



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 06:25 PM EDT

PDB ID : 6YFC
Title : Virus-like particle of bacteriophage AVE019
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 3.25 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

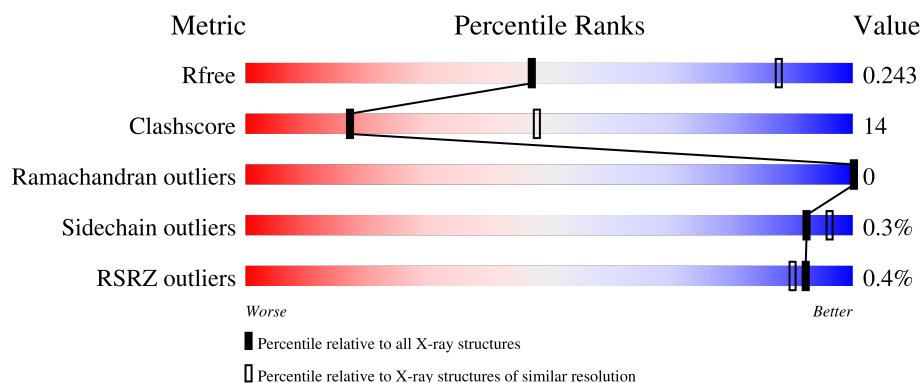
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1619 (3.28-3.20)
Clashscore	141614	1755 (3.28-3.20)
Ramachandran outliers	138981	1728 (3.28-3.20)
Sidechain outliers	138945	1727 (3.28-3.20)
RSRZ outliers	127900	1567 (3.28-3.20)

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	124	<div> <div>69%</div> <div>31%</div> </div>
1	AB	124	<div> <div>2%</div> <div>60%</div> <div>34%</div> <div>6%</div> </div>
1	AC	124	<div> <div>70%</div> <div>30%</div> </div>
1	AD	124	<div> <div>%</div> <div>69%</div> <div>31%</div> </div>
1	AE	124	<div> <div>2%</div> <div>57%</div> <div>36%</div> <div>6%</div> </div>


























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Mol	Chain	Length	Quality of chain
1	AF	124	
1	AG	124	
1	AH	124	
1	AI	124	
1	AJ	124	
1	AK	124	
1	AL	124	
1	AM	124	
1	AN	124	
1	AO	124	
1	AP	124	
1	AQ	124	
1	AR	124	
1	AS	124	
1	AT	124	
1	AU	124	
1	AV	124	
1	AW	124	
1	AX	124	
1	AY	124	
1	AZ	124	
1	BA	124	
1	BB	124	
1	BC	124	
1	BD	124	



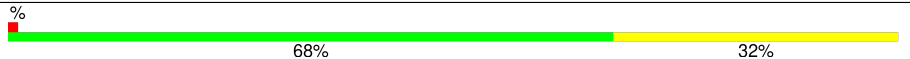
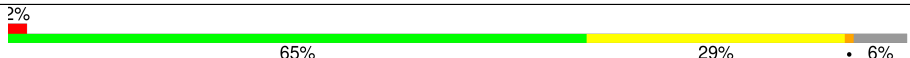
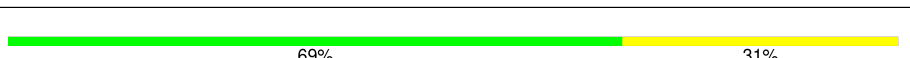
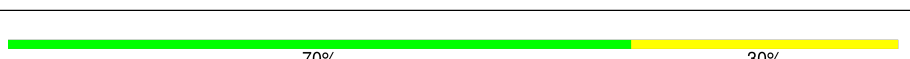
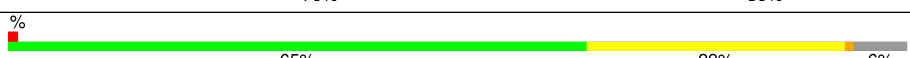
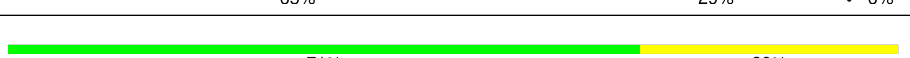
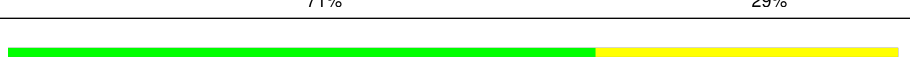

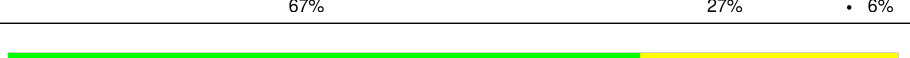







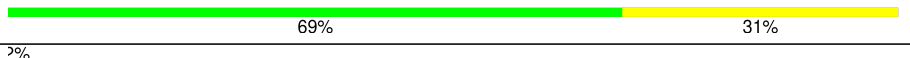
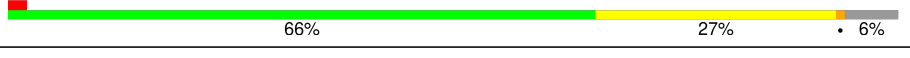

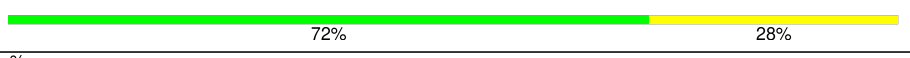



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Mol	Chain	Length	Quality of chain
1	BE	124	
1	BF	124	
1	BG	124	
1	BH	124	
1	BI	124	
1	BJ	124	
1	BK	124	
1	BL	124	
1	BM	124	
1	BN	124	
1	BO	124	
1	BP	124	
1	BQ	124	
1	BR	124	
1	BS	124	
1	BT	124	
1	BU	124	
1	BV	124	
1	BW	124	
1	BX	124	
1	BY	124	
1	BZ	124	
1	CA	124	
1	CB	124	
1	CC	124	







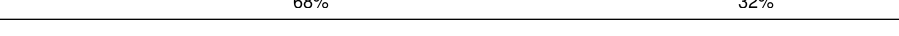
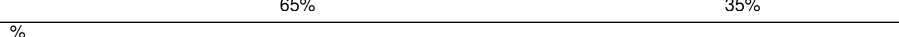
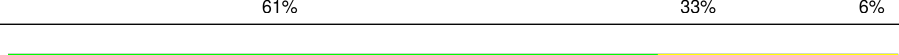
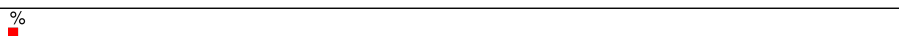




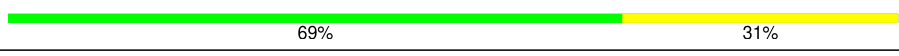






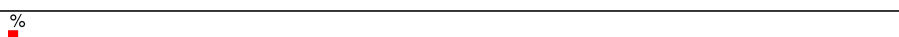
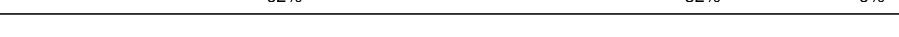


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Mol	Chain	Length	Quality of chain
1	CD	124	
1	CE	124	
1	CF	124	
1	CG	124	
1	CH	124	
1	CI	124	
1	CJ	124	
1	CK	124	
1	CL	124	
1	CM	124	
1	CN	124	
1	CO	124	
1	CP	124	
1	CQ	124	
1	CR	124	
1	CS	124	
1	CT	124	
1	CU	124	
1	CV	124	
1	CW	124	
1	CX	124	
1	CY	124	
1	CZ	124	
1	DA	124	
1	DB	124	

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Mol	Chain	Length	Quality of chain
1	DC	124	% 
1	DD	124	
1	DE	124	% 
1	DF	124	
1	DG	124	
1	DH	124	
1	DI	124	
1	DJ	124	
1	DK	124	% 
1	DL	124	
1	DM	124	% 
1	DN	124	% 
1	DO	124	
1	DP	124	
1	DQ	124	2% 
1	DR	124	
1	DS	124	
1	DT	124	% 
1	DU	124	
1	DV	124	
1	DW	124	
1	DX	124	
1	DY	124	
1	DZ	124	% 
1	EA	124	



















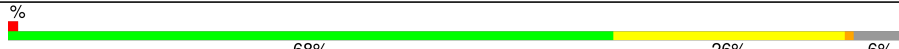






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Mol	Chain	Length	Quality of chain
1	EB	124	
1	EC	124	
1	ED	124	
1	EE	124	
1	EF	124	
1	EG	124	
1	EH	124	
1	EI	124	
1	EJ	124	
1	EK	124	
1	EL	124	
1	EM	124	
1	EN	124	
1	EO	124	
1	EP	124	
1	EQ	124	
1	ER	124	
1	ES	124	
1	ET	124	
1	EU	124	
1	EV	124	
1	EW	124	
1	EX	124	
1	EY	124	
1	EZ	124	












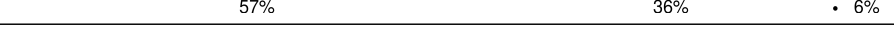







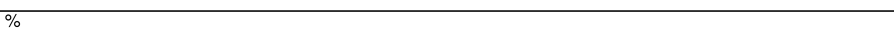

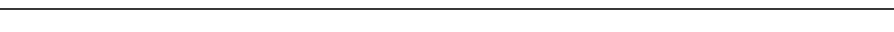
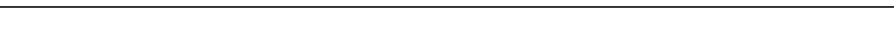


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Mol	Chain	Length	Quality of chain
1	FA	124	% 
1	FB	124	
1	FC	124	% 
1	FD	124	
1	FE	124	
1	FF	124	
1	FG	124	% 
1	FH	124	
1	FI	124	
1	FJ	124	% 
1	FK	124	
1	FL	124	
1	FM	124	
1	FN	124	
1	FO	124	
1	FP	124	
1	FQ	124	
1	FR	124	
1	FS	124	% 
1	FT	124	
1	FU	124	% 
1	FV	124	4% 
1	FW	124	
1	FX	124	
1	FY	124	% 

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Mol	Chain	Length	Quality of chain
1	FZ	124	 71%29%
1	GA	124	 62%38%
1	GB	124	 64%30%6%
1	GC	124	 70%30%
1	GD	124	 69%31%
1	GE	124	 59%35%6%
1	GF	124	 68%32%
1	GG	124	 66%34%
1	GH	124	 65%30%6%
1	GI	124	 69%31%
1	GJ	124	 68%32%
1	GK	124	 57%36%6%
1	GL	124	 68%32%
1	GM	124	 65%35%
1	GN	124	 64%30%6%
1	GO	124	 67%33%
1	GP	124	 70%30%
1	GQ	124	 64%31%6%
1	GR	124	 71%29%
1	GS	124	 71%29%
1	GT	124	 65%29%6%
1	GU	124	 69%31%
1	GV	124	 69%31%
1	GW	124	 65%29%6%
1	GX	124	 72%28%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 169260 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	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AB	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	AC	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AD	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AE	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	AF	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AG	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AH	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	AI	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AJ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AK	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	AL	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AM	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AN	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	AO	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AP	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	AR	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AS	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AT	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	AU	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AV	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AW	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	AX	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AY	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	AZ	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	BA	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BB	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BC	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	BD	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BE	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BF	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	BG	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BH	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BI	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	BJ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BK	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BL	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	BM	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BN	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BO	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	BP	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BQ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BR	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	BS	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BT	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BU	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	BV	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BW	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BX	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	BY	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	BZ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CA	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	CB	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CC	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CD	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	CE	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CF	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CG	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	CH	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CI	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CJ	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	CK	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CL	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CM	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	CN	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CO	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CP	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	CQ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CR	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CS	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	CT	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CU	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CV	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	CW	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CX	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	CY	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	CZ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DA	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DB	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	DC	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DD	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DE	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	DF	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DG	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DH	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	DI	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DJ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DK	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	DL	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DM	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DN	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	DO	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DP	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DQ	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	DR	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DS	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DT	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	DU	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DV	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DW	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	DX	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DY	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	DZ	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	EA	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EB	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EC	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	ED	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EE	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EF	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	EG	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EH	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EI	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	EJ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EK	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EL	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	EM	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EN	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EO	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	EP	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EQ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	ER	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	ES	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	ET	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EU	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	EV	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EW	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EX	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	EY	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	EZ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FA	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	FB	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FC	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FD	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	FE	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FF	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FG	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	FH	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FI	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FJ	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	FK	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FL	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	FM	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	FN	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FO	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FP	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	FQ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FR	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FS	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	FT	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FU	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FV	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	FW	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FX	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	FY	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	FZ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GA	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GB	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	GC	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GD	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GE	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	GF	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GG	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	GH	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	GI	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GJ	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GK	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	GL	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GM	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GN	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	GO	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GP	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GQ	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	GR	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GS	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GT	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	GU	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GV	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			
1	GW	117	Total	C	N	O	S	0	0	0
			910	569	157	180	4			
1	GX	124	Total	C	N	O	S	0	0	0
			955	594	165	192	4			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AA	1	Total	Ca	0	0
			1	1		
2	AD	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AG	1	Total 1	Ca 1	0	0
2	AJ	1	Total 1	Ca 1	0	0
2	AM	1	Total 1	Ca 1	0	0
2	AP	1	Total 1	Ca 1	0	0
2	AS	1	Total 1	Ca 1	0	0
2	AV	1	Total 1	Ca 1	0	0
2	AY	1	Total 1	Ca 1	0	0
2	BB	1	Total 1	Ca 1	0	0
2	BE	1	Total 1	Ca 1	0	0
2	BH	1	Total 1	Ca 1	0	0
2	BK	1	Total 1	Ca 1	0	0
2	BN	1	Total 1	Ca 1	0	0
2	BQ	1	Total 1	Ca 1	0	0
2	BT	1	Total 1	Ca 1	0	0
2	BW	1	Total 1	Ca 1	0	0
2	BZ	1	Total 1	Ca 1	0	0
2	CC	1	Total 1	Ca 1	0	0
2	CF	1	Total 1	Ca 1	0	0
2	CI	1	Total 1	Ca 1	0	0
2	CL	1	Total 1	Ca 1	0	0
2	CO	1	Total 1	Ca 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	CR	1	Total 1	Ca 1	0	0
2	CU	1	Total 1	Ca 1	0	0
2	CX	1	Total 1	Ca 1	0	0
2	DA	1	Total 1	Ca 1	0	0
2	DD	1	Total 1	Ca 1	0	0
2	DG	1	Total 1	Ca 1	0	0
2	DJ	1	Total 1	Ca 1	0	0
2	DM	1	Total 1	Ca 1	0	0
2	DP	1	Total 1	Ca 1	0	0
2	DS	1	Total 1	Ca 1	0	0
2	DV	1	Total 1	Ca 1	0	0
2	DY	1	Total 1	Ca 1	0	0
2	EB	1	Total 1	Ca 1	0	0
2	EE	1	Total 1	Ca 1	0	0
2	EH	1	Total 1	Ca 1	0	0
2	EK	1	Total 1	Ca 1	0	0
2	EN	1	Total 1	Ca 1	0	0
2	EQ	1	Total 1	Ca 1	0	0
2	ET	1	Total 1	Ca 1	0	0
2	EW	1	Total 1	Ca 1	0	0
2	EZ	1	Total 1	Ca 1	0	0

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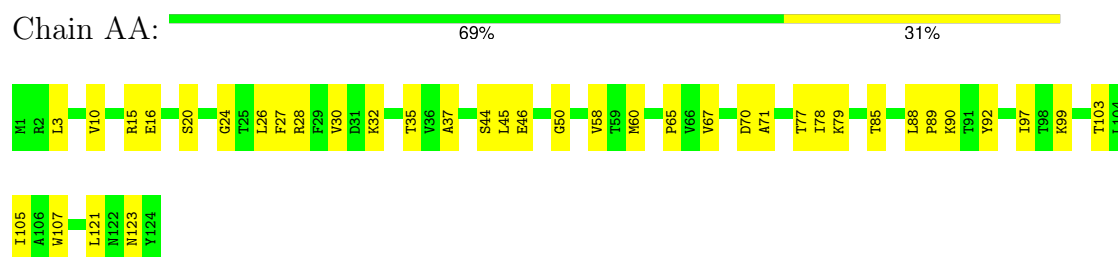
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	FC	1	Total 1	Ca 1	0	0
2	FF	1	Total 1	Ca 1	0	0
2	FI	1	Total 1	Ca 1	0	0
2	FL	1	Total 1	Ca 1	0	0
2	FO	1	Total 1	Ca 1	0	0
2	FR	1	Total 1	Ca 1	0	0
2	FU	1	Total 1	Ca 1	0	0
2	FX	1	Total 1	Ca 1	0	0
2	GA	1	Total 1	Ca 1	0	0
2	GD	1	Total 1	Ca 1	0	0
2	GG	1	Total 1	Ca 1	0	0
2	GJ	1	Total 1	Ca 1	0	0
2	GM	1	Total 1	Ca 1	0	0
2	GP	1	Total 1	Ca 1	0	0
2	GS	1	Total 1	Ca 1	0	0
2	GV	1	Total 1	Ca 1	0	0

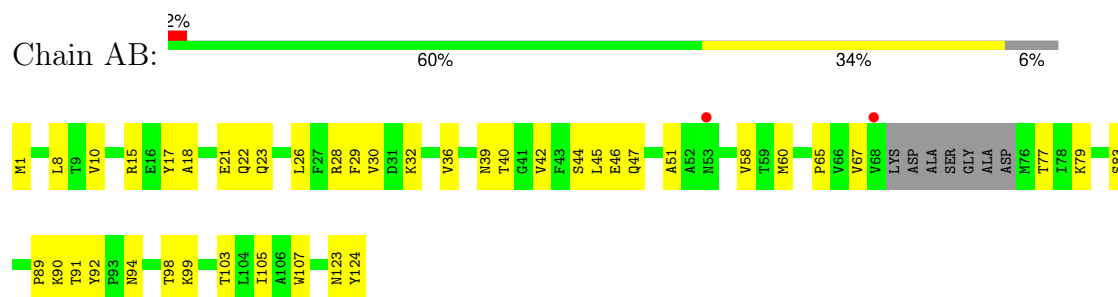
3 Residue-property plots [i](#)

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.

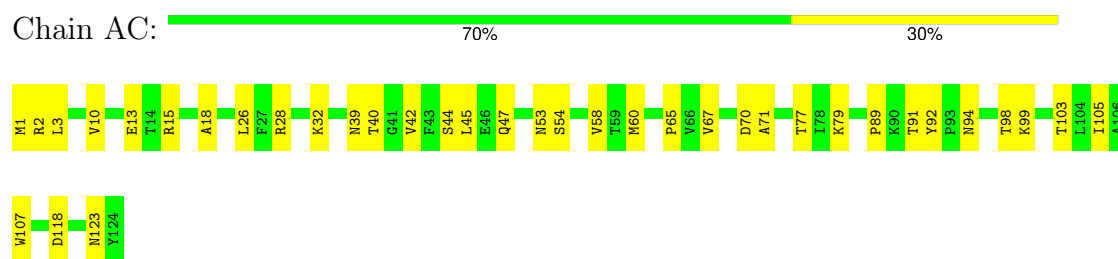
- Molecule 1: coat protein



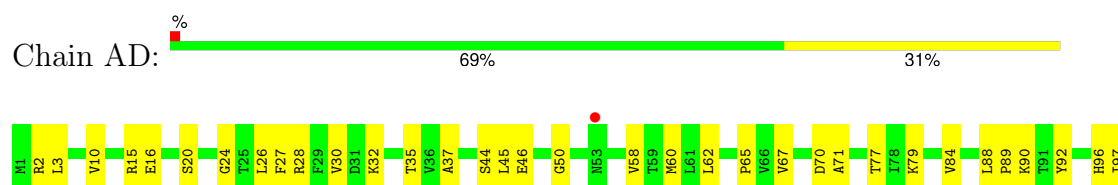
- Molecule 1: coat protein



- Molecule 1: coat protein

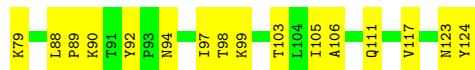


- Molecule 1: coat protein

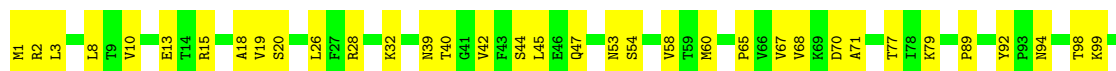




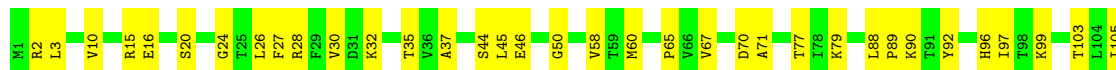
- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein



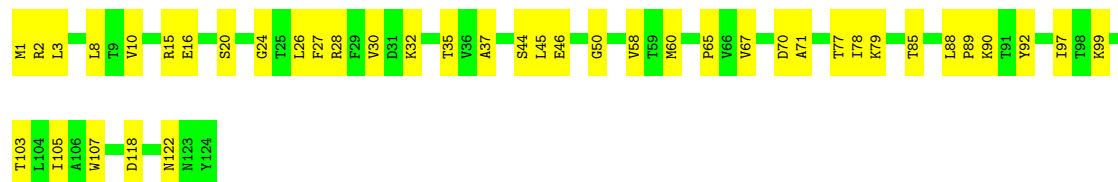
- Molecule 1: coat protein





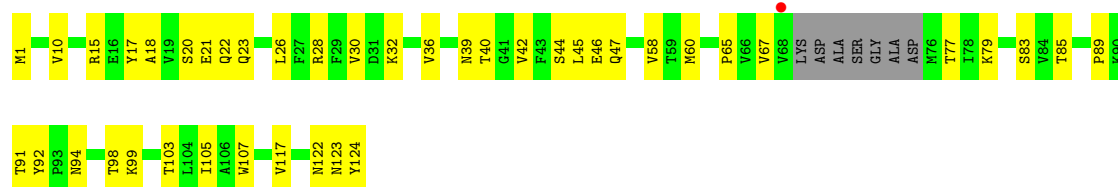
- Molecule 1: coat protein

Chain AJ: 67% 33%



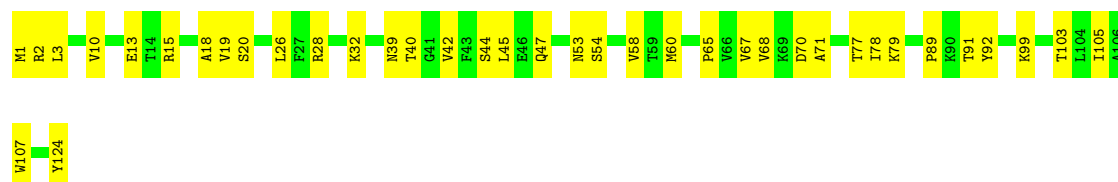
- Molecule 1: coat protein

Chain AK: 60% 34% 6%



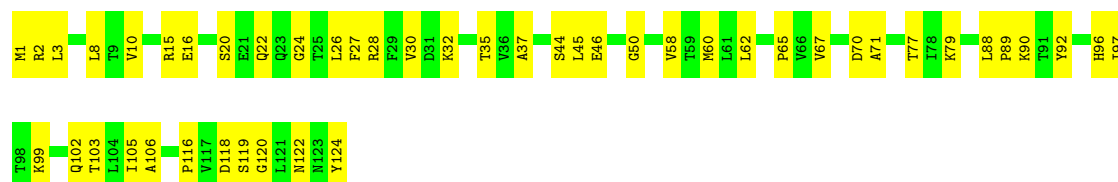
- Molecule 1: coat protein

Chain AL: 69% 31%



- Molecule 1: coat protein

Chain AM: 62% 38%



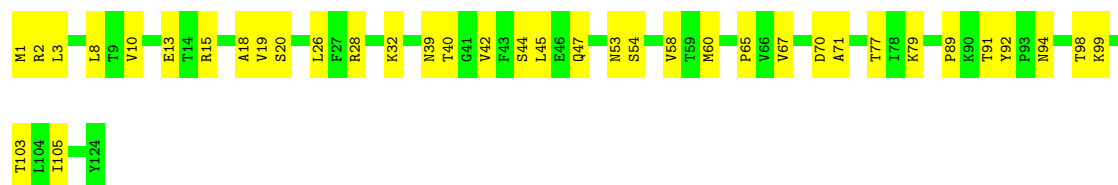
- Molecule 1: coat protein

Chain AN: 



- Molecule 1: coat protein

Chain AO: 



- Molecule 1: coat protein

Chain AP: 



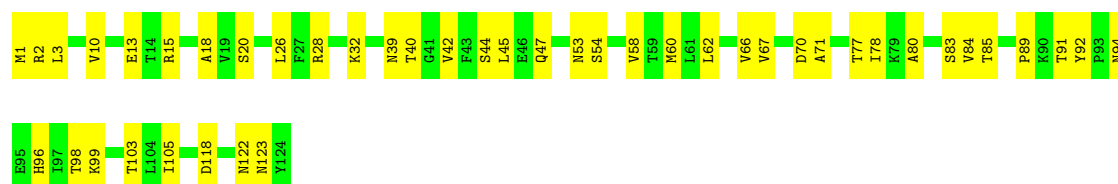
- Molecule 1: coat protein

Chain AQ: 

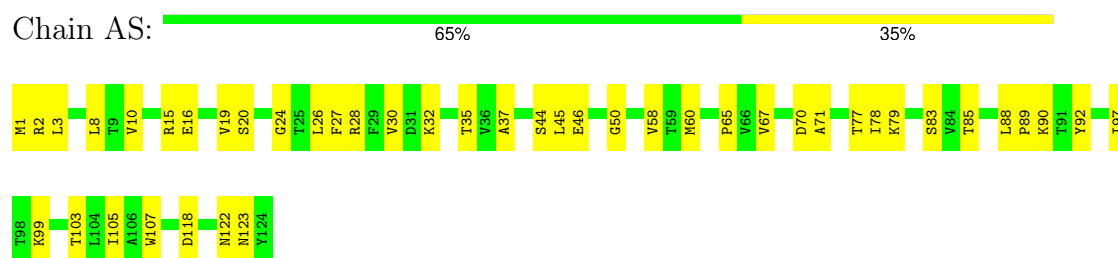


- Molecule 1: coat protein

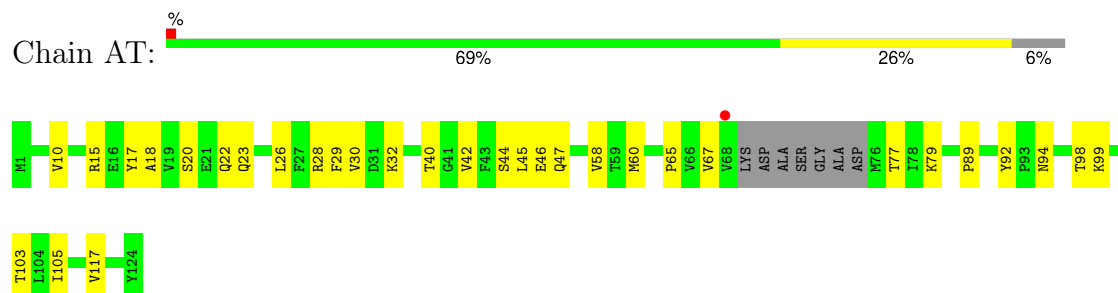
Chain AR: 



