB3	2.20	0.40
1:DV:36:THR:HG23	1:GE:110:VAL:HB	2.03	0.40
1:EE:6:SER:OG	1:EG:11:PRO:HB3	2.20	0.40
1:EN:3:THR:OG1	1:EN:20:THR:HG22	2.21	0.40
1:ES:104:ASN:OD1	1:ES:113:VAL:HB	2.21	0.40
1:FL:3:THR:OG1	1:FL:20:THR:HG22	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FL:30:PRO:HB3	1:FL:53:TYR:HA	2.04	0.40
1:FS:21:GLY:H	1:GP:89:ARG:HH22	1.69	0.40
1:GE:32:LEU:CD1	1:GE:49:ILE:HG23	2.48	0.40
1:GF:16:ILE:HG23	1:GF:33:VAL:HG22	2.02	0.40
1:GG:3:THR:OG1	1:GG:20:THR:HG22	2.21	0.40
1:GI:104:ASN:OD1	1:GI:113:VAL:HB	2.21	0.40
1:GJ:4:LYS:HG2	1:GJ:17:TYR:CE1	2.56	0.40
1:ID:2:ILE:HD13	1:ID:32:LEU:HD23	2.02	0.40
1:IG:44:ASN:CB	1:IG:78:LEU:HA	2.51	0.40
1:II:6:SER:OG	1:IK:11:PRO:HB3	2.20	0.40
1:IK:104:ASN:OD1	1:IK:113:VAL:HB	2.21	0.40
1:IL:3:THR:OG1	1:IL:20:THR:HG22	2.21	0.40
1:IL:4:LYS:HG2	1:IL:17:TYR:CE1	2.56	0.40
1:IT:86:GLU:OE1	1:IT:86:GLU:N	2.53	0.40
1:IU:110:VAL:HB	1:JE:36:THR:HG23	2.02	0.40
1:JH:44:ASN:CB	1:JH:78:LEU:HA	2.51	0.40
1:JP:3:THR:OG1	1:JP:20:THR:HG22	2.21	0.40
1:JU:32:LEU:CD1	1:JU:49:ILE:HG23	2.46	0.40
1:JW:2:ILE:HD13	1:JW:32:LEU:HD23	2.02	0.40
1:KE:4:LYS:HG2	1:KE:17:TYR:CE1	2.56	0.40
1:KH:6:SER:OG	1:KJ:11:PRO:HB3	2.20	0.40
1:AQ:93:GLU:OE1	1:FU:2:ILE:HG23	2.22	0.40
1:AR:16:ILE:HG23	1:AR:33:VAL:HG22	2.02	0.40
1:AY:102:LYS:HG3	1:EI:91:LEU:CD1	2.51	0.40
1:BB:3:THR:OG1	1:BB:20:THR:HG22	2.21	0.40
1:BK:6:SER:OG	1:BM:11:PRO:HB3	2.20	0.40
1:BM:106:ILE:HD13	1:EY:88:LEU:HD21	2.03	0.40
1:BQ:4:LYS:HG2	1:BQ:17:TYR:CE1	2.56	0.40
1:BQ:6:SER:OG	1:BS:11:PRO:HB3	2.20	0.40
1:BW:3:THR:OG1	1:BW:20:THR:HG22	2.21	0.40
1:BY:47:TYR:HE1	1:FK:109:ASN:O	2.04	0.40
1:BZ:30:PRO:HB3	1:BZ:53:TYR:HA	2.04	0.40
1:CL:6:SER:OG	1:CN:11:PRO:HB3	2.20	0.40
1:CN:102:LYS:HG2	1:FZ:88:LEU:CD2	2.51	0.40
1:DA:3:THR:OG1	1:DA:20:THR:HG22	2.21	0.40
1:DA:78:LEU:HD12	1:DE:69:ILE:HG12	2.03	0.40
1:DF:86:GLU:OE1	1:DF:86:GLU:N	2.53	0.40
1:DP:4:LYS:HG2	1:DP:17:TYR:CE1	2.56	0.40
1:DP:106:ILE:HG21	1:GW:88:LEU:HG	2.03	0.40
1:DS:4:LYS:HG2	1:DS:17:TYR:CE1	2.56	0.40
1:DX:104:ASN:OD1	1:DX:113:VAL:HB	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EK:3:THR:OG1	1:EK:20:THR:HG22	2.21	0.40
1:FF:30:PRO:HB3	1:FF:53:TYR:HA	2.04	0.40
1:FO:2:ILE:HD13	1:FO:32:LEU:HD23	2.02	0.40
1:FR:3:THR:OG1	1:FR:20:THR:HG22	2.21	0.40
1:FW:86:GLU:OE1	1:FW:86:GLU:N	2.53	0.40
1:FW:104:ASN:OD1	1:FW:113:VAL:HB	2.21	0.40
1:GD:4:LYS:HG2	1:GD:17:TYR:CE1	2.56	0.40
1:GL:104:ASN:OD1	1:GL:113:VAL:HB	2.21	0.40
1:HB:99:THR:HG22	1:HX:95:VAL:HG11	2.04	0.40
1:HN:71:ALA:HB2	1:HR:75:PHE:HD1	1.85	0.40
1:HT:71:ALA:HA	1:IM:74:SER:O	2.20	0.40
1:HZ:109:ASN:O	1:KC:47:TYR:HE1	2.05	0.40
1:IB:32:LEU:CD1	1:IB:49:ILE:HG23	2.46	0.40
1:IG:2:ILE:HD13	1:IG:32:LEU:HD23	2.02	0.40
1:IN:104:ASN:OD1	1:IN:113:VAL:HB	2.21	0.40
1:IP:2:ILE:HD13	1:IP:32:LEU:HD23	2.02	0.40
1:IP:44:ASN:CB	1:IP:78:LEU:HA	2.51	0.40
1:IU:4:LYS:HG2	1:IU:17:TYR:CE1	2.56	0.40
1:IX:73:LEU:HD22	1:JB:98:ILE:HD11	2.03	0.40
1:IZ:32:LEU:CD1	1:IZ:49:ILE:HG23	2.46	0.40
1:JD:3:THR:OG1	1:JD:20:THR:HG22	2.21	0.40
1:JH:83:ASN:OD1	1:JP:55:LEU:HD13	2.21	0.40
1:JM:30:PRO:HB3	1:JM:53:TYR:HA	2.04	0.40
1:JS:2:ILE:HD13	1:JS:32:LEU:HD23	2.02	0.40
1:JT:69:ILE:HG12	1:KH:78:LEU:HD12	2.04	0.40
1:JT:108:GLY:O	1:KH:45:ILE:HD13	2.21	0.40
1:KI:44:ASN:CB	1:KI:78:LEU:HA	2.51	0.40
1:AF:104:ASN:OD1	1:AF:113:VAL:HB	2.21	0.40
1:AM:3:THR:OG1	1:AM:20:THR:HG22	2.21	0.40
1:AM:6:SER:OG	1:AO:11:PRO:HB3	2.20	0.40
1:AP:3:THR:OG1	1:AP:20:THR:HG22	2.21	0.40
1:AP:30:PRO:HB3	1:AP:53:TYR:HA	2.04	0.40
1:AP:73:LEU:CD2	1:BU:98:ILE:HD11	2.51	0.40
1:AY:47:TYR:CZ	1:EI:105:ILE:HG12	2.57	0.40
1:BH:3:THR:OG1	1:BH:20:THR:HG22	2.21	0.40
1:BK:4:LYS:HG2	1:BK:17:TYR:CE1	2.56	0.40
1:BN:3:THR:OG1	1:BN:20:THR:HG22	2.21	0.40
1:BY:32:LEU:CD1	1:BY:49:ILE:HG23	2.46	0.40
1:CC:30:PRO:HB3	1:CC:53:TYR:HA	2.04	0.40
1:CY:110:VAL:HG12	1:GG:11:PRO:O	2.21	0.40
1:CZ:104:ASN:OD1	1:CZ:113:VAL:HB	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DF:95:VAL:HG11	1:GR:99:THR:HG23	2.03	0.40
1:DI:104:ASN:OD1	1:DI:113:VAL:HB	2.21	0.40
1:DS:30:PRO:HB3	1:DS:53:TYR:HA	2.04	0.40
1:EH:76:THR:HG23	1:EO:70:ARG:O	2.21	0.40
1:ET:30:PRO:HB3	1:ET:53:TYR:HA	2.04	0.40
1:EU:44:ASN:CB	1:EU:78:LEU:HA	2.51	0.40
1:FO:4:LYS:HG2	1:FO:17:TYR:CE1	2.56	0.40
1:FR:24:VAL:HB	1:FR:25:PRO:HD2	2.04	0.40
1:FX:3:THR:OG1	1:FX:20:THR:HG22	2.21	0.40
1:GB:2:ILE:HD13	1:GB:32:LEU:HD23	2.02	0.40
1:GM:3:THR:OG1	1:GM:20:THR:HG22	2.21	0.40
1:GN:2:ILE:HD13	1:GN:32:LEU:HD23	2.02	0.40
1:GX:16:ILE:HG23	1:GX:33:VAL:HG22	2.02	0.40
1:HA:16:ILE:HG23	1:HA:33:VAL:HG22	2.02	0.40
1:HD:16:ILE:HG23	1:HD:33:VAL:HG22	2.02	0.40
1:HE:3:THR:OG1	1:HE:20:THR:HG22	2.21	0.40
1:HH:4:LYS:HG2	1:HH:17:TYR:CE1	2.56	0.40
1:IC:4:LYS:HG2	1:IC:17:TYR:CE1	2.56	0.40
1:IC:6:SER:OG	1:IE:11:PRO:HB3	2.20	0.40
1:IF:4:LYS:HG2	1:IF:17:TYR:CE1	2.56	0.40
1:IF:30:PRO:HB3	1:IF:53:TYR:HA	2.04	0.40
1:IO:24:VAL:HB	1:IO:25:PRO:HD2	2.04	0.40
1:IR:4:LYS:HG2	1:IR:17:TYR:CE1	2.56	0.40
1:IU:24:VAL:HB	1:IU:25:PRO:HD2	2.04	0.40
1:IX:4:LYS:HG2	1:IX:17:TYR:CE1	2.56	0.40
1:IX:73:LEU:HB2	1:JB:73:LEU:HD12	2.03	0.40
1:JA:112:THR:HG23	1:JQ:17:TYR:OH	2.22	0.40
1:JJ:3:THR:OG1	1:JJ:20:THR:HG22	2.21	0.40
1:JJ:30:PRO:HB3	1:JJ:53:TYR:HA	2.04	0.40
1:JT:2:ILE:HD13	1:JT:32:LEU:HD23	2.02	0.40
1:JX:32:LEU:CD1	1:JX:49:ILE:HG23	2.46	0.40
1:KB:24:VAL:HB	1:KB:25:PRO:HD2	2.04	0.40
1:KH:3:THR:OG1	1:KH:20:THR:HG22	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	112/115 (97%)	112 (100%)	0	0	100	100
1	AB	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	AC	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	AD	112/115 (97%)	112 (100%)	0	0	100	100
1	AE	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	AF	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	AG	112/115 (97%)	112 (100%)	0	0	100	100
1	AH	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	AI	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	AJ	112/115 (97%)	112 (100%)	0	0	100	100
1	AK	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	AL	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	AM	112/115 (97%)	112 (100%)	0	0	100	100
1	AN	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	AO	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	AP	112/115 (97%)	112 (100%)	0	0	100	100
1	AQ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	AR	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	AS	112/115 (97%)	112 (100%)	0	0	100	100
1	AT	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	AU	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	AV	112/115 (97%)	112 (100%)	0	0	100	100
1	AW	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	AX	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	AY	112/115 (97%)	112 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AZ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	BA	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	BB	112/115 (97%)	112 (100%)	0	0	100	100
1	BC	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	BD	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	BE	112/115 (97%)	112 (100%)	0	0	100	100
1	BF	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	BG	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	BH	112/115 (97%)	112 (100%)	0	0	100	100
1	BI	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	BJ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	BK	112/115 (97%)	112 (100%)	0	0	100	100
1	BL	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	BM	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	BN	112/115 (97%)	112 (100%)	0	0	100	100
1	BO	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	BP	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	BQ	112/115 (97%)	112 (100%)	0	0	100	100
1	BR	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	BS	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	BT	112/115 (97%)	112 (100%)	0	0	100	100
1	BU	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	BV	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	BW	112/115 (97%)	112 (100%)	0	0	100	100
1	BX	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	BY	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	BZ	112/115 (97%)	112 (100%)	0	0	100	100
1	CA	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	CB	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	CC	112/115 (97%)	112 (100%)	0	0	100	100
1	CD	112/115 (97%)	111 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CE	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	CF	112/115 (97%)	112 (100%)	0	0	100	100
1	CG	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	CH	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	CI	112/115 (97%)	112 (100%)	0	0	100	100
1	CJ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	CK	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	CL	112/115 (97%)	112 (100%)	0	0	100	100
1	CM	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	CN	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	CO	112/115 (97%)	112 (100%)	0	0	100	100
1	CP	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	CQ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	CR	112/115 (97%)	112 (100%)	0	0	100	100
1	CS	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	CT	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	CU	112/115 (97%)	112 (100%)	0	0	100	100
1	CV	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	CW	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	CX	112/115 (97%)	112 (100%)	0	0	100	100
1	CY	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	CZ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	DA	112/115 (97%)	112 (100%)	0	0	100	100
1	DB	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	DC	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	DD	112/115 (97%)	112 (100%)	0	0	100	100
1	DE	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	DF	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	DG	112/115 (97%)	112 (100%)	0	0	100	100
1	DH	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	DI	112/115 (97%)	110 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DJ	112/115 (97%)	112 (100%)	0	0	100	100
1	DK	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	DL	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	DM	112/115 (97%)	112 (100%)	0	0	100	100
1	DN	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	DO	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	DP	112/115 (97%)	112 (100%)	0	0	100	100
1	DQ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	DR	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	DS	112/115 (97%)	112 (100%)	0	0	100	100
1	DT	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	DU	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	DV	112/115 (97%)	112 (100%)	0	0	100	100
1	DW	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	DX	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	DY	112/115 (97%)	112 (100%)	0	0	100	100
1	DZ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	EA	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	EB	112/115 (97%)	112 (100%)	0	0	100	100
1	EC	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	ED	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	EE	112/115 (97%)	112 (100%)	0	0	100	100
1	EF	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	EG	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	EH	112/115 (97%)	112 (100%)	0	0	100	100
1	EI	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	EJ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	EK	112/115 (97%)	112 (100%)	0	0	100	100
1	EL	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	EM	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	EN	112/115 (97%)	112 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EO	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	EP	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	EQ	112/115 (97%)	112 (100%)	0	0	100	100
1	ER	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	ES	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	ET	112/115 (97%)	112 (100%)	0	0	100	100
1	EU	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	EV	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	EW	112/115 (97%)	112 (100%)	0	0	100	100
1	EX	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	EY	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	EZ	112/115 (97%)	112 (100%)	0	0	100	100
1	FA	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	FB	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	FC	112/115 (97%)	112 (100%)	0	0	100	100
1	FD	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	FE	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	FF	112/115 (97%)	112 (100%)	0	0	100	100
1	FG	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	FH	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	FI	112/115 (97%)	112 (100%)	0	0	100	100
1	FJ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	FK	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	FL	112/115 (97%)	112 (100%)	0	0	100	100
1	FM	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	FN	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	FO	112/115 (97%)	112 (100%)	0	0	100	100
1	FP	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	FQ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	FR	112/115 (97%)	112 (100%)	0	0	100	100
1	FS	112/115 (97%)	111 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	FT	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	FU	112/115 (97%)	112 (100%)	0	0	100	100
1	FV	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	FW	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	FX	112/115 (97%)	112 (100%)	0	0	100	100
1	FY	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	FZ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	GA	112/115 (97%)	112 (100%)	0	0	100	100
1	GB	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	GC	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	GD	112/115 (97%)	112 (100%)	0	0	100	100
1	GE	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	GF	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	GG	112/115 (97%)	112 (100%)	0	0	100	100
1	GH	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	GI	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	GJ	112/115 (97%)	112 (100%)	0	0	100	100
1	GK	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	GL	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	GM	112/115 (97%)	112 (100%)	0	0	100	100
1	GN	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	GO	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	GP	112/115 (97%)	112 (100%)	0	0	100	100
1	GQ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	GR	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	GS	112/115 (97%)	112 (100%)	0	0	100	100
1	GT	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	GU	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	GV	112/115 (97%)	112 (100%)	0	0	100	100
1	GW	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	GX	112/115 (97%)	110 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GY	112/115 (97%)	112 (100%)	0	0	100	100
1	GZ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	HA	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	HB	112/115 (97%)	112 (100%)	0	0	100	100
1	HC	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	HD	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	HE	112/115 (97%)	112 (100%)	0	0	100	100
1	HF	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	HG	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	HH	112/115 (97%)	112 (100%)	0	0	100	100
1	HI	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	HJ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	HK	112/115 (97%)	112 (100%)	0	0	100	100
1	HL	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	HM	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	HN	112/115 (97%)	112 (100%)	0	0	100	100
1	HO	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	HP	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	HQ	112/115 (97%)	112 (100%)	0	0	100	100
1	HR	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	HS	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	HT	112/115 (97%)	112 (100%)	0	0	100	100
1	HU	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	HV	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	HW	112/115 (97%)	112 (100%)	0	0	100	100
1	HX	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	HY	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	HZ	112/115 (97%)	112 (100%)	0	0	100	100
1	IA	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	IB	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	IC	112/115 (97%)	112 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	ID	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	IE	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	IF	112/115 (97%)	112 (100%)	0	0	100	100
1	IG	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	IH	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	II	112/115 (97%)	112 (100%)	0	0	100	100
1	IJ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	IK	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	IL	112/115 (97%)	112 (100%)	0	0	100	100
1	IM	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	IN	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	IO	112/115 (97%)	112 (100%)	0	0	100	100
1	IP	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	IQ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	IR	112/115 (97%)	112 (100%)	0	0	100	100
1	IS	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	IT	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	IU	112/115 (97%)	112 (100%)	0	0	100	100
1	IV	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	IW	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	IX	112/115 (97%)	112 (100%)	0	0	100	100
1	IY	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	IZ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	JA	112/115 (97%)	112 (100%)	0	0	100	100
1	JB	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	JC	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	JD	112/115 (97%)	112 (100%)	0	0	100	100
1	JE	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	JF	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	JG	112/115 (97%)	112 (100%)	0	0	100	100
1	JH	112/115 (97%)	111 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	JI	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	JJ	112/115 (97%)	112 (100%)	0	0	100	100
1	JK	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	JL	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	JM	112/115 (97%)	112 (100%)	0	0	100	100
1	JN	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	JO	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	JP	112/115 (97%)	112 (100%)	0	0	100	100
1	JQ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	JR	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	JS	112/115 (97%)	112 (100%)	0	0	100	100
1	JT	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	JU	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	JV	112/115 (97%)	112 (100%)	0	0	100	100
1	JW	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	JX	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	JY	112/115 (97%)	112 (100%)	0	0	100	100
1	JZ	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	KA	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	KB	112/115 (97%)	112 (100%)	0	0	100	100
1	KC	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	KD	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	KE	112/115 (97%)	112 (100%)	0	0	100	100
1	KF	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	KG	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
1	KH	112/115 (97%)	112 (100%)	0	0	100	100
1	KI	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
1	KJ	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
All	All	30240/31050 (97%)	29970 (99%)	270 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	97/98 (99%)	97 (100%)	0	100	100
1	AB	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	AC	97/98 (99%)	97 (100%)	0	100	100
1	AD	97/98 (99%)	97 (100%)	0	100	100
1	AE	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	AF	97/98 (99%)	97 (100%)	0	100	100
1	AG	97/98 (99%)	97 (100%)	0	100	100
1	AH	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	AI	97/98 (99%)	97 (100%)	0	100	100
1	AJ	97/98 (99%)	97 (100%)	0	100	100
1	AK	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	AL	97/98 (99%)	97 (100%)	0	100	100
1	AM	97/98 (99%)	97 (100%)	0	100	100
1	AN	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	AO	97/98 (99%)	97 (100%)	0	100	100
1	AP	97/98 (99%)	97 (100%)	0	100	100
1	AQ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	AR	97/98 (99%)	97 (100%)	0	100	100
1	AS	97/98 (99%)	97 (100%)	0	100	100
1	AT	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	AU	97/98 (99%)	97 (100%)	0	100	100
1	AV	97/98 (99%)	97 (100%)	0	100	100
1	AW	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	AX	97/98 (99%)	97 (100%)	0	100	100
1	AY	97/98 (99%)	97 (100%)	0	100	100
1	AZ	97/98 (99%)	96 (99%)	1 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	97/98 (99%)	97 (100%)	0	100	100
1	BB	97/98 (99%)	97 (100%)	0	100	100
1	BC	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	BD	97/98 (99%)	97 (100%)	0	100	100
1	BE	97/98 (99%)	97 (100%)	0	100	100
1	BF	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	BG	97/98 (99%)	97 (100%)	0	100	100
1	BH	97/98 (99%)	97 (100%)	0	100	100
1	BI	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	BJ	97/98 (99%)	97 (100%)	0	100	100
1	BK	97/98 (99%)	97 (100%)	0	100	100
1	BL	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	BM	97/98 (99%)	97 (100%)	0	100	100
1	BN	97/98 (99%)	97 (100%)	0	100	100
1	BO	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	BP	97/98 (99%)	97 (100%)	0	100	100
1	BQ	97/98 (99%)	97 (100%)	0	100	100
1	BR	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	BS	97/98 (99%)	97 (100%)	0	100	100
1	BT	97/98 (99%)	97 (100%)	0	100	100
1	BU	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	BV	97/98 (99%)	97 (100%)	0	100	100
1	BW	97/98 (99%)	97 (100%)	0	100	100
1	BX	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	BY	97/98 (99%)	97 (100%)	0	100	100
1	BZ	97/98 (99%)	97 (100%)	0	100	100
1	CA	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	CB	97/98 (99%)	97 (100%)	0	100	100
1	CC	97/98 (99%)	97 (100%)	0	100	100
1	CD	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	CE	97/98 (99%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CF	97/98 (99%)	97 (100%)	0	100	100
1	CG	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	CH	97/98 (99%)	97 (100%)	0	100	100
1	CI	97/98 (99%)	97 (100%)	0	100	100
1	CJ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	CK	97/98 (99%)	97 (100%)	0	100	100
1	CL	97/98 (99%)	97 (100%)	0	100	100
1	CM	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	CN	97/98 (99%)	97 (100%)	0	100	100
1	CO	97/98 (99%)	97 (100%)	0	100	100
1	CP	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	CQ	97/98 (99%)	97 (100%)	0	100	100
1	CR	97/98 (99%)	97 (100%)	0	100	100
1	CS	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	CT	97/98 (99%)	97 (100%)	0	100	100
1	CU	97/98 (99%)	97 (100%)	0	100	100
1	CV	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	CW	97/98 (99%)	97 (100%)	0	100	100
1	CX	97/98 (99%)	97 (100%)	0	100	100
1	CY	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	CZ	97/98 (99%)	97 (100%)	0	100	100
1	DA	97/98 (99%)	97 (100%)	0	100	100
1	DB	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	DC	97/98 (99%)	97 (100%)	0	100	100
1	DD	97/98 (99%)	97 (100%)	0	100	100
1	DE	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	DF	97/98 (99%)	97 (100%)	0	100	100
1	DG	97/98 (99%)	97 (100%)	0	100	100
1	DH	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	DI	97/98 (99%)	97 (100%)	0	100	100
1	DJ	97/98 (99%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DK	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	DL	97/98 (99%)	97 (100%)	0	100	100
1	DM	97/98 (99%)	97 (100%)	0	100	100
1	DN	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	DO	97/98 (99%)	97 (100%)	0	100	100
1	DP	97/98 (99%)	97 (100%)	0	100	100
1	DQ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	DR	97/98 (99%)	97 (100%)	0	100	100
1	DS	97/98 (99%)	97 (100%)	0	100	100
1	DT	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	DU	97/98 (99%)	97 (100%)	0	100	100
1	DV	97/98 (99%)	97 (100%)	0	100	100
1	DW	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	DX	97/98 (99%)	97 (100%)	0	100	100
1	DY	97/98 (99%)	97 (100%)	0	100	100
1	DZ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	EA	97/98 (99%)	97 (100%)	0	100	100
1	EB	97/98 (99%)	97 (100%)	0	100	100
1	EC	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	ED	97/98 (99%)	97 (100%)	0	100	100
1	EE	97/98 (99%)	97 (100%)	0	100	100
1	EF	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	EG	97/98 (99%)	97 (100%)	0	100	100
1	EH	97/98 (99%)	97 (100%)	0	100	100
1	EI	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	EJ	97/98 (99%)	97 (100%)	0	100	100
1	EK	97/98 (99%)	97 (100%)	0	100	100
1	EL	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	EM	97/98 (99%)	97 (100%)	0	100	100
1	EN	97/98 (99%)	97 (100%)	0	100	100
1	EO	97/98 (99%)	96 (99%)	1 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	EP	97/98 (99%)	97 (100%)	0	100	100
1	EQ	97/98 (99%)	97 (100%)	0	100	100
1	ER	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	ES	97/98 (99%)	97 (100%)	0	100	100
1	ET	97/98 (99%)	97 (100%)	0	100	100
1	EU	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	EV	97/98 (99%)	97 (100%)	0	100	100
1	EW	97/98 (99%)	97 (100%)	0	100	100
1	EX	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	EY	97/98 (99%)	97 (100%)	0	100	100
1	EZ	97/98 (99%)	97 (100%)	0	100	100
1	FA	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	FB	97/98 (99%)	97 (100%)	0	100	100
1	FC	97/98 (99%)	97 (100%)	0	100	100
1	FD	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	FE	97/98 (99%)	97 (100%)	0	100	100
1	FF	97/98 (99%)	97 (100%)	0	100	100
1	FG	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	FH	97/98 (99%)	97 (100%)	0	100	100
1	FI	97/98 (99%)	97 (100%)	0	100	100
1	FJ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	FK	97/98 (99%)	97 (100%)	0	100	100
1	FL	97/98 (99%)	97 (100%)	0	100	100
1	FM	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	FN	97/98 (99%)	97 (100%)	0	100	100
1	FO	97/98 (99%)	97 (100%)	0	100	100
1	FP	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	FQ	97/98 (99%)	97 (100%)	0	100	100
1	FR	97/98 (99%)	97 (100%)	0	100	100
1	FS	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	FT	97/98 (99%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	FU	97/98 (99%)	97 (100%)	0	100	100
1	FV	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	FW	97/98 (99%)	97 (100%)	0	100	100
1	FX	97/98 (99%)	97 (100%)	0	100	100
1	FY	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	FZ	97/98 (99%)	97 (100%)	0	100	100
1	GA	97/98 (99%)	97 (100%)	0	100	100
1	GB	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	GC	97/98 (99%)	97 (100%)	0	100	100
1	GD	97/98 (99%)	97 (100%)	0	100	100
1	GE	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	GF	97/98 (99%)	97 (100%)	0	100	100
1	GG	97/98 (99%)	97 (100%)	0	100	100
1	GH	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	GI	97/98 (99%)	97 (100%)	0	100	100
1	GJ	97/98 (99%)	97 (100%)	0	100	100
1	GK	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	GL	97/98 (99%)	97 (100%)	0	100	100
1	GM	97/98 (99%)	97 (100%)	0	100	100
1	GN	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	GO	97/98 (99%)	97 (100%)	0	100	100
1	GP	97/98 (99%)	97 (100%)	0	100	100
1	GQ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	GR	97/98 (99%)	97 (100%)	0	100	100
1	GS	97/98 (99%)	97 (100%)	0	100	100
1	GT	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	GU	97/98 (99%)	97 (100%)	0	100	100
1	GV	97/98 (99%)	97 (100%)	0	100	100
1	GW	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	GX	97/98 (99%)	97 (100%)	0	100	100
1	GY	97/98 (99%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	GZ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	HA	97/98 (99%)	97 (100%)	0	100	100
1	HB	97/98 (99%)	97 (100%)	0	100	100
1	HC	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	HD	97/98 (99%)	97 (100%)	0	100	100
1	HE	97/98 (99%)	97 (100%)	0	100	100
1	HF	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	HG	97/98 (99%)	97 (100%)	0	100	100
1	HH	97/98 (99%)	97 (100%)	0	100	100
1	HI	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	HJ	97/98 (99%)	97 (100%)	0	100	100
1	HK	97/98 (99%)	97 (100%)	0	100	100
1	HL	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	HM	97/98 (99%)	97 (100%)	0	100	100
1	HN	97/98 (99%)	97 (100%)	0	100	100
1	HO	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	HP	97/98 (99%)	97 (100%)	0	100	100
1	HQ	97/98 (99%)	97 (100%)	0	100	100
1	HR	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	HS	97/98 (99%)	97 (100%)	0	100	100
1	HT	97/98 (99%)	97 (100%)	0	100	100
1	HU	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	HV	97/98 (99%)	97 (100%)	0	100	100
1	HW	97/98 (99%)	97 (100%)	0	100	100
1	HX	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	HY	97/98 (99%)	97 (100%)	0	100	100
1	HZ	97/98 (99%)	97 (100%)	0	100	100
1	IA	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	IB	97/98 (99%)	97 (100%)	0	100	100
1	IC	97/98 (99%)	97 (100%)	0	100	100
1	ID	97/98 (99%)	96 (99%)	1 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	IE	97/98 (99%)	97 (100%)	0	100	100
1	IF	97/98 (99%)	97 (100%)	0	100	100
1	IG	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	IH	97/98 (99%)	97 (100%)	0	100	100
1	II	97/98 (99%)	97 (100%)	0	100	100
1	IJ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	IK	97/98 (99%)	97 (100%)	0	100	100
1	IL	97/98 (99%)	97 (100%)	0	100	100
1	IM	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	IN	97/98 (99%)	97 (100%)	0	100	100
1	IO	97/98 (99%)	97 (100%)	0	100	100
1	IP	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	IQ	97/98 (99%)	97 (100%)	0	100	100
1	IR	97/98 (99%)	97 (100%)	0	100	100
1	IS	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	IT	97/98 (99%)	97 (100%)	0	100	100
1	IU	97/98 (99%)	97 (100%)	0	100	100
1	IV	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	IW	97/98 (99%)	97 (100%)	0	100	100
1	IX	97/98 (99%)	97 (100%)	0	100	100
1	IY	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	IZ	97/98 (99%)	97 (100%)	0	100	100
1	JA	97/98 (99%)	97 (100%)	0	100	100
1	JB	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	JC	97/98 (99%)	97 (100%)	0	100	100
1	JD	97/98 (99%)	97 (100%)	0	100	100
1	JE	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	JF	97/98 (99%)	97 (100%)	0	100	100
1	JG	97/98 (99%)	97 (100%)	0	100	100
1	JH	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	JI	97/98 (99%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	JJ	97/98 (99%)	97 (100%)	0	100	100
1	JK	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	JL	97/98 (99%)	97 (100%)	0	100	100
1	JM	97/98 (99%)	97 (100%)	0	100	100
1	JN	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	JO	97/98 (99%)	97 (100%)	0	100	100
1	JP	97/98 (99%)	97 (100%)	0	100	100
1	JQ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	JR	97/98 (99%)	97 (100%)	0	100	100
1	JS	97/98 (99%)	97 (100%)	0	100	100
1	JT	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	JU	97/98 (99%)	97 (100%)	0	100	100
1	JV	97/98 (99%)	97 (100%)	0	100	100
1	JW	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	JX	97/98 (99%)	97 (100%)	0	100	100
1	JY	97/98 (99%)	97 (100%)	0	100	100
1	JZ	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	KA	97/98 (99%)	97 (100%)	0	100	100
1	KB	97/98 (99%)	97 (100%)	0	100	100
1	KC	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	KD	97/98 (99%)	97 (100%)	0	100	100
1	KE	97/98 (99%)	97 (100%)	0	100	100
1	KF	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	KG	97/98 (99%)	97 (100%)	0	100	100
1	KH	97/98 (99%)	97 (100%)	0	100	100
1	KI	97/98 (99%)	96 (99%)	1 (1%)	68	75
1	KJ	97/98 (99%)	97 (100%)	0	100	100
All	All	26190/26460 (99%)	26100 (100%)	90 (0%)	86	84