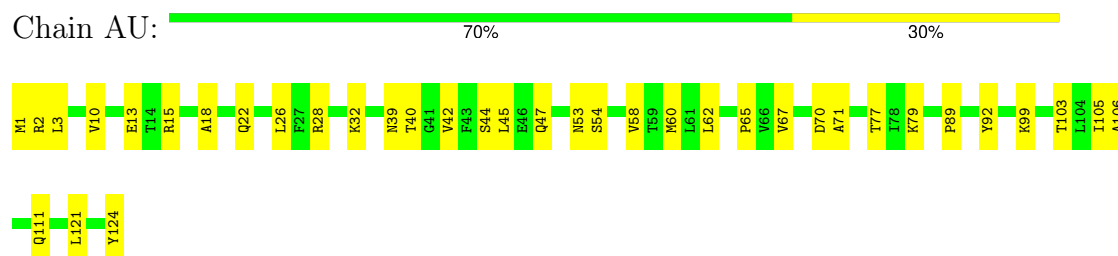
- Molecule 1: coat protein



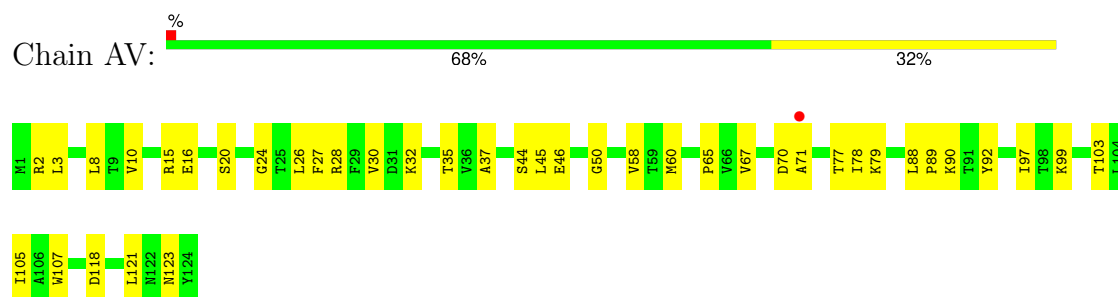
- Molecule 1: coat protein



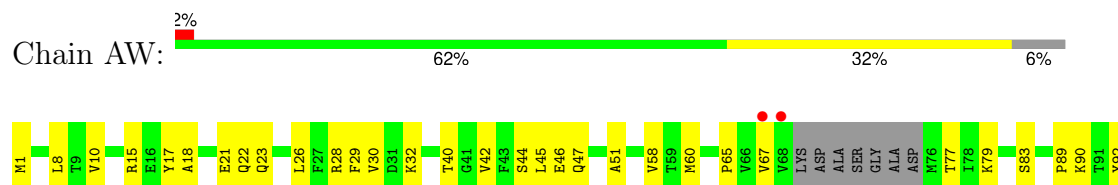
- Molecule 1: coat protein



- Molecule 1: coat protein



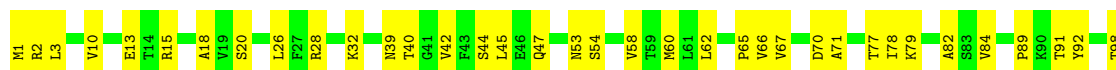
- Molecule 1: coat protein





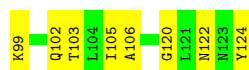
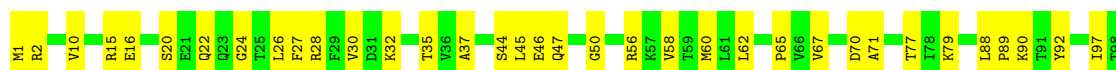
- Molecule 1: coat protein

Chain AX: 65% 35%



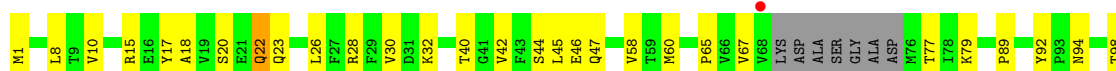
- Molecule 1: coat protein

Chain AY: 65% 35%



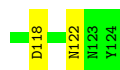
- Molecule 1: coat protein

Chain AZ: 66% 27% 6%



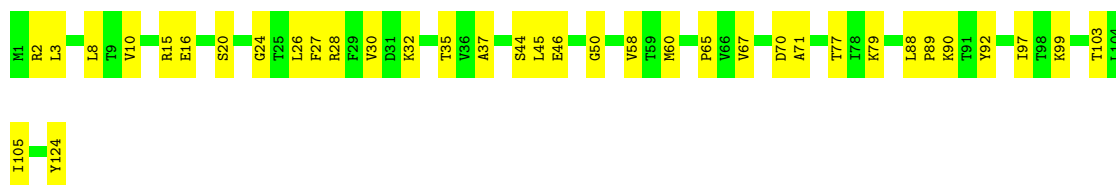
- Molecule 1: coat protein

Chain BA: 70% 30%



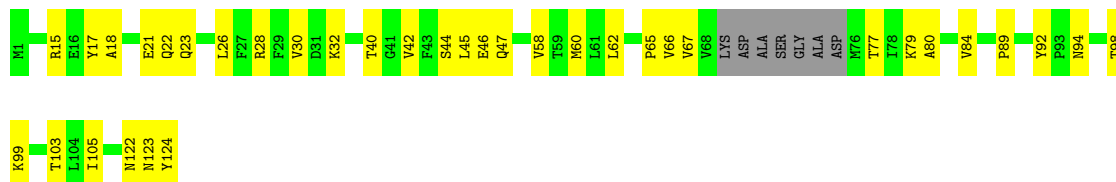
- Molecule 1: coat protein

Chain BB: 71% 29%



- Molecule 1: coat protein

Chain BC:



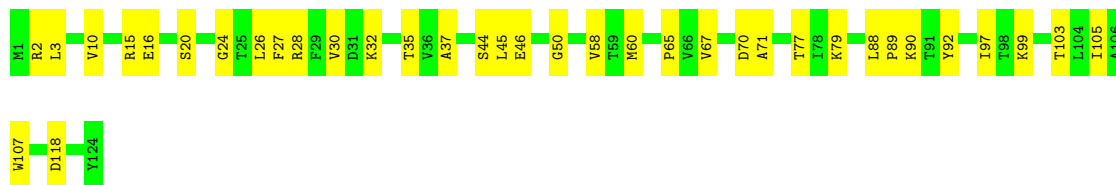
- Molecule 1: coat protein

Chain BD:



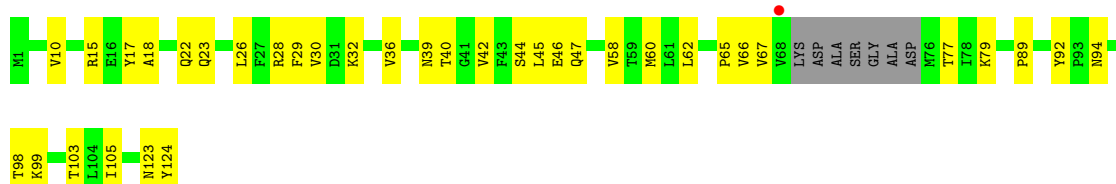
- Molecule 1: coat protein

Chain BE:



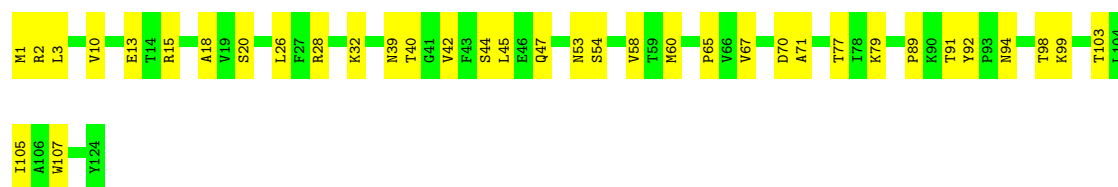
- Molecule 1: coat protein

Chain BF:



- Molecule 1: coat protein

Chain BG:  71% 29%



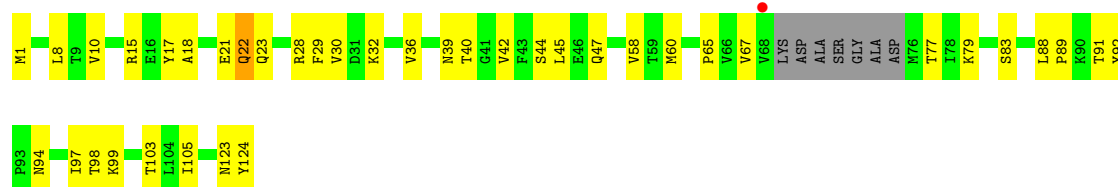
- Molecule 1: coat protein

Chain BH:  70% 30%



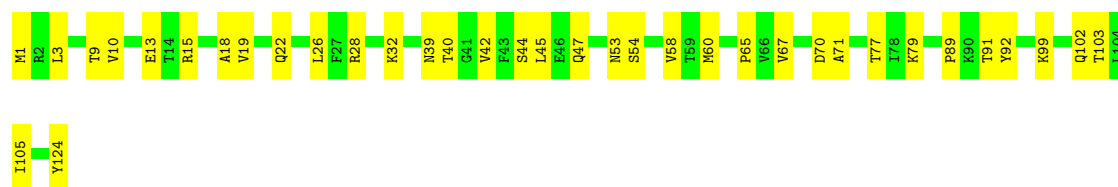
- Molecule 1: coat protein

Chain BI:  63% 31% 6%



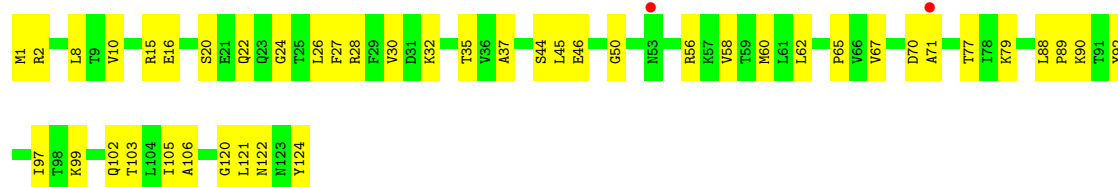
- Molecule 1: coat protein

Chain BJ:  71% 29%

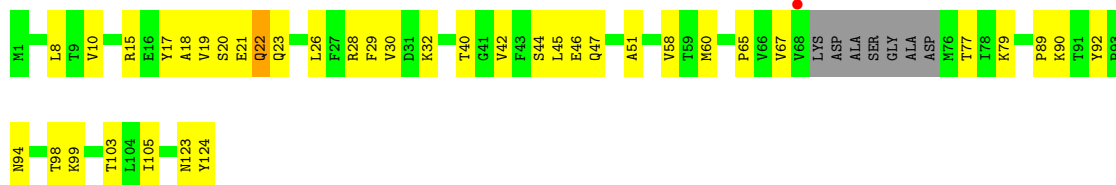


- Molecule 1: coat protein

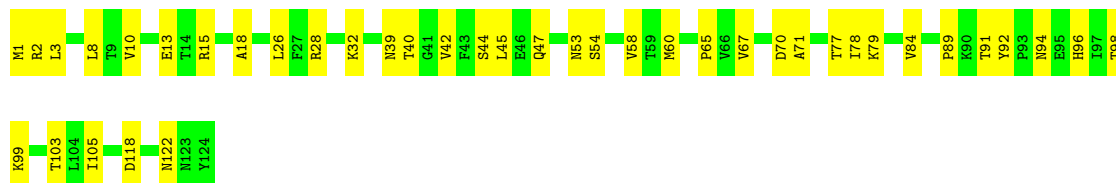
Chain BK:  65% 35% 2%



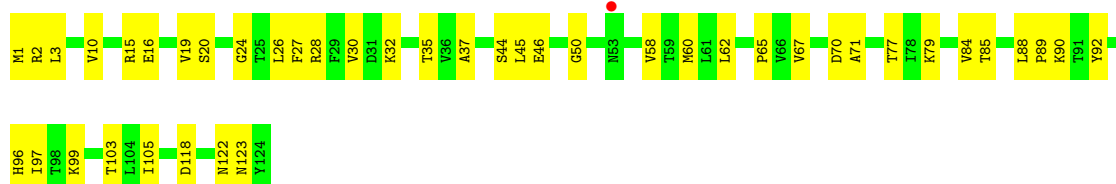
- Molecule 1: coat protein



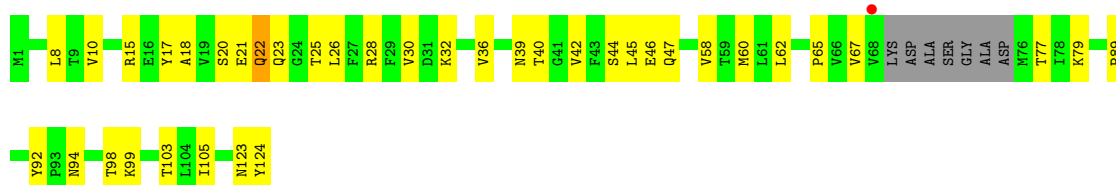
- Molecule 1: coat protein



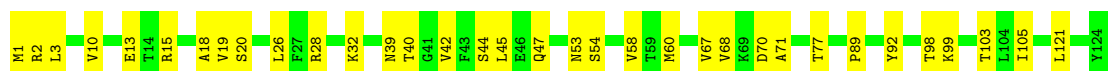
- Molecule 1: coat protein



- Molecule 1: coat protein

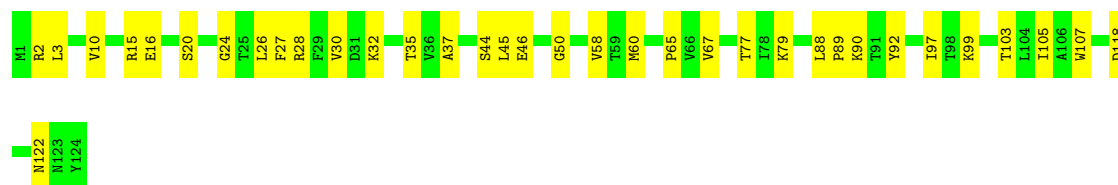


- Molecule 1: coat protein

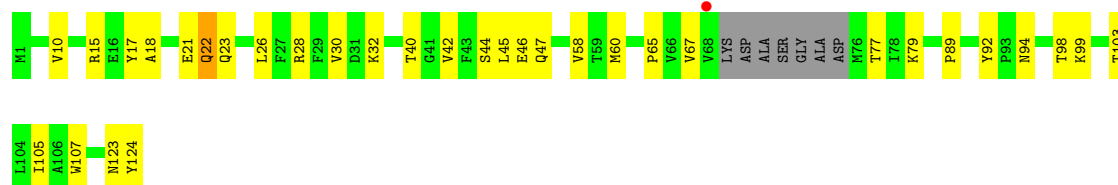


- Molecule 1: coat protein





- Molecule 1: coat protein



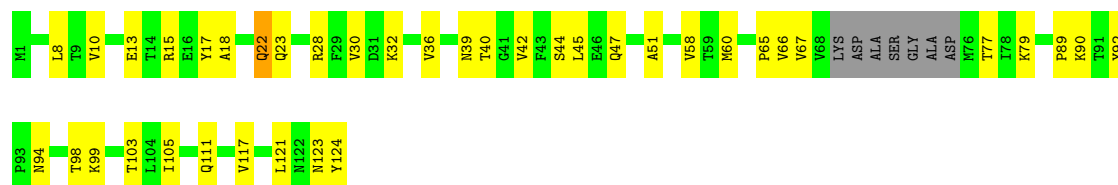
- Molecule 1: coat protein



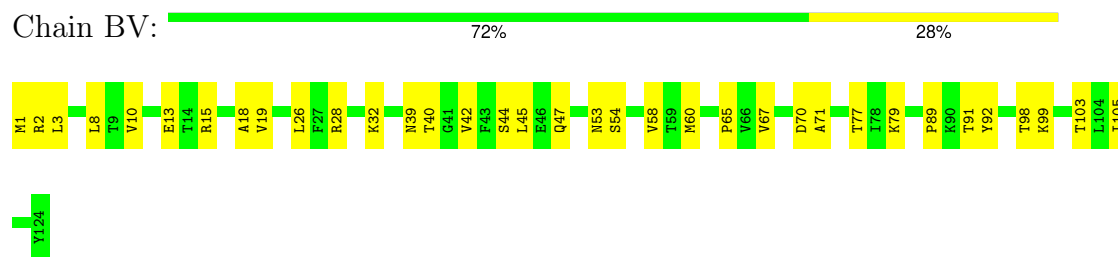
- Molecule 1: coat protein



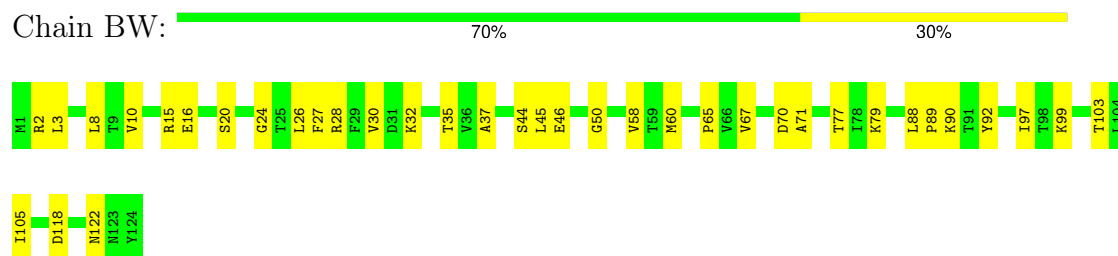
- Molecule 1: coat protein



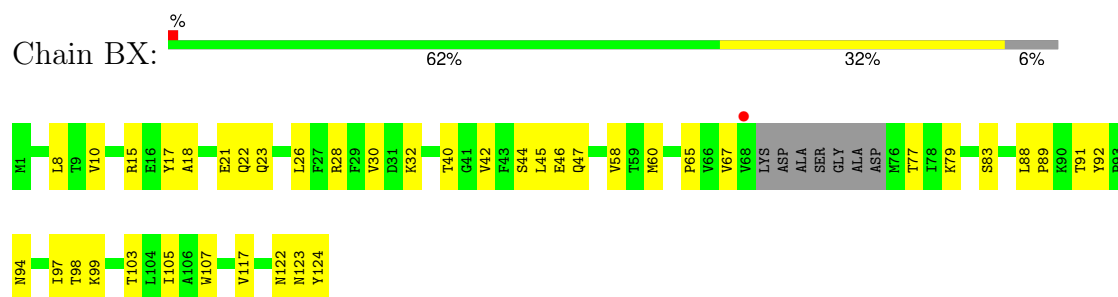
- Molecule 1: coat protein



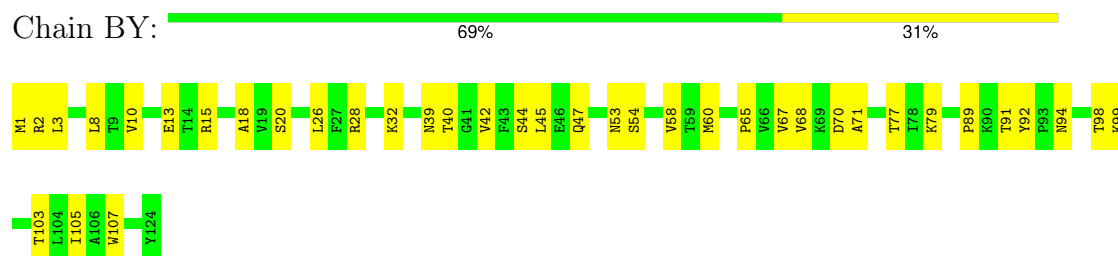
- Molecule 1: coat protein



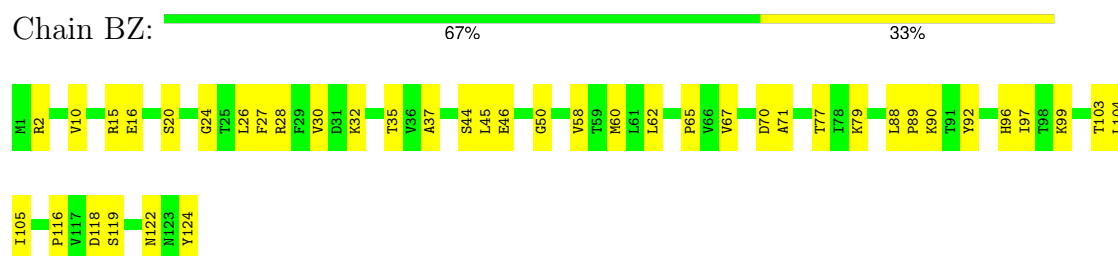
- Molecule 1: coat protein



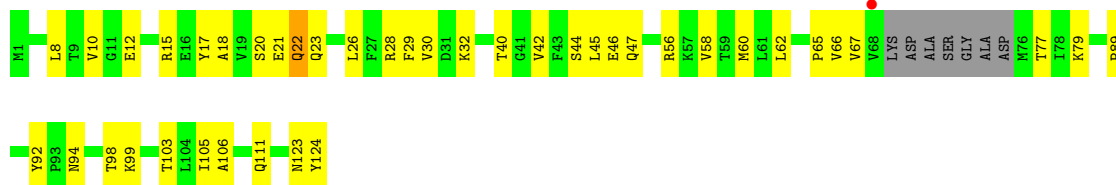
- Molecule 1: coat protein



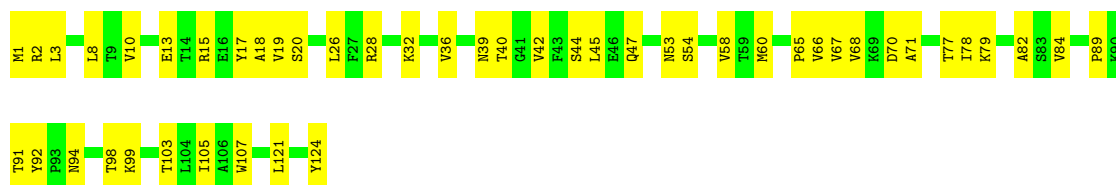
- Molecule 1: coat protein



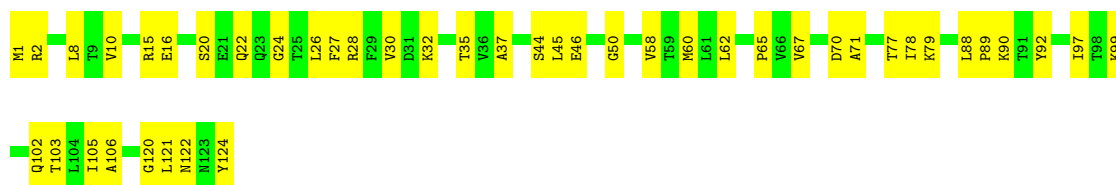
- Molecule 1: coat protein



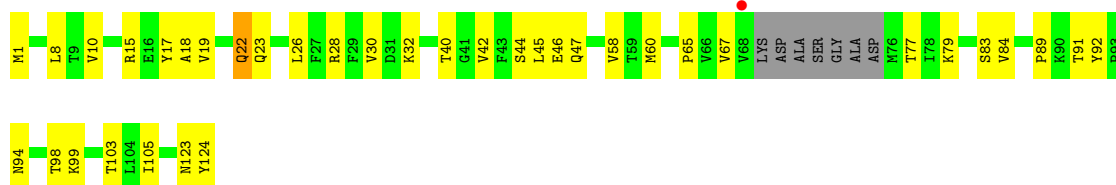
- Molecule 1: coat protein



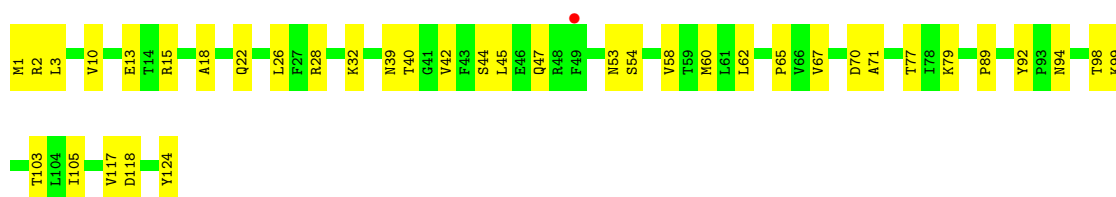
- Molecule 1: coat protein



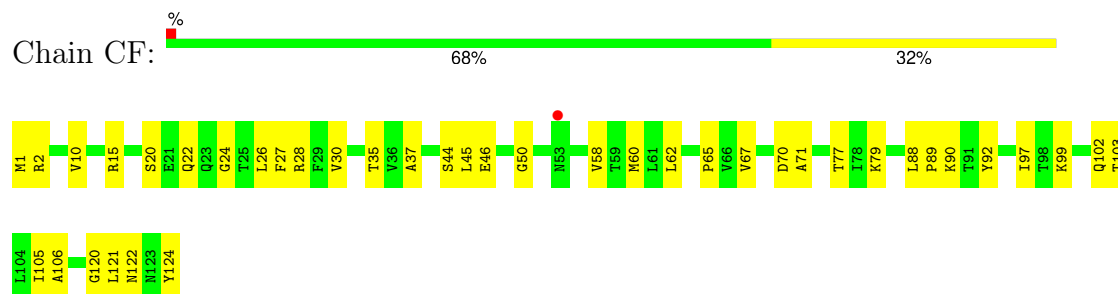
- Molecule 1: coat protein



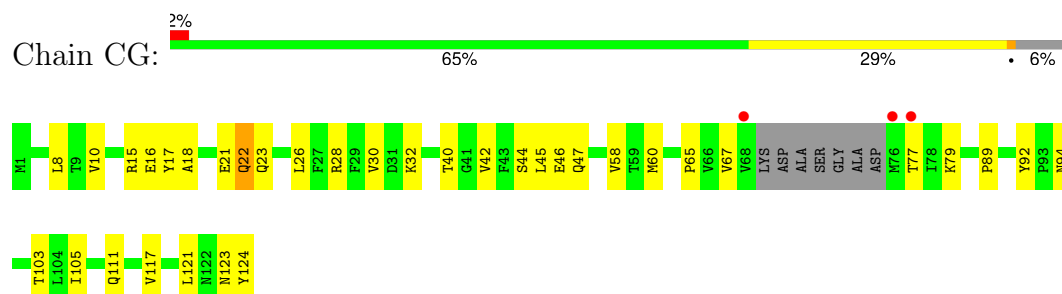
- Molecule 1: coat protein



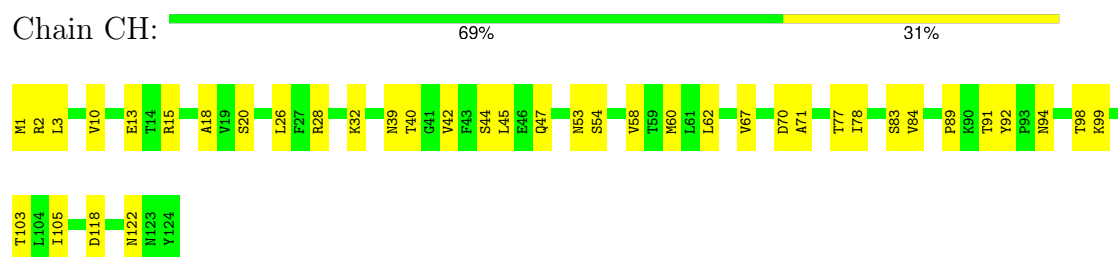
- Molecule 1: coat protein



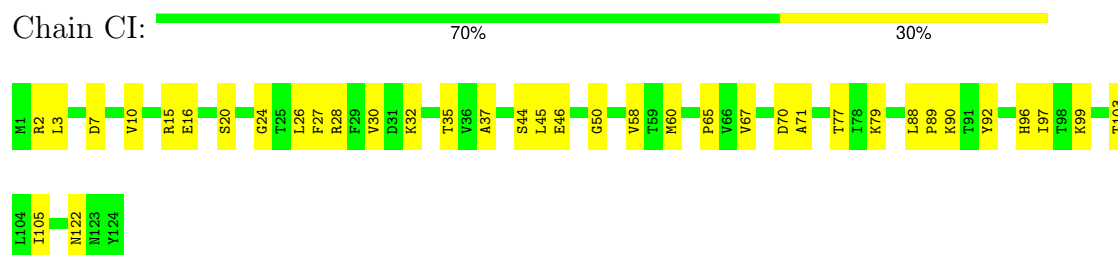
- Molecule 1: coat protein



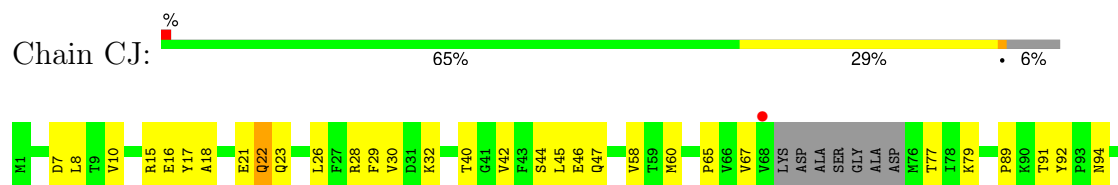
- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein