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AB	66	LEU

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Mol	Chain	Res	Type
1	AE	66	LEU
1	AH	66	LEU
1	AK	66	LEU
1	AN	66	LEU
1	AQ	66	LEU
1	AT	66	LEU
1	AW	66	LEU
1	AZ	66	LEU
1	BC	66	LEU
1	BF	66	LEU
1	BI	66	LEU
1	BL	66	LEU
1	BO	66	LEU
1	BR	66	LEU
1	BU	66	LEU
1	BX	66	LEU
1	CA	66	LEU
1	CD	66	LEU
1	CG	66	LEU
1	CJ	66	LEU
1	CM	66	LEU
1	CP	66	LEU
1	CS	66	LEU
1	CV	66	LEU
1	CY	66	LEU
1	DB	66	LEU
1	DE	66	LEU
1	DH	66	LEU
1	DK	66	LEU
1	DN	66	LEU
1	DQ	66	LEU
1	DT	66	LEU
1	DW	66	LEU
1	DZ	66	LEU
1	EC	66	LEU
1	EF	66	LEU
1	EI	66	LEU
1	EL	66	LEU
1	EO	66	LEU
1	ER	66	LEU
1	EU	66	LEU
1	EX	66	LEU

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Mol	Chain	Res	Type
1	FA	66	LEU
1	FD	66	LEU
1	FG	66	LEU
1	FJ	66	LEU
1	FM	66	LEU
1	FP	66	LEU
1	FS	66	LEU
1	FV	66	LEU
1	FY	66	LEU
1	GB	66	LEU
1	GE	66	LEU
1	GH	66	LEU
1	GK	66	LEU
1	GN	66	LEU
1	GQ	66	LEU
1	GT	66	LEU
1	GW	66	LEU
1	GZ	66	LEU
1	HC	66	LEU
1	HF	66	LEU
1	HI	66	LEU
1	HL	66	LEU
1	HO	66	LEU
1	HR	66	LEU
1	HU	66	LEU
1	HX	66	LEU
1	IA	66	LEU
1	ID	66	LEU
1	IG	66	LEU
1	IJ	66	LEU
1	IM	66	LEU
1	IP	66	LEU
1	IS	66	LEU
1	IV	66	LEU
1	IY	66	LEU
1	JB	66	LEU
1	JE	66	LEU
1	JH	66	LEU
1	JK	66	LEU
1	JN	66	LEU
1	JQ	66	LEU
1	JT	66	LEU

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Mol	Chain	Res	Type
1	JW	66	LEU
1	JZ	66	LEU
1	KC	66	LEU
1	KF	66	LEU
1	KI	66	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (445) such sidechains are listed below:

Mol	Chain	Res	Type
1	AB	44	ASN
1	AB	67	ASN
1	AC	44	ASN
1	AC	109	ASN
1	AD	44	ASN
1	AE	44	ASN
1	AE	67	ASN
1	AF	109	ASN
1	AG	44	ASN
1	AH	44	ASN
1	AH	83	ASN
1	AI	44	ASN
1	AI	83	ASN
1	AI	109	ASN
1	AJ	44	ASN
1	AK	44	ASN
1	AK	67	ASN
1	AK	83	ASN
1	AL	44	ASN
1	AL	109	ASN
1	AM	44	ASN
1	AN	44	ASN
1	AN	67	ASN
1	AN	83	ASN
1	AO	44	ASN
1	AO	109	ASN
1	AP	44	ASN
1	AQ	44	ASN
1	AQ	67	ASN
1	AQ	83	ASN
1	AR	44	ASN
1	AR	109	ASN
1	AS	44	ASN

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Mol	Chain	Res	Type
1	AT	44	ASN
1	AT	67	ASN
1	AU	44	ASN
1	AW	44	ASN
1	AW	83	ASN
1	AX	44	ASN
1	AX	109	ASN
1	AY	44	ASN
1	AZ	67	ASN
1	BA	44	ASN
1	BA	83	ASN
1	BA	109	ASN
1	BB	44	ASN
1	BC	44	ASN
1	BC	67	ASN
1	BD	44	ASN
1	BD	109	ASN
1	BE	44	ASN
1	BF	44	ASN
1	BF	67	ASN
1	BG	44	ASN
1	BG	109	ASN
1	BH	44	ASN
1	BI	44	ASN
1	BI	67	ASN
1	BI	83	ASN
1	BJ	44	ASN
1	BJ	109	ASN
1	BK	44	ASN
1	BL	67	ASN
1	BL	83	ASN
1	BM	44	ASN
1	BN	44	ASN
1	BO	44	ASN
1	BO	83	ASN
1	BP	44	ASN
1	BP	109	ASN
1	BR	44	ASN
1	BR	67	ASN
1	BR	83	ASN
1	BS	109	ASN
1	BT	44	ASN

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Mol	Chain	Res	Type
1	BU	67	ASN
1	BV	44	ASN
1	BV	109	ASN
1	BW	83	ASN
1	BX	67	ASN
1	BY	44	ASN
1	BY	83	ASN
1	BY	109	ASN
1	BZ	44	ASN
1	CA	44	ASN
1	CA	67	ASN
1	CB	109	ASN
1	CC	83	ASN
1	CD	44	ASN
1	CD	67	ASN
1	CD	83	ASN
1	CE	109	ASN
1	CF	44	ASN
1	CF	83	ASN
1	CG	44	ASN
1	CG	67	ASN
1	CG	83	ASN
1	CH	44	ASN
1	CI	44	ASN
1	CJ	44	ASN
1	CJ	67	ASN
1	CK	109	ASN
1	CL	83	ASN
1	CM	44	ASN
1	CM	67	ASN
1	CM	83	ASN
1	CN	44	ASN
1	CN	109	ASN
1	CO	44	ASN
1	CP	44	ASN
1	CP	67	ASN
1	CP	83	ASN
1	CQ	44	ASN
1	CR	44	ASN
1	CS	44	ASN
1	CS	67	ASN
1	CT	109	ASN

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Mol	Chain	Res	Type
1	CV	44	ASN
1	CV	67	ASN
1	CV	83	ASN
1	CW	44	ASN
1	CW	109	ASN
1	CX	44	ASN
1	CX	83	ASN
1	CY	44	ASN
1	CY	67	ASN
1	CZ	44	ASN
1	CZ	109	ASN
1	DA	44	ASN
1	DB	44	ASN
1	DB	67	ASN
1	DB	83	ASN
1	DC	44	ASN
1	DC	109	ASN
1	DD	44	ASN
1	DE	44	ASN
1	DE	67	ASN
1	DE	83	ASN
1	DG	44	ASN
1	DH	44	ASN
1	DH	67	ASN
1	DH	83	ASN
1	DI	109	ASN
1	DJ	44	ASN
1	DK	44	ASN
1	DK	67	ASN
1	DK	83	ASN
1	DL	109	ASN
1	DM	44	ASN
1	DM	83	ASN
1	DN	44	ASN
1	DN	67	ASN
1	DN	83	ASN
1	DO	109	ASN
1	DQ	44	ASN
1	DQ	67	ASN
1	DQ	83	ASN
1	DR	109	ASN
1	DT	44	ASN