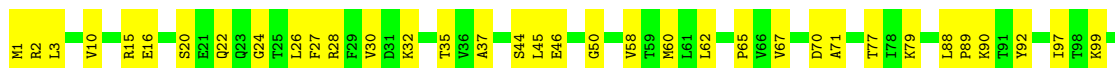
- Molecule 1: coat protein

Chain CK: 71% 29%



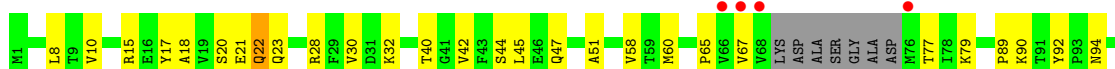
- Molecule 1: coat protein

Chain CL: 66% 34%



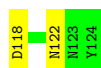
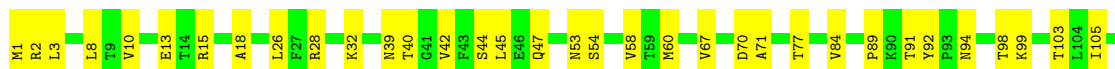
- Molecule 1: coat protein

Chain CM: 3% 67% 27% 6%



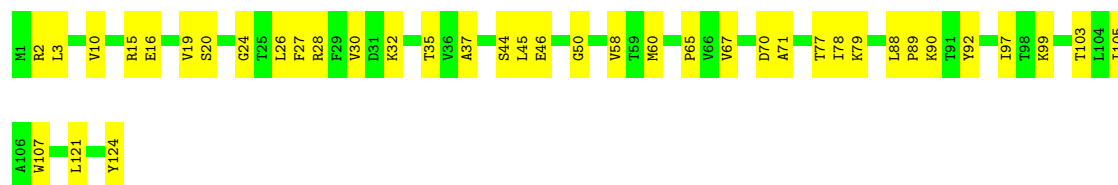
- Molecule 1: coat protein

Chain CN: 71% 29%

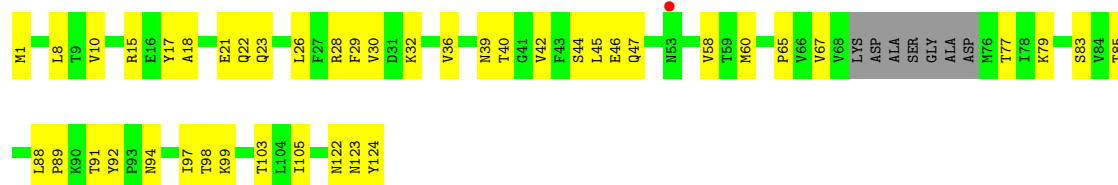


- Molecule 1: coat protein

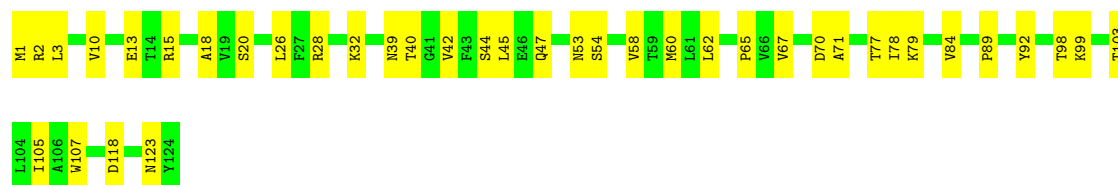
Chain CO: 69% 31%



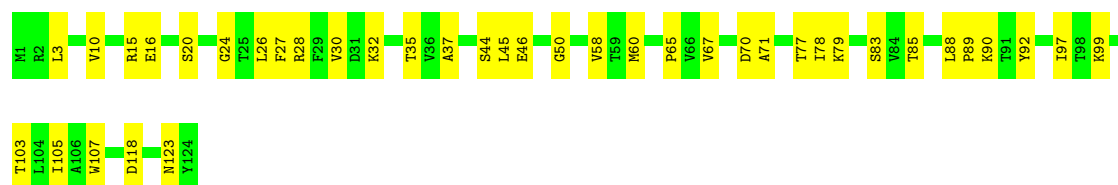
- Molecule 1: coat protein



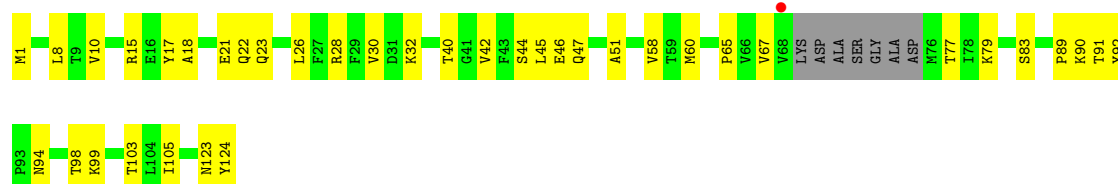
- Molecule 1: coat protein



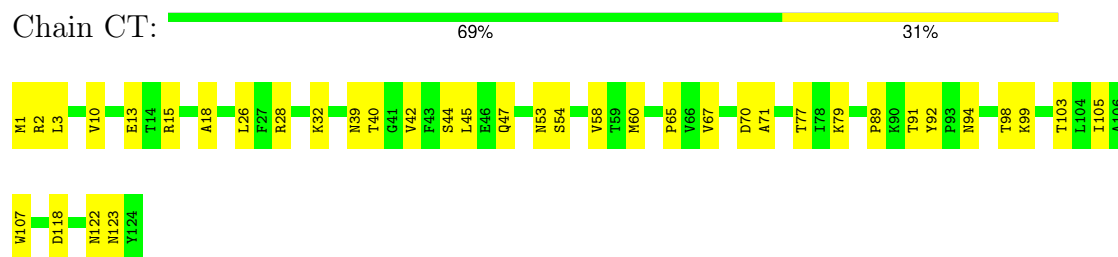
- Molecule 1: coat protein



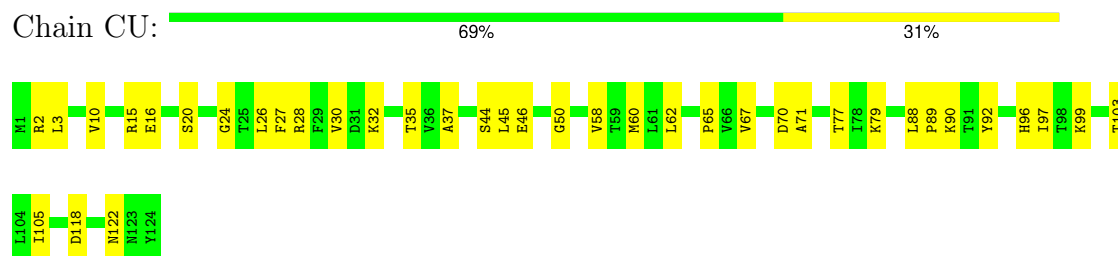
- Molecule 1: coat protein



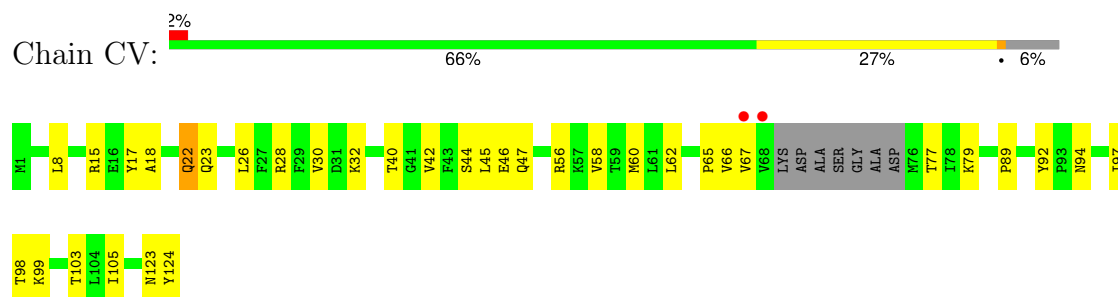
- Molecule 1: coat protein



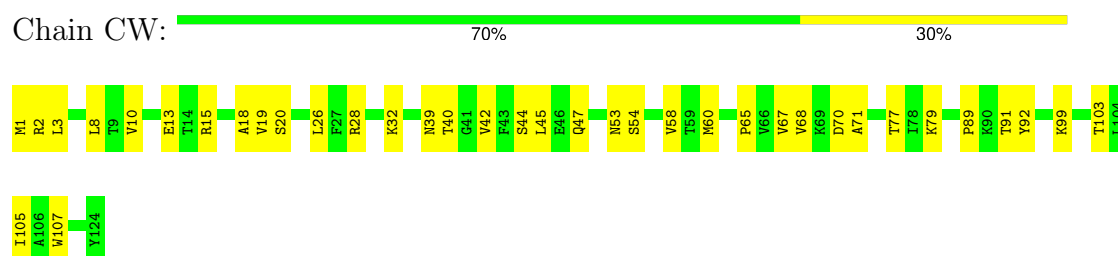
- Molecule 1: coat protein



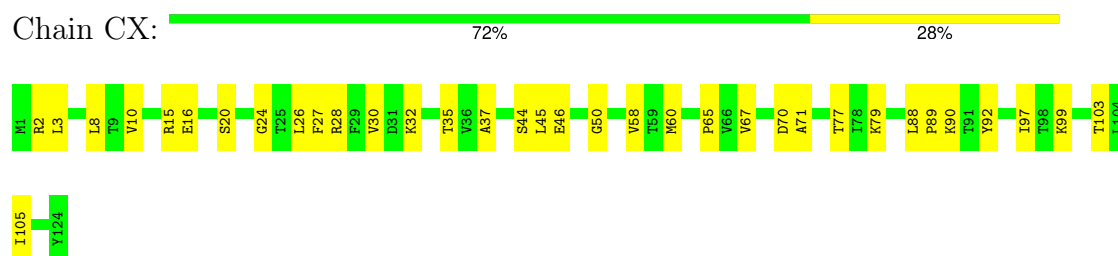
- Molecule 1: coat protein



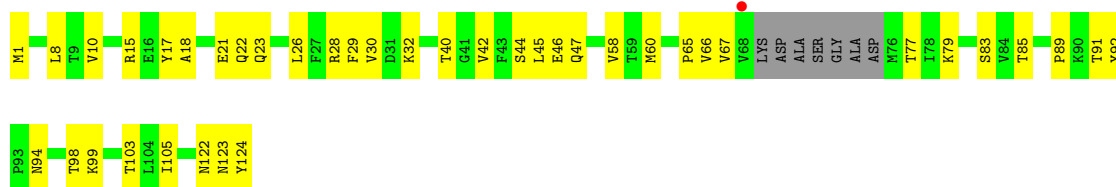
- Molecule 1: coat protein



- Molecule 1: coat protein



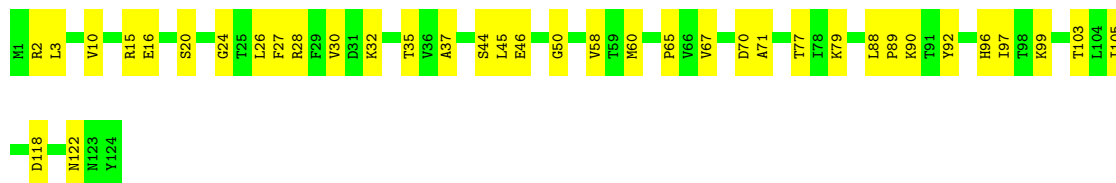
- Molecule 1: coat protein



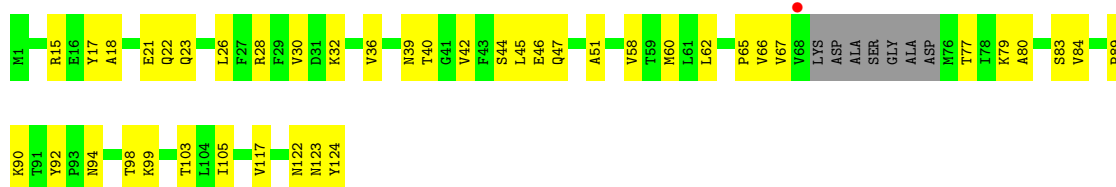
- Molecule 1: coat protein



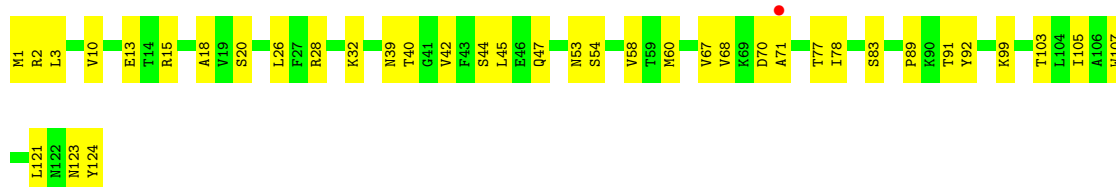
- Molecule 1: coat protein



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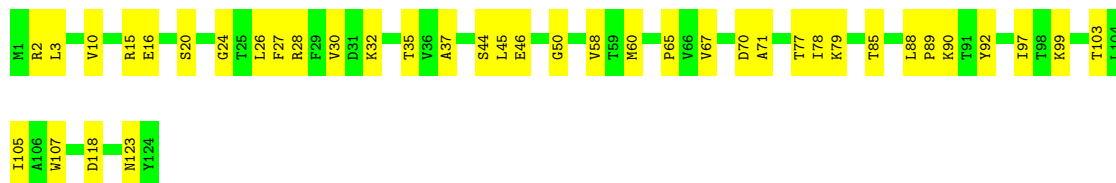


- Molecule 1: coat protein



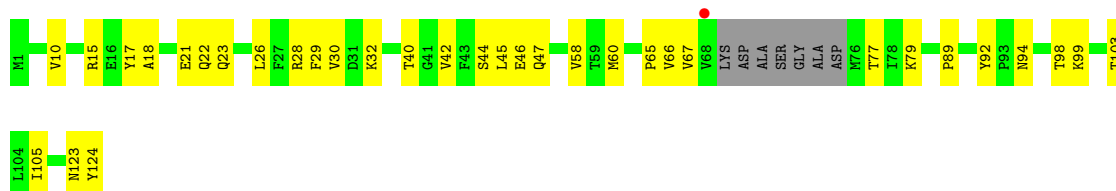
- Molecule 1: coat protein

Chain DD:  69% 31%



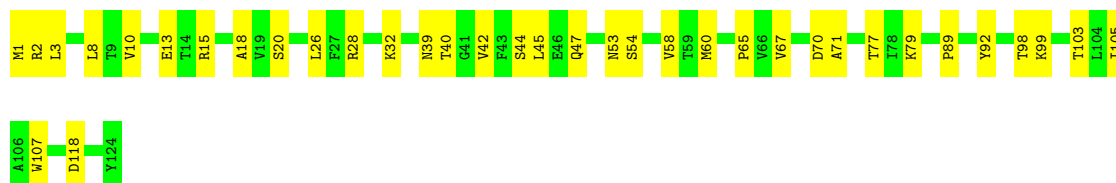
- Molecule 1: coat protein

Chain DE:  % 67% 27% 6%



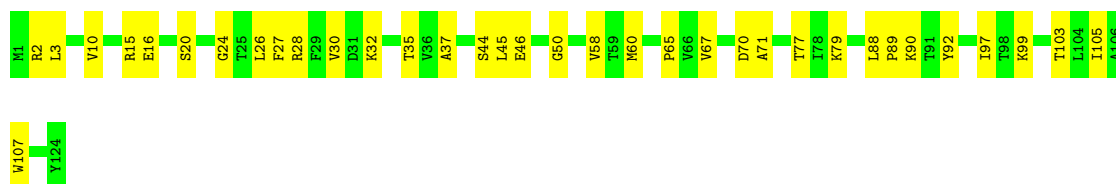
- Molecule 1: coat protein

Chain DF:  71% 29%



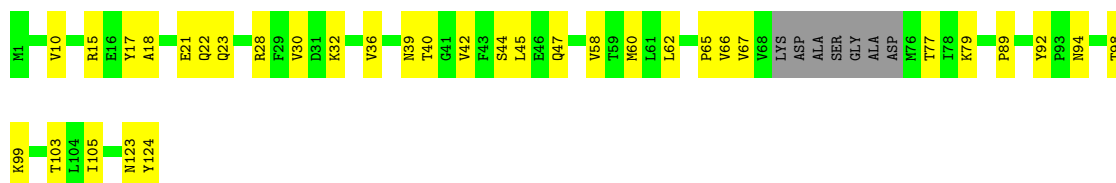
- Molecule 1: coat protein

Chain DG:  72% 28%



- Molecule 1: coat protein

Chain DH:  67% 27% 6%



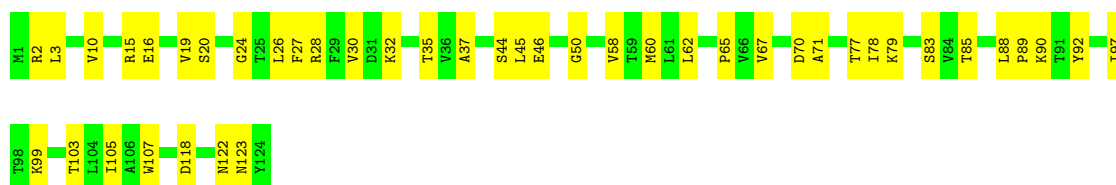
- Molecule 1: coat protein

Chain DI:  68% 32%



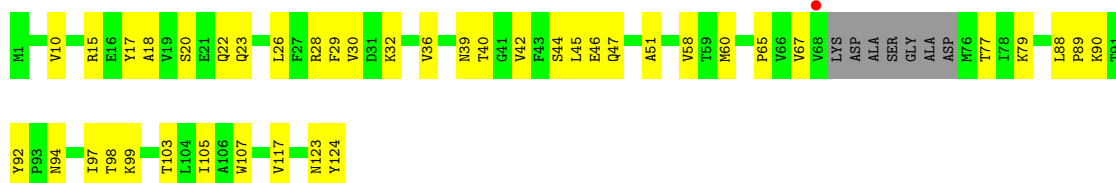
- Molecule 1: coat protein

Chain DJ:  65% 35%



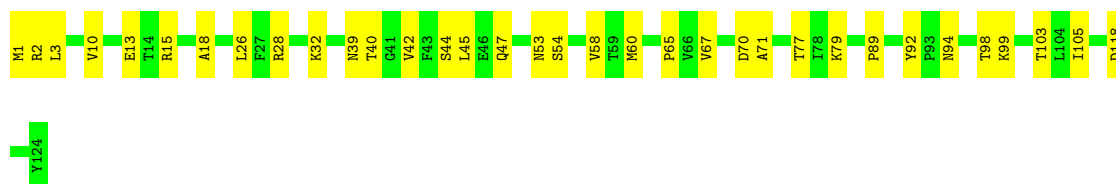
- Molecule 1: coat protein

Chain DK:  % 61% 33% 6%



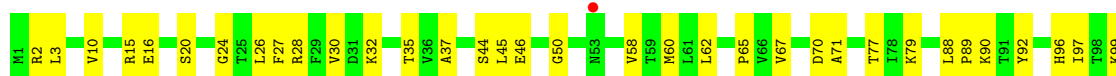
- Molecule 1: coat protein

Chain DL:  73% 27%



- Molecule 1: coat protein

Chain DM:  % 69% 31%

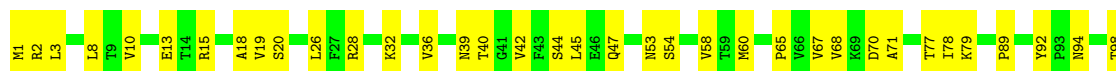




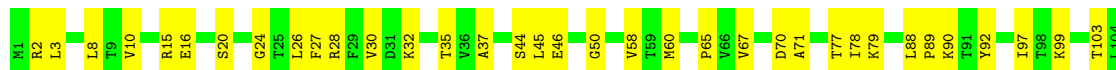
- Molecule 1: coat protein



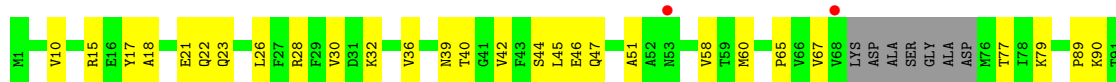
- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein

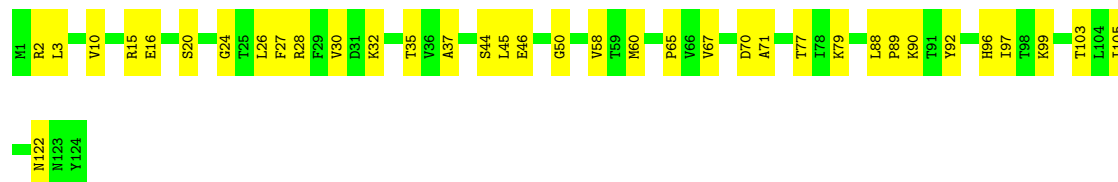


- Molecule 1: coat protein

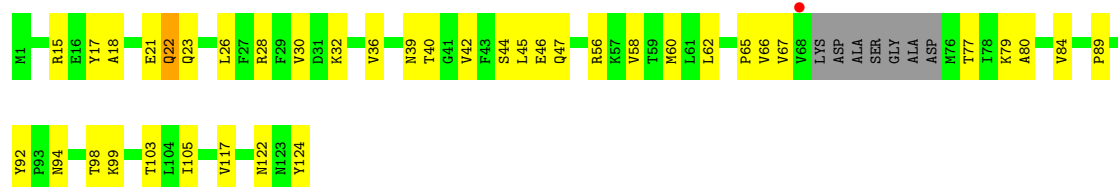




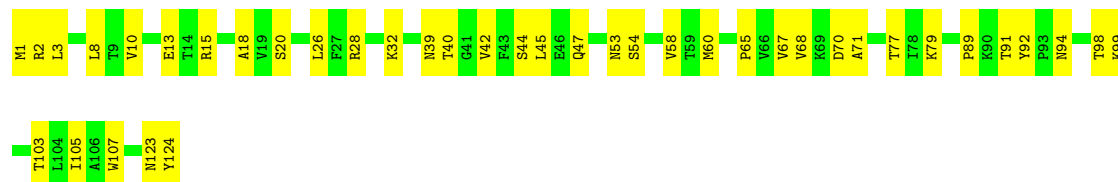
- Molecule 1: coat protein



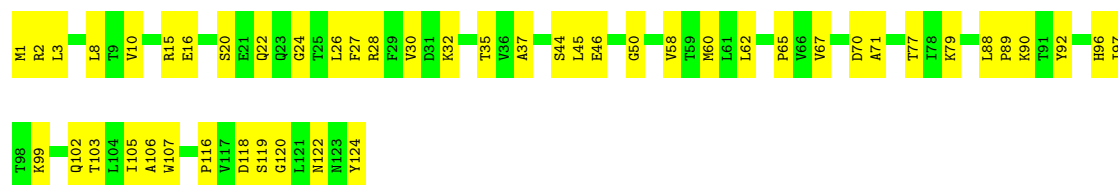
- Molecule 1: coat protein



- Molecule 1: coat protein

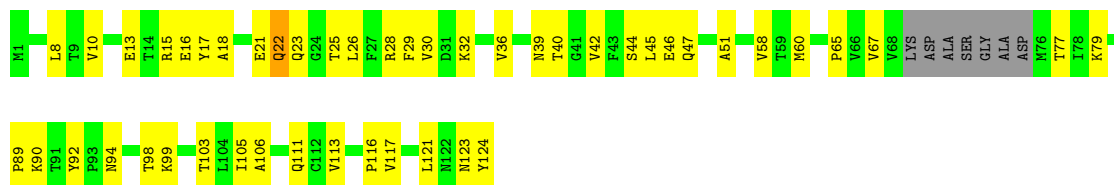


- Molecule 1: coat protein



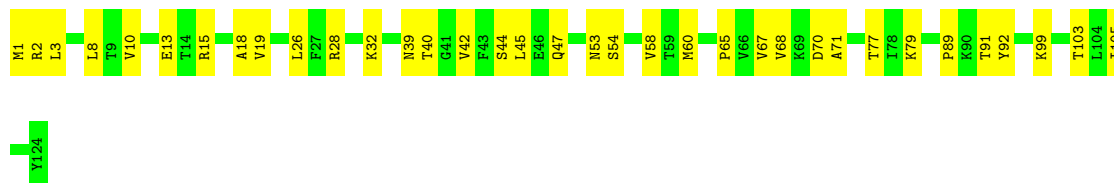
- Molecule 1: coat protein

Chain DW:  56% 37% 6%



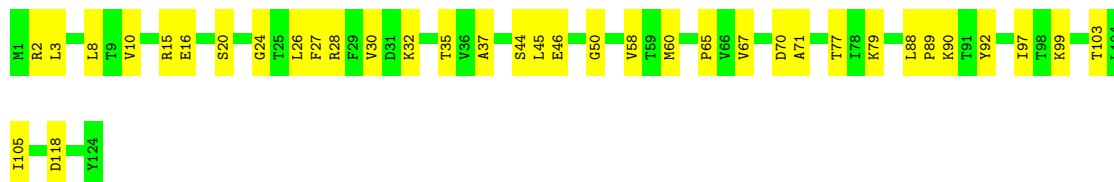
- Molecule 1: coat protein

Chain DX:  72% 28%



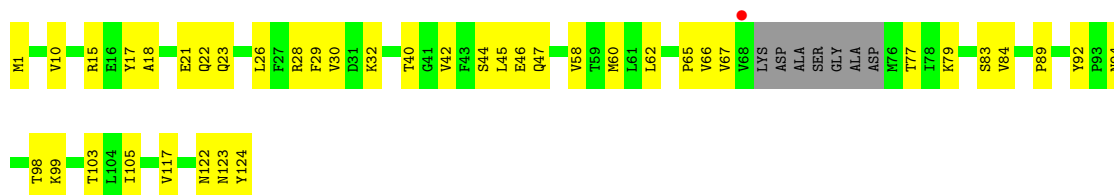
- Molecule 1: coat protein

Chain DY:  71% 29%



- Molecule 1: coat protein

Chain DZ:  62% 32% 6%



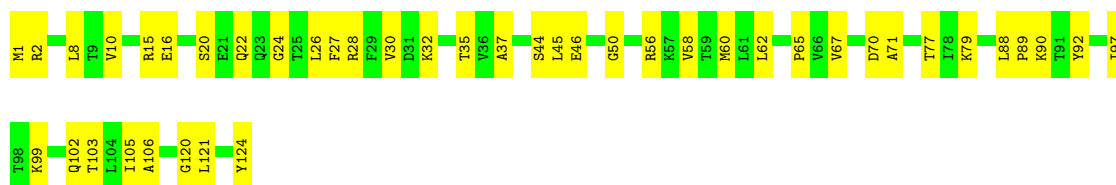
- Molecule 1: coat protein

Chain EA:  73% 27%

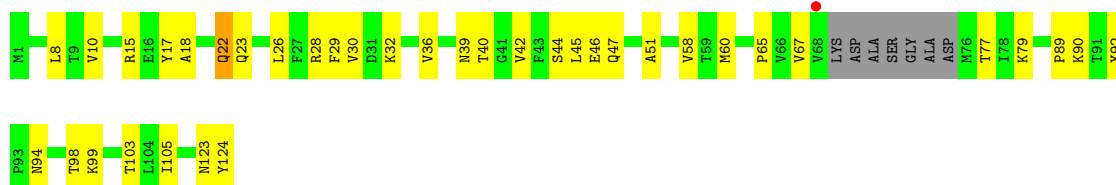


- Molecule 1: coat protein

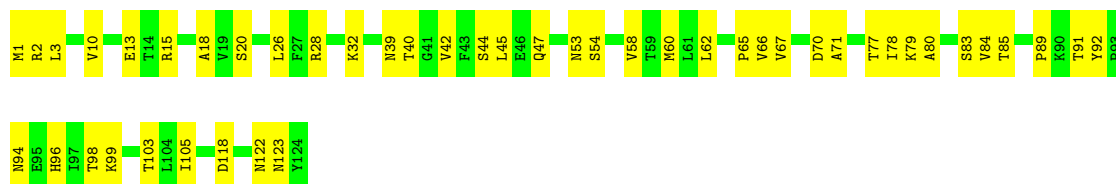
Chain EB:  65% 35%



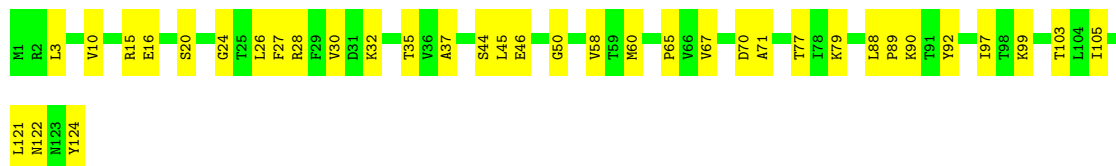
- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein



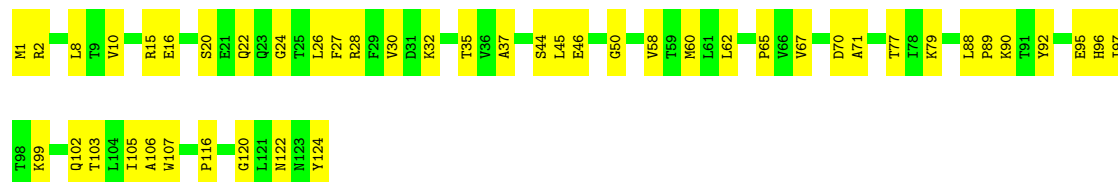
- Molecule 1: coat protein





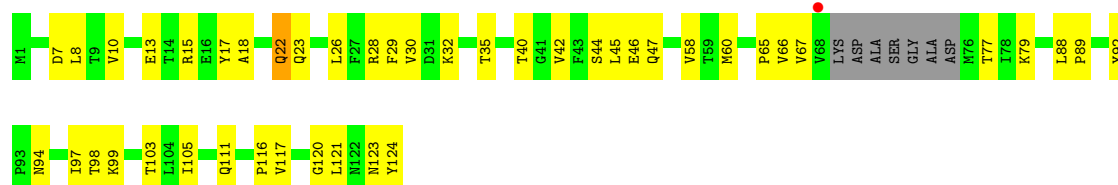
- Molecule 1: coat protein

Chain EH: 63% 37%



- Molecule 1: coat protein

Chain EI: % 59% 35% 6%



- Molecule 1: coat protein

Chain EJ: 68% 32%

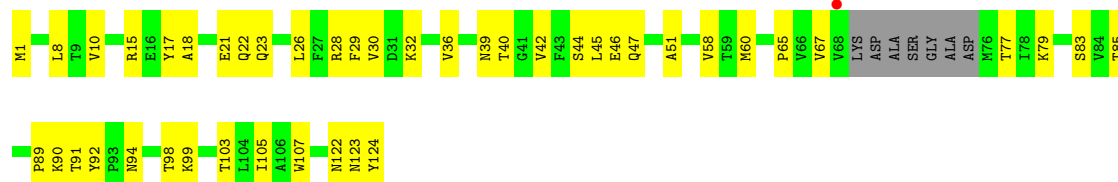


- Molecule 1: coat protein

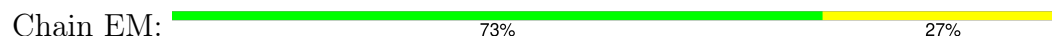
Chain EK: 71% 29%



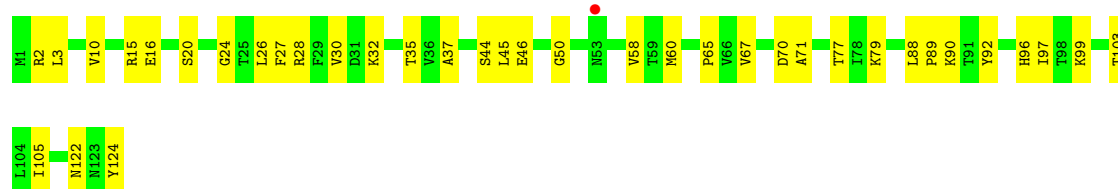
- Molecule 1: coat protein



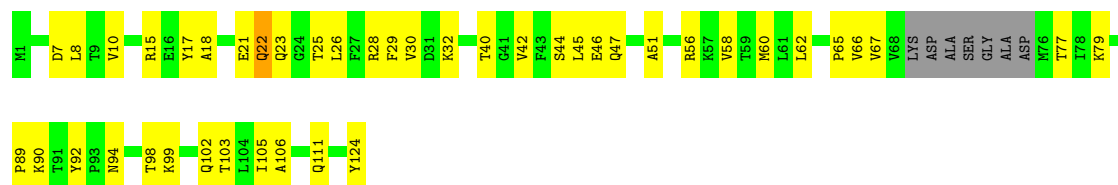
- Molecule 1: coat protein



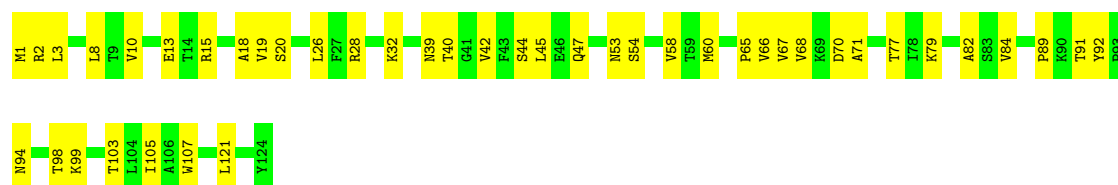
- Molecule 1: coat protein



- Molecule 1: coat protein

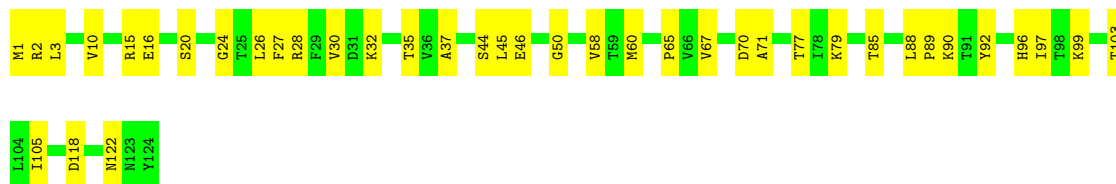


- Molecule 1: coat protein



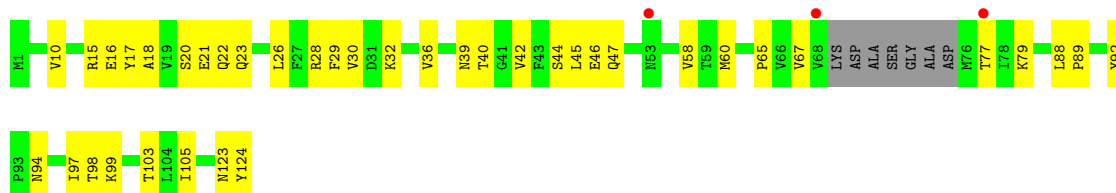
- Molecule 1: coat protein

Chain EQ:  69% 31%



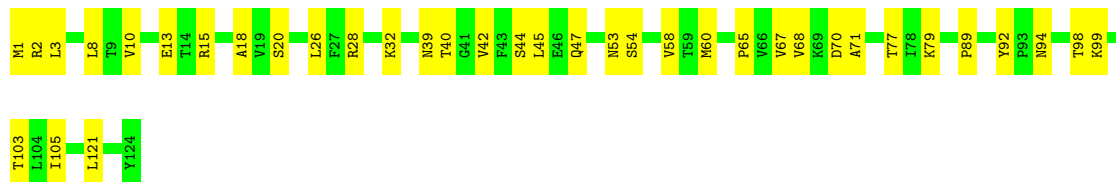
- Molecule 1: coat protein

Chain ER:  2% 63% 31% 6%



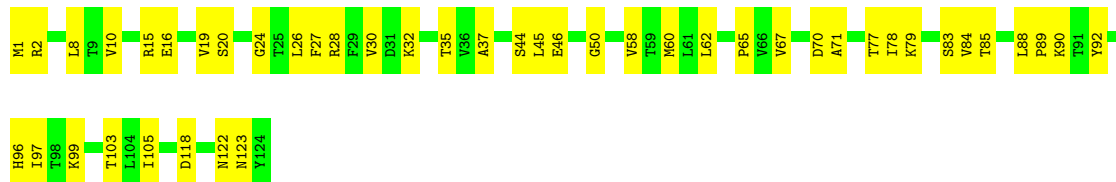
- Molecule 1: coat protein

Chain ES:  70% 30%



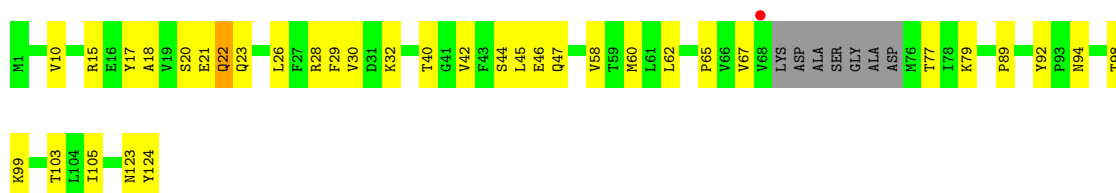
- Molecule 1: coat protein

Chain ET:  64% 36%

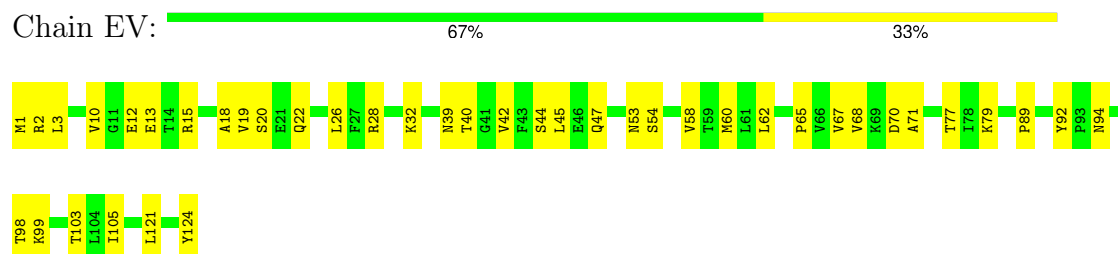


- Molecule 1: coat protein

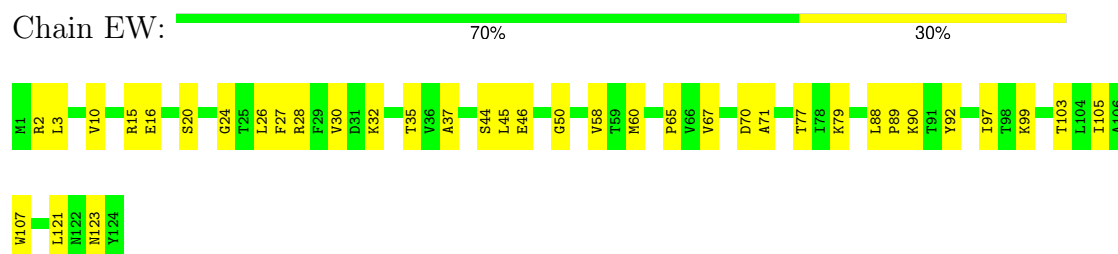
Chain EU:  66% 27% 6%



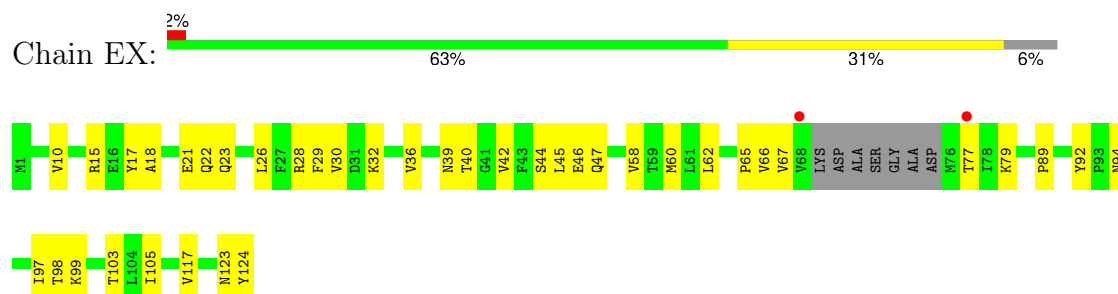
- Molecule 1: coat protein



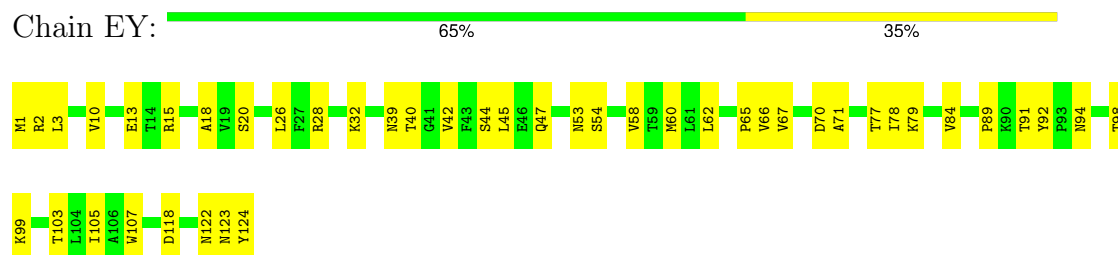
- Molecule 1: coat protein



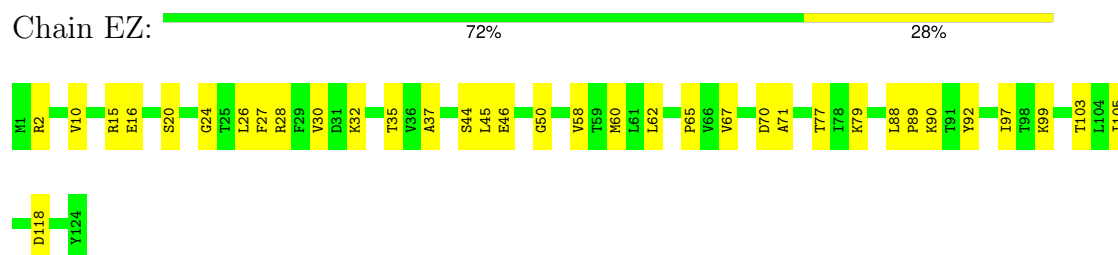
- Molecule 1: coat protein



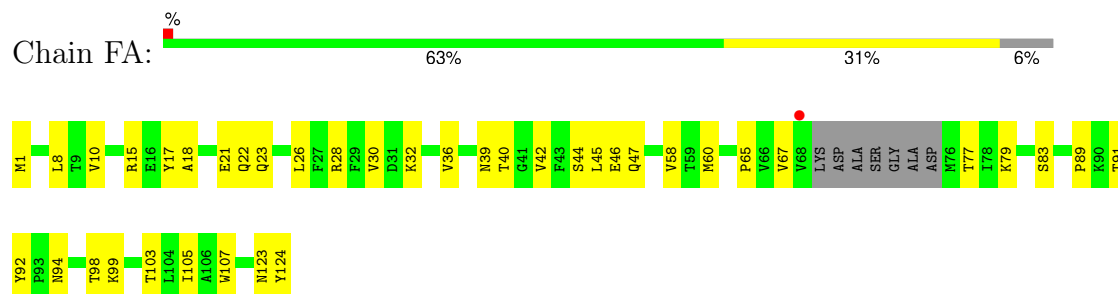
- Molecule 1: coat protein



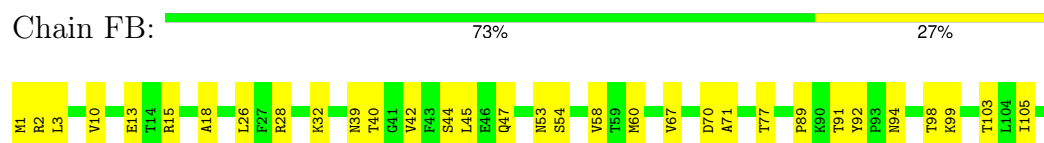
- Molecule 1: coat protein



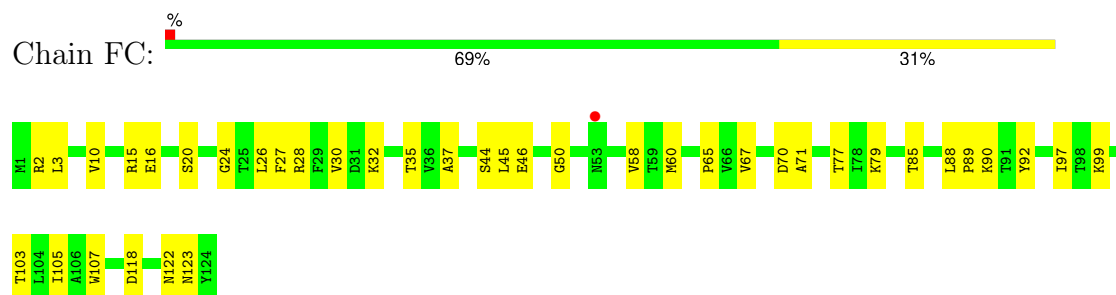
- Molecule 1: coat protein



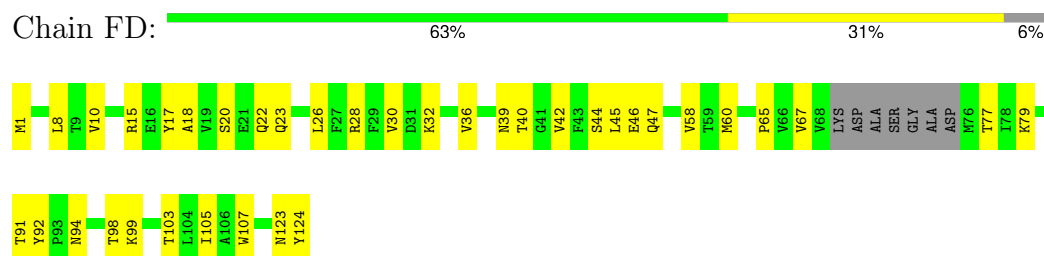
- Molecule 1: coat protein



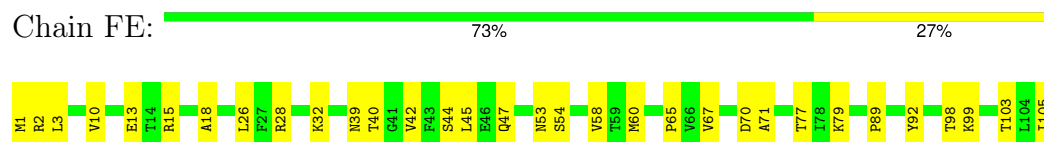
- Molecule 1: coat protein



- Molecule 1: coat protein

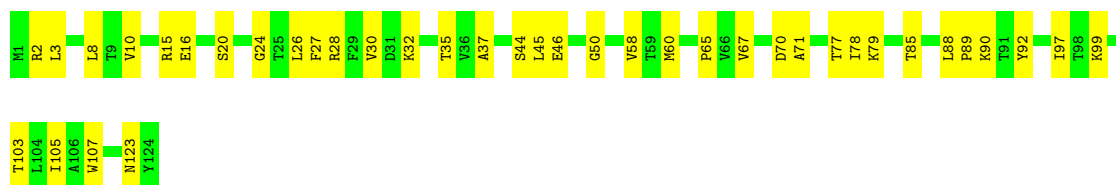


- Molecule 1: coat protein

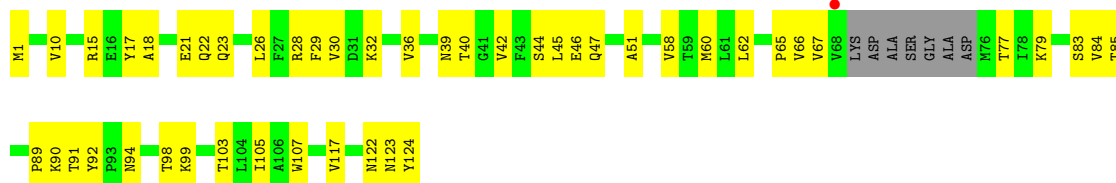


- Molecule 1: coat protein

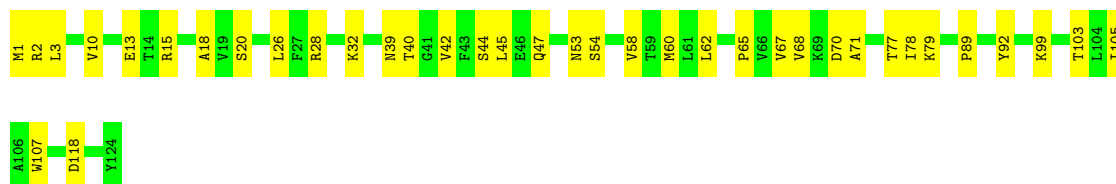




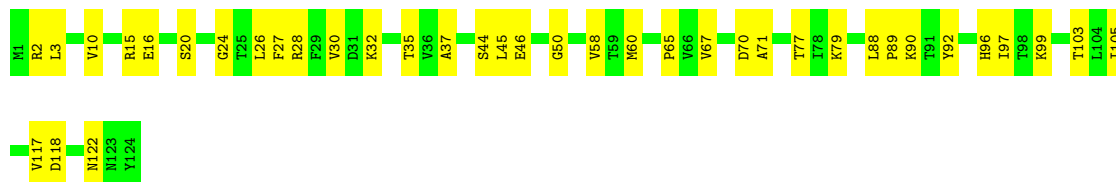
- Molecule 1: coat protein



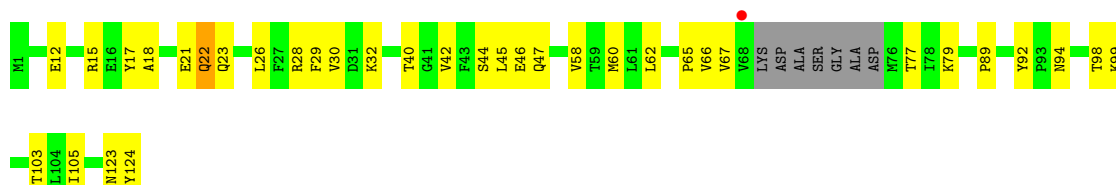
- Molecule 1: coat protein



- Molecule 1: coat protein

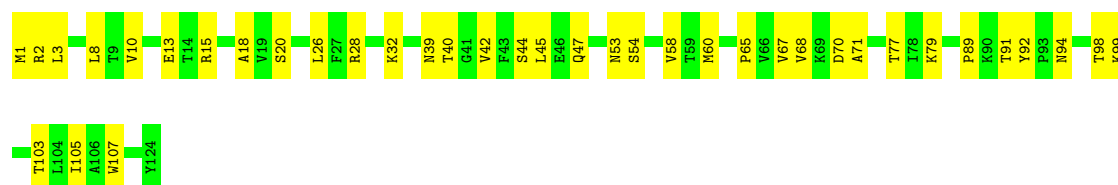


- Molecule 1: coat protein



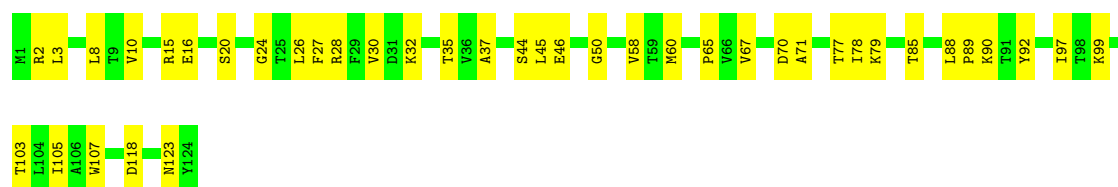
- Molecule 1: coat protein

Chain FK:  69% 31%



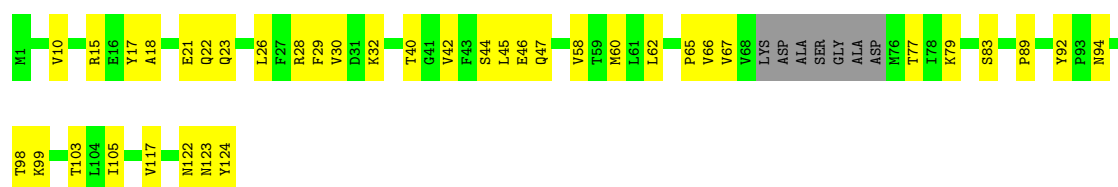
- Molecule 1: coat protein

Chain FL:  68% 32%



- Molecule 1: coat protein

Chain FM:  64% 31% 6%



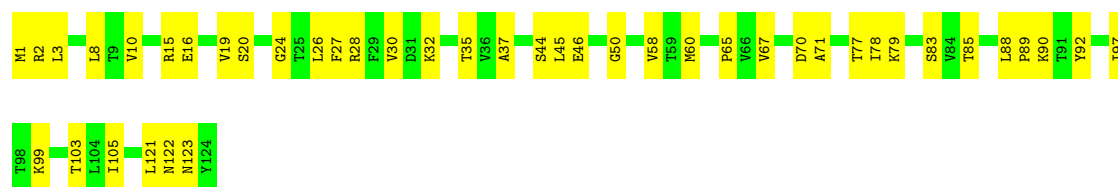
- Molecule 1: coat protein

Chain FN:  69% 31%



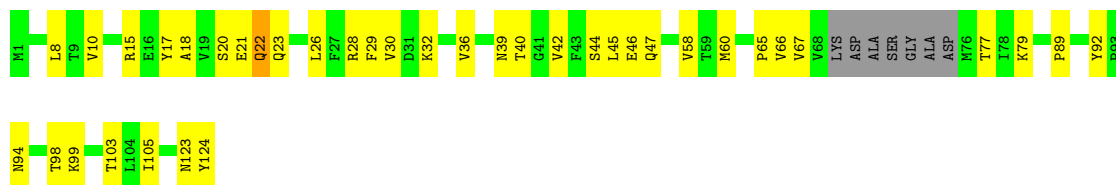
- Molecule 1: coat protein

Chain FO:  65% 35%



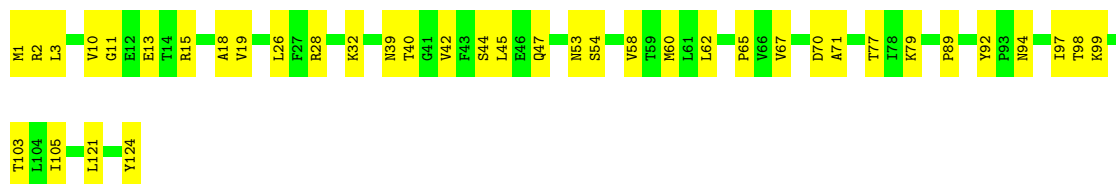
- Molecule 1: coat protein

Chain FP:  64% 30% • 6%



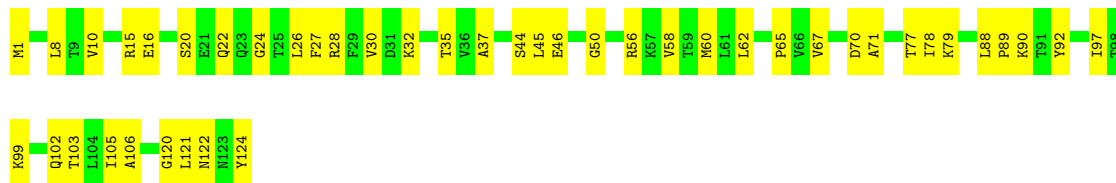
• Molecule 1: coat protein

Chain FQ:  69% 31%



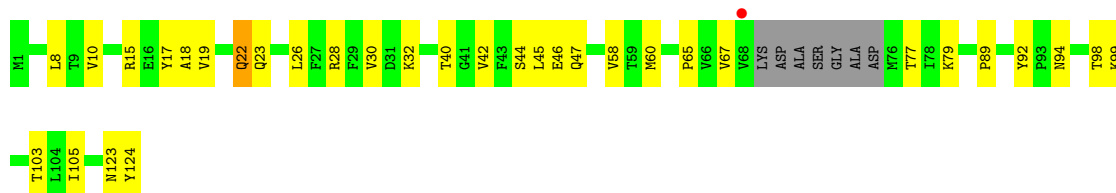
• Molecule 1: coat protein

Chain FR:  65% 35%



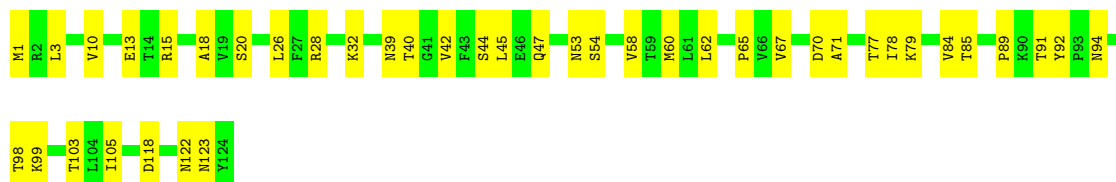
• Molecule 1: coat protein

Chain FS:  68% 26% • 6%

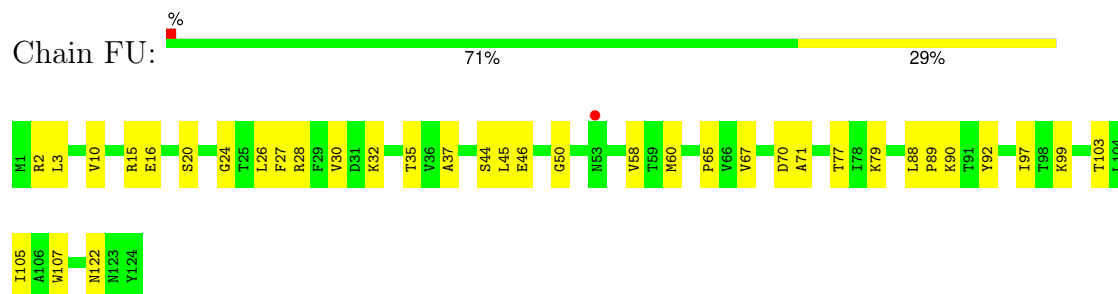


• Molecule 1: coat protein

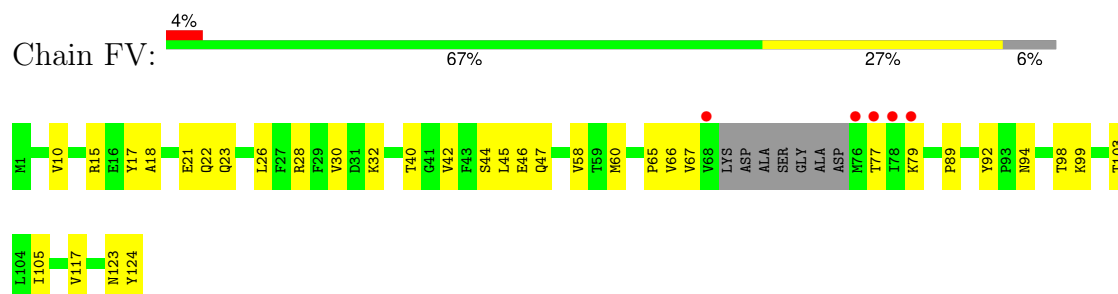
Chain FT:  67% 33%



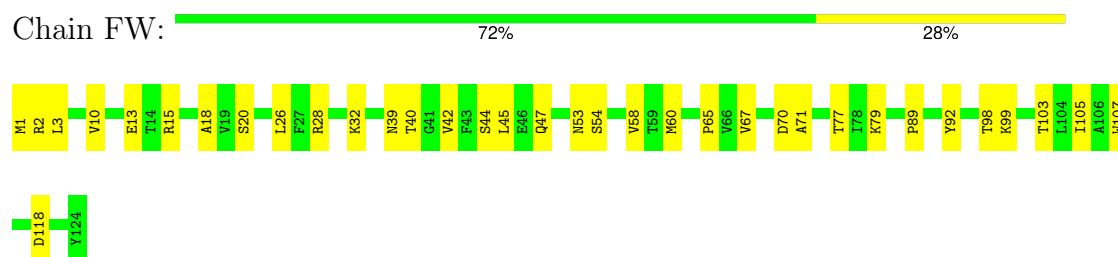
- Molecule 1: coat protein



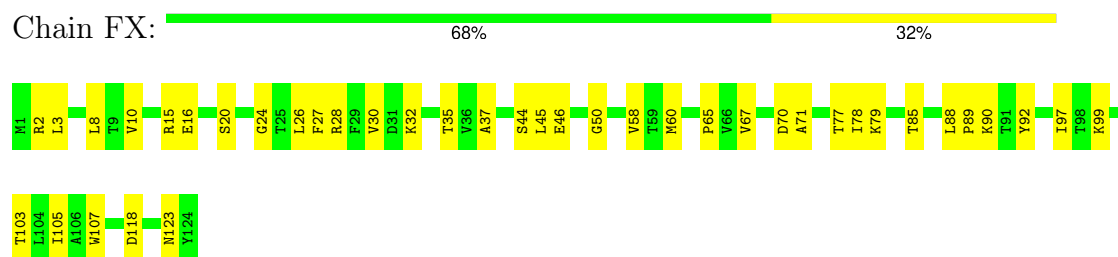
- Molecule 1: coat protein



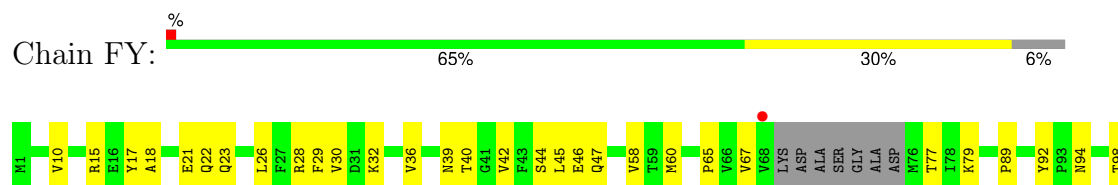
- Molecule 1: coat protein



- Molecule 1: coat protein



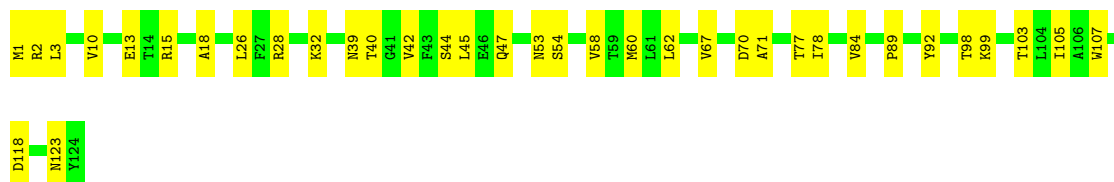
- Molecule 1: coat protein





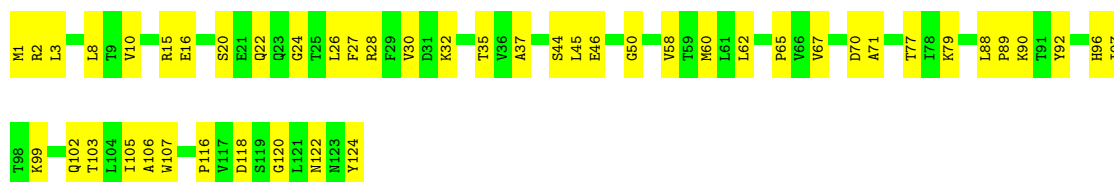
- Molecule 1: coat protein

Chain FZ: 71% 29%



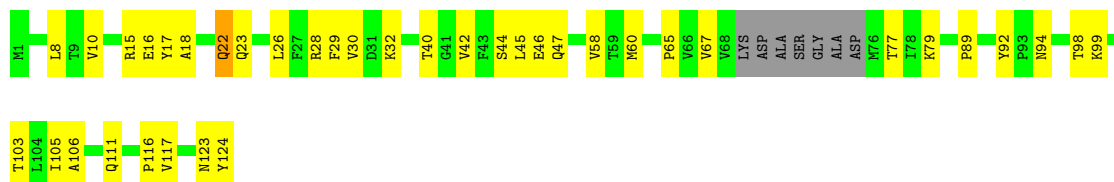
- Molecule 1: coat protein

Chain GA: 62% 38%



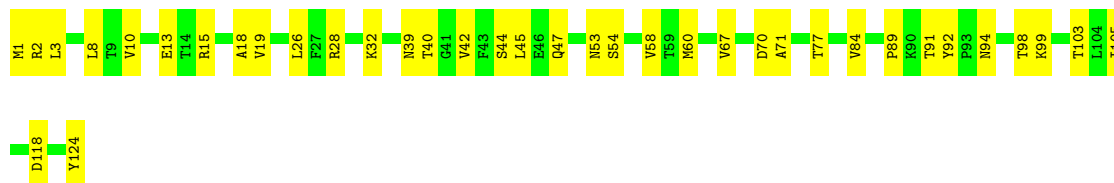
- Molecule 1: coat protein

Chain GB: 64% 30% 6%



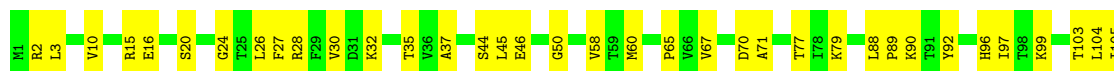
- Molecule 1: coat protein

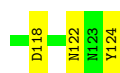
Chain GC: 70% 30%



- Molecule 1: coat protein

Chain GD: 69% 31%

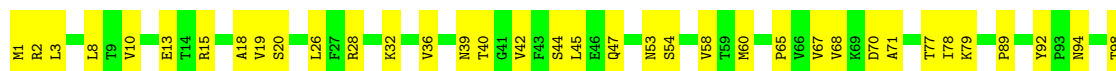




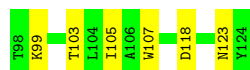
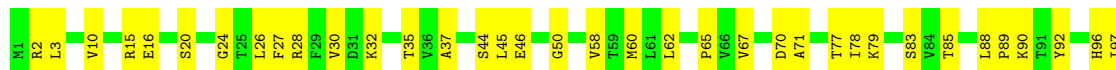
- Molecule 1: coat protein



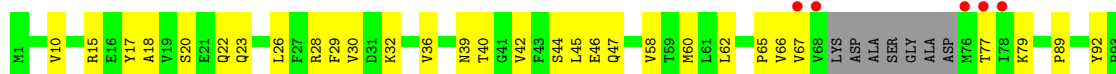
- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein





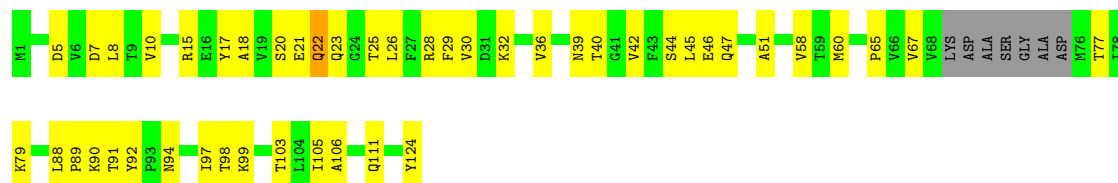
- Molecule 1: coat protein

Chain GJ: 68% 32%



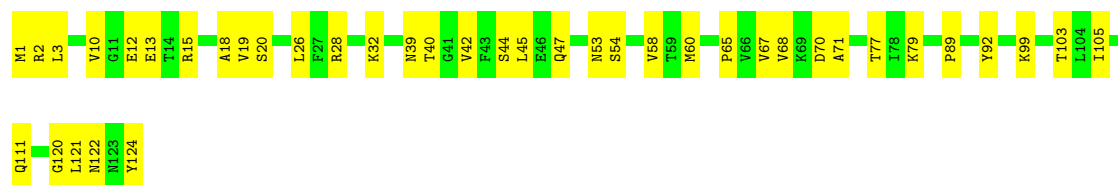
- Molecule 1: coat protein

Chain GK: 57% 36% 6%



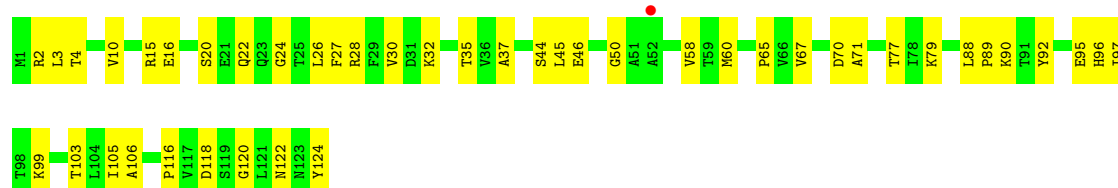
- Molecule 1: coat protein

Chain GL: 68% 32%



- Molecule 1: coat protein

Chain GM: 65% 35%



- Molecule 1: coat protein

Chain GN:  64% 30% 6%



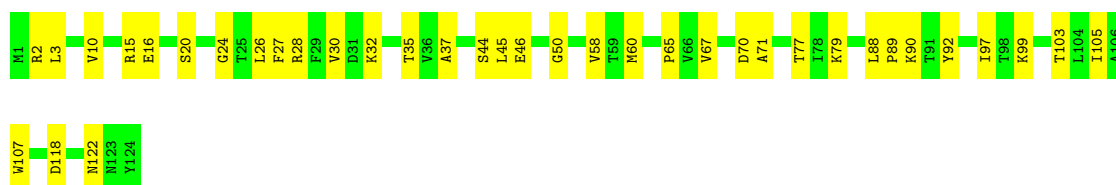
• Molecule 1: coat protein

Chain GO:  67% 33%