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Mol	Chain	Res	Type
1	DT	67	ASN
1	DT	83	ASN
1	DU	109	ASN
1	DW	44	ASN
1	DW	67	ASN
1	DX	109	ASN
1	DY	44	ASN
1	DZ	67	ASN
1	EA	44	ASN
1	EA	109	ASN
1	EB	44	ASN
1	EC	44	ASN
1	EC	67	ASN
1	ED	109	ASN
1	EE	83	ASN
1	EF	44	ASN
1	EF	67	ASN
1	EH	44	ASN
1	EI	44	ASN
1	EI	67	ASN
1	EI	83	ASN
1	EJ	44	ASN
1	EJ	109	ASN
1	EK	44	ASN
1	EK	67	ASN
1	EL	44	ASN
1	EL	67	ASN
1	EL	83	ASN
1	EM	109	ASN
1	EO	44	ASN
1	EP	109	ASN
1	ER	44	ASN
1	ER	67	ASN
1	ES	109	ASN
1	ET	44	ASN
1	EU	44	ASN
1	EU	67	ASN
1	EU	83	ASN
1	EV	44	ASN
1	EV	109	ASN
1	EW	44	ASN
1	EW	67	ASN

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Mol	Chain	Res	Type
1	EX	44	ASN
1	EX	67	ASN
1	EX	83	ASN
1	EY	44	ASN
1	EY	109	ASN
1	EZ	44	ASN
1	FA	44	ASN
1	FA	67	ASN
1	FA	83	ASN
1	FB	44	ASN
1	FB	109	ASN
1	FD	44	ASN
1	FD	83	ASN
1	FE	44	ASN
1	FF	44	ASN
1	FG	44	ASN
1	FG	67	ASN
1	FH	44	ASN
1	FH	109	ASN
1	FI	44	ASN
1	FI	83	ASN
1	FJ	44	ASN
1	FJ	67	ASN
1	FJ	83	ASN
1	FK	44	ASN
1	FK	109	ASN
1	FM	44	ASN
1	FM	67	ASN
1	FN	44	ASN
1	FN	109	ASN
1	FO	44	ASN
1	FO	67	ASN
1	FP	44	ASN
1	FP	67	ASN
1	FP	83	ASN
1	FQ	44	ASN
1	FQ	109	ASN
1	FS	44	ASN
1	FS	67	ASN
1	FT	44	ASN
1	FT	83	ASN
1	FT	109	ASN

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Mol	Chain	Res	Type
1	FU	44	ASN
1	FV	44	ASN
1	FV	67	ASN
1	FW	109	ASN
1	FX	67	ASN
1	FY	44	ASN
1	FY	67	ASN
1	FY	83	ASN
1	FZ	44	ASN
1	FZ	109	ASN
1	GA	44	ASN
1	GA	83	ASN
1	GB	44	ASN
1	GB	67	ASN
1	GB	83	ASN
1	GC	109	ASN
1	GD	83	ASN
1	GE	44	ASN
1	GE	67	ASN
1	GE	83	ASN
1	GF	44	ASN
1	GF	109	ASN
1	GG	44	ASN
1	GH	44	ASN
1	GH	83	ASN
1	GI	44	ASN
1	GI	109	ASN
1	GJ	44	ASN
1	GK	44	ASN
1	GK	67	ASN
1	GL	109	ASN
1	GM	83	ASN
1	GN	67	ASN
1	GN	83	ASN
1	GO	44	ASN
1	GO	83	ASN
1	GO	109	ASN
1	GP	44	ASN
1	GP	83	ASN
1	GQ	44	ASN
1	GQ	67	ASN
1	GQ	83	ASN

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Mol	Chain	Res	Type
1	GR	44	ASN
1	GR	109	ASN
1	GS	44	ASN
1	GT	67	ASN
1	GT	83	ASN
1	GU	44	ASN
1	GV	44	ASN
1	GW	44	ASN
1	GW	83	ASN
1	GX	44	ASN
1	GX	109	ASN
1	GY	83	ASN
1	GZ	44	ASN
1	GZ	67	ASN
1	GZ	83	ASN
1	HA	44	ASN
1	HA	109	ASN
1	HC	44	ASN
1	HC	67	ASN
1	HC	83	ASN
1	HD	44	ASN
1	HD	83	ASN
1	HD	109	ASN
1	HF	44	ASN
1	HF	67	ASN
1	HF	83	ASN
1	HG	109	ASN
1	HH	44	ASN
1	HH	83	ASN
1	HI	44	ASN
1	HI	83	ASN
1	HJ	109	ASN
1	HK	44	ASN
1	HL	44	ASN
1	HL	67	ASN
1	HL	83	ASN
1	HM	83	ASN
1	HM	109	ASN
1	HN	44	ASN
1	HO	44	ASN
1	HO	67	ASN
1	HO	83	ASN

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Mol	Chain	Res	Type
1	HP	44	ASN
1	HP	109	ASN
1	HR	44	ASN
1	HR	67	ASN
1	HS	44	ASN
1	HS	109	ASN
1	HT	44	ASN
1	HT	83	ASN
1	HU	44	ASN
1	HU	67	ASN
1	HU	83	ASN
1	HV	44	ASN
1	HV	109	ASN
1	HW	44	ASN
1	HX	44	ASN
1	HX	67	ASN
1	HX	83	ASN
1	HY	109	ASN
1	HZ	44	ASN
1	IA	44	ASN
1	IA	67	ASN
1	IA	83	ASN
1	IB	109	ASN
1	ID	44	ASN
1	ID	67	ASN
1	ID	83	ASN
1	IE	109	ASN
1	IF	44	ASN
1	IF	83	ASN
1	IG	44	ASN
1	IH	44	ASN
1	IH	109	ASN
1	II	44	ASN
1	IJ	44	ASN
1	IJ	67	ASN
1	IJ	83	ASN
1	IK	44	ASN
1	IK	109	ASN
1	IL	44	ASN
1	IM	67	ASN
1	IN	83	ASN
1	IO	44	ASN

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Mol	Chain	Res	Type
1	IP	44	ASN
1	IP	67	ASN
1	IP	83	ASN
1	IQ	44	ASN
1	IQ	109	ASN
1	IR	44	ASN
1	IS	44	ASN
1	IS	67	ASN
1	IT	44	ASN
1	IT	109	ASN
1	IU	44	ASN
1	IV	67	ASN
1	IW	44	ASN
1	IY	44	ASN
1	IY	67	ASN
1	IY	83	ASN
1	IZ	44	ASN
1	IZ	109	ASN
1	JA	44	ASN
1	JB	44	ASN
1	JB	67	ASN
1	JC	44	ASN
1	JC	109	ASN
1	JE	44	ASN
1	JE	67	ASN
1	JE	83	ASN
1	JF	44	ASN
1	JH	44	ASN
1	JH	67	ASN
1	JI	83	ASN
1	JI	109	ASN
1	JJ	83	ASN
1	JK	44	ASN
1	JK	67	ASN
1	JK	83	ASN
1	JL	44	ASN
1	JL	109	ASN
1	JN	44	ASN
1	JO	44	ASN
1	JO	109	ASN
1	JP	44	ASN
1	JP	67	ASN