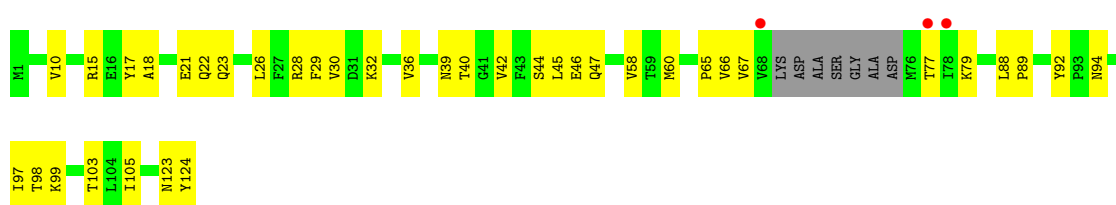
• Molecule 1: coat protein

Chain GP:  70% 30%



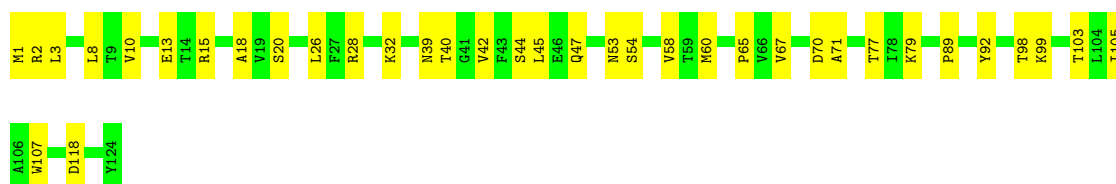
• Molecule 1: coat protein

Chain GQ:  2% 64% 31% 6%

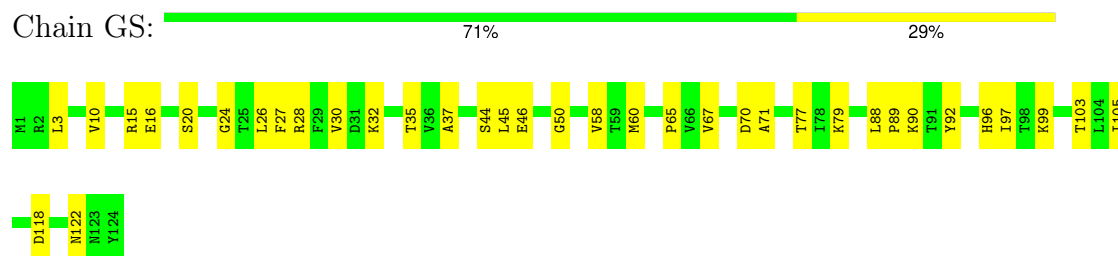


• Molecule 1: coat protein

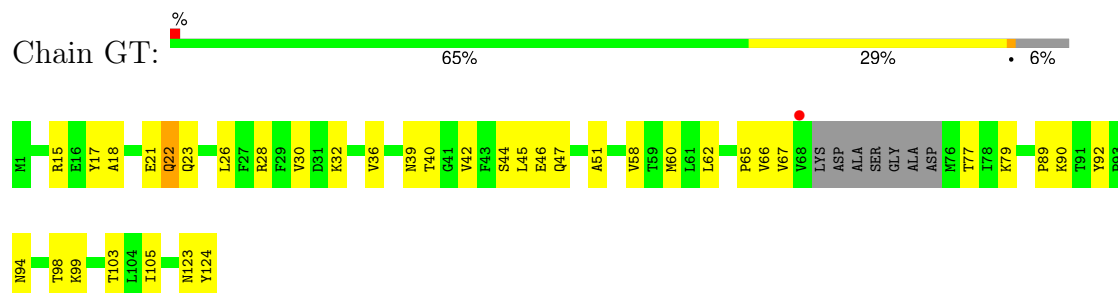
Chain GR:  71% 29%



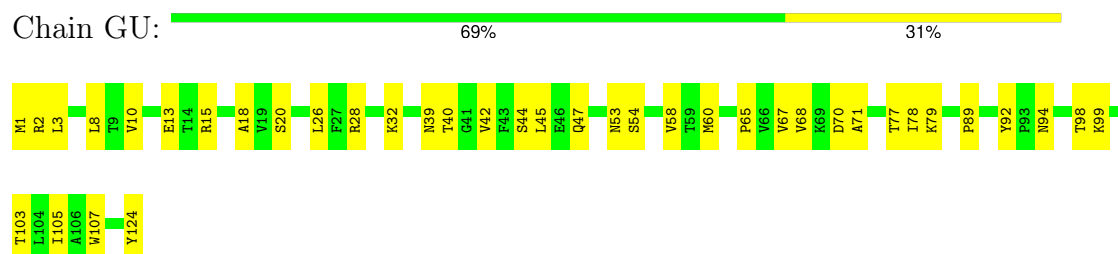
- Molecule 1: coat protein



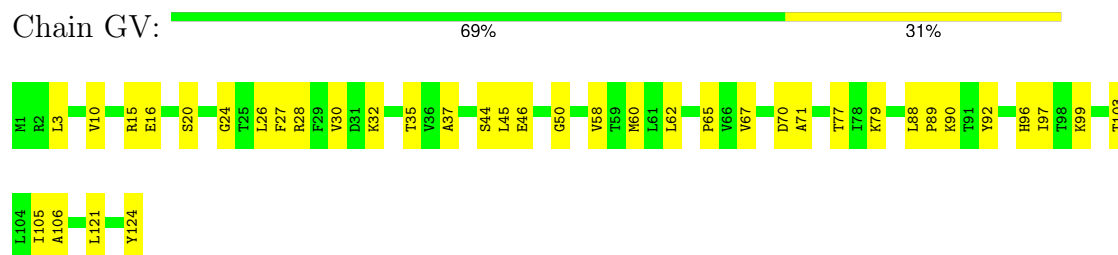
- Molecule 1: coat protein



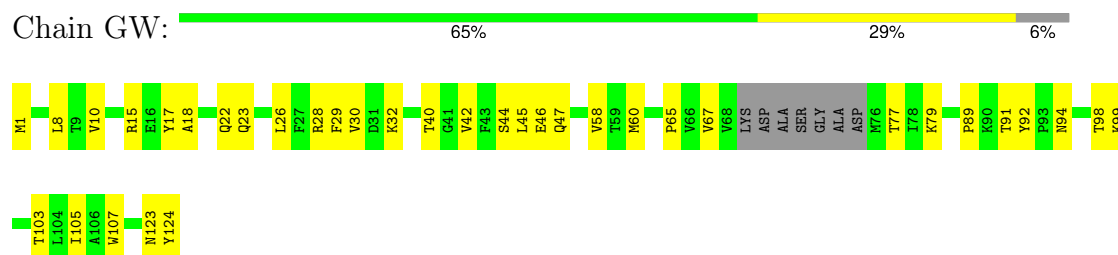
- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	269.42Å 277.20Å 277.44Å 103.91° 117.39° 106.96°	Depositor
Resolution (Å)	49.27 – 3.25 49.26 – 3.25	Depositor EDS
% Data completeness (in resolution range)	92.9 (49.27-3.25) 94.2 (49.26-3.25)	Depositor EDS
R_{merge}	0.37	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 3.25Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.241 , 0.239 0.244 , 0.243	Depositor DCC
R_{free} test set	10021 reflections (1.10%)	wwPDB-VP
Wilson B-factor (Å ²)	89.3	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 68.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.026 for k,h,-h-k-l 0.026 for l,-h-k-l,h 0.026 for -h-k-l,l,k	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	169260	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.33	0/969	0.56	0/1314
1	AB	0.33	0/923	0.55	0/1251
1	AC	0.32	0/969	0.55	0/1314
1	AD	0.33	0/969	0.56	0/1314
1	AE	0.33	0/923	0.55	0/1251
1	AF	0.33	0/969	0.55	0/1314
1	AG	0.33	0/969	0.56	0/1314
1	AH	0.33	0/923	0.55	0/1251
1	AI	0.33	0/969	0.55	0/1314
1	AJ	0.33	0/969	0.56	0/1314
1	AK	0.33	0/923	0.55	0/1251
1	AL	0.33	0/969	0.55	0/1314
1	AM	0.33	0/969	0.56	0/1314
1	AN	0.33	0/923	0.55	0/1251
1	AO	0.32	0/969	0.55	0/1314
1	AP	0.33	0/969	0.56	0/1314
1	AQ	0.33	0/923	0.55	0/1251
1	AR	0.33	0/969	0.55	0/1314
1	AS	0.33	0/969	0.56	0/1314
1	AT	0.33	0/923	0.55	0/1251
1	AU	0.32	0/969	0.55	0/1314
1	AV	0.33	0/969	0.56	0/1314
1	AW	0.33	0/923	0.55	0/1251
1	AX	0.32	0/969	0.55	0/1314
1	AY	0.33	0/969	0.56	0/1314
1	AZ	0.33	0/923	0.55	0/1251
1	BA	0.32	0/969	0.55	0/1314
1	BB	0.33	0/969	0.56	0/1314
1	BC	0.33	0/923	0.55	0/1251
1	BD	0.33	0/969	0.55	0/1314
1	BE	0.33	0/969	0.56	0/1314
1	BF	0.33	0/923	0.55	0/1251

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BG	0.32	0/969	0.55	0/1314
1	BH	0.33	0/969	0.56	0/1314
1	BI	0.33	0/923	0.55	0/1251
1	BJ	0.33	0/969	0.55	0/1314
1	BK	0.33	0/969	0.56	0/1314
1	BL	0.33	0/923	0.55	0/1251
1	BM	0.32	0/969	0.55	0/1314
1	BN	0.33	0/969	0.56	0/1314
1	BO	0.33	0/923	0.55	0/1251
1	BP	0.32	0/969	0.55	0/1314
1	BQ	0.33	0/969	0.56	0/1314
1	BR	0.33	0/923	0.55	0/1251
1	BS	0.32	0/969	0.55	0/1314
1	BT	0.33	0/969	0.56	0/1314
1	BU	0.33	0/923	0.55	0/1251
1	BV	0.32	0/969	0.55	0/1314
1	BW	0.33	0/969	0.56	0/1314
1	BX	0.33	0/923	0.55	0/1251
1	BY	0.32	0/969	0.55	0/1314
1	BZ	0.33	0/969	0.56	0/1314
1	CA	0.33	0/923	0.55	0/1251
1	CB	0.32	0/969	0.55	0/1314
1	CC	0.33	0/969	0.56	0/1314
1	CD	0.33	0/923	0.55	0/1251
1	CE	0.32	0/969	0.55	0/1314
1	CF	0.33	0/969	0.56	0/1314
1	CG	0.33	0/923	0.55	0/1251
1	CH	0.32	0/969	0.55	0/1314
1	CI	0.33	0/969	0.56	0/1314
1	CJ	0.33	0/923	0.55	0/1251
1	CK	0.32	0/969	0.55	0/1314
1	CL	0.33	0/969	0.56	0/1314
1	CM	0.33	0/923	0.55	0/1251
1	CN	0.32	0/969	0.55	0/1314
1	CO	0.33	0/969	0.55	0/1314
1	CP	0.33	0/923	0.55	0/1251
1	CQ	0.32	0/969	0.55	0/1314
1	CR	0.33	0/969	0.56	0/1314
1	CS	0.33	0/923	0.55	0/1251
1	CT	0.32	0/969	0.55	0/1314
1	CU	0.33	0/969	0.56	0/1314
1	CV	0.33	0/923	0.55	0/1251
1	CW	0.33	0/969	0.55	0/1314

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CX	0.33	0/969	0.56	0/1314
1	CY	0.33	0/923	0.55	0/1251
1	CZ	0.32	0/969	0.55	0/1314
1	DA	0.33	0/969	0.56	0/1314
1	DB	0.33	0/923	0.55	0/1251
1	DC	0.32	0/969	0.55	0/1314
1	DD	0.33	0/969	0.56	0/1314
1	DE	0.33	0/923	0.55	0/1251
1	DF	0.32	0/969	0.55	0/1314
1	DG	0.33	0/969	0.56	0/1314
1	DH	0.33	0/923	0.55	0/1251
1	DI	0.33	0/969	0.55	0/1314
1	DJ	0.33	0/969	0.56	0/1314
1	DK	0.33	0/923	0.55	0/1251
1	DL	0.32	0/969	0.55	0/1314
1	DM	0.33	0/969	0.56	0/1314
1	DN	0.33	0/923	0.55	0/1251
1	DO	0.32	0/969	0.55	0/1314
1	DP	0.33	0/969	0.56	0/1314
1	DQ	0.33	0/923	0.55	0/1251
1	DR	0.33	0/969	0.55	0/1314
1	DS	0.33	0/969	0.56	0/1314
1	DT	0.33	0/923	0.55	0/1251
1	DU	0.32	0/969	0.55	0/1314
1	DV	0.33	0/969	0.56	0/1314
1	DW	0.33	0/923	0.55	0/1251
1	DX	0.33	0/969	0.55	0/1314
1	DY	0.33	0/969	0.56	0/1314
1	DZ	0.33	0/923	0.55	0/1251
1	EA	0.33	0/969	0.55	0/1314
1	EB	0.33	0/969	0.56	0/1314
1	EC	0.33	0/923	0.55	0/1251
1	ED	0.32	0/969	0.55	0/1314
1	EE	0.33	0/969	0.56	0/1314
1	EF	0.33	0/923	0.55	0/1251
1	EG	0.32	0/969	0.55	0/1314
1	EH	0.33	0/969	0.56	0/1314
1	EI	0.33	0/923	0.55	0/1251
1	EJ	0.33	0/969	0.55	0/1314
1	EK	0.33	0/969	0.56	0/1314
1	EL	0.33	0/923	0.55	0/1251
1	EM	0.32	0/969	0.55	0/1314
1	EN	0.33	0/969	0.56	0/1314