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Mol	Chain	Res	Type
1	JP	83	ASN
1	JQ	44	ASN
1	JQ	67	ASN
1	JQ	83	ASN
1	JR	44	ASN
1	JR	109	ASN
1	JS	83	ASN
1	JT	44	ASN
1	JT	67	ASN
1	JT	83	ASN
1	JU	44	ASN
1	JW	44	ASN
1	JW	67	ASN
1	JW	83	ASN
1	JX	44	ASN
1	JX	109	ASN
1	JZ	67	ASN
1	JZ	83	ASN
1	KA	109	ASN
1	KB	44	ASN
1	KC	44	ASN
1	KC	67	ASN
1	KC	83	ASN
1	KD	109	ASN
1	KE	44	ASN
1	KF	44	ASN
1	KF	83	ASN
1	KG	44	ASN
1	KG	83	ASN
1	KH	83	ASN
1	KI	67	ASN
1	KI	83	ASN
1	KJ	44	ASN
1	KJ	109	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [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](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	AA	114/115 (99%)	0.51	6 (5%)	32 24	44, 67, 100, 129	0
1	AB	114/115 (99%)	0.54	8 (7%)	22 18	39, 66, 99, 114	0
1	AC	114/115 (99%)	0.75	10 (8%)	15 14	40, 68, 111, 175	0
1	AD	114/115 (99%)	0.47	7 (6%)	27 21	44, 67, 100, 129	0
1	AE	114/115 (99%)	0.69	10 (8%)	15 14	39, 66, 99, 114	0
1	AF	114/115 (99%)	0.67	9 (7%)	18 16	40, 68, 111, 175	0
1	AG	114/115 (99%)	0.77	14 (12%)	8 9	44, 67, 100, 129	0
1	AH	114/115 (99%)	0.54	6 (5%)	32 24	39, 66, 99, 114	0
1	AI	114/115 (99%)	0.62	7 (6%)	27 21	40, 68, 111, 175	0
1	AJ	114/115 (99%)	0.50	4 (3%)	47 34	44, 67, 100, 129	0
1	AK	114/115 (99%)	0.50	6 (5%)	32 24	39, 66, 99, 114	0
1	AL	114/115 (99%)	0.65	7 (6%)	27 21	40, 68, 111, 175	0
1	AM	114/115 (99%)	0.64	10 (8%)	15 14	44, 67, 100, 129	0
1	AN	114/115 (99%)	0.37	5 (4%)	39 28	39, 66, 99, 114	0
1	AO	114/115 (99%)	0.33	3 (2%)	57 42	40, 68, 111, 175	0
1	AP	114/115 (99%)	1.18	22 (19%)	3 4	44, 67, 100, 129	0
1	AQ	114/115 (99%)	0.75	8 (7%)	22 18	39, 66, 99, 114	0
1	AR	114/115 (99%)	0.98	16 (14%)	6 8	40, 68, 111, 175	0
1	AS	114/115 (99%)	1.00	13 (11%)	10 10	44, 67, 100, 129	0
1	AT	114/115 (99%)	0.51	7 (6%)	27 21	39, 66, 99, 114	0
1	AU	114/115 (99%)	0.87	15 (13%)	7 8	40, 68, 111, 175	0
1	AV	114/115 (99%)	0.73	7 (6%)	27 21	44, 67, 100, 129	0
1	AW	114/115 (99%)	0.44	3 (2%)	57 42	39, 66, 99, 114	0
1	AX	114/115 (99%)	0.66	5 (4%)	39 28	40, 68, 111, 175	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	114/115 (99%)	0.94	14 (12%) 8 9	44, 67, 100, 129	0
1	AZ	114/115 (99%)	1.04	17 (14%) 5 7	39, 66, 99, 114	0
1	BA	114/115 (99%)	1.12	21 (18%) 3 5	40, 68, 111, 175	0
1	BB	114/115 (99%)	0.75	10 (8%) 15 14	44, 67, 100, 129	0
1	BC	114/115 (99%)	0.48	4 (3%) 47 34	39, 66, 99, 114	0
1	BD	114/115 (99%)	0.69	10 (8%) 15 14	40, 68, 111, 175	0
1	BE	114/115 (99%)	0.63	8 (7%) 22 18	44, 67, 100, 129	0
1	BF	114/115 (99%)	0.64	4 (3%) 47 34	39, 66, 99, 114	0
1	BG	114/115 (99%)	0.76	10 (8%) 15 14	40, 68, 111, 175	0
1	BH	114/115 (99%)	0.37	4 (3%) 47 34	44, 67, 100, 129	0
1	BI	114/115 (99%)	0.61	7 (6%) 27 21	39, 66, 99, 114	0
1	BJ	114/115 (99%)	0.45	6 (5%) 32 24	40, 68, 111, 175	0
1	BK	114/115 (99%)	0.43	4 (3%) 47 34	44, 67, 100, 129	0
1	BL	114/115 (99%)	0.42	2 (1%) 67 53	39, 66, 99, 114	0
1	BM	114/115 (99%)	0.62	9 (7%) 18 16	40, 68, 111, 175	0
1	BN	114/115 (99%)	0.31	2 (1%) 67 53	44, 67, 100, 129	0
1	BO	114/115 (99%)	0.27	3 (2%) 57 42	39, 66, 99, 114	0
1	BP	114/115 (99%)	0.55	7 (6%) 27 21	40, 68, 111, 175	0
1	BQ	114/115 (99%)	0.70	8 (7%) 22 18	44, 67, 100, 129	0
1	BR	114/115 (99%)	0.59	4 (3%) 47 34	39, 66, 99, 114	0
1	BS	114/115 (99%)	0.38	3 (2%) 57 42	40, 68, 111, 175	0
1	BT	114/115 (99%)	0.95	16 (14%) 6 8	44, 67, 100, 129	0
1	BU	114/115 (99%)	1.08	25 (21%) 2 4	39, 66, 99, 114	0
1	BV	114/115 (99%)	0.99	15 (13%) 7 8	40, 68, 111, 175	0
1	BW	114/115 (99%)	0.38	4 (3%) 47 34	44, 67, 100, 129	0
1	BX	114/115 (99%)	0.58	4 (3%) 47 34	39, 66, 99, 114	0
1	BY	114/115 (99%)	0.83	11 (9%) 13 13	40, 68, 111, 175	0
1	BZ	114/115 (99%)	0.76	8 (7%) 22 18	44, 67, 100, 129	0
1	CA	114/115 (99%)	0.33	6 (5%) 32 24	39, 66, 99, 114	0
1	CB	114/115 (99%)	0.57	9 (7%) 18 16	40, 68, 111, 175	0
1	CC	114/115 (99%)	0.41	6 (5%) 32 24	44, 67, 100, 129	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	CD	114/115 (99%)	0.57	4 (3%) 47 34	39, 66, 99, 114	0
1	CE	114/115 (99%)	0.38	10 (8%) 15 14	40, 68, 111, 175	0
1	CF	114/115 (99%)	0.21	1 (0%) 81 68	44, 67, 100, 129	0
1	CG	114/115 (99%)	0.54	6 (5%) 32 24	39, 66, 99, 114	0
1	CH	114/115 (99%)	0.78	11 (9%) 13 13	40, 68, 111, 175	0
1	CI	114/115 (99%)	0.85	11 (9%) 13 13	44, 67, 100, 129	0
1	CJ	114/115 (99%)	0.94	13 (11%) 10 10	39, 66, 99, 114	0
1	CK	114/115 (99%)	1.19	24 (21%) 2 4	40, 68, 111, 175	0
1	CL	114/115 (99%)	0.55	4 (3%) 47 34	44, 67, 100, 129	0
1	CM	114/115 (99%)	0.62	6 (5%) 32 24	39, 66, 99, 114	0
1	CN	114/115 (99%)	0.46	6 (5%) 32 24	40, 68, 111, 175	0
1	CO	114/115 (99%)	0.90	9 (7%) 18 16	44, 67, 100, 129	0
1	CP	114/115 (99%)	0.71	11 (9%) 13 13	39, 66, 99, 114	0
1	CQ	114/115 (99%)	0.61	9 (7%) 18 16	40, 68, 111, 175	0
1	CR	114/115 (99%)	0.52	4 (3%) 47 34	44, 67, 100, 129	0
1	CS	114/115 (99%)	0.31	3 (2%) 57 42	39, 66, 99, 114	0
1	CT	114/115 (99%)	0.48	11 (9%) 13 13	40, 68, 111, 175	0
1	CU	114/115 (99%)	0.62	10 (8%) 15 14	44, 67, 100, 129	0
1	CV	114/115 (99%)	0.50	10 (8%) 15 14	39, 66, 99, 114	0
1	CW	114/115 (99%)	0.42	7 (6%) 27 21	40, 68, 111, 175	0
1	CX	114/115 (99%)	0.35	4 (3%) 47 34	44, 67, 100, 129	0
1	CY	114/115 (99%)	0.61	6 (5%) 32 24	39, 66, 99, 114	0
1	CZ	114/115 (99%)	0.60	8 (7%) 22 18	40, 68, 111, 175	0
1	DA	114/115 (99%)	0.39	5 (4%) 39 28	44, 67, 100, 129	0
1	DB	114/115 (99%)	0.33	3 (2%) 57 42	39, 66, 99, 114	0
1	DC	114/115 (99%)	0.30	3 (2%) 57 42	40, 68, 111, 175	0
1	DD	114/115 (99%)	0.46	5 (4%) 39 28	44, 67, 100, 129	0
1	DE	114/115 (99%)	0.35	4 (3%) 47 34	39, 66, 99, 114	0
1	DF	114/115 (99%)	0.39	4 (3%) 47 34	40, 68, 111, 175	0
1	DG	114/115 (99%)	0.45	2 (1%) 67 53	44, 67, 100, 129	0
1	DH	114/115 (99%)	0.56	6 (5%) 32 24	39, 66, 99, 114	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	DI	114/115 (99%)	0.63	7 (6%) 27 21	40, 68, 111, 175	0
1	DJ	114/115 (99%)	0.64	10 (8%) 15 14	44, 67, 100, 129	0
1	DK	114/115 (99%)	0.44	4 (3%) 47 34	39, 66, 99, 114	0
1	DL	114/115 (99%)	0.42	3 (2%) 57 42	40, 68, 111, 175	0
1	DM	114/115 (99%)	0.60	4 (3%) 47 34	44, 67, 100, 129	0
1	DN	114/115 (99%)	0.75	13 (11%) 10 10	39, 66, 99, 114	0
1	DO	114/115 (99%)	0.64	6 (5%) 32 24	40, 68, 111, 175	0
1	DP	114/115 (99%)	0.37	6 (5%) 32 24	44, 67, 100, 129	0
1	DQ	114/115 (99%)	0.45	7 (6%) 27 21	39, 66, 99, 114	0
1	DR	114/115 (99%)	0.57	8 (7%) 22 18	40, 68, 111, 175	0
1	DS	114/115 (99%)	0.42	5 (4%) 39 28	44, 67, 100, 129	0
1	DT	114/115 (99%)	0.54	5 (4%) 39 28	39, 66, 99, 114	0
1	DU	114/115 (99%)	0.61	9 (7%) 18 16	40, 68, 111, 175	0
1	DV	114/115 (99%)	0.58	3 (2%) 57 42	44, 67, 100, 129	0
1	DW	114/115 (99%)	0.53	8 (7%) 22 18	39, 66, 99, 114	0
1	DX	114/115 (99%)	0.51	8 (7%) 22 18	40, 68, 111, 175	0
1	DY	114/115 (99%)	0.57	11 (9%) 13 13	44, 67, 100, 129	0
1	DZ	114/115 (99%)	0.24	2 (1%) 67 53	39, 66, 99, 114	0
1	EA	114/115 (99%)	0.38	4 (3%) 47 34	40, 68, 111, 175	0
1	EB	114/115 (99%)	1.06	13 (11%) 10 10	44, 67, 100, 129	0
1	EC	114/115 (99%)	0.66	8 (7%) 22 18	39, 66, 99, 114	0
1	ED	114/115 (99%)	0.90	11 (9%) 13 13	40, 68, 111, 175	0
1	EE	114/115 (99%)	0.66	8 (7%) 22 18	44, 67, 100, 129	0
1	EF	114/115 (99%)	0.86	15 (13%) 7 8	39, 66, 99, 114	0
1	EG	114/115 (99%)	0.93	13 (11%) 10 10	40, 68, 111, 175	0
1	EH	114/115 (99%)	1.15	20 (17%) 4 5	44, 67, 100, 129	0
1	EI	114/115 (99%)	0.90	15 (13%) 7 8	39, 66, 99, 114	0
1	EJ	114/115 (99%)	0.88	13 (11%) 10 10	40, 68, 111, 175	0
1	EK	114/115 (99%)	0.72	4 (3%) 47 34	44, 67, 100, 129	0
1	EL	114/115 (99%)	0.78	13 (11%) 10 10	39, 66, 99, 114	0
1	EM	114/115 (99%)	0.87	10 (8%) 15 14	40, 68, 111, 175	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	EN	114/115 (99%)	1.16	18 (15%) 5 6	44, 67, 100, 129	0
1	EO	114/115 (99%)	0.67	7 (6%) 27 21	39, 66, 99, 114	0
1	EP	114/115 (99%)	0.82	10 (8%) 15 14	40, 68, 111, 175	0
1	EQ	114/115 (99%)	0.74	9 (7%) 18 16	44, 67, 100, 129	0
1	ER	114/115 (99%)	0.54	8 (7%) 22 18	39, 66, 99, 114	0
1	ES	114/115 (99%)	0.78	10 (8%) 15 14	40, 68, 111, 175	0
1	ET	114/115 (99%)	0.57	4 (3%) 47 34	44, 67, 100, 129	0
1	EU	114/115 (99%)	0.54	7 (6%) 27 21	39, 66, 99, 114	0
1	EV	114/115 (99%)	0.47	3 (2%) 57 42	40, 68, 111, 175	0
1	EW	114/115 (99%)	0.82	8 (7%) 22 18	44, 67, 100, 129	0
1	EX	114/115 (99%)	0.76	10 (8%) 15 14	39, 66, 99, 114	0
1	EY	114/115 (99%)	0.80	16 (14%) 6 8	40, 68, 111, 175	0
1	EZ	114/115 (99%)	0.65	8 (7%) 22 18	44, 67, 100, 129	0
1	FA	114/115 (99%)	0.51	6 (5%) 32 24	39, 66, 99, 114	0
1	FB	114/115 (99%)	0.61	11 (9%) 13 13	40, 68, 111, 175	0
1	FC	114/115 (99%)	0.49	3 (2%) 57 42	44, 67, 100, 129	0
1	FD	114/115 (99%)	0.53	4 (3%) 47 34	39, 66, 99, 114	0
1	FE	114/115 (99%)	0.44	3 (2%) 57 42	40, 68, 111, 175	0
1	FF	114/115 (99%)	0.37	4 (3%) 47 34	44, 67, 100, 129	0
1	FG	114/115 (99%)	0.53	9 (7%) 18 16	39, 66, 99, 114	0
1	FH	114/115 (99%)	0.80	12 (10%) 11 12	40, 68, 111, 175	0
1	FI	114/115 (99%)	0.75	8 (7%) 22 18	44, 67, 100, 129	0
1	FJ	114/115 (99%)	0.94	13 (11%) 10 10	39, 66, 99, 114	0
1	FK	114/115 (99%)	0.66	7 (6%) 27 21	40, 68, 111, 175	0
1	FL	114/115 (99%)	0.54	8 (7%) 22 18	44, 67, 100, 129	0
1	FM	114/115 (99%)	0.63	7 (6%) 27 21	39, 66, 99, 114	0
1	FN	114/115 (99%)	0.65	14 (12%) 8 9	40, 68, 111, 175	0
1	FO	114/115 (99%)	0.52	5 (4%) 39 28	44, 67, 100, 129	0
1	FP	114/115 (99%)	0.31	4 (3%) 47 34	39, 66, 99, 114	0
1	FQ	114/115 (99%)	0.45	5 (4%) 39 28	40, 68, 111, 175	0
1	FR	114/115 (99%)	0.79	9 (7%) 18 16	44, 67, 100, 129	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	FS	114/115 (99%)	0.34	5 (4%) 39 28	39, 66, 99, 114	0
1	FT	114/115 (99%)	0.93	18 (15%) 5 6	40, 68, 111, 175	0
1	FU	114/115 (99%)	0.86	10 (8%) 15 14	44, 67, 100, 129	0
1	FV	114/115 (99%)	0.78	9 (7%) 18 16	39, 66, 99, 114	0
1	FW	114/115 (99%)	1.03	13 (11%) 10 10	40, 68, 111, 175	0
1	FX	114/115 (99%)	0.58	4 (3%) 47 34	44, 67, 100, 129	0
1	FY	114/115 (99%)	0.39	2 (1%) 67 53	39, 66, 99, 114	0
1	FZ	114/115 (99%)	0.59	4 (3%) 47 34	40, 68, 111, 175	0
1	GA	114/115 (99%)	0.68	9 (7%) 18 16	44, 67, 100, 129	0
1	GB	114/115 (99%)	1.00	17 (14%) 5 7	39, 66, 99, 114	0
1	GC	114/115 (99%)	0.68	10 (8%) 15 14	40, 68, 111, 175	0
1	GD	114/115 (99%)	0.55	5 (4%) 39 28	44, 67, 100, 129	0
1	GE	114/115 (99%)	0.45	4 (3%) 47 34	39, 66, 99, 114	0
1	GF	114/115 (99%)	0.65	6 (5%) 32 24	40, 68, 111, 175	0
1	GG	114/115 (99%)	0.41	3 (2%) 57 42	44, 67, 100, 129	0
1	GH	114/115 (99%)	0.72	8 (7%) 22 18	39, 66, 99, 114	0
1	GI	114/115 (99%)	0.43	2 (1%) 67 53	40, 68, 111, 175	0
1	GJ	114/115 (99%)	0.27	6 (5%) 32 24	44, 67, 100, 129	0
1	GK	114/115 (99%)	0.45	8 (7%) 22 18	39, 66, 99, 114	0
1	GL	114/115 (99%)	0.68	13 (11%) 10 10	40, 68, 111, 175	0
1	GM	114/115 (99%)	0.44	4 (3%) 47 34	44, 67, 100, 129	0
1	GN	114/115 (99%)	0.31	5 (4%) 39 28	39, 66, 99, 114	0
1	GO	114/115 (99%)	0.44	5 (4%) 39 28	40, 68, 111, 175	0
1	GP	114/115 (99%)	0.54	9 (7%) 18 16	44, 67, 100, 129	0
1	GQ	114/115 (99%)	0.44	3 (2%) 57 42	39, 66, 99, 114	0
1	GR	114/115 (99%)	0.41	4 (3%) 47 34	40, 68, 111, 175	0
1	GS	114/115 (99%)	0.60	4 (3%) 47 34	44, 67, 100, 129	0
1	GT	114/115 (99%)	0.72	12 (10%) 11 12	39, 66, 99, 114	0
1	GU	114/115 (99%)	0.61	8 (7%) 22 18	40, 68, 111, 175	0
1	GV	114/115 (99%)	0.41	7 (6%) 27 21	44, 67, 100, 129	0
1	GW	114/115 (99%)	0.27	2 (1%) 67 53	39, 66, 99, 114	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	GX	114/115 (99%)	0.51	5 (4%) 39 28	40, 68, 111, 175	0
1	GY	114/115 (99%)	0.83	15 (13%) 7 8	44, 67, 100, 129	0
1	GZ	114/115 (99%)	1.04	14 (12%) 8 9	39, 66, 99, 114	0
1	HA	114/115 (99%)	0.84	8 (7%) 22 18	40, 68, 111, 175	0
1	HB	114/115 (99%)	0.24	2 (1%) 67 53	44, 67, 100, 129	0
1	HC	114/115 (99%)	0.14	1 (0%) 81 68	39, 66, 99, 114	0
1	HD	114/115 (99%)	0.38	6 (5%) 32 24	40, 68, 111, 175	0
1	HE	114/115 (99%)	1.17	20 (17%) 4 5	44, 67, 100, 129	0
1	HF	114/115 (99%)	0.83	8 (7%) 22 18	39, 66, 99, 114	0
1	HG	114/115 (99%)	1.22	20 (17%) 4 5	40, 68, 111, 175	0
1	HH	114/115 (99%)	0.44	4 (3%) 47 34	44, 67, 100, 129	0
1	HI	114/115 (99%)	1.01	17 (14%) 5 7	39, 66, 99, 114	0
1	HJ	114/115 (99%)	0.40	4 (3%) 47 34	40, 68, 111, 175	0
1	HK	114/115 (99%)	0.41	4 (3%) 47 34	44, 67, 100, 129	0
1	HL	114/115 (99%)	0.36	4 (3%) 47 34	39, 66, 99, 114	0
1	HM	114/115 (99%)	0.33	4 (3%) 47 34	40, 68, 111, 175	0
1	HN	114/115 (99%)	1.29	22 (19%) 3 4	44, 67, 100, 129	0
1	HO	114/115 (99%)	0.80	8 (7%) 22 18	39, 66, 99, 114	0
1	HP	114/115 (99%)	0.94	14 (12%) 8 9	40, 68, 111, 175	0
1	HQ	114/115 (99%)	1.07	22 (19%) 3 4	44, 67, 100, 129	0
1	HR	114/115 (99%)	1.13	18 (15%) 5 6	39, 66, 99, 114	0
1	HS	114/115 (99%)	1.33	24 (21%) 2 4	40, 68, 111, 175	0
1	HT	114/115 (99%)	0.90	10 (8%) 15 14	44, 67, 100, 129	0
1	HU	114/115 (99%)	1.22	29 (25%) 1 3	39, 66, 99, 114	0
1	HV	114/115 (99%)	1.06	18 (15%) 5 6	40, 68, 111, 175	0
1	HW	114/115 (99%)	0.46	4 (3%) 47 34	44, 67, 100, 129	0
1	HX	114/115 (99%)	0.21	2 (1%) 67 53	39, 66, 99, 114	0
1	HY	114/115 (99%)	0.42	3 (2%) 57 42	40, 68, 111, 175	0
1	HZ	114/115 (99%)	0.32	1 (0%) 81 68	44, 67, 100, 129	0
1	IA	114/115 (99%)	0.56	7 (6%) 27 21	39, 66, 99, 114	0
1	IB	114/115 (99%)	0.41	6 (5%) 32 24	40, 68, 111, 175	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	IC	114/115 (99%)	0.51	4 (3%)	47	34	44, 67, 100, 129	0
1	ID	114/115 (99%)	0.35	3 (2%)	57	42	39, 66, 99, 114	0
1	IE	114/115 (99%)	0.68	10 (8%)	15	14	40, 68, 111, 175	0
1	IF	114/115 (99%)	0.70	5 (4%)	39	28	44, 67, 100, 129	0
1	IG	114/115 (99%)	0.38	5 (4%)	39	28	39, 66, 99, 114	0
1	IH	114/115 (99%)	0.46	7 (6%)	27	21	40, 68, 111, 175	0
1	II	114/115 (99%)	0.32	3 (2%)	57	42	44, 67, 100, 129	0
1	IJ	114/115 (99%)	0.52	7 (6%)	27	21	39, 66, 99, 114	0
1	IK	114/115 (99%)	0.48	7 (6%)	27	21	40, 68, 111, 175	0
1	IL	114/115 (99%)	0.45	2 (1%)	67	53	44, 67, 100, 129	0
1	IM	114/115 (99%)	0.82	12 (10%)	11	12	39, 66, 99, 114	0
1	IN	114/115 (99%)	0.80	13 (11%)	10	10	40, 68, 111, 175	0
1	IO	114/115 (99%)	0.64	8 (7%)	22	18	44, 67, 100, 129	0
1	IP	114/115 (99%)	0.63	8 (7%)	22	18	39, 66, 99, 114	0
1	IQ	114/115 (99%)	1.00	18 (15%)	5	6	40, 68, 111, 175	0
1	IR	114/115 (99%)	1.04	16 (14%)	6	8	44, 67, 100, 129	0
1	IS	114/115 (99%)	1.03	13 (11%)	10	10	39, 66, 99, 114	0
1	IT	114/115 (99%)	1.13	15 (13%)	7	8	40, 68, 111, 175	0
1	IU	114/115 (99%)	0.72	11 (9%)	13	13	44, 67, 100, 129	0
1	IV	114/115 (99%)	0.42	2 (1%)	67	53	39, 66, 99, 114	0
1	IW	114/115 (99%)	0.55	4 (3%)	47	34	40, 68, 111, 175	0
1	IX	114/115 (99%)	0.59	4 (3%)	47	34	44, 67, 100, 129	0
1	IY	114/115 (99%)	0.36	3 (2%)	57	42	39, 66, 99, 114	0
1	IZ	114/115 (99%)	0.45	5 (4%)	39	28	40, 68, 111, 175	0
1	JA	114/115 (99%)	0.81	14 (12%)	8	9	44, 67, 100, 129	0
1	JB	114/115 (99%)	0.50	8 (7%)	22	18	39, 66, 99, 114	0
1	JC	114/115 (99%)	0.92	10 (8%)	15	14	40, 68, 111, 175	0
1	JD	114/115 (99%)	1.09	18 (15%)	5	6	44, 67, 100, 129	0
1	JE	114/115 (99%)	0.39	7 (6%)	27	21	39, 66, 99, 114	0
1	JF	114/115 (99%)	0.57	4 (3%)	47	34	40, 68, 111, 175	0
1	JG	114/115 (99%)	0.44	5 (4%)	39	28	44, 67, 100, 129	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	JH	114/115 (99%)	0.41	9 (7%) 18 16	39, 66, 99, 114	0
1	JI	114/115 (99%)	0.62	11 (9%) 13 13	40, 68, 111, 175	0
1	JJ	114/115 (99%)	0.98	18 (15%) 5 6	44, 67, 100, 129	0
1	JK	114/115 (99%)	1.21	24 (21%) 2 4	39, 66, 99, 114	0
1	JL	114/115 (99%)	1.37	24 (21%) 2 4	40, 68, 111, 175	0
1	JM	114/115 (99%)	1.38	28 (24%) 2 3	44, 67, 100, 129	0
1	JN	114/115 (99%)	0.85	13 (11%) 10 10	39, 66, 99, 114	0
1	JO	114/115 (99%)	0.90	14 (12%) 8 9	40, 68, 111, 175	0
1	JP	114/115 (99%)	0.48	5 (4%) 39 28	44, 67, 100, 129	0
1	JQ	114/115 (99%)	0.77	12 (10%) 11 12	39, 66, 99, 114	0
1	JR	114/115 (99%)	0.53	5 (4%) 39 28	40, 68, 111, 175	0
1	JS	114/115 (99%)	0.16	3 (2%) 57 42	44, 67, 100, 129	0
1	JT	114/115 (99%)	0.50	5 (4%) 39 28	39, 66, 99, 114	0
1	JU	114/115 (99%)	0.56	7 (6%) 27 21	40, 68, 111, 175	0
1	JV	114/115 (99%)	0.72	7 (6%) 27 21	44, 67, 100, 129	0
1	JW	114/115 (99%)	0.52	9 (7%) 18 16	39, 66, 99, 114	0
1	JX	114/115 (99%)	0.44	2 (1%) 67 53	40, 68, 111, 175	0
1	JY	114/115 (99%)	0.75	9 (7%) 18 16	44, 67, 100, 129	0
1	JZ	114/115 (99%)	1.03	19 (16%) 4 6	39, 66, 99, 114	0
1	KA	114/115 (99%)	0.76	9 (7%) 18 16	40, 68, 111, 175	0
1	KB	114/115 (99%)	0.44	4 (3%) 47 34	44, 67, 100, 129	0
1	KC	114/115 (99%)	0.40	5 (4%) 39 28	39, 66, 99, 114	0
1	KD	114/115 (99%)	0.57	10 (8%) 15 14	40, 68, 111, 175	0
1	KE	114/115 (99%)	0.56	5 (4%) 39 28	44, 67, 100, 129	0
1	KF	114/115 (99%)	0.39	2 (1%) 67 53	39, 66, 99, 114	0
1	KG	114/115 (99%)	0.64	6 (5%) 32 24	40, 68, 111, 175	0
1	KH	114/115 (99%)	0.57	9 (7%) 18 16	44, 67, 100, 129	0
1	KI	114/115 (99%)	0.46	3 (2%) 57 42	39, 66, 99, 114	0
1	KJ	114/115 (99%)	0.48	4 (3%) 47 34	40, 68, 111, 175	0
All	All	30780/31050 (99%)	0.64	2280 (7%) 20 17	39, 67, 105, 175	0

All (2280) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	FT	85	ASP	8.8
1	DO	57	SER	8.3
1	HR	62	ALA	6.9
1	IF	114	THR	6.8
1	EB	62	ALA	6.7
1	AC	50	ALA	6.4
1	HN	6	SER	6.3
1	JK	74	SER	6.2
1	HG	50	ALA	6.1
1	JL	10	GLY	6.1
1	IT	34	ALA	6.1
1	CK	34	ALA	5.9
1	JM	101	ASN	5.6
1	JT	114	THR	5.4
1	EQ	57	SER	5.4
1	IR	74	SER	5.4
1	CK	74	SER	5.3
1	BJ	42	GLY	5.3
1	AP	95	VAL	5.3
1	HN	50	ALA	5.2
1	HS	34	ALA	5.2
1	JL	15	SER	5.2
1	BD	44	ASN	5.2
1	IQ	13	GLY	5.2
1	HE	1	SER	5.1
1	JQ	33	VAL	5.1
1	IQ	34	ALA	5.0
1	EU	107	ASP	5.0
1	HI	95	VAL	5.0
1	EH	108	GLY	5.0
1	FN	60	ASP	5.0
1	EH	109	ASN	5.0
1	FN	59	VAL	4.9
1	DJ	44	ASN	4.9
1	DM	6	SER	4.9
1	AC	61	GLY	4.8
1	IO	42	GLY	4.8
1	EY	66	LEU	4.8
1	EJ	9	ALA	4.7
1	IR	15	SER	4.7
1	FN	42	GLY	4.7
1	JI	85	ASP	4.7
1	GB	74	SER	4.7

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Mol	Chain	Res	Type	RSRZ
1	IR	6	SER	4.7
1	IJ	114	THR	4.7
1	GL	41	ALA	4.7
1	JN	82	ILE	4.6
1	FW	6	SER	4.6
1	AZ	99	THR	4.6
1	JO	3	THR	4.6
1	FW	74	SER	4.6
1	DI	9	ALA	4.6
1	ED	66	LEU	4.6
1	GF	62	ALA	4.5
1	EB	108	GLY	4.5
1	IE	61	GLY	4.5
1	JZ	74	SER	4.5
1	HE	76	THR	4.5
1	JJ	42	GLY	4.4
1	IM	80	SER	4.4
1	CZ	44	ASN	4.4
1	JD	103	ALA	4.4
1	FD	99	THR	4.4
1	HR	1	SER	4.4
1	CK	54	PRO	4.4
1	CK	13	GLY	4.4
1	CH	44	ASN	4.4
1	DA	44	ASN	4.4
1	HT	106	ILE	4.4
1	GZ	6	SER	4.4
1	HG	35	THR	4.3
1	HS	6	SER	4.3
1	FJ	42	GLY	4.3
1	JZ	76	THR	4.3
1	HU	34	ALA	4.3
1	AY	108	GLY	4.3
1	JY	10	GLY	4.3
1	KC	108	GLY	4.3
1	IH	64	VAL	4.3
1	BA	108	GLY	4.3
1	EU	44	ASN	4.3
1	AP	33	VAL	4.3
1	CH	23	THR	4.2
1	FL	37	THR	4.2
1	AO	80	SER	4.2

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Mol	Chain	Res	Type	RSRZ
1	FZ	67	ASN	4.2
1	HS	87	LYS	4.2
1	JL	50	ALA	4.2
1	EG	112	THR	4.2
1	HI	92	ASP	4.2
1	HU	97	PHE	4.2
1	EI	108	GLY	4.2
1	JL	7	GLU	4.2
1	HG	75	PHE	4.2
1	AR	62	ALA	4.2
1	FB	82	ILE	4.2
1	AY	114	THR	4.2
1	KG	64	VAL	4.2
1	CE	111	LEU	4.2
1	HE	82	ILE	4.2
1	DJ	17	TYR	4.2
1	IQ	50	ALA	4.1
1	AZ	13	GLY	4.1
1	CZ	23	THR	4.1
1	FV	62	ALA	4.1
1	HE	57	SER	4.1
1	GZ	62	ALA	4.1
1	EX	6	SER	4.1
1	JK	6	SER	4.1
1	GB	76	THR	4.1
1	CG	112	THR	4.1
1	AQ	82	ILE	4.1
1	EA	44	ASN	4.0
1	HG	51	VAL	4.0
1	HV	82	ILE	4.0
1	AM	41	ALA	4.0
1	FT	41	ALA	4.0
1	HJ	11	PRO	4.0
1	BY	59	VAL	4.0
1	HG	34	ALA	4.0
1	JM	103	ALA	4.0
1	CE	113	VAL	4.0
1	BU	1	SER	4.0
1	CK	50	ALA	4.0
1	HG	47	TYR	4.0
1	HY	64	VAL	4.0
1	AM	44	ASN	4.0

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Mol	Chain	Res	Type	RSRZ
1	BD	68	THR	3.9
1	HN	33	VAL	3.9
1	BY	61	GLY	3.9
1	EH	112	THR	3.9
1	BB	44	ASN	3.9
1	HN	76	THR	3.9
1	HS	46	GLU	3.9
1	HT	7	GLU	3.9
1	BV	62	ALA	3.9
1	GR	3	THR	3.9
1	GL	23	THR	3.8
1	KC	114	THR	3.8
1	DX	96	SER	3.8
1	FJ	107	ASP	3.8
1	HU	8	SER	3.8
1	HP	62	ALA	3.8
1	BS	3	THR	3.8
1	FO	61	GLY	3.8
1	JM	75	PHE	3.8
1	HV	62	ALA	3.8
1	HQ	74	SER	3.8
1	EN	113	VAL	3.8
1	JR	113	VAL	3.8
1	GB	13	GLY	3.8
1	JO	82	ILE	3.8
1	JJ	11	PRO	3.8
1	BA	113	VAL	3.8
1	JL	54	PRO	3.8
1	JL	78	LEU	3.8
1	GY	50	ALA	3.7
1	HS	62	ALA	3.7
1	BI	6	SER	3.7
1	DF	15	SER	3.7
1	AD	42	GLY	3.7
1	AH	114	THR	3.7
1	EB	114	THR	3.7
1	EE	23	THR	3.7
1	KI	95	VAL	3.7
1	JV	15	SER	3.7
1	HV	42	GLY	3.7
1	JO	84	THR	3.7
1	HG	77	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	EY	67	ASN	3.7
1	CL	21	GLY	3.7
1	IS	62	ALA	3.7
1	JQ	50	ALA	3.7
1	GH	95	VAL	3.7
1	GL	82	ILE	3.7
1	CR	101	ASN	3.7
1	EL	44	ASN	3.7
1	IS	63	ASN	3.7
1	HV	61	GLY	3.7
1	GE	1	SER	3.7
1	AV	114	THR	3.7
1	GU	82	ILE	3.7
1	KD	63	ASN	3.7
1	FH	61	GLY	3.7
1	HQ	92	ASP	3.6
1	HU	33	VAL	3.6
1	HI	99	THR	3.6
1	FY	82	ILE	3.6
1	GS	10	GLY	3.6
1	GZ	101	ASN	3.6
1	BD	46	GLU	3.6
1	HN	34	ALA	3.6
1	JL	51	VAL	3.6
1	JM	112	THR	3.6
1	KA	82	ILE	3.6
1	IH	108	GLY	3.6
1	AY	25	PRO	3.6
1	CW	44	ASN	3.6
1	JC	63	ASN	3.6
1	AD	113	VAL	3.6
1	EZ	9	ALA	3.6
1	IR	9	ALA	3.6
1	HJ	28	TYR	3.6
1	AP	74	SER	3.6
1	AD	111	LEU	3.6
1	BA	78	LEU	3.6
1	DS	4	LYS	3.6
1	HQ	3	THR	3.6
1	HQ	16	ILE	3.6
1	IB	42	GLY	3.6
1	AS	41	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	GC	104	ASN	3.6
1	JD	111	LEU	3.6
1	BB	43	THR	3.6
1	CI	21	GLY	3.6
1	CU	50	ALA	3.6
1	GL	62	ALA	3.6
1	IZ	111	LEU	3.6
1	CV	42	GLY	3.5
1	JM	108	GLY	3.5
1	CC	64	VAL	3.5
1	EQ	62	ALA	3.5
1	IC	26	ALA	3.5
1	BM	82	ILE	3.5
1	JJ	98	ILE	3.5
1	BL	1	SER	3.5
1	JR	112	THR	3.5
1	AI	65	ALA	3.5
1	BZ	101	ASN	3.5
1	JI	44	ASN	3.5
1	EH	114	THR	3.5
1	IQ	76	THR	3.5
1	EC	57	SER	3.5
1	HE	74	SER	3.5
1	HN	8	SER	3.5
1	IU	1	SER	3.5
1	ES	61	GLY	3.5
1	FM	13	GLY	3.5
1	GC	59	VAL	3.5
1	FW	62	ALA	3.5
1	IE	9	ALA	3.5
1	EH	111	LEU	3.5
1	EJ	44	ASN	3.5
1	BB	4	LYS	3.5
1	HH	37	THR	3.5
1	AV	113	VAL	3.5
1	EO	14	GLN	3.5
1	BK	6	SER	3.5
1	BF	107	ASP	3.5
1	GQ	107	ASP	3.5
1	JZ	62	ALA	3.5
1	HI	16	ILE	3.5
1	HN	69	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	DQ	44	ASN	3.5
1	ED	101	ASN	3.5
1	EP	114	THR	3.5
1	IB	113	VAL	3.5
1	IT	56	VAL	3.5
1	FT	77	ALA	3.5
1	HN	15	SER	3.5
1	JR	111	LEU	3.5
1	JP	25	PRO	3.5
1	GA	81	VAL	3.4
1	BA	61	GLY	3.4
1	EJ	23	THR	3.4
1	EV	3	THR	3.4
1	GD	50	ALA	3.4
1	DT	57	SER	3.4
1	IZ	82	ILE	3.4
1	DG	5	TYR	3.4
1	EK	10	GLY	3.4
1	JG	42	GLY	3.4
1	JH	111	LEU	3.4
1	ES	62	ALA	3.4
1	GU	9	ALA	3.4
1	AE	80	SER	3.4
1	GT	1	SER	3.4
1	AP	92	ASP	3.4
1	BR	92	ASP	3.4
1	BD	56	VAL	3.4
1	EM	61	GLY	3.4
1	FV	13	GLY	3.4
1	HE	42	GLY	3.4
1	AF	3	THR	3.4
1	IG	109	ASN	3.4
1	IH	44	ASN	3.4
1	JN	44	ASN	3.4
1	HN	16	ILE	3.4
1	GR	11	PRO	3.4
1	GZ	30	PRO	3.4
1	GB	4	LYS	3.4
1	AP	6	SER	3.4
1	DT	74	SER	3.4
1	FJ	96	SER	3.4
1	EN	53	TYR	3.4