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	EO	0.33	0/923	0.55	0/1251
1	EP	0.32	0/969	0.55	0/1314
1	EQ	0.33	0/969	0.56	0/1314
1	ER	0.33	0/923	0.55	0/1251
1	ES	0.32	0/969	0.55	0/1314
1	ET	0.33	0/969	0.56	0/1314
1	EU	0.33	0/923	0.55	0/1251
1	EV	0.33	0/969	0.55	0/1314
1	EW	0.33	0/969	0.56	0/1314
1	EX	0.33	0/923	0.55	0/1251
1	EY	0.32	0/969	0.55	0/1314
1	EZ	0.33	0/969	0.56	0/1314
1	FA	0.33	0/923	0.55	0/1251
1	FB	0.32	0/969	0.55	0/1314
1	FC	0.33	0/969	0.56	0/1314
1	FD	0.33	0/923	0.55	0/1251
1	FE	0.32	0/969	0.55	0/1314
1	FF	0.33	0/969	0.56	0/1314
1	FG	0.33	0/923	0.55	0/1251
1	FH	0.32	0/969	0.55	0/1314
1	FI	0.33	0/969	0.56	0/1314
1	FJ	0.33	0/923	0.55	0/1251
1	FK	0.32	0/969	0.55	0/1314
1	FL	0.33	0/969	0.56	0/1314
1	FM	0.33	0/923	0.55	0/1251
1	FN	0.32	0/969	0.55	0/1314
1	FO	0.33	0/969	0.56	0/1314
1	FP	0.33	0/923	0.55	0/1251
1	FQ	0.33	0/969	0.55	0/1314
1	FR	0.33	0/969	0.56	0/1314
1	FS	0.33	0/923	0.55	0/1251
1	FT	0.32	0/969	0.55	0/1314
1	FU	0.33	0/969	0.56	0/1314
1	FV	0.33	0/923	0.55	0/1251
1	FW	0.32	0/969	0.55	0/1314
1	FX	0.33	0/969	0.56	0/1314
1	FY	0.33	0/923	0.55	0/1251
1	FZ	0.33	0/969	0.55	0/1314
1	GA	0.33	0/969	0.56	0/1314
1	GB	0.33	0/923	0.55	0/1251
1	GC	0.32	0/969	0.55	0/1314
1	GD	0.33	0/969	0.56	0/1314
1	GE	0.33	0/923	0.55	0/1251

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GF	0.32	0/969	0.55	0/1314
1	GG	0.33	0/969	0.56	0/1314
1	GH	0.33	0/923	0.55	0/1251
1	GI	0.32	0/969	0.55	0/1314
1	GJ	0.33	0/969	0.56	0/1314
1	GK	0.33	0/923	0.55	0/1251
1	GL	0.33	0/969	0.55	0/1314
1	GM	0.33	0/969	0.56	0/1314
1	GN	0.33	0/923	0.55	0/1251
1	GO	0.33	0/969	0.55	0/1314
1	GP	0.33	0/969	0.56	0/1314
1	GQ	0.33	0/923	0.55	0/1251
1	GR	0.32	0/969	0.55	0/1314
1	GS	0.33	0/969	0.56	0/1314
1	GT	0.33	0/923	0.55	0/1251
1	GU	0.32	0/969	0.55	0/1314
1	GV	0.33	0/969	0.56	0/1314
1	GW	0.33	0/923	0.55	0/1251
1	GX	0.32	0/969	0.55	0/1314
All	All	0.33	0/171660	0.55	0/232740

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	955	0	947	31	0
1	AB	910	0	907	37	0
1	AC	955	0	947	36	0
1	AD	955	0	947	33	0
1	AE	910	0	907	48	0
1	AF	955	0	947	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AG	955	0	947	32	0
1	AH	910	0	907	36	0
1	AI	955	0	947	37	0
1	AJ	955	0	947	35	0
1	AK	910	0	907	37	0
1	AL	955	0	947	32	0
1	AM	955	0	947	46	0
1	AN	910	0	907	51	2
1	AO	955	0	947	30	0
1	AP	955	0	947	40	0
1	AQ	910	0	907	34	0
1	AR	955	0	947	45	0
1	AS	955	0	947	37	0
1	AT	910	0	907	27	0
1	AU	955	0	947	33	0
1	AV	955	0	947	37	0
1	AW	910	0	907	34	0
1	AX	955	0	947	39	0
1	AY	955	0	947	44	0
1	AZ	910	0	907	31	0
1	BA	955	0	947	33	0
1	BB	955	0	947	29	0
1	BC	910	0	907	33	0
1	BD	955	0	947	40	0
1	BE	955	0	947	30	0
1	BF	910	0	907	32	0
1	BG	955	0	947	29	0
1	BH	955	0	947	37	2
1	BI	910	0	907	33	0
1	BJ	955	0	947	30	1
1	BK	955	0	947	48	0
1	BL	910	0	907	35	0
1	BM	955	0	947	41	0
1	BN	955	0	947	42	0
1	BO	910	0	907	37	0
1	BP	955	0	947	29	0
1	BQ	955	0	947	30	0
1	BR	910	0	907	28	0
1	BS	955	0	947	29	0
1	BT	955	0	947	47	1
1	BU	910	0	907	41	1
1	BV	955	0	947	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BW	955	0	947	31	0
1	BX	910	0	907	36	0
1	BY	955	0	947	31	0
1	BZ	955	0	947	39	0
1	CA	910	0	907	45	1
1	CB	955	0	947	44	0
1	CC	955	0	947	44	0
1	CD	910	0	907	37	0
1	CE	955	0	947	30	0
1	CF	955	0	947	39	0
1	CG	910	0	907	42	1
1	CH	955	0	947	37	0
1	CI	955	0	947	30	1
1	CJ	910	0	907	30	3
1	CK	955	0	947	30	0
1	CL	955	0	947	41	0
1	CM	910	0	907	31	0
1	CN	955	0	947	33	0
1	CO	955	0	947	31	0
1	CP	910	0	907	38	0
1	CQ	955	0	947	35	0
1	CR	955	0	947	36	0
1	CS	910	0	907	32	0
1	CT	955	0	947	36	0
1	CU	955	0	947	33	0
1	CV	910	0	907	35	0
1	CW	955	0	947	32	0
1	CX	955	0	947	30	0
1	CY	910	0	907	36	0
1	CZ	955	0	947	37	0
1	DA	955	0	947	29	0
1	DB	910	0	907	40	0
1	DC	955	0	947	43	0
1	DD	955	0	947	31	0
1	DE	910	0	907	29	0
1	DF	955	0	947	31	0
1	DG	955	0	947	28	0
1	DH	910	0	907	32	0
1	DI	955	0	947	39	0
1	DJ	955	0	947	35	0
1	DK	910	0	907	33	0
1	DL	955	0	947	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DM	955	0	947	33	0
1	DN	910	0	907	45	1
1	DO	955	0	947	41	0
1	DP	955	0	947	31	0
1	DQ	910	0	907	32	0
1	DR	955	0	947	34	0
1	DS	955	0	947	29	0
1	DT	910	0	907	39	0
1	DU	955	0	947	38	0
1	DV	955	0	947	50	1
1	DW	910	0	907	53	1
1	DX	955	0	947	29	0
1	DY	955	0	947	29	0
1	DZ	910	0	907	42	0
1	EA	955	0	947	29	0
1	EB	955	0	947	44	0
1	EC	910	0	907	34	0
1	ED	955	0	947	46	0
1	EE	955	0	947	33	0
1	EF	910	0	907	36	0
1	EG	955	0	947	33	3
1	EH	955	0	947	50	1
1	EI	910	0	907	47	3
1	EJ	955	0	947	36	0
1	EK	955	0	947	28	3
1	EL	910	0	907	39	0
1	EM	955	0	947	31	0
1	EN	955	0	947	32	0
1	EO	910	0	907	48	1
1	EP	955	0	947	43	0
1	EQ	955	0	947	36	0
1	ER	910	0	907	29	1
1	ES	955	0	947	30	0
1	ET	955	0	947	46	0
1	EU	910	0	907	32	0
1	EV	955	0	947	35	1
1	EW	955	0	947	31	0
1	EX	910	0	907	37	0
1	EY	955	0	947	44	0
1	EZ	955	0	947	29	0
1	FA	910	0	907	34	0
1	FB	955	0	947	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	FC	955	0	947	32	0
1	FD	910	0	907	32	0
1	FE	955	0	947	28	0
1	FF	955	0	947	31	0
1	FG	910	0	907	48	0
1	FH	955	0	947	31	0
1	FI	955	0	947	36	0
1	FJ	910	0	907	32	2
1	FK	955	0	947	31	0
1	FL	955	0	947	34	0
1	FM	910	0	907	37	0
1	FN	955	0	947	40	0
1	FO	955	0	947	37	0
1	FP	910	0	907	32	0
1	FQ	955	0	947	33	3
1	FR	955	0	947	48	0
1	FS	910	0	907	33	0
1	FT	955	0	947	37	0
1	FU	955	0	947	30	0
1	FV	910	0	907	30	0
1	FW	955	0	947	29	0
1	FX	955	0	947	35	0
1	FY	910	0	907	31	0
1	FZ	955	0	947	33	0
1	GA	955	0	947	47	1
1	GB	910	0	907	44	2
1	GC	955	0	947	34	0
1	GD	955	0	947	38	0
1	GE	910	0	907	50	1
1	GF	955	0	947	40	0
1	GG	955	0	947	34	0
1	GH	910	0	907	31	0
1	GI	955	0	947	32	0
1	GJ	955	0	947	38	0
1	GK	910	0	907	46	2
1	GL	955	0	947	39	2
1	GM	955	0	947	40	3
1	GN	910	0	907	38	3
1	GO	955	0	947	44	0
1	GP	955	0	947	31	0
1	GQ	910	0	907	31	0
1	GR	955	0	947	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GS	955	0	947	30	0
1	GT	910	0	907	34	0
1	GU	955	0	947	38	0
1	GV	955	0	947	30	0
1	GW	910	0	907	31	0
1	GX	955	0	947	28	0
2	AA	1	0	0	0	0
2	AD	1	0	0	0	0
2	AG	1	0	0	0	0
2	AJ	1	0	0	0	0
2	AM	1	0	0	0	0
2	AP	1	0	0	0	0
2	AS	1	0	0	0	0
2	AV	1	0	0	0	0
2	AY	1	0	0	0	0
2	BB	1	0	0	0	0
2	BE	1	0	0	0	0
2	BH	1	0	0	0	0
2	BK	1	0	0	0	0
2	BN	1	0	0	0	0
2	BQ	1	0	0	0	0
2	BT	1	0	0	0	0
2	BW	1	0	0	0	0
2	BZ	1	0	0	0	0
2	CC	1	0	0	0	0
2	CF	1	0	0	0	0
2	CI	1	0	0	0	0
2	CL	1	0	0	0	0
2	CO	1	0	0	0	0
2	CR	1	0	0	0	0
2	CU	1	0	0	0	0
2	CX	1	0	0	0	0
2	DA	1	0	0	0	0
2	DD	1	0	0	0	0
2	DG	1	0	0	0	0
2	DJ	1	0	0	0	0
2	DM	1	0	0	0	0
2	DP	1	0	0	0	0
2	DS	1	0	0	0	0
2	DV	1	0	0	0	0
2	DY	1	0	0	0	0
2	EB	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	EE	1	0	0	0	0
2	EH	1	0	0	0	0
2	EK	1	0	0	0	0
2	EN	1	0	0	0	0
2	EQ	1	0	0	0	0
2	ET	1	0	0	0	0
2	EW	1	0	0	0	0
2	EZ	1	0	0	0	0
2	FC	1	0	0	0	0
2	FF	1	0	0	0	0
2	FI	1	0	0	0	0
2	FL	1	0	0	0	0
2	FO	1	0	0	0	0
2	FR	1	0	0	0	0
2	FU	1	0	0	0	0
2	FX	1	0	0	0	0
2	GA	1	0	0	0	0
2	GD	1	0	0	0	0
2	GG	1	0	0	0	0
2	GJ	1	0	0	0	0
2	GM	1	0	0	0	0
2	GP	1	0	0	0	0
2	GS	1	0	0	0	0
2	GV	1	0	0	0	0
All	All	169260	0	168060	4697	24

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 14.