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Mol	Chain	Res	Type	RSRZ
1	GL	59	VAL	3.4
1	HE	81	VAL	3.4
1	JM	50	ALA	3.4
1	BH	37	THR	3.4
1	IR	76	THR	3.4
1	AG	74	SER	3.4
1	AM	56	VAL	3.4
1	HI	34	ALA	3.4
1	EF	39	ASN	3.3
1	HR	101	ASN	3.3
1	IK	63	ASN	3.3
1	JD	110	VAL	3.3
1	FN	62	ALA	3.3
1	JL	102	LYS	3.3
1	HN	98	ILE	3.3
1	HG	101	ASN	3.3
1	HI	88	LEU	3.3
1	EM	1	SER	3.3
1	HE	62	ALA	3.3
1	HG	61	GLY	3.3
1	JJ	82	ILE	3.3
1	JL	34	ALA	3.3
1	FT	84	THR	3.3
1	GK	23	THR	3.3
1	BP	44	ASN	3.3
1	GJ	111	LEU	3.3
1	CK	33	VAL	3.3
1	ES	33	VAL	3.3
1	CV	40	LYS	3.3
1	IR	46	GLU	3.3
1	BE	15	SER	3.3
1	DI	61	GLY	3.3
1	IU	82	ILE	3.3
1	JC	71	ALA	3.3
1	BA	28	TYR	3.3
1	FR	60	ASP	3.3
1	JY	76	THR	3.3
1	JC	66	LEU	3.3
1	CK	101	ASN	3.3
1	BU	69	ILE	3.3
1	HP	82	ILE	3.3
1	BT	21	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	EY	61	GLY	3.3
1	FE	28	TYR	3.3
1	HE	107	ASP	3.3
1	JH	107	ASP	3.3
1	AE	68	THR	3.3
1	BE	99	THR	3.3
1	DI	112	THR	3.3
1	DV	112	THR	3.3
1	EQ	55	LEU	3.3
1	GT	76	THR	3.3
1	HI	91	LEU	3.3
1	HW	43	THR	3.3
1	FL	38	VAL	3.3
1	GZ	4	LYS	3.3
1	AB	83	ASN	3.3
1	AC	101	ASN	3.3
1	CN	104	ASN	3.3
1	BV	13	GLY	3.3
1	EP	108	GLY	3.3
1	CN	28	TYR	3.2
1	HO	47	TYR	3.2
1	JZ	6	SER	3.2
1	HR	4	LYS	3.2
1	AR	64	VAL	3.2
1	AP	50	ALA	3.2
1	BU	62	ALA	3.2
1	CW	65	ALA	3.2
1	FW	47	TYR	3.2
1	AS	96	SER	3.2
1	CO	74	SER	3.2
1	CV	4	LYS	3.2
1	DU	66	LEU	3.2
1	IR	8	SER	3.2
1	IN	110	VAL	3.2
1	EA	43	THR	3.2
1	EI	112	THR	3.2
1	KH	106	ILE	3.2
1	HM	46	GLU	3.2
1	AY	5	TYR	3.2
1	AK	57	SER	3.2
1	HQ	95	VAL	3.2
1	HU	6	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	JT	80	SER	3.2
1	DD	14	GLN	3.2
1	AG	3	THR	3.2
1	HI	107	ASP	3.2
1	BU	82	ILE	3.2
1	BI	34	ALA	3.2
1	ES	50	ALA	3.2
1	HS	10	GLY	3.2
1	GS	93	GLU	3.2
1	CG	111	LEU	3.2
1	HV	111	LEU	3.2
1	EH	110	VAL	3.2
1	FI	80	SER	3.2
1	BM	76	THR	3.2
1	HD	29	MET	3.2
1	HS	112	THR	3.2
1	JD	41	ALA	3.2
1	JQ	34	ALA	3.2
1	EW	21	GLY	3.2
1	KJ	61	GLY	3.2
1	GO	44	ASN	3.2
1	CO	47	TYR	3.2
1	HS	25	PRO	3.2
1	JO	113	VAL	3.2
1	BG	57	SER	3.2
1	DD	106	ILE	3.2
1	GT	8	SER	3.2
1	HU	74	SER	3.2
1	JI	82	ILE	3.2
1	HV	3	THR	3.2
1	IK	9	ALA	3.2
1	JM	35	THR	3.2
1	IA	73	LEU	3.1
1	EK	101	ASN	3.1
1	FK	63	ASN	3.1
1	FT	44	ASN	3.1
1	JA	5	TYR	3.1
1	CB	82	ILE	3.1
1	GZ	98	ILE	3.1
1	KA	98	ILE	3.1
1	AP	15	SER	3.1
1	BO	68	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	BR	41	ALA	3.1
1	CD	34	ALA	3.1
1	IF	4	LYS	3.1
1	HA	74	SER	3.1
1	IP	6	SER	3.1
1	JY	6	SER	3.1
1	CH	92	ASP	3.1
1	CW	61	GLY	3.1
1	HU	92	ASP	3.1
1	IO	21	GLY	3.1
1	IU	108	GLY	3.1
1	CU	72	ASN	3.1
1	IM	44	ASN	3.1
1	JM	47	TYR	3.1
1	BT	82	ILE	3.1
1	FW	82	ILE	3.1
1	BV	34	ALA	3.1
1	IS	65	ALA	3.1
1	JL	9	ALA	3.1
1	BT	76	THR	3.1
1	GY	3	THR	3.1
1	HW	112	THR	3.1
1	JG	111	LEU	3.1
1	KD	112	THR	3.1
1	CV	107	ASP	3.1
1	HE	89	ARG	3.1
1	CQ	44	ASN	3.1
1	DS	72	ASN	3.1
1	EL	82	ILE	3.1
1	HN	52	ASN	3.1
1	HX	82	ILE	3.1
1	IE	63	ASN	3.1
1	AZ	50	ALA	3.1
1	CO	61	GLY	3.1
1	DY	114	THR	3.1
1	EF	68	THR	3.1
1	BD	1	SER	3.1
1	KA	15	SER	3.1
1	GH	82	ILE	3.1
1	HU	49	ILE	3.1
1	HK	44	ASN	3.1
1	EH	103	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	FZ	9	ALA	3.1
1	AR	61	GLY	3.1
1	CB	84	THR	3.1
1	EU	108	GLY	3.1
1	HI	36	THR	3.1
1	AY	110	VAL	3.1
1	IQ	33	VAL	3.1
1	KD	22	VAL	3.1
1	AM	4	LYS	3.1
1	FG	93	GLU	3.1
1	FU	93	GLU	3.1
1	EL	85	ASP	3.1
1	JL	49	ILE	3.1
1	AT	44	ASN	3.0
1	BU	52	ASN	3.0
1	CH	103	ALA	3.0
1	CJ	26	ALA	3.0
1	FP	44	ASN	3.0
1	EI	14	GLN	3.0
1	HS	61	GLY	3.0
1	CZ	90	VAL	3.0
1	EF	110	VAL	3.0
1	EH	113	VAL	3.0
1	FZ	8	SER	3.0
1	KE	96	SER	3.0
1	EW	62	ALA	3.0
1	FA	44	ASN	3.0
1	HR	67	ASN	3.0
1	JR	61	GLY	3.0
1	DN	95	VAL	3.0
1	EL	114	THR	3.0
1	BT	16	ILE	3.0
1	CI	2	ILE	3.0
1	CL	82	ILE	3.0
1	EH	106	ILE	3.0
1	GU	6	SER	3.0
1	HQ	6	SER	3.0
1	AX	103	ALA	3.0
1	BB	85	ASP	3.0
1	KB	111	LEU	3.0
1	ED	34	ALA	3.0
1	KD	9	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	AG	4	LYS	3.0
1	GV	44	ASN	3.0
1	HG	13	GLY	3.0
1	BC	112	THR	3.0
1	ID	112	THR	3.0
1	JU	3	THR	3.0
1	GA	7	GLU	3.0
1	GY	82	ILE	3.0
1	HP	98	ILE	3.0
1	AQ	1	SER	3.0
1	EN	8	SER	3.0
1	HU	15	SER	3.0
1	CR	62	ALA	3.0
1	ED	9	ALA	3.0
1	CG	108	GLY	3.0
1	DR	42	GLY	3.0
1	EY	13	GLY	3.0
1	EJ	22	VAL	3.0
1	HV	113	VAL	3.0
1	CM	72	ASN	3.0
1	DR	44	ASN	3.0
1	EG	101	ASN	3.0
1	AR	76	THR	3.0
1	BA	84	THR	3.0
1	DQ	37	THR	3.0
1	DU	36	THR	3.0
1	AR	69	ILE	3.0
1	CH	2	ILE	3.0
1	AS	7	GLU	3.0
1	DY	7	GLU	3.0
1	FK	46	GLU	3.0
1	BN	9	ALA	3.0
1	FQ	8	SER	3.0
1	FQ	9	ALA	3.0
1	GF	96	SER	3.0
1	HG	15	SER	3.0
1	HY	6	SER	3.0
1	JL	8	SER	3.0
1	BB	17	TYR	3.0
1	EF	40	LYS	3.0
1	IT	5	TYR	3.0
1	DU	61	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	GU	10	GLY	3.0
1	FM	97	PHE	3.0
1	AU	44	ASN	3.0
1	DP	109	ASN	3.0
1	ED	67	ASN	3.0
1	FA	109	ASN	3.0
1	GE	67	ASN	3.0
1	GN	104	ASN	3.0
1	HQ	83	ASN	3.0
1	EC	45	ILE	3.0
1	EN	114	THR	3.0
1	HV	2	ILE	3.0
1	DU	78	LEU	2.9
1	IB	111	LEU	2.9
1	EG	65	ALA	2.9
1	IY	4	LYS	2.9
1	ER	57	SER	2.9
1	BM	10	GLY	2.9
1	CZ	22	VAL	2.9
1	IN	59	VAL	2.9
1	EQ	107	ASP	2.9
1	IX	107	ASP	2.9
1	EF	97	PHE	2.9
1	AR	98	ILE	2.9
1	FT	82	ILE	2.9
1	FU	82	ILE	2.9
1	AP	35	THR	2.9
1	BA	43	THR	2.9
1	CQ	112	THR	2.9
1	GD	76	THR	2.9
1	EG	103	ALA	2.9
1	AU	64	VAL	2.9
1	BA	22	VAL	2.9
1	EH	6	SER	2.9
1	EQ	1	SER	2.9
1	FM	15	SER	2.9
1	AJ	21	GLY	2.9
1	BM	61	GLY	2.9
1	GO	61	GLY	2.9
1	EW	85	ASP	2.9
1	AG	16	ILE	2.9
1	CH	82	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
1	CO	43	THR	2.9
1	EF	84	THR	2.9
1	GL	3	THR	2.9
1	IT	112	THR	2.9
1	JK	65	ALA	2.9
1	EN	110	VAL	2.9
1	EH	105	ILE	2.9
1	CX	66	LEU	2.9
1	GX	66	LEU	2.9
1	FH	102	LYS	2.9
1	JD	107	ASP	2.9
1	CK	84	THR	2.9
1	CW	83	ASN	2.9
1	EG	3	THR	2.9
1	EG	36	THR	2.9
1	EN	84	THR	2.9
1	GC	67	ASN	2.9
1	HE	18	THR	2.9
1	GK	103	ALA	2.9
1	GN	109	ASN	2.9
1	JD	68	THR	2.9
1	BV	26	ALA	2.9
1	BW	26	ALA	2.9
1	BY	62	ALA	2.9
1	JF	44	ASN	2.9
1	HF	22	VAL	2.9
1	HU	51	VAL	2.9
1	AS	111	LEU	2.9
1	DT	6	SER	2.9
1	EW	57	SER	2.9
1	FU	6	SER	2.9
1	GC	111	LEU	2.9
1	IZ	15	SER	2.9
1	JN	4	LYS	2.9
1	FB	107	ASP	2.9
1	AX	3	THR	2.9
1	FU	112	THR	2.9
1	IN	103	ALA	2.9
1	JW	114	THR	2.9
1	FV	93	GLU	2.9
1	IA	72	ASN	2.9
1	JO	109	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	JQ	39	ASN	2.9
1	FW	58	VAL	2.9
1	HT	81	VAL	2.9
1	CK	61	GLY	2.9
1	EU	19	PHE	2.9
1	FI	28	TYR	2.9
1	IQ	97	PHE	2.9
1	JJ	28	TYR	2.9
1	EB	82	ILE	2.9
1	CO	14	GLN	2.8
1	DL	80	SER	2.8
1	EB	74	SER	2.8
1	FU	15	SER	2.8
1	GB	15	SER	2.8
1	BZ	114	THR	2.8
1	EO	43	THR	2.8
1	HQ	33	VAL	2.8
1	HV	22	VAL	2.8
1	JH	81	VAL	2.8
1	AN	4	LYS	2.8
1	BV	61	GLY	2.8
1	CT	66	LEU	2.8
1	FA	108	GLY	2.8
1	FW	61	GLY	2.8
1	CQ	6	SER	2.8
1	FI	15	SER	2.8
1	ID	57	SER	2.8
1	IX	6	SER	2.8
1	AC	9	ALA	2.8
1	JI	77	ALA	2.8
1	JJ	62	ALA	2.8
1	HE	11	PRO	2.8
1	BV	60	ASP	2.8
1	IN	107	ASP	2.8
1	IS	76	THR	2.8
1	JA	114	THR	2.8
1	JM	36	THR	2.8
1	GU	72	ASN	2.8
1	HV	4	LYS	2.8
1	CP	82	ILE	2.8
1	EQ	82	ILE	2.8
1	GH	61	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	GI	61	GLY	2.8
1	IK	61	GLY	2.8
1	JD	82	ILE	2.8
1	FR	28	TYR	2.8
1	HR	5	TYR	2.8
1	IM	14	GLN	2.8
1	JL	79	GLN	2.8
1	AP	26	ALA	2.8
1	CB	9	ALA	2.8
1	CI	9	ALA	2.8
1	HO	1	SER	2.8
1	JF	80	SER	2.8
1	CS	112	THR	2.8
1	EB	107	ASP	2.8
1	EO	112	THR	2.8
1	EY	76	THR	2.8
1	EZ	113	VAL	2.8
1	AP	93	GLU	2.8
1	CH	85	ASP	2.8
1	FD	107	ASP	2.8
1	FQ	114	THR	2.8
1	FT	3	THR	2.8
1	AS	44	ASN	2.8
1	HA	42	GLY	2.8
1	HR	13	GLY	2.8
1	IK	44	ASN	2.8
1	JM	29	MET	2.8
1	JM	72	ASN	2.8
1	ET	28	TYR	2.8
1	KF	47	TYR	2.8
1	DJ	103	ALA	2.8
1	BJ	113	VAL	2.8
1	BP	57	SER	2.8
1	CU	48	LYS	2.8
1	HI	6	SER	2.8
1	IS	4	LYS	2.8
1	IS	81	VAL	2.8
1	JM	74	SER	2.8
1	EL	46	GLU	2.8
1	GQ	99	THR	2.8
1	IM	7	GLU	2.8
1	AR	19	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
1	CP	107	ASP	2.8
1	FM	92	ASP	2.8
1	FV	107	ASP	2.8
1	GB	16	ILE	2.8
1	GL	60	ASP	2.8
1	JM	49	ILE	2.8
1	AL	61	GLY	2.8
1	KI	61	GLY	2.8
1	FD	63	ASN	2.8
1	IN	52	ASN	2.8
1	IO	67	ASN	2.8
1	JC	101	ASN	2.8
1	AC	17	TYR	2.8
1	AQ	47	TYR	2.8
1	JL	47	TYR	2.8
1	AK	65	ALA	2.8
1	FP	77	ALA	2.8
1	DY	4	LYS	2.8
1	HO	14	GLN	2.8
1	EX	1	SER	2.8
1	FT	80	SER	2.8
1	AJ	82	ILE	2.8
1	AP	99	THR	2.8
1	BV	112	THR	2.8
1	CR	82	ILE	2.8
1	HQ	82	ILE	2.8
1	BJ	60	ASP	2.7
1	DX	21	GLY	2.7
1	FG	108	GLY	2.7
1	HA	61	GLY	2.7
1	IV	108	GLY	2.7
1	AG	72	ASN	2.7
1	EG	44	ASN	2.7
1	IU	101	ASN	2.7
1	BY	28	TYR	2.7
1	DU	47	TYR	2.7
1	DR	70	ARG	2.7
1	GY	71	ALA	2.7
1	JK	26	ALA	2.7
1	JU	48	LYS	2.7
1	JW	103	ALA	2.7
1	BN	14	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	BT	95	VAL	2.7
1	EH	27	GLN	2.7
1	GL	27	GLN	2.7
1	JK	33	VAL	2.7
1	DP	111	LEU	2.7
1	EN	111	LEU	2.7
1	JQ	88	LEU	2.7
1	BS	15	SER	2.7
1	CV	82	ILE	2.7
1	DO	6	SER	2.7
1	ED	97	PHE	2.7
1	JF	76	THR	2.7
1	JQ	76	THR	2.7
1	DI	13	GLY	2.7
1	JV	10	GLY	2.7
1	AE	107	ASP	2.7
1	CE	60	ASP	2.7
1	AX	44	ASN	2.7
1	II	101	ASN	2.7
1	JH	109	ASN	2.7
1	BB	103	ALA	2.7
1	BU	71	ALA	2.7
1	GS	50	ALA	2.7
1	HQ	65	ALA	2.7
1	AX	59	VAL	2.7
1	DN	113	VAL	2.7
1	FQ	64	VAL	2.7
1	JV	79	GLN	2.7
1	BA	82	ILE	2.7
1	CK	97	PHE	2.7
1	FK	82	ILE	2.7
1	CX	7	GLU	2.7
1	BD	61	GLY	2.7
1	CY	8	SER	2.7
1	EG	80	SER	2.7
1	FR	76	THR	2.7
1	IR	35	THR	2.7
1	IT	57	SER	2.7
1	IU	76	THR	2.7
1	AG	92	ASP	2.7
1	AS	53	TYR	2.7
1	HV	28	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	ET	72	ASN	2.7
1	GA	44	ASN	2.7
1	HI	63	ASN	2.7
1	JE	63	ASN	2.7
1	JM	52	ASN	2.7
1	JX	9	ALA	2.7
1	KD	44	ASN	2.7
1	GB	33	VAL	2.7
1	GN	113	VAL	2.7
1	AY	106	ILE	2.7
1	GA	105	ILE	2.7
1	AG	7	GLU	2.7
1	AI	61	GLY	2.7
1	DP	7	GLU	2.7
1	HP	61	GLY	2.7
1	IY	7	GLU	2.7
1	AT	68	THR	2.7
1	CK	76	THR	2.7
1	HD	114	THR	2.7
1	AR	6	SER	2.7
1	EX	57	SER	2.7
1	IC	96	SER	2.7
1	IP	80	SER	2.7
1	FN	85	ASP	2.7
1	AA	55	LEU	2.7
1	AY	64	VAL	2.7
1	EJ	59	VAL	2.7
1	FJ	113	VAL	2.7
1	AY	44	ASN	2.7
1	BV	44	ASN	2.7
1	FN	63	ASN	2.7
1	JD	101	ASN	2.7
1	HA	82	ILE	2.7
1	HG	79	GLN	2.7
1	GY	89	ARG	2.7
1	AU	61	GLY	2.7
1	BJ	40	LYS	2.7
1	DM	10	GLY	2.7
1	AT	3	THR	2.7
1	DN	112	THR	2.7
1	DQ	23	THR	2.7
1	EH	43	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	HE	3	THR	2.7
1	CD	74	SER	2.7
1	DH	57	SER	2.7
1	EF	15	SER	2.7
1	FA	80	SER	2.7
1	GT	57	SER	2.7
1	AI	62	ALA	2.7
1	FH	9	ALA	2.7
1	FH	34	ALA	2.7
1	GY	103	ALA	2.7
1	JU	9	ALA	2.7
1	CJ	5	TYR	2.7
1	EC	81	VAL	2.7
1	IB	28	TYR	2.7
1	EP	60	ASP	2.7
1	GB	92	ASP	2.7
1	GC	60	ASP	2.7
1	AP	44	ASN	2.7
1	HN	109	ASN	2.7
1	JK	72	ASN	2.7
1	AI	27	GLN	2.6
1	AP	27	GLN	2.6
1	CK	79	GLN	2.6
1	KC	14	GLN	2.6
1	AQ	4	LYS	2.6
1	AY	21	GLY	2.6
1	CE	61	GLY	2.6
1	AD	114	THR	2.6
1	BA	3	THR	2.6
1	HQ	76	THR	2.6
1	KE	18	THR	2.6
1	AB	38	VAL	2.6
1	BG	6	SER	2.6
1	BV	6	SER	2.6
1	CB	88	LEU	2.6
1	EA	64	VAL	2.6
1	FJ	77	ALA	2.6
1	GT	62	ALA	2.6
1	HG	88	LEU	2.6
1	IS	80	SER	2.6
1	JH	80	SER	2.6
1	KA	74	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	FN	28	TYR	2.6
1	EN	60	ASP	2.6
1	GI	106	ILE	2.6
1	HS	82	ILE	2.6
1	KD	82	ILE	2.6
1	DW	101	ASN	2.6
1	EH	19	PHE	2.6
1	IJ	40	LYS	2.6
1	JZ	75	PHE	2.6
1	KJ	101	ASN	2.6
1	CQ	13	GLY	2.6
1	EZ	108	GLY	2.6
1	FN	61	GLY	2.6
1	IE	13	GLY	2.6
1	AF	23	THR	2.6
1	DR	23	THR	2.6
1	GA	43	THR	2.6
1	HO	76	THR	2.6
1	IQ	68	THR	2.6
1	AX	111	LEU	2.6
1	BA	62	ALA	2.6
1	CP	77	ALA	2.6
1	CT	34	ALA	2.6
1	DU	62	ALA	2.6
1	FC	81	VAL	2.6
1	FZ	66	LEU	2.6
1	GP	9	ALA	2.6
1	IQ	9	ALA	2.6
1	JD	88	LEU	2.6
1	JK	22	VAL	2.6
1	KH	26	ALA	2.6
1	AA	57	SER	2.6
1	AH	1	SER	2.6
1	BZ	74	SER	2.6
1	DO	15	SER	2.6
1	JY	74	SER	2.6
1	BD	106	ILE	2.6
1	DG	82	ILE	2.6
1	EZ	105	ILE	2.6
1	FN	40	LYS	2.6
1	HI	94	ILE	2.6
1	IG	4	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	IQ	54	PRO	2.6
1	AZ	60	ASP	2.6
1	IS	107	ASP	2.6
1	JD	85	ASP	2.6
1	BR	44	ASN	2.6
1	GZ	72	ASN	2.6
1	FF	42	GLY	2.6
1	JH	108	GLY	2.6
1	AB	93	GLU	2.6
1	BT	46	GLU	2.6
1	IP	93	GLU	2.6
1	JB	93	GLU	2.6
1	AB	65	ALA	2.6
1	AL	84	THR	2.6
1	FI	78	LEU	2.6
1	CI	62	ALA	2.6
1	EG	110	VAL	2.6
1	FL	114	THR	2.6
1	HE	35	THR	2.6
1	HU	35	THR	2.6
1	JA	62	ALA	2.6
1	BT	6	SER	2.6
1	EM	82	ILE	2.6
1	EW	6	SER	2.6
1	HG	17	TYR	2.6
1	HN	17	TYR	2.6
1	BQ	107	ASP	2.6
1	CH	107	ASP	2.6
1	GT	107	ASP	2.6
1	HL	14	GLN	2.6
1	IQ	79	GLN	2.6
1	AZ	67	ASN	2.6
1	CF	63	ASN	2.6
1	CN	108	GLY	2.6
1	GL	44	ASN	2.6
1	IE	109	ASN	2.6
1	JD	21	GLY	2.6
1	HN	7	GLU	2.6
1	CM	34	ALA	2.6
1	EB	58	VAL	2.6
1	DB	112	THR	2.6
1	ER	71	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	GL	22	VAL	2.6
1	HH	81	VAL	2.6
1	HT	64	VAL	2.6
1	FT	18	THR	2.6
1	GL	103	ALA	2.6
1	GZ	23	THR	2.6
1	IT	62	ALA	2.6
1	JK	76	THR	2.6
1	JR	3	THR	2.6
1	KE	23	THR	2.6
1	HX	4	LYS	2.6
1	AF	82	ILE	2.6
1	BP	82	ILE	2.6
1	DB	11	PRO	2.6
1	DN	1	SER	2.6
1	JY	15	SER	2.6
1	KH	1	SER	2.6
1	BU	61	GLY	2.6
1	GC	107	ASP	2.6
1	KB	108	GLY	2.6
1	EZ	104	ASN	2.6
1	FB	44	ASN	2.6
1	HF	83	ASN	2.6
1	HV	63	ASN	2.6
1	EP	111	LEU	2.6
1	GH	88	LEU	2.6
1	HU	73	LEU	2.6
1	FO	7	GLU	2.6
1	AC	34	ALA	2.6
1	CE	62	ALA	2.6
1	FC	65	ALA	2.6
1	FS	64	VAL	2.6
1	GJ	113	VAL	2.6
1	HE	100	ALA	2.6
1	JQ	4	LYS	2.6
1	CY	112	THR	2.6
1	KG	68	THR	2.6
1	EF	82	ILE	2.5
1	IZ	12	ILE	2.5
1	BE	1	SER	2.5
1	BT	74	SER	2.5
1	DH	6	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	DH	74	SER	2.5
1	EL	1	SER	2.5
1	GD	6	SER	2.5
1	IS	57	SER	2.5
1	JA	96	SER	2.5
1	CU	13	GLY	2.5
1	GF	61	GLY	2.5
1	GL	61	GLY	2.5
1	HL	61	GLY	2.5
1	JY	13	GLY	2.5
1	HR	111	LEU	2.5
1	JT	111	LEU	2.5
1	AF	44	ASN	2.5
1	AM	85	ASP	2.5
1	CK	95	VAL	2.5
1	HK	60	ASP	2.5
1	JU	22	VAL	2.5
1	JV	101	ASN	2.5
1	JZ	33	VAL	2.5
1	JZ	107	ASP	2.5
1	DW	62	ALA	2.5
1	IN	62	ALA	2.5
1	BP	3	THR	2.5
1	CY	114	THR	2.5
1	EJ	3	THR	2.5
1	GA	106	ILE	2.5
1	IR	82	ILE	2.5
1	JO	37	THR	2.5
1	KH	2	ILE	2.5
1	AF	28	TYR	2.5
1	AV	28	TYR	2.5
1	FR	5	TYR	2.5
1	HR	47	TYR	2.5
1	CG	61	GLY	2.5
1	EJ	42	GLY	2.5
1	GY	6	SER	2.5
1	HG	74	SER	2.5
1	IK	88	LEU	2.5
1	IQ	15	SER	2.5
1	JO	108	GLY	2.5
1	JZ	57	SER	2.5
1	FO	14	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	AW	70	ARG	2.5
1	EL	40	LYS	2.5
1	CM	33	VAL	2.5
1	DX	58	VAL	2.5
1	FR	24	VAL	2.5
1	JK	24	VAL	2.5
1	AH	72	ASN	2.5
1	AM	7	GLU	2.5
1	BA	44	ASN	2.5
1	BB	9	ALA	2.5
1	CG	44	ASN	2.5
1	EI	7	GLU	2.5
1	EN	34	ALA	2.5
1	EP	109	ASN	2.5
1	EZ	109	ASN	2.5
1	IM	109	ASN	2.5
1	CA	82	ILE	2.5
1	AL	76	THR	2.5
1	BA	76	THR	2.5
1	BJ	3	THR	2.5
1	CD	76	THR	2.5
1	EI	68	THR	2.5
1	IU	114	THR	2.5
1	GP	19	PHE	2.5
1	HA	53	TYR	2.5
1	JK	5	TYR	2.5
1	FJ	40	LYS	2.5
1	GL	40	LYS	2.5
1	IA	13	GLY	2.5
1	JN	40	LYS	2.5
1	BQ	6	SER	2.5
1	CA	1	SER	2.5
1	JK	27	GLN	2.5
1	BX	95	VAL	2.5
1	DS	22	VAL	2.5
1	AB	9	ALA	2.5
1	HU	77	ALA	2.5
1	JC	9	ALA	2.5
1	BT	7	GLU	2.5
1	CA	44	ASN	2.5
1	GP	109	ASN	2.5
1	IS	82	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	JA	107	ASP	2.5
1	AU	114	THR	2.5
1	CK	99	THR	2.5
1	CU	99	THR	2.5
1	GK	68	THR	2.5
1	HQ	84	THR	2.5
1	CL	5	TYR	2.5
1	CP	4	LYS	2.5
1	HT	53	TYR	2.5
1	JZ	28	TYR	2.5
1	KE	4	LYS	2.5
1	EX	10	GLY	2.5
1	FO	13	GLY	2.5
1	CJ	81	VAL	2.5
1	ED	64	VAL	2.5
1	HG	110	VAL	2.5
1	HK	56	VAL	2.5
1	HN	51	VAL	2.5
1	HP	58	VAL	2.5
1	JM	90	VAL	2.5
1	AP	71	ALA	2.5
1	BG	34	ALA	2.5
1	BR	9	ALA	2.5
1	BZ	103	ALA	2.5
1	CK	9	ALA	2.5
1	DT	34	ALA	2.5
1	DU	15	SER	2.5
1	EH	100	ALA	2.5
1	FP	80	SER	2.5
1	FU	8	SER	2.5
1	JO	9	ALA	2.5
1	JQ	71	ALA	2.5
1	KD	1	SER	2.5
1	AK	93	GLU	2.5
1	FU	106	ILE	2.5
1	IM	106	ILE	2.5
1	IS	29	MET	2.5
1	AB	72	ASN	2.5
1	AY	109	ASN	2.5
1	BU	67	ASN	2.5
1	EE	44	ASN	2.5
1	FM	52	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	FS	44	ASN	2.5
1	HE	44	ASN	2.5
1	JL	97	PHE	2.5
1	JZ	72	ASN	2.5
1	JZ	101	ASN	2.5
1	AP	3	THR	2.5
1	BT	3	THR	2.5
1	DN	76	THR	2.5
1	EC	112	THR	2.5
1	FF	18	THR	2.5
1	JL	66	LEU	2.5
1	EB	5	TYR	2.5
1	HH	5	TYR	2.5
1	JC	47	TYR	2.5
1	JK	47	TYR	2.5
1	CM	13	GLY	2.5
1	HU	13	GLY	2.5
1	AD	56	VAL	2.5
1	BF	79	GLN	2.5
1	CE	14	GLN	2.5
1	JC	79	GLN	2.5
1	FG	65	ALA	2.4
1	JK	50	ALA	2.4
1	JY	26	ALA	2.4
1	EO	2	ILE	2.4
1	GY	49	ILE	2.4
1	HP	6	SER	2.4
1	HR	82	ILE	2.4
1	JJ	57	SER	2.4
1	AF	46	GLU	2.4
1	JC	97	PHE	2.4
1	AC	63	ASN	2.4
1	BY	67	ASN	2.4
1	CY	109	ASN	2.4
1	EF	67	ASN	2.4
1	EY	109	ASN	2.4
1	HL	63	ASN	2.4
1	IN	44	ASN	2.4
1	JV	72	ASN	2.4
1	CK	73	LEU	2.4
1	DI	76	THR	2.4
1	EY	35	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	FN	3	THR	2.4
1	IU	111	LEU	2.4
1	KH	20	THR	2.4
1	FV	54	PRO	2.4
1	CJ	58	VAL	2.4
1	ET	59	VAL	2.4
1	JZ	56	VAL	2.4
1	BE	9	ALA	2.4
1	CO	79	GLN	2.4
1	DA	103	ALA	2.4
1	GB	34	ALA	2.4
1	IF	103	ALA	2.4
1	IY	9	ALA	2.4
1	HP	69	ILE	2.4
1	HS	98	ILE	2.4
1	AZ	8	SER	2.4
1	EY	46	GLU	2.4
1	GP	7	GLU	2.4
1	HD	80	SER	2.4
1	HR	74	SER	2.4
1	AU	19	PHE	2.4
1	AZ	4	LYS	2.4
1	KG	40	LYS	2.4
1	CN	111	LEU	2.4
1	DO	73	LEU	2.4
1	HN	78	LEU	2.4
1	JK	73	LEU	2.4
1	CE	104	ASN	2.4
1	CO	112	THR	2.4
1	DF	52	ASN	2.4
1	DY	3	THR	2.4
1	DZ	44	ASN	2.4
1	EB	84	THR	2.4
1	EF	109	ASN	2.4
1	EH	67	ASN	2.4
1	EN	44	ASN	2.4
1	FK	83	ASN	2.4
1	HM	114	THR	2.4
1	HO	67	ASN	2.4
1	EJ	92	ASP	2.4
1	HS	76	THR	2.4
1	IJ	107	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	JI	23	THR	2.4
1	AF	61	GLY	2.4
1	AU	53	TYR	2.4
1	IZ	110	VAL	2.4
1	AI	82	ILE	2.4
1	IT	82	ILE	2.4
1	JK	71	ALA	2.4
1	JW	82	ILE	2.4
1	KD	62	ALA	2.4
1	JA	4	LYS	2.4
1	JK	93	GLU	2.4
1	EE	6	SER	2.4
1	EO	80	SER	2.4
1	GB	6	SER	2.4
1	GZ	57	SER	2.4
1	HS	74	SER	2.4
1	JA	74	SER	2.4
1	KH	6	SER	2.4
1	BC	111	LEU	2.4
1	BZ	88	LEU	2.4
1	IA	88	LEU	2.4
1	KH	111	LEU	2.4
1	AQ	84	THR	2.4
1	AU	43	THR	2.4
1	BA	104	ASN	2.4
1	DJ	23	THR	2.4
1	EN	18	THR	2.4
1	ES	99	THR	2.4
1	FK	44	ASN	2.4
1	GF	3	THR	2.4
1	GP	44	ASN	2.4
1	HG	52	ASN	2.4
1	HQ	99	THR	2.4
1	HT	25	PRO	2.4
1	HV	39	ASN	2.4
1	IR	72	ASN	2.4
1	JG	39	ASN	2.4
1	JG	109	ASN	2.4
1	KJ	67	ASN	2.4
1	AR	81	VAL	2.4
1	AU	60	ASP	2.4