All (4697) 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:BK:15:ARG:HH11	1:DW:103:THR:HG21	1.14	1.12
1:EB:15:ARG:HH11	1:GB:103:THR:HG21	1.17	1.08
1:FP:103:THR:HG21	1:GV:15:ARG:HH11	1.16	1.07
1:CG:103:THR:HG21	1:CL:15:ARG:HH11	1.19	1.05
1:AE:103:THR:HG21	1:GA:15:ARG:HH11	1.23	1.03
1:EH:15:ARG:HH11	1:EO:103:THR:HG21	1.17	1.03
1:AN:103:THR:HG21	1:FR:15:ARG:HH11	1.25	1.02
1:AP:15:ARG:HH11	1:BU:103:THR:HG21	1.19	1.02
1:AY:15:ARG:HH11	1:EI:103:THR:HG21	1.28	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:103:THR:HG22	1:EP:10:VAL:HG21	1.46	0.98
1:AD:15:ARG:HH11	1:BC:103:THR:HG21	1.28	0.97
1:CC:15:ARG:HH11	1:GK:103:THR:HG21	1.30	0.95
1:CY:103:THR:HG21	1:GG:15:ARG:HH11	1.31	0.94
1:AZ:103:THR:HG21	1:EW:15:ARG:HH11	1.33	0.93
1:CF:15:ARG:HH11	1:GN:103:THR:HG21	1.31	0.93
1:BT:15:ARG:HH11	1:DN:103:THR:HG21	1.33	0.92
1:DV:15:ARG:HH11	1:GE:103:THR:HG21	1.33	0.92
1:AN:10:VAL:HG21	1:FR:103:THR:HG22	1.51	0.91
1:CJ:103:THR:HG21	1:CO:15:ARG:HH11	1.34	0.91
1:AY:22:GLN:NE2	1:EI:124:TYR:HA	1.86	0.91
1:AM:15:ARG:HH11	1:CA:103:THR:HG21	1.36	0.90
1:AY:103:THR:HG22	1:EI:10:VAL:HG21	1.51	0.90
1:AP:103:THR:HG22	1:BU:10:VAL:HG21	1.53	0.89
1:EK:15:ARG:HH11	1:ER:103:THR:HG21	1.37	0.89
1:BK:22:GLN:NE2	1:DW:124:TYR:HA	1.87	0.89
1:BK:103:THR:HG22	1:DW:10:VAL:HG21	1.55	0.89
1:EE:15:ARG:HH11	1:EU:103:THR:HG21	1.38	0.89
1:EH:124:TYR:OXT	1:EO:22:GLN:NE2	2.06	0.88
1:BJ:103:THR:HG21	1:EV:15:ARG:HH11	1.39	0.88
1:BT:124:TYR:OXT	1:DN:22:GLN:NE2	2.07	0.88
1:CP:103:THR:HG21	1:DJ:15:ARG:HH11	1.38	0.88
1:CD:103:THR:HG21	1:CR:15:ARG:HH11	1.38	0.88
1:DM:15:ARG:HH11	1:GT:103:THR:HG21	1.36	0.88
1:AU:15:ARG:NH1	1:EG:103:THR:HG21	1.89	0.87
1:DC:103:THR:HG22	1:GO:10:VAL:HG21	1.56	0.87
1:CQ:105:ILE:HG23	1:GC:105:ILE:HG23	1.54	0.87
1:CU:15:ARG:HH11	1:DH:103:THR:HG21	1.40	0.87
1:BH:15:ARG:HH11	1:BO:103:THR:HG21	1.39	0.87
1:CI:15:ARG:HH11	1:GH:103:THR:HG21	1.40	0.86
1:AA:15:ARG:HH11	1:BI:103:THR:HG21	1.38	0.86
1:CB:10:VAL:HG21	1:FN:103:THR:HG22	1.58	0.86
1:BK:15:ARG:NH1	1:DW:103:THR:HG21	1.90	0.86
1:AH:103:THR:HG21	1:GD:15:ARG:HH11	1.41	0.86
1:EN:15:ARG:HH11	1:FJ:103:THR:HG21	1.39	0.86
1:AV:103:THR:HG22	1:EF:10:VAL:HG21	1.58	0.85
1:DL:105:ILE:HG23	1:GX:105:ILE:HG23	1.57	0.85
1:BJ:103:THR:HG21	1:EV:15:ARG:NH1	1.90	0.85
1:AU:15:ARG:HH11	1:EG:103:THR:HG21	1.40	0.85
1:CV:103:THR:HG21	1:GM:15:ARG:HH11	1.42	0.85
1:CG:124:TYR:HA	1:CL:22:GLN:NE2	1.91	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:22:GLN:HB3	1:DW:124:TYR:HB2	1.59	0.84
1:FP:103:THR:HG21	1:GV:15:ARG:NH1	1.90	0.84
1:AT:103:THR:HG21	1:EZ:15:ARG:HH11	1.42	0.84
1:BB:15:ARG:HH11	1:BR:103:THR:HG21	1.41	0.84
1:ET:105:ILE:HG23	1:FG:105:ILE:HG23	1.59	0.84
1:BN:15:ARG:HH11	1:DZ:103:THR:HG21	1.42	0.84
1:AG:15:ARG:HH11	1:BF:103:THR:HG21	1.43	0.84
1:AA:103:THR:HG22	1:BI:10:VAL:HG21	1.60	0.84
1:AV:15:ARG:HH11	1:EF:103:THR:HG21	1.43	0.83
1:CH:105:ILE:HG23	1:FT:105:ILE:HG23	1.60	0.83
1:FV:103:THR:HG21	1:GS:15:ARG:HH11	1.41	0.83
1:CD:124:TYR:OXT	1:CT:2:ARG:NH1	2.11	0.83
1:CG:103:THR:HG21	1:CL:15:ARG:NH1	1.93	0.83
1:AW:103:THR:HG21	1:FC:15:ARG:HH11	1.43	0.83
1:CD:10:VAL:HG21	1:CR:103:THR:HG22	1.58	0.83
1:EB:15:ARG:NH1	1:GB:103:THR:HG21	1.94	0.83
1:DV:124:TYR:OXT	1:GE:22:GLN:NE2	2.12	0.83
1:CZ:103:THR:HG21	1:GL:15:ARG:HH11	1.43	0.82
1:AS:105:ILE:HG23	1:EL:105:ILE:HG23	1.59	0.82
1:CT:103:THR:HG22	1:GF:10:VAL:HG21	1.61	0.82
1:CT:105:ILE:HG23	1:GF:105:ILE:HG23	1.60	0.82
1:BD:105:ILE:HG23	1:EP:105:ILE:HG23	1.62	0.82
1:CN:105:ILE:HG23	1:FZ:105:ILE:HG23	1.62	0.82
1:DB:105:ILE:HG23	1:GJ:105:ILE:HG23	1.60	0.82
1:DS:15:ARG:HH11	1:GQ:103:THR:HG21	1.42	0.82
1:EH:124:TYR:C	1:EO:22:GLN:HE21	1.83	0.82
1:BQ:105:ILE:HG23	1:EC:105:ILE:HG23	1.62	0.82
1:BZ:105:ILE:HG23	1:DT:105:ILE:HG23	1.62	0.82
1:EQ:105:ILE:HG23	1:FM:105:ILE:HG23	1.61	0.82
1:AZ:10:VAL:HG21	1:EW:103:THR:HG22	1.60	0.81
1:EH:15:ARG:NH1	1:EO:103:THR:HG21	1.95	0.81
1:AF:105:ILE:HG23	1:DR:105:ILE:HG23	1.61	0.81
1:AM:105:ILE:HG23	1:CA:105:ILE:HG23	1.62	0.81
1:AQ:10:VAL:HG21	1:FU:103:THR:HG22	1.62	0.81
1:AU:103:THR:HG21	1:EG:15:ARG:NH1	1.95	0.81
1:AX:105:ILE:HG23	1:EJ:105:ILE:HG23	1.62	0.81
1:BE:103:THR:HG22	1:BL:10:VAL:HG21	1.61	0.81
1:DC:15:ARG:HH11	1:GO:103:THR:HG21	1.44	0.81
1:DR:2:ARG:NH1	1:GW:124:TYR:OXT	2.14	0.81
1:AJ:105:ILE:HG23	1:BX:105:ILE:HG23	1.60	0.81
1:BP:105:ILE:HG23	1:FB:105:ILE:HG23	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FS:105:ILE:HG23	1:GP:105:ILE:HG23	1.63	0.81
1:AB:124:TYR:OXT	1:FZ:2:ARG:NH1	2.14	0.81
1:AP:15:ARG:NH1	1:BU:103:THR:HG21	1.95	0.81
1:CS:103:THR:HG21	1:DD:15:ARG:HH11	1.45	0.81
1:FS:103:THR:HG21	1:GP:15:ARG:HH11	1.45	0.81
1:AL:15:ARG:HH11	1:DX:103:THR:HG21	1.46	0.81
1:AO:103:THR:HG21	1:EA:15:ARG:HH11	1.45	0.81
1:AX:15:ARG:NH1	1:EJ:103:THR:HG21	1.96	0.81
1:BQ:103:THR:HG22	1:EC:10:VAL:HG21	1.61	0.81
1:BW:105:ILE:HG23	1:DQ:105:ILE:HG23	1.63	0.81
1:BZ:15:ARG:HH11	1:DT:103:THR:HG21	1.46	0.81
1:CE:105:ILE:HG23	1:FQ:105:ILE:HG23	1.60	0.80
1:BE:105:ILE:HG23	1:BL:105:ILE:HG23	1.63	0.80
1:AQ:103:THR:HG21	1:FU:15:ARG:HH11	1.47	0.80
1:CM:103:THR:HG21	1:DG:15:ARG:HH11	1.46	0.80
1:AU:103:THR:HG21	1:EG:15:ARG:HH11	1.47	0.80
1:CK:105:ILE:HG23	1:FW:105:ILE:HG23	1.64	0.80
1:FD:124:TYR:OXT	1:FH:2:ARG:NH1	2.13	0.80
1:AX:2:ARG:NH1	1:EF:124:TYR:OXT	2.14	0.80
1:DB:103:THR:HG22	1:GJ:10:VAL:HG21	1.64	0.80
1:BQ:15:ARG:HH11	1:EC:103:THR:HG21	1.46	0.80
1:AC:103:THR:HG22	1:DO:10:VAL:HG21	1.64	0.79
1:EB:22:GLN:NE2	1:GB:124:TYR:HA	1.97	0.79
1:FA:124:TYR:OXT	1:FN:2:ARG:NH1	2.13	0.79
1:FD:103:THR:HG21	1:FF:15:ARG:HH11	1.47	0.79
1:AT:105:ILE:HG23	1:EZ:105:ILE:HG23	1.64	0.79
1:EX:103:THR:HG21	1:FI:15:ARG:HH11	1.47	0.79
1:CU:105:ILE:HG23	1:DH:105:ILE:HG23	1.64	0.79
1:EB:103:THR:HG22	1:GB:10:VAL:HG21	1.62	0.79
1:AL:15:ARG:NH1	1:DX:103:THR:HG21	1.97	0.79
1:AO:103:THR:HG21	1:EA:15:ARG:NH1	1.96	0.79
1:DP:15:ARG:HH11	1:GW:103:THR:HG21	1.48	0.79
1:AK:103:THR:HG21	1:FO:15:ARG:HH11	1.45	0.79
1:CZ:15:ARG:NH1	1:GL:103:THR:HG21	1.96	0.79
1:DA:15:ARG:HH11	1:DE:103:THR:HG21	1.47	0.79
1:DP:103:THR:HG22	1:GW:10:VAL:HG21	1.65	0.79
1:AK:124:TYR:OXT	1:FQ:2:ARG:NH1	2.15	0.79
1:DI:105:ILE:HG23	1:GU:105:ILE:HG23	1.65	0.79
1:EQ:15:ARG:HH11	1:FM:103:THR:HG21	1.48	0.79
1:BV:103:THR:HG21	1:FH:15:ARG:NH1	1.98	0.78
1:CY:124:TYR:OXT	1:GI:2:ARG:NH1	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:2:ARG:NH1	1:EL:124:TYR:OXT	2.16	0.78
1:FA:103:THR:HG21	1:FL:15:ARG:HH11	1.47	0.78
1:AW:105:ILE:HG23	1:FC:105:ILE:HG23	1.65	0.78
1:CS:105:ILE:HG23	1:DD:105:ILE:HG23	1.66	0.78
1:BP:2:ARG:NH1	1:DZ:124:TYR:OXT	2.16	0.78
1:CB:15:ARG:HH11	1:FN:103:THR:HG21	1.47	0.78
1:EE:105:ILE:HG23	1:EU:105:ILE:HG23	1.66	0.78
1:CB:103:THR:HG21	1:FN:15:ARG:HH11	1.48	0.78
1:AS:15:ARG:HH11	1:EL:103:THR:HG21	1.48	0.78
1:AN:105:ILE:HG23	1:FR:105:ILE:HG23	1.66	0.78
1:ET:15:ARG:HH11	1:FG:103:THR:HG21	1.49	0.78
1:DF:105:ILE:HG23	1:GR:105:ILE:HG23	1.65	0.77
1:BA:103:THR:HG21	1:EM:15:ARG:NH1	1.99	0.77
1:BV:103:THR:HG21	1:FH:15:ARG:HH11	1.49	0.77
1:BT:22:GLN:NE2	1:DN:124:TYR:HA	2.00	0.77
1:CZ:15:ARG:HH11	1:GL:103:THR:HG21	1.49	0.77
1:DY:15:ARG:HH11	1:FY:103:THR:HG21	1.49	0.77
1:AQ:105:ILE:HG23	1:FU:105:ILE:HG23	1.64	0.77
1:AI:10:VAL:HG21	1:DU:103:THR:HG22	1.66	0.77
1:AI:103:THR:HG22	1:DU:10:VAL:HG21	1.65	0.77
1:BM:105:ILE:HG23	1:EY:105:ILE:HG23	1.66	0.77
1:AF:10:VAL:HG21	1:DR:103:THR:HG22	1.67	0.77
1:EI:22:GLN:HB3	1:EO:124:TYR:HB2	1.66	0.77
1:AB:103:THR:HG21	1:FX:15:ARG:HH11	1.48	0.77
1:AL:103:THR:HG22	1:DX:10:VAL:HG21	1.66	0.77
1:AR:105:ILE:HG23	1:ED:105:ILE:HG23	1.66	0.77
1:DC:15:ARG:NH1	1:GO:103:THR:HG21	2.00	0.77
1:DV:22:GLN:NE2	1:GE:124:TYR:HA	2.00	0.77
1:BN:105:ILE:HG23	1:DZ:105:ILE:HG23	1.67	0.76
1:AK:105:ILE:HG23	1:FO:105:ILE:HG23	1.67	0.76
1:CW:105:ILE:HG23	1:GI:105:ILE:HG23	1.66	0.76
1:AE:103:THR:HG21	1:GA:15:ARG:NH1	2.00	0.76
1:BW:15:ARG:HH11	1:DQ:103:THR:HG21	1.50	0.76
1:CB:68:VAL:HG11	1:FN:91:THR:HG22	1.67	0.76
1:BJ:15:ARG:HH11	1:EV:103:THR:HG21	1.50	0.76
1:CP:105:ILE:HG23	1:DJ:105:ILE:HG23	1.67	0.76
1:AO:10:VAL:HG21	1:EA:103:THR:HG22	1.67	0.76
1:CF:105:ILE:HG23	1:GN:105:ILE:HG23	1.67	0.76
1:AD:96:HIS:CG	1:BC:66:VAL:HG21	2.21	0.76
1:AN:124:TYR:HB2	1:FS:22:GLN:HB3	1.66	0.76
1:AP:22:GLN:NE2	1:BU:124:TYR:HA	2.00	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:105:ILE:HG23	1:GK:105:ILE:HG23	1.66	0.76
1:CE:103:THR:HG21	1:FQ:15:ARG:NH1	2.01	0.76
1:AS:10:VAL:HG21	1:EL:103:THR:HG22	1.67	0.76
1:BH:105:ILE:HG23	1:BO:105:ILE:HG23	1.67	0.76
1:CC:10:VAL:HG21	1:GK:103:THR:HG22	1.65	0.75
1:AB:105:ILE:HG23	1:FX:105:ILE:HG23	1.67	0.75
1:BA:103:THR:HG21	1:EM:15:ARG:HH11	1.50	0.75
1:BH:10:VAL:HG21	1:BO:103:THR:HG22	1.66	0.75
1:DV:105:ILE:HG23	1:GE:105:ILE:HG23	1.68	0.75
1:AY:105:ILE:HG23	1:EI:105:ILE:HG23	1.66	0.75
1:DB:103:THR:HG21	1:GJ:15:ARG:HH11	1.50	0.75
1:AK:103:THR:HG22	1:FO:10:VAL:HG21	1.69	0.75
1:AZ:22:GLN:HB3	1:EI:124:TYR:HB2	1.68	0.75
1:DC:2:ARG:NH1	1:DE:124:TYR:OXT	2.19	0.75
1:EX:105:ILE:HG23	1:FI:105:ILE:HG23	1.67	0.75
1:AC:105:ILE:HG23	1:DO:105:ILE:HG23	1.67	0.75
1:EE:10:VAL:HG21	1:EU:103:THR:HG22	1.69	0.75
1:AX:103:THR:HG22	1:EJ:10:VAL:HG21	1.68	0.75
1:CP:124:TYR:OXT	1:DL:2:ARG:NH1	2.20	0.75
1:FP:15:ARG:NH1	1:GV:103:THR:HG21	2.02	0.75
1:AX:103:THR:HG21	1:EJ:15:ARG:HH11	1.51	0.75
1:CV:105:ILE:HG23	1:GM:105:ILE:HG23	1.69	0.75
1:EK:105:ILE:HG23	1:ER:105:ILE:HG23	1.69	0.75
1:BF:18:ALA:HB2	1:BF:32:LYS:HE3	1.69	0.75
1:CD:18:ALA:HB2	1:CD:32:LYS:HE3	1.69	0.75
1:AI:105:ILE:HG23	1:DU:105:ILE:HG23	1.68	0.74
1:AX:15:ARG:HH11	1:EJ:103:THR:HG21	1.50	0.74
1:CG:18:ALA:HB2	1:CG:32:LYS:HE3	1.69	0.74
1:CQ:103:THR:HG22	1:GC:10:VAL:HG21	1.67	0.74
1:DQ:18:ALA:HB2	1:DQ:32:LYS:HE3	1.69	0.74
1:EU:18:ALA:HB2	1:EU:32:LYS:HE3	1.69	0.74
1:AK:18:ALA:HB2	1:AK:32:LYS:HE3	1.69	0.74
1:CA:18:ALA:HB2	1:CA:32:LYS:HE3	1.70	0.74
1:CN:103:THR:HG21	1:FZ:15:ARG:NH1	2.02	0.74
1:CX:105:ILE:HG23	1:DK:105:ILE:HG23	1.68	0.74
1:DI:103:THR:HG22	1:GU:10:VAL:HG21	1.69	0.74
1:FV:18:ALA:HB2	1:FV:32:LYS:HE3	1.69	0.74
1:GN:18:ALA:HB2	1:GN:32:LYS:HE3	1.69	0.74
1:AN:103:THR:HG22	1:FR:10:VAL:HG21	1.70	0.74
1:BJ:15:ARG:NH1	1:EV:103:THR:HG21	2.02	0.74
1:BO:18:ALA:HB2	1:BO:32:LYS:HE3	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GB:18:ALA:HB2	1:GB:32:LYS:HE3	1.69	0.74
1:DC:68:VAL:HG11	1:GO:91:THR:HG22	1.68	0.74
1:DZ:18:ALA:HB2	1:DZ:32:LYS:HE3	1.69	0.74
1:AB:18:ALA:HB2	1:AB:32:LYS:HE3	1.70	0.74
1:AG:105:ILE:HG23	1:BF:105:ILE:HG23	1.70	0.74
1:DB:18:ALA:HB2	1:DB:32:LYS:HE3	1.69	0.74
1:DN:18:ALA:HB2	1:DN:32:LYS:HE3	1.69	0.74
1:GQ:18:ALA:HB2	1:GQ:32:LYS:HE3	1.69	0.74
1:AJ:10:VAL:HG21	1:BX:103:THR:HG22	1.70	0.74
1:DP:105:ILE:HG23	1:GW:105:ILE:HG23	1.69	0.74
1:DW:18:ALA:HB2	1:DW:32:LYS:HE3	1.69	0.74
1:EI:18:ALA:HB2	1:EI:32:LYS:HE3	1.70	0.74
1:GW:18:ALA:HB2	1:GW:32:LYS:HE3	1.70	0.74
1:AR:15:ARG:NH1	1:ED:103:THR:HG21	2.02	0.74
1:CM:10:VAL:HG21	1:DG:103:THR:HG22	1.69	0.74
1:CZ:103:THR:HG21	1:GL:15:ARG:NH1	2.01	0.74
1:DH:18:ALA:HB2	1:DH:32:LYS:HE3	1.69	0.74
1:EO:18:ALA:HB2	1:EO:32:LYS:HE3	1.69	0.74
1:BM:103:THR:HG21	1:EY:15:ARG:NH1	2.03	0.74
1:BV:10:VAL:HG21	1:FH:103:THR:HG22	1.70	0.74
1:CH:15:ARG:HH11	1:FT:103:THR:HG21	1.53	0.74
1:AW:18:ALA:HB2	1:AW:32:LYS:HE3	1.70	0.74
1:BD:91:THR:HG22	1:EP:68:VAL:HG11	1.70	0.74
1:FJ:18:ALA:HB2	1:FJ:32:LYS:HE3	1.69	0.74
1:BR:18:ALA:HB2	1:BR:32:LYS:HE3	1.70	0.74
1:CJ:105:ILE:HG23	1:CO:105:ILE:HG23	1.70	0.73
1:FG:18:ALA:HB2	1:FG:32:LYS:HE3	1.69	0.73
1:AL:2:ARG:NH1	1:BX:124:TYR:OXT	2.22	0.73
1:BG:105:ILE:HG23	1:ES:105:ILE:HG23	1.70	0.73
1:BI:18:ALA:HB2	1:BI:32:LYS:HE3	1.69	0.73
1:CZ:103:THR:HG22	1:GL:10:VAL:HG21	1.70	0.73
1:DA:105:ILE:HG23	1:DE:105:ILE:HG23	1.70	0.73
1:DT:18:ALA:HB2	1:DT:32:LYS:HE3	1.69	0.73
1:EC:18:ALA:HB2	1:EC:32:LYS:HE3	1.69	0.73
1:FD:18:ALA:HB2	1:FD:32:LYS:HE3	1.70	0.73
1:GT:18:ALA:HB2	1:GT:32:LYS:HE3	1.70	0.73
1:AH:18:ALA:HB2	1:AH:32:LYS:HE3	1.69	0.73
1:BC:18:ALA:HB2	1:BC:32:LYS:HE3	1.69	0.73
1:BT:124:TYR:C	1:DN:22:GLN:HE21	1.90	0.73
1:CM:18:ALA:HB2	1:CM:32:LYS:HE3	1.69	0.73
1:CS:18:ALA:HB2	1:CS:32:LYS:HE3	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:18:ALA:HB2	1:BL:32:LYS:HE3	1.69	0.73
1:BS:105:ILE:HG23	1:FE:105:ILE:HG23	1.69	0.73
1:CN:103:THR:HG21	1:FZ:15:ARG:HH11	1.54	0.73
1:CX:15:ARG:HH11	1:DK:103:THR:HG21	1.54	0.73
1:AT:18:ALA:HB2	1:AT:32:LYS:HE3	1.69	0.73
1:BG:103:THR:HG21	1:ES:15:ARG:HH11	1.51	0.73
1:DE:18:ALA:HB2	1:DE:32:LYS:HE3	1.69	0.73
1:DY:105:ILE:HG23	1:FY:105:ILE:HG23	1.69	0.73
1:EX:18:ALA:HB2	1:EX:32:LYS:HE3	1.70	0.73
1:AZ:18:ALA:HB2	1:AZ:32:LYS:HE3	1.69	0.73
1:BJ:105:ILE:HG23	1:EV:105:ILE:HG23	1.71	0.73
1:FD:105:ILE:HG23	1:FF:105:ILE:HG23	1.70	0.73
1:FP:18:ALA:HB2	1:FP:32:LYS:HE3	1.69	0.73
1:AE:124:TYR:HA	1:GA:22:GLN:NE2	2.03	0.73
1:CE:103:THR:HG21	1:FQ:15:ARG:HH11	1.53	0.73
1:CM:123:ASN:HB3	1:DG:3:LEU:HG	1.70	0.73
1:CY:18:ALA:HB2	1:CY:32:LYS:HE3	1.69	0.73
1:FS:18:ALA:HB2	1:FS:32:LYS:HE3	1.69	0.73
1:AH:105:ILE:HG23	1:GD:105:ILE:HG23	1.71	0.73
1:AQ:18:ALA:HB2	1:AQ:32:LYS:HE3	1.69	0.73
1:BT:105:ILE:HG23	1:DN:105:ILE:HG23	1.69	0.73
1:CB:103:THR:HG21	1:FN:15:ARG:NH1	2.02	0.73
1:CJ:10:VAL:HG21	1:CO:103:THR:HG22	1.68	0.73
1:FA:18:ALA:HB2	1:FA:32:LYS:HE3	1.69	0.73
1:AA:105:ILE:HG23	1:BI:105:ILE:HG23	1.69	0.73
1:BP:15:ARG:HH11	1:FB:103:THR:HG21	1.52	0.73
1:CJ:18:ALA:HB2	1:CJ:32:LYS:HE3	1.70	0.73
1:AC:103:THR:HG21	1:DO:15:ARG:HH11	1.54	0.72
1:AE:18:ALA:HB2	1:AE:32:LYS:HE3	1.69	0.72
1:AN:18:ALA:HB2	1:AN:32:LYS:HE3	1.70	0.72
1:GH:18:ALA:HB2	1:GH:32:LYS:HE3	1.69	0.72
1:AR:103:THR:HG21	1:ED:15:ARG:NH1	2.04	0.72
1:AS:103:THR:HG22	1:EL:10:VAL:HG21	1.70	0.72
1:BU:18:ALA:HB2	1:BU:32:LYS:HE3	1.69	0.72
1:BV:105:ILE:HG23	1:FH:105:ILE:HG23	1.70	0.72
1:BX:18:ALA:HB2	1:BX:32:LYS:HE3	1.69	0.72
1:BY:105:ILE:HG23	1:FK:105:ILE:HG23	1.69	0.72
1:EL:18:ALA:HB2	1:EL:32:LYS:HE3	1.69	0.72
1:FM:15:ARG:NH2	1:FM:17:TYR:OH	2.23	0.72
1:GE:18:ALA:HB2	1:GE:32:LYS:HE3	1.69	0.72
1:AB:10:VAL:HG21	1:FX:103:THR:HG22	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:15:ARG:NH2	1:AH:17:TYR:OH	2.23	0.72
1:AK:15:ARG:NH2	1:AK:17:TYR:OH	2.23	0.72
1:AT:15:ARG:NH2	1:AT:17:TYR:OH	2.23	0.72
1:BI:15:ARG:NH2	1:BI:17:TYR:OH	2.23	0.72
1:GN:15:ARG:NH2	1:GN:17:TYR:OH	2.23	0.72
1:GQ:15:ARG:NH2	1:GQ:17:TYR:OH	2.23	0.72
1:BO:15:ARG:NH2	1:BO:17:TYR:OH	2.23	0.72
1:CD:15:ARG:NH2	1:CD:17:TYR:OH	2.23	0.72
1:CV:18:ALA:HB2	1:CV:32:LYS:HE3	1.70	0.72
1:DK:15:ARG:NH2	1:DK:17:TYR:OH	2.23	0.72
1:DZ:15:ARG:NH2	1:DZ:17:TYR:OH	2.23	0.72
1:ER:18:ALA:HB2	1:ER:32:LYS:HE3	1.70	0.72
1:FD:103:THR:HG22	1:FF:10:VAL:HG21	1.72	0.72
1:FS:15:ARG:NH2	1:FS:17:TYR:OH	2.23	0.72
1:AZ:15:ARG:NH2	1:AZ:17:TYR:OH	2.23	0.72
1:BA:105:ILE:HG23	1:EM:105:ILE:HG23	1.70	0.72
1:BX:15:ARG:NH2	1:BX:17:TYR:OH	2.23	0.72
1:DT:15:ARG:NH2	1:DT:17:TYR:OH	2.23	0.72
1:EL:15:ARG:NH2	1:EL:17:TYR:OH	2.23	0.72
1:FM:18:ALA:HB2	1:FM:32:LYS:HE3	1.69	0.72
1:FV:15:ARG:NH2	1:FV:17:TYR:OH	2.23	0.72
1:FY:18:ALA:HB2	1:FY:32:LYS:HE3	1.69	0.72
1:AQ:15:ARG:NH2	1:AQ:17:TYR:OH	2.23	0.72
1:BC:15:ARG:NH2	1:BC:17:TYR:OH	2.23	0.72
1:BR:15:ARG:NH2	1:BR:17:TYR:OH	2.23	0.72
1:CG:15:ARG:NH2	1:CG:17:TYR:OH	2.23	0.72
1:DW:15:ARG:NH2	1:DW:17:TYR:OH	2.23	0.72
1:AH:66:VAL:HG21	1:GD:96:HIS:CG	2.25	0.72
1:CA:15:ARG:NH2	1:CA:17:TYR:OH	2.23	0.72
1:CY:15:ARG:NH2	1:CY:17:TYR:OH	2.23	0.72
1:DH:15:ARG:NH2	1:DH:17:TYR:OH	2.23	0.72
1:DQ:15:ARG:NH2	1:DQ:17:TYR:OH	2.23	0.72
1:EF:18:ALA:HB2	1:EF:32:LYS:HE3	1.70	0.72
1:GE:15:ARG:NH2	1:GE:17:TYR:OH	2.23	0.72
1:GH:15:ARG:NH2	1:GH:17:TYR:OH	2.23	0.72
1:GW:15:ARG:NH2	1:GW:17:TYR:OH	2.23	0.72
1:AE:15:ARG:NH2	1:AE:17:TYR:OH	2.23	0.72
1:AN:15:ARG:NH2	1:AN:17:TYR:OH	2.23	0.72
1:BL:15:ARG:NH2	1:BL:17:TYR:OH	2.23	0.72
1:CJ:15:ARG:NH2	1:CJ:17:TYR:OH	2.23	0.72
1:CS:15:ARG:NH2	1:CS:17:TYR:OH	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EH:106:ALA:HB1	1:EO:8:LEU:HD22	1.72	0.72
1:EI:15:ARG:NH2	1:EI:17:TYR:OH	2.23	0.72
1:FP:15:ARG:NH2	1:FP:17:TYR:OH	2.23	0.72
1:FS:10:VAL:HG21	1:GP:103:THR:HG22	1.70	0.72
1:CP:15:ARG:NH2	1:CP:17:TYR:OH	2.23	0.72
1:CW:10:VAL:HG21	1:GI:103:THR:HG22	1.70	0.72
1:DK:18:ALA:HB2	1:DK:32:LYS:HE3	1.70	0.72
1:EC:22:GLN:HB3	1:GB:124:TYR:HB2	1.69	0.72
1:CM:15:ARG:NH2	1:CM:17:TYR:OH	2.23	0.71
1:CP:18:ALA:HB2	1:CP:32:LYS:HE3	1.69	0.71
1:CZ:105:ILE:HG23	1:GL:105:ILE:HG23	1.72	0.71
1:EC:15:ARG:NH2	1:EC:17:TYR:OH	2.23	0.71
1:EX:15:ARG:NH2	1:EX:17:TYR:OH	2.23	0.71
1:FA:10:VAL:HG21	1:FL:103:THR:HG22	1.72	0.71
1:FA:105:ILE:HG23	1:FL:105:ILE:HG23	1.71	0.71
1:GB:15:ARG:NH2	1:GB:17:TYR:OH	2.23	0.71
1:AB:15:ARG:NH2	1:AB:17:TYR:OH	2.23	0.71
1:AU:105:ILE:HG23	1:EG:105:ILE:HG23	1.72	0.71
1:DB:15:ARG:NH2	1:DB:17:TYR:OH	2.23	0.71
1:FA:15:ARG:NH2	1:FA:17:TYR:OH	2.23	0.71
1:AL:105:ILE:HG23	1:DX:105:ILE:HG23	1.72	0.71
1:AW:15:ARG:NH2	1:AW:17:TYR:OH	2.23	0.71
1:BD:15:ARG:HH11	1:EP:103:THR:HG21	1.54	0.71
1:BY:103:THR:HG22	1:FK:10:VAL:HG21	1.70	0.71
1:EF:15:ARG:NH2	1:EF:17:TYR:OH	2.23	0.71
1:FJ:15:ARG:NH2	1:FJ:17:TYR:OH	2.23	0.71
1:GK:15:ARG:NH2	1:GK:17:TYR:OH	2.23	0.71
1:AD:15:ARG:NH1	1:BC:103:THR:HG21	2.04	0.71
1:BF:15:ARG:NH2	1:BF:17:TYR:OH	2.23	0.71
1:DE:15:ARG:NH2	1:DE:17:TYR:OH	2.23	0.71
1:EU:15:ARG:NH2	1:EU:17:TYR:OH	2.23	0.71
1:GK:18:ALA:HB2	1:GK:32:LYS:HE3	1.70	0.71
1:DN:15:ARG:NH2	1:DN:17:TYR:OH	2.23	0.71
1:EH:22:GLN:NE2	1:EO:124:TYR:HA	2.05	0.71
1:FG:15:ARG:NH2	1:FG:17:TYR:OH	2.23	0.71
1:AO:105:ILE:HG23	1:EA:105:ILE:HG23	1.73	0.71
1:AY:15:ARG:NH1	1:EI:103:THR:HG21	2.03	0.71
1:BU:15:ARG:NH2	1:BU:17:TYR:OH	2.23	0.71
1:BW:10:VAL:HG21	1:DQ:103:THR:HG22	1.72	0.71
1:CW:103:THR:HG22	1:GI:10:VAL:HG21	1.72	0.71
1:CV:15:ARG:NH2	1:CV:17:TYR:OH	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FY:15:ARG:NH2	1:FY:17:TYR:OH	2.23	0.71
1:BE:15:ARG:HH11	1:BL:103:THR:HG21	1.55	0.71
1:DC:103:THR:HG21	1:GO:15:ARG:HH11	1.56	0.71
1:GT:15:ARG:NH2	1:GT:17:TYR:OH	2.23	0.71
1:BM:103:THR:HG21	1:EY:15:ARG:HH11	1.56	0.71
1:ER:15:ARG:NH2	1:ER:17:TYR:OH	2.23	0.71
1:EV:2:ARG:NH1	1:FG:124:TYR:OXT	2.23	0.71
1:DM:105:ILE:HG23	1:GT:105:ILE:HG23	1.72	0.70