1	BY	64	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	FH	38	VAL	2.4
1	GA	85	ASP	2.4
1	HU	85	ASP	2.4
1	HV	59	VAL	2.4
1	JI	22	VAL	2.4
1	DQ	108	GLY	2.4
1	JZ	5	TYR	2.4
1	AB	34	ALA	2.4
1	AB	71	ALA	2.4
1	AD	82	ILE	2.4
1	AH	82	ILE	2.4
1	BK	9	ALA	2.4
1	CZ	2	ILE	2.4
1	EJ	82	ILE	2.4
1	ER	65	ALA	2.4
1	HF	50	ALA	2.4
1	AE	4	LYS	2.4
1	BU	14	GLN	2.4
1	HI	48	LYS	2.4
1	HN	27	GLN	2.4
1	HU	14	GLN	2.4
1	AP	88	LEU	2.4
1	BM	74	SER	2.4
1	CO	80	SER	2.4
1	HN	74	SER	2.4
1	AU	112	THR	2.4
1	AV	24	VAL	2.4
1	CC	110	VAL	2.4
1	CW	114	THR	2.4
1	DC	64	VAL	2.4
1	EI	23	THR	2.4
1	FI	99	THR	2.4
1	GX	37	THR	2.4
1	HR	3	THR	2.4
1	IF	90	VAL	2.4
1	IM	56	VAL	2.4
1	IN	113	VAL	2.4
1	JB	112	THR	2.4
1	JW	58	VAL	2.4
1	JZ	54	PRO	2.4
1	FQ	63	ASN	2.4
1	GJ	39	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	IF	44	ASN	2.4
1	EE	17	TYR	2.4
1	EI	107	ASP	2.4
1	EL	107	ASP	2.4
1	AR	82	ILE	2.4
1	BU	26	ALA	2.4
1	GN	106	ILE	2.4
1	HU	17	TYR	2.4
1	II	50	ALA	2.4
1	JU	103	ALA	2.4
1	AY	4	LYS	2.4
1	HQ	89	ARG	2.4
1	AT	14	GLN	2.4
1	BY	111	LEU	2.4
1	HI	66	LEU	2.4
1	AZ	7	GLU	2.4
1	DQ	46	GLU	2.4
1	BA	57	SER	2.4
1	BV	1	SER	2.4
1	IT	74	SER	2.4
1	BD	81	VAL	2.4
1	BH	81	VAL	2.4
1	DA	56	VAL	2.4
1	EL	11	PRO	2.4
1	HP	24	VAL	2.4
1	IP	38	VAL	2.4
1	JM	113	VAL	2.4
1	AL	35	THR	2.3
1	AS	43	THR	2.3
1	BU	21	GLY	2.3
1	CJ	114	THR	2.3
1	CU	10	GLY	2.3
1	DO	112	THR	2.3
1	FG	3	THR	2.3
1	FL	108	GLY	2.3
1	FU	76	THR	2.3
1	HN	10	GLY	2.3
1	IC	112	THR	2.3
1	IJ	18	THR	2.3
1	JA	108	GLY	2.3
1	JE	3	THR	2.3
1	AF	41	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	AS	4	LYS	2.3
1	BF	62	ALA	2.3
1	BT	103	ALA	2.3
1	CJ	77	ALA	2.3
1	CV	9	ALA	2.3
1	DX	62	ALA	2.3
1	EM	83	ASN	2.3
1	EO	39	ASN	2.3
1	ER	67	ASN	2.3
1	FT	9	ALA	2.3
1	FW	70	ARG	2.3
1	HN	49	ILE	2.3
1	IN	82	ILE	2.3
1	IU	44	ASN	2.3
1	JC	50	ALA	2.3
1	JK	44	ASN	2.3
1	KB	109	ASN	2.3
1	JL	17	TYR	2.3
1	AE	66	LEU	2.3
1	DP	14	GLN	2.3
1	HS	27	GLN	2.3
1	IT	73	LEU	2.3
1	FX	7	GLU	2.3
1	IM	81	VAL	2.3
1	JE	113	VAL	2.3
1	JN	56	VAL	2.3
1	JN	90	VAL	2.3
1	BG	15	SER	2.3
1	CS	57	SER	2.3
1	FJ	57	SER	2.3
1	FW	1	SER	2.3
1	GC	11	PRO	2.3
1	JD	96	SER	2.3
1	AE	112	THR	2.3
1	BG	112	THR	2.3
1	BJ	68	THR	2.3
1	BU	102	LYS	2.3
1	CB	61	GLY	2.3
1	CI	10	GLY	2.3
1	EN	42	GLY	2.3
1	ER	10	GLY	2.3
1	DW	82	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	DY	103	ALA	2.3
1	EL	41	ALA	2.3
1	EV	82	ILE	2.3
1	FB	114	THR	2.3
1	FT	68	THR	2.3
1	FW	112	THR	2.3
1	GX	108	GLY	2.3
1	HD	37	THR	2.3
1	HU	4	LYS	2.3
1	JE	4	LYS	2.3
1	IT	49	ILE	2.3
1	JA	84	THR	2.3
1	IR	34	ALA	2.3
1	JB	45	ILE	2.3
1	JK	35	THR	2.3
1	AL	62	ALA	2.3
1	GD	34	ALA	2.3
1	JQ	49	ILE	2.3
1	ET	104	ASN	2.3
1	EY	63	ASN	2.3
1	FH	28	TYR	2.3
1	FV	53	TYR	2.3
1	HB	44	ASN	2.3
1	IG	104	ASN	2.3
1	JL	5	TYR	2.3
1	AU	92	ASP	2.3
1	JL	73	LEU	2.3
1	BE	79	GLN	2.3
1	HF	93	GLU	2.3
1	HQ	7	GLU	2.3
1	EP	64	VAL	2.3
1	FL	81	VAL	2.3
1	GH	33	VAL	2.3
1	GP	81	VAL	2.3
1	HE	33	VAL	2.3
1	IB	22	VAL	2.3
1	IX	22	VAL	2.3
1	HU	48	LYS	2.3
1	CJ	25	PRO	2.3
1	EF	11	PRO	2.3
1	HL	11	PRO	2.3
1	AY	57	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	BL	6	SER	2.3
1	DN	82	ILE	2.3
1	CE	114	THR	2.3
1	CM	50	ALA	2.3
1	EF	9	ALA	2.3
1	EF	114	THR	2.3
1	EU	1	SER	2.3
1	GB	80	SER	2.3
1	GC	112	THR	2.3
1	GF	18	THR	2.3
1	GG	114	THR	2.3
1	HF	15	SER	2.3
1	HS	16	ILE	2.3
1	JD	108	GLY	2.3
1	JM	10	GLY	2.3
1	HY	114	THR	2.3
1	IA	71	ALA	2.3
1	IQ	71	ALA	2.3
1	IW	114	THR	2.3
1	JI	3	THR	2.3
1	JM	34	ALA	2.3
1	JN	103	ALA	2.3
1	JZ	71	ALA	2.3
1	KH	112	THR	2.3
1	IW	17	TYR	2.3
1	ED	52	ASN	2.3
1	EX	55	LEU	2.3
1	GB	52	ASN	2.3
1	GM	39	ASN	2.3
1	GX	111	LEU	2.3
1	HO	32	LEU	2.3
1	HR	109	ASN	2.3
1	JP	44	ASN	2.3
1	JQ	52	ASN	2.3
1	KG	55	LEU	2.3
1	HV	19	PHE	2.3
1	BT	92	ASP	2.3
1	FB	60	ASP	2.3
1	BU	79	GLN	2.3
1	BE	46	GLU	2.3
1	DF	81	VAL	2.3
1	EB	59	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	GM	113	VAL	2.3
1	JJ	81	VAL	2.3
1	EU	70	ARG	2.3
1	FR	30	PRO	2.3
1	BP	108	GLY	2.3
1	HA	21	GLY	2.3
1	BP	62	ALA	2.3
1	FH	103	ALA	2.3
1	FX	62	ALA	2.3
1	IB	62	ALA	2.3
1	DL	37	THR	2.3
1	EC	76	THR	2.3
1	EP	112	THR	2.3
1	EY	74	SER	2.3
1	FI	68	THR	2.3
1	GH	99	THR	2.3
1	GK	112	THR	2.3
1	IO	3	THR	2.3
1	JL	6	SER	2.3
1	JN	1	SER	2.3
1	AE	111	LEU	2.3
1	BX	88	LEU	2.3
1	CM	73	LEU	2.3
1	CZ	66	LEU	2.3
1	EI	111	LEU	2.3
1	JO	88	LEU	2.3
1	EL	17	TYR	2.3
1	FT	17	TYR	2.3
1	JJ	5	TYR	2.3
1	CC	19	PHE	2.3
1	BC	52	ASN	2.3
1	FY	44	ASN	2.3
1	HU	72	ASN	2.3
1	IJ	44	ASN	2.3
1	IP	44	ASN	2.3
1	JT	44	ASN	2.3
1	AR	107	ASP	2.3
1	AZ	107	ASP	2.3
1	BZ	60	ASP	2.3
1	JS	60	ASP	2.3
1	GV	4	LYS	2.3
1	BV	22	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	CP	90	VAL	2.3
1	DM	33	VAL	2.3
1	FL	7	GLU	2.3
1	GA	46	GLU	2.3
1	AT	82	ILE	2.3
1	CS	45	ILE	2.3
1	DX	82	ILE	2.3
1	HA	11	PRO	2.3
1	JX	82	ILE	2.3
1	AL	9	ALA	2.3
1	AQ	50	ALA	2.3
1	BG	61	GLY	2.3
1	BU	13	GLY	2.3
1	CI	13	GLY	2.3
1	FH	10	GLY	2.3
1	HF	34	ALA	2.3
1	HF	65	ALA	2.3
1	HS	21	GLY	2.3
1	IH	41	ALA	2.3
1	IK	65	ALA	2.3
1	IU	103	ALA	2.3
1	AC	35	THR	2.3
1	AS	114	THR	2.3
1	CQ	114	THR	2.3
1	CT	99	THR	2.3
1	CV	23	THR	2.3
1	DK	36	THR	2.3
1	EA	112	THR	2.3
1	FA	68	THR	2.3
1	GP	68	THR	2.3
1	HJ	3	THR	2.3
1	HU	36	THR	2.3
1	IH	112	THR	2.3
1	JA	91	LEU	2.3
1	CH	1	SER	2.3
1	EC	1	SER	2.3
1	FM	8	SER	2.3
1	GD	15	SER	2.3
1	GT	74	SER	2.3
1	HW	74	SER	2.3
1	IO	1	SER	2.3
1	JA	1	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	AS	17	TYR	2.3
1	CH	53	TYR	2.3
1	EW	5	TYR	2.3
1	HU	47	TYR	2.3
1	AK	44	ASN	2.3
1	AN	44	ASN	2.3
1	BQ	109	ASN	2.3
1	CJ	44	ASN	2.3
1	DU	67	ASN	2.3
1	CB	27	GLN	2.3
1	ED	79	GLN	2.3
1	HP	4	LYS	2.3
1	AS	92	ASP	2.3
1	CK	22	VAL	2.3
1	DW	22	VAL	2.3
1	FR	107	ASP	2.3
1	IO	59	VAL	2.3
1	JL	59	VAL	2.3
1	BM	46	GLU	2.2
1	CG	7	GLU	2.2
1	CK	86	GLU	2.2
1	CC	69	ILE	2.2
1	DJ	82	ILE	2.2
1	DR	82	ILE	2.2
1	EM	49	ILE	2.2
1	JP	106	ILE	2.2
1	BA	41	ALA	2.2
1	EY	9	ALA	2.2
1	FN	9	ALA	2.2
1	HH	108	GLY	2.2
1	JK	10	GLY	2.2
1	KD	103	ALA	2.2
1	HM	66	LEU	2.2
1	II	78	LEU	2.2
1	AG	76	THR	2.2
1	AN	97	PHE	2.2
1	BK	76	THR	2.2
1	BU	75	PHE	2.2
1	CI	75	PHE	2.2
1	CP	18	THR	2.2
1	CT	97	PHE	2.2
1	EF	112	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	EZ	112	THR	2.2
1	GM	18	THR	2.2
1	HN	3	THR	2.2
1	IR	99	THR	2.2
1	JM	76	THR	2.2
1	BZ	1	SER	2.2
1	FR	1	SER	2.2
1	IQ	74	SER	2.2
1	JQ	6	SER	2.2
1	GO	70	ARG	2.2
1	AE	81	VAL	2.2
1	BY	39	ASN	2.2
1	BY	63	ASN	2.2
1	CB	52	ASN	2.2
1	CH	22	VAL	2.2
1	CT	67	ASN	2.2
1	EI	109	ASN	2.2
1	EN	39	ASN	2.2
1	FG	38	VAL	2.2
1	HS	22	VAL	2.2
1	CY	7	GLU	2.2
1	ES	60	ASP	2.2
1	FO	86	GLU	2.2
1	HB	7	GLU	2.2
1	HU	107	ASP	2.2
1	BA	45	ILE	2.2
1	AH	62	ALA	2.2
1	CA	21	GLY	2.2
1	CN	62	ALA	2.2
1	CP	11	PRO	2.2
1	DW	50	ALA	2.2
1	DX	34	ALA	2.2
1	EM	62	ALA	2.2
1	FB	11	PRO	2.2
1	GK	111	LEU	2.2
1	GZ	26	ALA	2.2
1	IQ	21	GLY	2.2
1	JC	62	ALA	2.2
1	JE	9	ALA	2.2
1	JY	50	ALA	2.2
1	JY	91	LEU	2.2
1	KI	88	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	BF	76	THR	2.2
1	BY	114	THR	2.2
1	CK	35	THR	2.2
1	CT	48	LYS	2.2
1	GW	4	LYS	2.2
1	IL	19	PHE	2.2
1	EY	3	THR	2.2
1	IN	99	THR	2.2
1	JJ	112	THR	2.2
1	EL	70	ARG	2.2
1	EX	70	ARG	2.2
1	FV	89	ARG	2.2
1	EP	1	SER	2.2
1	GJ	1	SER	2.2
1	IQ	8	SER	2.2
1	AG	33	VAL	2.2
1	BB	56	VAL	2.2
1	BQ	113	VAL	2.2
1	GG	110	VAL	2.2
1	HR	113	VAL	2.2
1	IM	110	VAL	2.2
1	DO	27	GLN	2.2
1	JN	14	GLN	2.2
1	DC	44	ASN	2.2
1	EH	101	ASN	2.2
1	FT	72	ASN	2.2
1	FU	83	ASN	2.2
1	IX	72	ASN	2.2
1	FN	82	ILE	2.2
1	GP	106	ILE	2.2
1	JH	106	ILE	2.2
1	CJ	107	ASP	2.2
1	AP	10	GLY	2.2
1	DH	34	ALA	2.2
1	DI	34	ALA	2.2
1	DU	10	GLY	2.2
1	EM	9	ALA	2.2
1	EX	78	LEU	2.2
1	FM	107	ASP	2.2
1	GH	92	ASP	2.2
1	JW	107	ASP	2.2
1	GO	62	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	GV	103	ALA	2.2
1	GY	61	GLY	2.2
1	IE	10	GLY	2.2
1	JV	9	ALA	2.2
1	KA	62	ALA	2.2
1	BU	4	LYS	2.2
1	GK	4	LYS	2.2
1	HS	75	PHE	2.2
1	IE	97	PHE	2.2
1	IJ	19	PHE	2.2
1	AT	112	THR	2.2
1	CB	3	THR	2.2
1	DJ	3	THR	2.2
1	ES	35	THR	2.2
1	FB	3	THR	2.2
1	GO	37	THR	2.2
1	HR	76	THR	2.2
1	HT	76	THR	2.2
1	IM	68	THR	2.2
1	JW	112	THR	2.2
1	DY	22	VAL	2.2
1	IN	64	VAL	2.2
1	AV	1	SER	2.2
1	FW	57	SER	2.2
1	GT	6	SER	2.2
1	IS	1	SER	2.2
1	JB	74	SER	2.2
1	JN	6	SER	2.2
1	KA	6	SER	2.2
1	EK	14	GLN	2.2
1	BH	106	ILE	2.2
1	CL	106	ILE	2.2
1	EN	94	ILE	2.2
1	FC	106	ILE	2.2
1	IO	82	ILE	2.2
1	JE	82	ILE	2.2
1	JZ	16	ILE	2.2
1	BP	7	GLU	2.2
1	BQ	104	ASN	2.2
1	CU	52	ASN	2.2
1	DV	44	ASN	2.2
1	DW	93	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	FF	72	ASN	2.2
1	GZ	63	ASN	2.2
1	HF	39	ASN	2.2
1	HU	52	ASN	2.2
1	JO	44	ASN	2.2
1	AG	50	ALA	2.2
1	AJ	54	PRO	2.2
1	AZ	71	ALA	2.2
1	BH	25	PRO	2.2
1	DI	10	GLY	2.2
1	DP	9	ALA	2.2
1	DR	103	ALA	2.2
1	DS	42	GLY	2.2
1	EV	62	ALA	2.2
1	GE	62	ALA	2.2
1	HU	50	ALA	2.2
1	IA	50	ALA	2.2
1	IP	26	ALA	2.2
1	JB	34	ALA	2.2
1	JZ	9	ALA	2.2
1	KC	29	MET	2.2
1	BG	85	ASP	2.2
1	DD	107	ASP	2.2
1	JJ	107	ASP	2.2
1	KA	87	LYS	2.2
1	AP	97	PHE	2.2
1	DJ	97	PHE	2.2
1	DK	19	PHE	2.2
1	AR	18	THR	2.2
1	BW	43	THR	2.2
1	CX	114	THR	2.2
1	FT	114	THR	2.2
1	GJ	43	THR	2.2
1	IQ	84	THR	2.2
1	JD	37	THR	2.2
1	AK	81	VAL	2.2
1	AL	33	VAL	2.2
1	AS	110	VAL	2.2
1	BD	38	VAL	2.2
1	BU	47	TYR	2.2
1	CE	64	VAL	2.2
1	DC	81	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	EG	56	VAL	2.2
1	FT	59	VAL	2.2
1	GZ	22	VAL	2.2
1	AP	16	ILE	2.2
1	BU	6	SER	2.2
1	BV	82	ILE	2.2
1	DN	96	SER	2.2
1	EW	74	SER	2.2
1	EW	82	ILE	2.2
1	FB	14	GLN	2.2
1	FD	8	SER	2.2
1	IN	57	SER	2.2
1	IP	27	GLN	2.2
1	JJ	96	SER	2.2
1	BI	88	LEU	2.2
1	EE	55	LEU	2.2
1	AA	4	LYS	2.2
1	AA	40	LYS	2.2
1	AA	62	ALA	2.2
1	AG	52	ASN	2.2
1	AT	39	ASN	2.2
1	AV	63	ASN	2.2
1	AZ	9	ALA	2.2
1	BI	52	ASN	2.2
1	CP	44	ASN	2.2
1	CT	9	ALA	2.2
1	DF	7	GLU	2.2
1	DS	62	ALA	2.2
1	EB	72	ASN	2.2
1	EP	44	ASN	2.2
1	EY	50	ALA	2.2
1	FG	26	ALA	2.2
1	FU	50	ALA	2.2
1	HJ	41	ALA	2.2
1	HQ	50	ALA	2.2
1	IG	63	ASN	2.2
1	JF	7	GLU	2.2
1	JK	21	GLY	2.2
1	JM	102	LYS	2.2
1	JV	4	LYS	2.2
1	KF	63	ASN	2.2
1	DN	54	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	ES	13	GLY	2.2
1	FB	21	GLY	2.2
1	FJ	108	GLY	2.2
1	HR	11	PRO	2.2
1	KG	61	GLY	2.2
1	AC	60	ASP	2.2
1	FH	97	PHE	2.2
1	HD	60	ASP	2.2
1	IN	60	ASP	2.2
1	AH	3	THR	2.1
1	BI	99	THR	2.1
1	CE	76	THR	2.1
1	CP	23	THR	2.1
1	CQ	113	VAL	2.1
1	ED	59	VAL	2.1
1	ER	113	VAL	2.1
1	FH	51	VAL	2.1
1	GC	113	VAL	2.1
1	GG	43	THR	2.1
1	IC	18	THR	2.1
1	IR	33	VAL	2.1
1	KH	114	THR	2.1
1	HA	5	TYR	2.1
1	DH	98	ILE	2.1
1	EM	16	ILE	2.1
1	KA	16	ILE	2.1
1	CW	88	LEU	2.1
1	GB	73	LEU	2.1
1	AG	8	SER	2.1
1	AR	4	LYS	2.1
1	AS	8	SER	2.1
1	CA	6	SER	2.1
1	CC	57	SER	2.1
1	CV	96	SER	2.1
1	DE	40	LYS	2.1
1	FX	4	LYS	2.1
1	GQ	15	SER	2.1
1	HG	48	LYS	2.1
1	AY	93	GLU	2.1
1	CK	71	ALA	2.1
1	DE	9	ALA	2.1
1	EQ	103	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	EY	34	ALA	2.1
1	FB	26	ALA	2.1
1	FH	71	ALA	2.1
1	FJ	103	ALA	2.1
1	GU	62	ALA	2.1
1	HI	96	SER	2.1
1	IE	15	SER	2.1
1	FP	70	ARG	2.1
1	GY	93	GLU	2.1
1	HK	7	GLU	2.1
1	IE	62	ALA	2.1
1	JD	100	ALA	2.1
1	JM	71	ALA	2.1
1	AN	42	GLY	2.1
1	AU	11	PRO	2.1
1	CU	61	GLY	2.1
1	GY	21	GLY	2.1
1	JO	61	GLY	2.1
1	AZ	44	ASN	2.1
1	BU	101	ASN	2.1
1	BW	109	ASN	2.1
1	DD	109	ASN	2.1
1	EB	101	ASN	2.1
1	EJ	63	ASN	2.1
1	EU	109	ASN	2.1
1	FV	72	ASN	2.1
1	GK	44	ASN	2.1
1	HV	104	ASN	2.1
1	IT	101	ASN	2.1
1	JL	67	ASN	2.1
1	JU	44	ASN	2.1
1	CC	107	ASP	2.1
1	DP	85	ASP	2.1
1	DQ	60	ASP	2.1
1	HS	107	ASP	2.1
1	AR	22	VAL	2.1
1	FN	113	VAL	2.1
1	FS	113	VAL	2.1
1	GX	22	VAL	2.1
1	JJ	22	VAL	2.1
1	BV	35	THR	2.1
1	DJ	99	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	EF	36	THR	2.1
1	FW	76	THR	2.1
1	GB	3	THR	2.1
1	GB	84	THR	2.1
1	GT	43	THR	2.1
1	GT	84	THR	2.1
1	HU	84	THR	2.1
1	IL	114	THR	2.1
1	IR	37	THR	2.1
1	BB	82	ILE	2.1
1	GV	17	TYR	2.1
1	IU	45	ILE	2.1
1	JK	69	ILE	2.1
1	JM	98	ILE	2.1
1	CA	4	LYS	2.1
1	DJ	4	LYS	2.1
1	DJ	32	LEU	2.1
1	EY	48	LYS	2.1
1	FA	4	LYS	2.1
1	JJ	48	LYS	2.1
1	JM	73	LEU	2.1
1	KA	91	LEU	2.1
1	BU	9	ALA	2.1
1	EN	26	ALA	2.1
1	EN	103	ALA	2.1
1	HN	103	ALA	2.1
1	KD	70	ARG	2.1
1	BG	1	SER	2.1
1	BM	6	SER	2.1
1	DN	57	SER	2.1
1	DX	61	GLY	2.1
1	EC	108	GLY	2.1
1	EN	96	SER	2.1
1	FG	6	SER	2.1
1	FI	7	GLU	2.1
1	FL	10	GLY	2.1
1	FS	46	GLU	2.1
1	GR	46	GLU	2.1
1	HE	96	SER	2.1
1	HO	93	GLU	2.1
1	HQ	86	GLU	2.1
1	HQ	93	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	IE	8	SER	2.1
1	IK	15	SER	2.1
1	IT	6	SER	2.1
1	IW	61	GLY	2.1
1	JI	42	GLY	2.1
1	CJ	67	ASN	2.1
1	CO	39	ASN	2.1
1	ER	44	ASN	2.1
1	HR	72	ASN	2.1
1	BX	33	VAL	2.1
1	BY	107	ASP	2.1
1	CP	92	ASP	2.1
1	EY	60	ASP	2.1
1	GE	60	ASP	2.1
1	HS	95	VAL	2.1
1	IM	58	VAL	2.1
1	JD	81	VAL	2.1
1	JN	107	ASP	2.1
1	AI	112	THR	2.1
1	AM	111	LEU	2.1
1	AZ	112	THR	2.1
1	CK	78	LEU	2.1
1	DT	35	THR	2.1
1	EE	88	LEU	2.1
1	EJ	111	LEU	2.1
1	EM	88	LEU	2.1
1	EQ	76	THR	2.1
1	EQ	112	THR	2.1
1	FR	111	LEU	2.1
1	HP	114	THR	2.1
1	HU	3	THR	2.1
1	IV	68	THR	2.1
1	JS	82	ILE	2.1
1	JM	17	TYR	2.1
1	AZ	70	ARG	2.1
1	BA	9	ALA	2.1
1	CQ	27	GLN	2.1
1	DN	62	ALA	2.1
1	DR	62	ALA	2.1
1	JN	34	ALA	2.1
1	AY	46	GLU	2.1
1	BB	42	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	CJ	10	GLY	2.1
1	DL	7	GLU	2.1
1	JL	13	GLY	2.1
1	AZ	6	SER	2.1
1	BE	74	SER	2.1
1	BK	15	SER	2.1
1	CI	8	SER	2.1
1	EI	19	PHE	2.1
1	EI	80	SER	2.1
1	EK	6	SER	2.1
1	EX	96	SER	2.1
1	JB	80	SER	2.1
1	JJ	1	SER	2.1
1	JZ	1	SER	2.1
1	AA	44	ASN	2.1
1	AW	44	ASN	2.1
1	BA	39	ASN	2.1
1	BS	67	ASN	2.1
1	CQ	109	ASN	2.1
1	EH	39	ASN	2.1
1	ES	101	ASN	2.1
1	GB	44	ASN	2.1
1	HE	72	ASN	2.1
1	HS	44	ASN	2.1
1	JD	109	ASN	2.1
1	JO	39	ASN	2.1
1	JS	63	ASN	2.1
1	JW	63	ASN	2.1
1	EI	56	VAL	2.1
1	EO	113	VAL	2.1
1	FE	59	VAL	2.1
1	FT	58	VAL	2.1
1	GA	22	VAL	2.1
1	HT	90	VAL	2.1
1	JO	110	VAL	2.1
1	JP	110	VAL	2.1
1	KJ	113	VAL	2.1
1	AN	40	LYS	2.1
1	BV	87	LYS	2.1
1	FN	4	LYS	2.1
1	HS	4	LYS	2.1
1	IO	4	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	JJ	4	LYS	2.1
1	AM	78	LEU	2.1
1	CP	12	ILE	2.1
1	CW	82	ILE	2.1
1	EZ	12	ILE	2.1
1	HG	32	LEU	2.1
1	ID	12	ILE	2.1
1	IG	111	LEU	2.1
1	IQ	66	LEU	2.1
1	JJ	78	LEU	2.1
1	JM	105	ILE	2.1
1	AG	70	ARG	2.1
1	AR	53	TYR	2.1
1	BU	20	THR	2.1
1	DQ	68	THR	2.1
1	DY	99	THR	2.1
1	EI	47	TYR	2.1
1	FE	114	THR	2.1
1	FJ	28	TYR	2.1
1	GC	68	THR	2.1
1	HD	3	THR	2.1
1	JE	47	TYR	2.1
1	JI	112	THR	2.1
1	JJ	76	THR	2.1
1	BU	77	ALA	2.1
1	ER	34	ALA	2.1
1	FF	9	ALA	2.1
1	EL	79	GLN	2.1
1	GU	14	GLN	2.1
1	AJ	42	GLY	2.1
1	CT	61	GLY	2.1
1	DD	108	GLY	2.1
1	FT	61	GLY	2.1
1	BI	97	PHE	2.1
1	FG	86	GLU	2.1
1	GT	54	PRO	2.1
1	HP	93	GLU	2.1
1	IQ	86	GLU	2.1
1	JA	7	GLU	2.1
1	JK	75	PHE	2.1
1	AQ	15	SER	2.1
1	FV	57	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	IW	57	SER	2.1
1	JL	74	SER	2.1
1	BZ	113	VAL	2.1
1	CQ	24	VAL	2.1
1	DY	110	VAL	2.1
1	EH	24	VAL	2.1
1	KB	24	VAL	2.1
1	BQ	72	ASN	2.1
1	BQ	101	ASN	2.1
1	BT	4	LYS	2.1
1	CD	39	ASN	2.1
1	HG	102	LYS	2.1
1	HM	44	ASN	2.1
1	HQ	39	ASN	2.1
1	HQ	52	ASN	2.1
1	IJ	63	ASN	2.1
1	JQ	72	ASN	2.1
1	AK	82	ILE	2.1
1	AR	70	ARG	2.1
1	BI	49	ILE	2.1
1	CR	78	LEU	2.1
1	CT	31	ARG	2.1
1	CY	111	LEU	2.1
1	GY	91	LEU	2.1
1	JA	89	ARG	2.1
1	BA	60	ASP	2.1
1	AI	114	THR	2.1
1	AU	3	THR	2.1
1	BT	112	THR	2.1
1	BU	29	MET	2.1
1	DX	60	ASP	2.1
1	EB	112	THR	2.1
1	EG	29	MET	2.1
1	GU	60	ASP	2.1
1	JD	92	ASP	2.1
1	KG	85	ASP	2.1
1	HP	23	THR	2.1
1	IH	37	THR	2.1
1	IP	3	THR	2.1
1	AP	34	ALA	2.1
1	BG	62	ALA	2.1
1	CU	77	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	DA	77	ALA	2.1
1	GS	26	ALA	2.1
1	HQ	71	ALA	2.1
1	JM	77	ALA	2.1
1	JO	26	ALA	2.1
1	JT	62	ALA	2.1
1	KE	9	ALA	2.1
1	AE	10	GLY	2.1
1	CI	42	GLY	2.1
1	EN	108	GLY	2.1
1	FK	27	GLN	2.1
1	GP	108	GLY	2.1
1	HR	61	GLY	2.1
1	IT	61	GLY	2.1
1	JB	21	GLY	2.1
1	JG	108	GLY	2.1
1	BA	75	PHE	2.1
1	BE	54	PRO	2.1
1	BG	46	GLU	2.1
1	DN	93	GLU	2.1
1	EX	93	GLU	2.1
1	GH	97	PHE	2.1
1	AO	38	VAL	2.0
1	CZ	59	VAL	2.0
1	DZ	4	LYS	2.0
1	EM	64	VAL	2.0
1	FL	64	VAL	2.0
1	GB	51	VAL	2.0
1	HW	102	LYS	2.0
1	IR	48	LYS	2.0
1	BT	8	SER	2.0
1	DM	74	SER	2.0
1	DW	6	SER	2.0
1	FS	80	SER	2.0
1	GY	15	SER	2.0
1	GZ	15	SER	2.0
1	HI	74	SER	2.0
1	AD	44	ASN	2.0
1	AG	67	ASN	2.0
1	AU	39	ASN	2.0
1	AU	88	LEU	2.0
1	BD	45	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	CB	66	LEU	2.0
1	CI	82	ILE	2.0
1	CJ	98	ILE	2.0
1	CN	67	ASN	2.0
1	DY	44	ASN	2.0
1	EG	52	ASN	2.0
1	EX	67	ASN	2.0
1	FH	101	ASN	2.0
1	FT	63	ASN	2.0
1	HC	104	ASN	2.0
1	HP	70	ARG	2.0
1	IH	39	ASN	2.0
1	IT	78	LEU	2.0
1	AV	60	ASP	2.0
1	BX	99	THR	2.0
1	DR	77	ALA	2.0
1	ED	47	TYR	2.0
1	EE	41	ALA	2.0
1	FB	9	ALA	2.0
1	FJ	100	ALA	2.0
1	GM	23	THR	2.0
1	GV	18	THR	2.0
1	GZ	50	ALA	2.0
1	HV	9	ALA	2.0
1	IR	71	ALA	2.0
1	KC	112	THR	2.0
1	CV	108	GLY	2.0
1	JM	79	GLN	2.0
1	JW	21	GLY	2.0
1	GY	11	PRO	2.0
1	BC	7	GLU	2.0
1	DE	7	GLU	2.0
1	DK	7	GLU	2.0
1	DN	48	LYS	2.0
1	IT	46	GLU	2.0
1	AO	64	VAL	2.0
1	AZ	95	VAL	2.0
1	BM	113	VAL	2.0
1	BV	38	VAL	2.0
1	DH	81	VAL	2.0
1	EJ	110	VAL	2.0
1	EP	58	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	FJ	56	VAL	2.0
1	GV	22	VAL	2.0
1	HP	59	VAL	2.0
1	JK	95	VAL	2.0
1	AQ	73	LEU	2.0
1	BM	31	ARG	2.0
1	BU	32	LEU	2.0
1	CK	32	LEU	2.0
1	CU	66	LEU	2.0
1	DK	111	LEU	2.0
1	DY	70	ARG	2.0
1	HS	111	LEU	2.0
1	JP	70	ARG	2.0
1	JZ	73	LEU	2.0
1	AE	106	ILE	2.0
1	BO	80	SER	2.0
1	CJ	57	SER	2.0
1	CK	15	SER	2.0
1	CT	15	SER	2.0
1	EI	57	SER	2.0
1	ES	80	SER	2.0
1	HI	49	ILE	2.0
1	HT	82	ILE	2.0
1	HZ	57	SER	2.0
1	IS	6	SER	2.0
1	JM	1	SER	2.0
1	AC	52	ASN	2.0
1	AF	83	ASN	2.0
1	AM	109	ASN	2.0
1	AZ	39	ASN	2.0
1	DV	63	ASN	2.0
1	FG	83	ASN	2.0
1	IU	109	ASN	2.0
1	JH	44	ASN	2.0
1	AM	103	ALA	2.0
1	AP	76	THR	2.0
1	BQ	84	THR	2.0
1	BU	84	THR	2.0
1	BW	65	ALA	2.0
1	CV	18	THR	2.0
1	CX	36	THR	2.0
1	CZ	3	THR	2.0

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Mol	Chain	Res	Type	RSRZ
1	DN	100	ALA	2.0
1	CK	53	TYR	2.0
1	DY	23	THR	2.0
1	EC	37	THR	2.0
1	EH	99	THR	2.0
1	EJ	43	THR	2.0
1	FJ	112	THR	2.0
1	FK	114	THR	2.0
1	GK	99	THR	2.0
1	GV	53	TYR	2.0
1	HO	114	THR	2.0
1	HT	43	THR	2.0
1	HU	9	ALA	2.0
1	HU	99	THR	2.0
1	IA	26	ALA	2.0
1	JH	23	THR	2.0
1	JI	103	ALA	2.0
1	JK	53	TYR	2.0
1	AW	107	ASP	2.0
1	DE	107	ASP	2.0
1	FI	107	ASP	2.0
1	FW	107	ASP	2.0
1	GF	107	ASP	2.0
1	HV	60	ASP	2.0
1	JI	92	ASP	2.0
1	DB	108	GLY	2.0
1	DW	13	GLY	2.0
1	EI	10	GLY	2.0
1	GR	61	GLY	2.0
1	GT	75	PHE	2.0
1	GW	19	PHE	2.0
1	IM	19	PHE	2.0
1	JW	97	PHE	2.0
1	BT	54	PRO	2.0
1	CI	4	LYS	2.0
1	CT	79	GLN	2.0
1	DA	79	GLN	2.0
1	EE	4	LYS	2.0
1	GJ	40	LYS	2.0
1	JN	11	PRO	2.0
1	AP	51	VAL	2.0
1	BO	46	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	AU	70	ARG	2.0
1	EG	113	VAL	2.0
1	GY	46	GLU	2.0
1	FX	70	ARG	2.0
1	HE	58	VAL	2.0
1	HQ	46	GLU	2.0
1	HS	64	VAL	2.0
1	JB	24	VAL	2.0
1	JU	59	VAL	2.0
1	GN	111	LEU	2.0
1	JA	82	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.