1:DP:10:VAL:HG21	1:GW:103:THR:HG22	1.70	0.70
1:FD:15:ARG:NH2	1:FD:17:TYR:OH	2.23	0.70
1:AD:105:ILE:HG23	1:BC:105:ILE:HG23	1.74	0.70
1:AJ:15:ARG:HH11	1:BX:103:THR:HG21	1.55	0.70
1:CG:10:VAL:HG21	1:CL:103:THR:HG22	1.71	0.70
1:EO:15:ARG:NH2	1:EO:17:TYR:OH	2.23	0.70
1:FV:105:ILE:HG23	1:GS:105:ILE:HG23	1.73	0.70
1:AR:15:ARG:HH11	1:ED:103:THR:HG21	1.55	0.70
1:AR:103:THR:HG21	1:ED:15:ARG:HH11	1.55	0.70
1:CH:103:THR:HG21	1:FT:15:ARG:NH1	2.05	0.70
1:CI:105:ILE:HG23	1:GH:105:ILE:HG23	1.72	0.70
1:EA:2:ARG:NH1	1:FY:124:TYR:OXT	2.24	0.70
1:BB:103:THR:HG21	1:BR:15:ARG:NH1	2.06	0.70
1:DV:124:TYR:C	1:GE:22:GLN:HE21	1.94	0.70
1:BD:2:ARG:NH1	1:BR:124:TYR:OXT	2.23	0.70
1:AW:124:TYR:OXT	1:FE:2:ARG:NH1	2.25	0.70
1:CE:15:ARG:NH1	1:FQ:103:THR:HG21	2.06	0.70
1:CS:124:TYR:OXT	1:DF:2:ARG:NH1	2.25	0.70
1:AE:105:ILE:HG23	1:GA:105:ILE:HG23	1.73	0.70
1:BA:15:ARG:NH1	1:EM:103:THR:HG21	2.07	0.70
1:DD:45:LEU:HD13	1:DD:60:MET:HG3	1.74	0.70
1:BG:15:ARG:HH11	1:ES:103:THR:HG21	1.56	0.69
1:FR:45:LEU:HD13	1:FR:60:MET:HG3	1.74	0.69
1:AM:124:TYR:OXT	1:CA:22:GLN:NE2	2.24	0.69
1:AA:45:LEU:HD13	1:AA:60:MET:HG3	1.74	0.69
1:AH:62:LEU:HD21	1:GD:103:THR:OG1	1.92	0.69
1:BH:45:LEU:HD13	1:BH:60:MET:HG3	1.75	0.69
1:BP:10:VAL:HG21	1:FB:103:THR:HG22	1.74	0.69
1:BV:15:ARG:HH11	1:FH:103:THR:HG21	1.57	0.69
1:CQ:15:ARG:NH1	1:GC:103:THR:HG21	2.07	0.69
1:DS:45:LEU:HD13	1:DS:60:MET:HG3	1.74	0.69
1:EQ:10:VAL:HG21	1:FM:103:THR:HG22	1.74	0.69
1:FU:45:LEU:HD13	1:FU:60:MET:HG3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GG:45:LEU:HD13	1:GG:60:MET:HG3	1.74	0.69
1:BN:45:LEU:HD13	1:BN:60:MET:HG3	1.75	0.69
1:BW:45:LEU:HD13	1:BW:60:MET:HG3	1.74	0.69
1:BY:2:ARG:NH1	1:DQ:124:TYR:OXT	2.25	0.69
1:CD:124:TYR:C	1:CT:2:ARG:HH12	1.96	0.69
1:CY:105:ILE:HG23	1:GG:105:ILE:HG23	1.74	0.69
1:DP:45:LEU:HD13	1:DP:60:MET:HG3	1.74	0.69
1:EB:45:LEU:HD13	1:EB:60:MET:HG3	1.74	0.69
1:FO:45:LEU:HD13	1:FO:60:MET:HG3	1.74	0.69
1:GD:45:LEU:HD13	1:GD:60:MET:HG3	1.74	0.69
1:GJ:45:LEU:HD13	1:GJ:60:MET:HG3	1.74	0.69
1:AJ:45:LEU:HD13	1:AJ:60:MET:HG3	1.75	0.69
1:BD:10:VAL:HG21	1:EP:103:THR:HG22	1.74	0.69
1:DI:10:VAL:HG21	1:GU:103:THR:HG22	1.74	0.69
1:AG:45:LEU:HD13	1:AG:60:MET:HG3	1.74	0.69
1:AL:103:THR:HG21	1:DX:15:ARG:HH11	1.56	0.69
1:AY:45:LEU:HD13	1:AY:60:MET:HG3	1.74	0.69
1:CF:10:VAL:HG21	1:GN:103:THR:HG22	1.73	0.69
1:CG:124:TYR:HB2	1:CM:22:GLN:HB3	1.73	0.69
1:CH:15:ARG:NH1	1:FT:103:THR:HG21	2.06	0.69
1:CQ:15:ARG:HH11	1:GC:103:THR:HG21	1.58	0.69
1:DY:45:LEU:HD13	1:DY:60:MET:HG3	1.74	0.69
1:EN:105:ILE:HG23	1:FJ:105:ILE:HG23	1.74	0.69
1:FF:45:LEU:HD13	1:FF:60:MET:HG3	1.74	0.69
1:GV:45:LEU:HD13	1:GV:60:MET:HG3	1.74	0.69
1:AV:45:LEU:HD13	1:AV:60:MET:HG3	1.74	0.69
1:BK:105:ILE:HG23	1:DW:105:ILE:HG23	1.75	0.69
1:BU:22:GLN:HB3	1:DN:124:TYR:HB2	1.75	0.69
1:GM:45:LEU:HD13	1:GM:60:MET:HG3	1.74	0.69
1:AI:103:THR:HG21	1:DU:15:ARG:HH11	1.57	0.69
1:AM:22:GLN:NE2	1:CA:124:TYR:HA	2.08	0.69
1:AM:99:LYS:HE2	1:CA:15:ARG:HH11	1.57	0.69
1:AO:15:ARG:HH11	1:EA:103:THR:HG21	1.57	0.69
1:AW:89:PRO:HG2	1:AW:92:TYR:HB2	1.75	0.69
1:BG:103:THR:HG21	1:ES:15:ARG:NH1	2.07	0.69
1:BQ:45:LEU:HD13	1:BQ:60:MET:HG3	1.74	0.69
1:BT:45:LEU:HD13	1:BT:60:MET:HG3	1.74	0.69
1:CG:89:PRO:HG2	1:CG:92:TYR:HB2	1.75	0.69
1:CI:10:VAL:HG21	1:GH:103:THR:HG22	1.74	0.69
1:CT:103:THR:HG21	1:GF:15:ARG:HH11	1.58	0.69
1:DC:105:ILE:HG23	1:GO:105:ILE:HG23	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EU:89:PRO:HG2	1:EU:92:TYR:HB2	1.75	0.69
1:GE:89:PRO:HG2	1:GE:92:TYR:HB2	1.75	0.69
1:GH:89:PRO:HG2	1:GH:92:TYR:HB2	1.75	0.69
1:GS:45:LEU:HD13	1:GS:60:MET:HG3	1.75	0.69
1:AE:22:GLN:NE2	1:GA:124:TYR:OXT	2.25	0.69
1:AP:45:LEU:HD13	1:AP:60:MET:HG3	1.74	0.69
1:CI:45:LEU:HD13	1:CI:60:MET:HG3	1.74	0.69
1:CY:89:PRO:HG2	1:CY:92:TYR:HB2	1.75	0.69
1:CZ:22:GLN:NE2	1:GL:124:TYR:HA	2.07	0.69
1:DK:89:PRO:HG2	1:DK:92:TYR:HB2	1.75	0.69
1:EC:89:PRO:HG2	1:EC:92:TYR:HB2	1.75	0.69
1:EW:45:LEU:HD13	1:EW:60:MET:HG3	1.74	0.69
1:AT:89:PRO:HG2	1:AT:92:TYR:HB2	1.75	0.69
1:BC:89:PRO:HG2	1:BC:92:TYR:HB2	1.75	0.69
1:BG:15:ARG:NH1	1:ES:103:THR:HG21	2.08	0.69
1:BL:89:PRO:HG2	1:BL:92:TYR:HB2	1.75	0.69
1:BZ:103:THR:OG1	1:DT:62:LEU:HD21	1.92	0.69
1:EX:89:PRO:HG2	1:EX:92:TYR:HB2	1.75	0.69
1:AM:45:LEU:HD13	1:AM:60:MET:HG3	1.74	0.68
1:BB:45:LEU:HD13	1:BB:60:MET:HG3	1.74	0.68
1:CA:89:PRO:HG2	1:CA:92:TYR:HB2	1.75	0.68
1:CS:89:PRO:HG2	1:CS:92:TYR:HB2	1.75	0.68
1:DG:45:LEU:HD13	1:DG:60:MET:HG3	1.74	0.68
1:DL:15:ARG:HH11	1:GX:103:THR:HG21	1.58	0.68
1:DM:96:HIS:CG	1:GT:66:VAL:HG21	2.28	0.68
1:EE:45:LEU:HD13	1:EE:60:MET:HG3	1.74	0.68
1:EH:1:MET:SD	1:EO:111:GLN:HB2	2.33	0.68
1:EQ:45:LEU:HD13	1:EQ:60:MET:HG3	1.74	0.68
1:ET:45:LEU:HD13	1:ET:60:MET:HG3	1.75	0.68
1:AN:124:TYR:HA	1:FR:22:GLN:NE2	2.08	0.68
1:AQ:22:GLN:HB3	1:BU:124:TYR:HB2	1.75	0.68
1:BZ:45:LEU:HD13	1:BZ:60:MET:HG3	1.74	0.68
1:CF:45:LEU:HD13	1:CF:60:MET:HG3	1.74	0.68
1:CX:10:VAL:HG21	1:DK:103:THR:HG22	1.74	0.68
1:DQ:89:PRO:HG2	1:DQ:92:TYR:HB2	1.75	0.68
1:DW:89:PRO:HG2	1:DW:92:TYR:HB2	1.75	0.68
1:FA:89:PRO:HG2	1:FA:92:TYR:HB2	1.75	0.68
1:FI:45:LEU:HD13	1:FI:60:MET:HG3	1.74	0.68
1:FP:89:PRO:HG2	1:FP:92:TYR:HB2	1.75	0.68
1:CV:89:PRO:HG2	1:CV:92:TYR:HB2	1.75	0.68
1:DN:89:PRO:HG2	1:DN:92:TYR:HB2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DV:45:LEU:HD13	1:DV:60:MET:HG3	1.74	0.68
1:EF:89:PRO:HG2	1:EF:92:TYR:HB2	1.75	0.68
1:EN:45:LEU:HD13	1:EN:60:MET:HG3	1.74	0.68
1:FJ:89:PRO:HG2	1:FJ:92:TYR:HB2	1.75	0.68
1:FY:89:PRO:HG2	1:FY:92:TYR:HB2	1.75	0.68
1:GW:89:PRO:HG2	1:GW:92:TYR:HB2	1.75	0.68
1:CJ:89:PRO:HG2	1:CJ:92:TYR:HB2	1.75	0.68
1:CX:45:LEU:HD13	1:CX:60:MET:HG3	1.74	0.68
1:DH:89:PRO:HG2	1:DH:92:TYR:HB2	1.75	0.68
1:EI:89:PRO:HG2	1:EI:92:TYR:HB2	1.75	0.68
1:FM:89:PRO:HG2	1:FM:92:TYR:HB2	1.75	0.68
1:FS:89:PRO:HG2	1:FS:92:TYR:HB2	1.75	0.68
1:GA:45:LEU:HD13	1:GA:60:MET:HG3	1.74	0.68
1:AE:89:PRO:HG2	1:AE:92:TYR:HB2	1.75	0.68
1:AS:45:LEU:HD13	1:AS:60:MET:HG3	1.75	0.68
1:DJ:45:LEU:HD13	1:DJ:60:MET:HG3	1.74	0.68
1:DT:89:PRO:HG2	1:DT:92:TYR:HB2	1.75	0.68
1:EB:103:THR:HG21	1:GB:15:ARG:NH1	2.09	0.68
1:EH:45:LEU:HD13	1:EH:60:MET:HG3	1.74	0.68
1:FX:45:LEU:HD13	1:FX:60:MET:HG3	1.74	0.68
1:AD:45:LEU:HD13	1:AD:60:MET:HG3	1.74	0.68
1:CP:10:VAL:HG21	1:DJ:103:THR:HG22	1.75	0.68
1:CR:45:LEU:HD13	1:CR:60:MET:HG3	1.74	0.68
1:ET:10:VAL:HG21	1:FG:103:THR:HG22	1.75	0.68
1:BA:15:ARG:HH11	1:EM:103:THR:HG21	1.57	0.68
1:CD:89:PRO:HG2	1:CD:92:TYR:HB2	1.75	0.68
1:CG:15:ARG:NH1	1:CL:103:THR:HG21	2.09	0.68
1:CM:124:TYR:OXT	1:DI:2:ARG:NH1	2.27	0.68
1:DV:99:LYS:HE2	1:GE:15:ARG:HH11	1.59	0.68
1:AB:89:PRO:HG2	1:AB:92:TYR:HB2	1.75	0.68
1:AQ:103:THR:HG22	1:FU:10:VAL:HG21	1.75	0.68
1:BI:89:PRO:HG2	1:BI:92:TYR:HB2	1.75	0.68
1:DM:45:LEU:HD13	1:DM:60:MET:HG3	1.74	0.68
1:DS:105:ILE:HG23	1:GQ:105:ILE:HG23	1.75	0.68
1:EZ:45:LEU:HD13	1:EZ:60:MET:HG3	1.74	0.68
1:AN:89:PRO:HG2	1:AN:92:TYR:HB2	1.75	0.68
1:BG:103:THR:HG22	1:ES:10:VAL:HG21	1.75	0.68
1:BU:89:PRO:HG2	1:BU:92:TYR:HB2	1.75	0.68
1:CW:15:ARG:HH11	1:GI:103:THR:HG21	1.57	0.68
1:DA:45:LEU:HD13	1:DA:60:MET:HG3	1.74	0.68
1:FD:89:PRO:HG2	1:FD:92:TYR:HB2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GB:89:PRO:HG2	1:GB:92:TYR:HB2	1.75	0.68
1:AB:103:THR:HG22	1:FX:10:VAL:HG21	1.74	0.68
1:AZ:105:ILE:HG23	1:EW:105:ILE:HG23	1.76	0.68
1:CU:10:VAL:HG21	1:DH:103:THR:HG22	1.75	0.68
1:DR:2:ARG:HH12	1:GW:124:TYR:C	1.97	0.68
1:EK:45:LEU:HD13	1:EK:60:MET:HG3	1.74	0.68
1:ER:89:PRO:HG2	1:ER:92:TYR:HB2	1.75	0.68
1:FL:45:LEU:HD13	1:FL:60:MET:HG3	1.74	0.68
1:BP:103:THR:HG21	1:FB:15:ARG:NH1	2.10	0.67
1:BY:103:THR:HG21	1:FK:15:ARG:HH11	1.59	0.67
1:CH:103:THR:HG21	1:FT:15:ARG:HH11	1.56	0.67
1:CU:45:LEU:HD13	1:CU:60:MET:HG3	1.74	0.67
1:FV:89:PRO:HG2	1:FV:92:TYR:HB2	1.75	0.67
1:AK:89:PRO:HG2	1:AK:92:TYR:HB2	1.75	0.67
1:AV:105:ILE:HG23	1:EF:105:ILE:HG23	1.74	0.67
1:CD:123:ASN:HB3	1:CR:3:LEU:HG	1.74	0.67
1:CO:45:LEU:HD13	1:CO:60:MET:HG3	1.75	0.67
1:DF:15:ARG:HH11	1:GR:103:THR:HG21	1.58	0.67
1:EB:105:ILE:HG23	1:GB:105:ILE:HG23	1.76	0.67
1:GQ:89:PRO:HG2	1:GQ:92:TYR:HB2	1.75	0.67
1:AP:105:ILE:HG23	1:BU:105:ILE:HG23	1.75	0.67
1:BK:45:LEU:HD13	1:BK:60:MET:HG3	1.74	0.67
1:BT:15:ARG:NH1	1:DN:103:THR:HG21	2.09	0.67
1:CB:15:ARG:NH1	1:FN:103:THR:HG21	2.09	0.67
1:CL:45:LEU:HD13	1:CL:60:MET:HG3	1.74	0.67
1:CN:10:VAL:HG21	1:FZ:103:THR:HG22	1.76	0.67
1:BE:45:LEU:HD13	1:BE:60:MET:HG3	1.74	0.67
1:BR:89:PRO:HG2	1:BR:92:TYR:HB2	1.75	0.67
1:CC:45:LEU:HD13	1:CC:60:MET:HG3	1.75	0.67
1:DC:20:SER:O	1:GJ:122:ASN:HB2	1.95	0.67
1:ES:2:ARG:NH1	1:FM:124:TYR:OXT	2.26	0.67
1:FC:45:LEU:HD13	1:FC:60:MET:HG3	1.74	0.67
1:FG:89:PRO:HG2	1:FG:92:TYR:HB2	1.75	0.67
1:BD:103:THR:HG21	1:EP:15:ARG:HH11	1.60	0.67
1:CM:89:PRO:HG2	1:CM:92:TYR:HB2	1.75	0.67
1:DB:124:TYR:OXT	1:GL:2:ARG:NH1	2.28	0.67
1:AH:89:PRO:HG2	1:AH:92:TYR:HB2	1.75	0.67
1:BD:91:THR:CG2	1:EP:68:VAL:HG11	2.24	0.67
1:BX:89:PRO:HG2	1:BX:92:TYR:HB2	1.75	0.67
1:CS:10:VAL:HG21	1:DD:103:THR:HG22	1.76	0.67
1:CX:20:SER:HA	1:GL:121:LEU:HD22	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:89:PRO:HG2	1:AQ:92:TYR:HB2	1.75	0.67
1:BY:15:ARG:HH11	1:FK:103:THR:HG21	1.60	0.67
1:CK:103:THR:HG21	1:FW:15:ARG:HH11	1.60	0.67
1:GP:45:LEU:HD13	1:GP:60:MET:HG3	1.74	0.67
1:AU:2:ARG:HH12	1:EL:124:TYR:C	1.98	0.67
1:BD:107:TRP:CE2	1:EP:8:LEU:HD11	2.30	0.67
1:BE:10:VAL:HG21	1:BL:103:THR:HG22	1.77	0.67
1:DB:89:PRO:HG2	1:DB:92:TYR:HB2	1.75	0.67
1:FD:124:TYR:C	1:FH:2:ARG:HH12	1.98	0.67
1:GK:89:PRO:HG2	1:GK:92:TYR:HB2	1.75	0.67
1:AI:15:ARG:HH11	1:DU:103:THR:HG21	1.59	0.67
1:BO:89:PRO:HG2	1:BO:92:TYR:HB2	1.75	0.67
1:BS:103:THR:HG21	1:FE:15:ARG:HH11	1.59	0.67
1:CM:15:ARG:NH1	1:DG:103:THR:HG21	2.10	0.67
1:CP:89:PRO:HG2	1:CP:92:TYR:HB2	1.75	0.67
1:AZ:89:PRO:HG2	1:AZ:92:TYR:HB2	1.75	0.67
1:BF:89:PRO:HG2	1:BF:92:TYR:HB2	1.75	0.67
1:CY:124:TYR:C	1:GI:2:ARG:HH12	1.98	0.67
1:BS:103:THR:HG21	1:FE:15:ARG:NH1	2.10	0.66
1:FA:124:TYR:C	1:FN:2:ARG:HH12	1.99	0.66
1:GT:89:PRO:HG2	1:GT:92:TYR:HB2	1.75	0.66
1:BI:65:PRO:HB3	1:BI:79:LYS:HG2	1.78	0.66
1:BP:15:ARG:NH1	1:FB:103:THR:HG21	2.09	0.66
1:EX:65:PRO:HB3	1:EX:79:LYS:HG2	1.78	0.66
1:CB:105:ILE:HG23	1:FN:105:ILE:HG23	1.77	0.66
1:CG:65:PRO:HB3	1:CG:79:LYS:HG2	1.78	0.66
1:CG:105:ILE:HG23	1:CL:105:ILE:HG23	1.77	0.66
1:CV:62:LEU:HD21	1:GM:103:THR:OG1	1.94	0.66
1:EF:65:PRO:HB3	1:EF:79:LYS:HG2	1.78	0.66
1:BB:3:LEU:HG	1:BR:123:ASN:HB3	1.77	0.66
1:CJ:103:THR:HG22	1:CO:10:VAL:HG21	1.76	0.66
1:FD:10:VAL:HG21	1:FF:103:THR:HG22	1.76	0.66
1:GN:89:PRO:HG2	1:GN:92:TYR:HB2	1.75	0.66
1:AH:103:THR:HG22	1:GD:10:VAL:HG21	1.76	0.66
1:CM:65:PRO:HB3	1:CM:79:LYS:HG2	1.78	0.66
1:CV:65:PRO:HB3	1:CV:79:LYS:HG2	1.78	0.66
1:DZ:89:PRO:HG2	1:DZ:92:TYR:HB2	1.75	0.66
1:EO:89:PRO:HG2	1:EO:92:TYR:HB2	1.75	0.66
1:GW:65:PRO:HB3	1:GW:79:LYS:HG2	1.78	0.66
1:AA:10:VAL:HG21	1:BI:103:THR:HG22	1.76	0.66
1:AB:65:PRO:HB3	1:AB:79:LYS:HG2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:91:THR:HG22	1:DU:68:VAL:HG11	1.77	0.66
1:AP:103:THR:HG21	1:BU:15:ARG:NH1	2.11	0.66
1:BP:103:THR:HG21	1:FB:15:ARG:HH11	1.59	0.66
1:DE:89:PRO:HG2	1:DE:92:TYR:HB2	1.75	0.66
1:DI:103:THR:HG21	1:GU:15:ARG:HH11	1.58	0.66
1:FM:65:PRO:HB3	1:FM:79:LYS:HG2	1.78	0.66
1:FP:65:PRO:HB3	1:FP:79:LYS:HG2	1.78	0.66
1:AQ:65:PRO:HB3	1:AQ:79:LYS:HG2	1.78	0.66
1:BO:65:PRO:HB3	1:BO:79:LYS:HG2	1.78	0.66
1:DU:2:ARG:NH1	1:GQ:124:TYR:OXT	2.29	0.66
1:DW:22:GLN:HB3	1:GE:124:TYR:HB2	1.77	0.66
1:EC:65:PRO:HB3	1:EC:79:LYS:HG2	1.78	0.66
1:EH:105:ILE:HG23	1:EO:105:ILE:HG23	1.76	0.66
1:EL:89:PRO:HG2	1:EL:92:TYR:HB2	1.75	0.66
1:EU:20:SER:O	1:FG:122:ASN:HB2	1.96	0.66
1:FS:65:PRO:HB3	1:FS:79:LYS:HG2	1.78	0.66
1:GE:65:PRO:HB3	1:GE:79:LYS:HG2	1.78	0.66
1:GK:65:PRO:HB3	1:GK:79:LYS:HG2	1.78	0.66
1:AE:65:PRO:HB3	1:AE:79:LYS:HG2	1.78	0.66
1:AH:65:PRO:HB3	1:AH:79:LYS:HG2	1.78	0.66
1:CD:65:PRO:HB3	1:CD:79:LYS:HG2	1.78	0.66
1:DK:65:PRO:HB3	1:DK:79:LYS:HG2	1.78	0.66
1:EU:65:PRO:HB3	1:EU:79:LYS:HG2	1.78	0.66
1:GH:65:PRO:HB3	1:GH:79:LYS:HG2	1.78	0.66
1:AD:103:THR:OG1	1:BC:62:LEU:HD21	1.95	0.66
1:AT:65:PRO:HB3	1:AT:79:LYS:HG2	1.78	0.66
1:AV:107:TRP:CE2	1:EF:8:LEU:HD11	2.30	0.66
1:BD:15:ARG:NH1	1:EP:103:THR:HG21	2.11	0.66
1:BF:65:PRO:HB3	1:BF:79:LYS:HG2	1.78	0.66
1:CS:65:PRO:HB3	1:CS:79:LYS:HG2	1.78	0.66
1:CV:22:GLN:NE2	1:GM:124:TYR:OXT	2.29	0.66
1:EI:65:PRO:HB3	1:EI:79:LYS:HG2	1.78	0.66
1:FA:103:THR:HG22	1:FL:10:VAL:HG21	1.78	0.66
1:FV:65:PRO:HB3	1:FV:79:LYS:HG2	1.78	0.66
1:AE:8:LEU:HD22	1:GA:106:ALA:HB1	1.76	0.66
1:AN:103:THR:HG21	1:FR:15:ARG:NH1	2.05	0.66
1:AW:65:PRO:HB3	1:AW:79:LYS:HG2	1.78	0.66
1:BX:65:PRO:HB3	1:BX:79:LYS:HG2	1.78	0.66
1:CK:103:THR:HG21	1:FW:15:ARG:NH1	2.11	0.66
1:DL:15:ARG:NH1	1:GX:103:THR:HG21	2.11	0.66
1:DZ:65:PRO:HB3	1:DZ:79:LYS:HG2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:122:ASN:HB2	1:BD:20:SER:O	1.95	0.65
1:AE:124:TYR:HB2	1:GB:22:GLN:HB3	1.77	0.65
1:AK:65:PRO:HB3	1:AK:79:LYS:HG2	1.78	0.65
1:AX:103:THR:HG21	1:EJ:15:ARG:NH1	2.10	0.65
1:BD:103:THR:HG22	1:EP:10:VAL:CG2	2.26	0.65
1:CK:15:ARG:HH11	1:FW:103:THR:HG21	1.61	0.65
1:DN:65:PRO:HB3	1:DN:79:LYS:HG2	1.78	0.65
1:DQ:65:PRO:HB3	1:DQ:79:LYS:HG2	1.78	0.65
1:EO:65:PRO:HB3	1:EO:79:LYS:HG2	1.78	0.65
1:AV:123:ASN:OD1	1:EF:1:MET:HG2	1.96	0.65
1:BK:103:THR:HG21	1:DW:15:ARG:NH1	2.11	0.65
1:DF:15:ARG:NH1	1:GR:103:THR:HG21	2.12	0.65
1:AZ:15:ARG:NH1	1:EW:103:THR:HG21	2.11	0.65
1:BU:65:PRO:HB3	1:BU:79:LYS:HG2	1.78	0.65
1:FY:65:PRO:HB3	1:FY:79:LYS:HG2	1.78	0.65
1:AB:124:TYR:C	1:FZ:2:ARG:HH12	1.99	0.65
1:BM:15:ARG:HH11	1:EY:103:THR:HG21	1.61	0.65
1:CA:65:PRO:HB3	1:CA:79:LYS:HG2	1.78	0.65
1:CM:105:ILE:HG23	1:DG:105:ILE:HG23	1.79	0.65
1:AJ:103:THR:HG22	1:BX:10:VAL:HG21	1.78	0.65
1:BL:65:PRO:HB3	1:BL:79:LYS:HG2	1.78	0.65
1:CC:103:THR:HG22	1:GK:10:VAL:HG21	1.78	0.65
1:DB:62:LEU:HD21	1:GJ:103:THR:OG1	1.97	0.65
1:DV:15:ARG:NH1	1:GE:103:THR:HG21	2.09	0.65
1:GT:65:PRO:HB3	1:GT:79:LYS:HG2	1.78	0.65
1:AM:10:VAL:HG21	1:CA:103:THR:HG22	1.78	0.65
1:BY:10:VAL:HG21	1:FK:103:THR:HG22	1.78	0.65
1:CE:15:ARG:HH11	1:FQ:103:THR:HG21	1.61	0.65
1:CY:103:THR:HG21	1:GG:15:ARG:NH1	2.08	0.65
1:DC:10:VAL:HG21	1:GO:103:THR:HG22	1.77	0.65
1:DT:65:PRO:HB3	1:DT:79:LYS:HG2	1.78	0.65
1:AF:15:ARG:HH11	1:DR:103:THR:HG21	1.62	0.65
1:AZ:65:PRO:HB3	1:AZ:79:LYS:HG2	1.78	0.65
1:BZ:96:HIS:CG	1:DT:66:VAL:HG21	2.32	0.65
1:CN:15:ARG:HH11	1:FZ:103:THR:HG21	1.61	0.65
1:DC:107:TRP:CE2	1:GO:8:LEU:HD11	2.31	0.65
1:FJ:65:PRO:HB3	1:FJ:79:LYS:HG2	1.78	0.65
1:BP:2:ARG:HH12	1:DZ:124:TYR:C	2.01	0.65
1:CV:66:VAL:HG21	1:GM:96:HIS:CG	2.32	0.65
1:EH:10:VAL:HG21	1:EO:103:THR:HG22	1.79	0.65
1:BB:10:VAL:HG21	1:BR:103:THR:HG22	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:58:VAL:HG11	1:DW:117:VAL:HG22	1.79	0.65
1:AC:15:ARG:NH1	1:DO:103:THR:HG21	2.12	0.64
1:CP:65:PRO:HB3	1:CP:79:LYS:HG2	1.78	0.64
1:EL:65:PRO:HB3	1:EL:79:LYS:HG2	1.78	0.64
1:AF:20:SER:O	1:GA:122:ASN:HB2	1.97	0.64
1:AN:22:GLN:HB3	1:CA:124:TYR:HB2	1.78	0.64
1:AN:65:PRO:HB3	1:AN:79:LYS:HG2	1.78	0.64
1:AV:10:VAL:HG21	1:EF:103:THR:HG22	1.78	0.64
1:AZ:103:THR:HG21	1:EW:15:ARG:NH1	2.09	0.64
1:BZ:99:LYS:HE2	1:DT:15:ARG:HH11	1.61	0.64
1:DH:65:PRO:HB3	1:DH:79:LYS:HG2	1.78	0.64
1:ER:65:PRO:HB3	1:ER:79:LYS:HG2	1.78	0.64
1:AC:2:ARG:NH1	1:BI:124:TYR:OXT	2.30	0.64
1:AT:10:VAL:HG21	1:EZ:103:THR:HG22	1.78	0.64
1:DE:65:PRO:HB3	1:DE:79:LYS:HG2	1.78	0.64
1:FG:65:PRO:HB3	1:FG:79:LYS:HG2	1.78	0.64
1:BR:65:PRO:HB3	1:BR:79:LYS:HG2	1.78	0.64
1:CS:103:THR:HG22	1:DD:10:VAL:HG21	1.79	0.64
1:DW:65:PRO:HB3	1:DW:79:LYS:HG2	1.78	0.64
1:AE:111:GLN:HB2	1:GA:1:MET:SD	2.36	0.64
1:CD:15:ARG:NH1	1:CR:103:THR:HG21	2.11	0.64
1:CV:15:ARG:HH11	1:GM:99:LYS:HE2	1.61	0.64
1:AI:2:ARG:NH1	1:BF:124:TYR:OXT	2.31	0.64
1:GQ:65:PRO:HB3	1:GQ:79:LYS:HG2	1.78	0.64
1:CD:105:ILE:HG23	1:CR:105:ILE:HG23	1.79	0.64
1:CJ:65:PRO:HB3	1:CJ:79:LYS:HG2	1.78	0.64
1:CF:15:ARG:NH1	1:GN:103:THR:HG21	2.10	0.64
1:CY:65:PRO:HB3	1:CY:79:LYS:HG2	1.78	0.64
1:DB:65:PRO:HB3	1:DB:79:LYS:HG2	1.78	0.64
1:FA:65:PRO:HB3	1:FA:79:LYS:HG2	1.78	0.64
1:FD:65:PRO:HB3	1:FD:79:LYS:HG2	1.78	0.64
1:AC:15:ARG:HH11	1:DO:103:THR:HG21	1.63	0.64
1:AX:2:ARG:HH12	1:EF:124:TYR:C	2.00	0.64
1:BC:65:PRO:HB3	1:BC:79:LYS:HG2	1.78	0.64
1:GB:65:PRO:HB3	1:GB:79:LYS:HG2	1.78	0.64
1:BS:15:ARG:HH11	1:FE:103:THR:HG21	1.61	0.64
1:BZ:122:ASN:HB2	1:DU:20:SER:O	1.98	0.64
1:CD:8:LEU:HD11	1:CR:107:TRP:CE2	2.33	0.64
1:DV:106:ALA:HB1	1:GE:8:LEU:HD22	1.78	0.64
1:CY:15:ARG:NH1	1:GG:103:THR:HG21	2.13	0.63
1:AH:67:VAL:HG22	1:AH:77:THR:HG22	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:67:VAL:HG22	1:BC:77:THR:HG22	1.81	0.63
1:CW:103:THR:HG21	1:GI:15:ARG:HH11	1.62	0.63
1:DW:67:VAL:HG22	1:DW:77:THR:HG22	1.81	0.63
1:AB:67:VAL:HG22	1:AB:77:THR:HG22	1.81	0.63
1:AK:124:TYR:C	1:FQ:2:ARG:HH12	2.01	0.63
1:BI:67:VAL:HG22	1:BI:77:THR:HG22	1.81	0.63
1:BU:67:VAL:HG22	1:BU:77:THR:HG22	1.81	0.63
1:CS:67:VAL:HG22	1:CS:77:THR:HG22	1.81	0.63
1:FA:67:VAL:HG22	1:FA:77:THR:HG22	1.81	0.63
1:GN:65:PRO:HB3	1:GN:79:LYS:HG2	1.78	0.63
1:AN:67:VAL:HG22	1:AN:77:THR:HG22	1.81	0.63
1:AZ:67:VAL:HG22	1:AZ:77:THR:HG22	1.81	0.63
1:BH:20:SER:HA	1:EV:121:LEU:HD22	1.80	0.63
1:CV:103:THR:HG22	1:GM:10:VAL:HG21	1.81	0.63
1:DH:67:VAL:HG22	1:DH:77:THR:HG22	1.81	0.63
1:DP:3:LEU:HG	1:GW:123:ASN:HB3	1.79	0.63
1:DY:10:VAL:HG21	1:FY:103:THR:HG22	1.79	0.63
1:FM:67:VAL:HG22	1:FM:77:THR:HG22	1.81	0.63
1:BH:124:TYR:OXT	1:BO:22:GLN:NE2	2.30	0.63
1:BS:15:ARG:NH1	1:FE:103:THR:HG21	2.13	0.63
1:CD:1:MET:HG2	1:CR:123:ASN:OD1	1.99	0.63
1:DQ:67:VAL:HG22	1:DQ:77:THR:HG22	1.81	0.63
1:DV:10:VAL:HG21	1:GE:103:THR:HG22	1.79	0.63
1:EK:15:ARG:NH1	1:ER:103:THR:HG21	2.13	0.63
1:FD:67:VAL:HG22	1:FD:77:THR:HG22	1.81	0.63
1:FY:67:VAL:HG22	1:FY:77:THR:HG22	1.81	0.63
1:GQ:67:VAL:HG22	1:GQ:77:THR:HG22	1.81	0.63
1:AM:106:ALA:HB1	1:CA:8:LEU:HD22	1.81	0.63
1:AS:89:PRO:HG2	1:AS:92:TYR:HB2	1.81	0.63
1:BK:89:PRO:HG2	1:BK:92:TYR:HB2	1.81	0.63
1:BZ:89:PRO:HG2	1:BZ:92:TYR:HB2	1.81	0.63
1:DM:89:PRO:HG2	1:DM:92:TYR:HB2	1.81	0.63
1:DN:67:VAL:HG22	1:DN:77:THR:HG22	1.81	0.63
1:FJ:67:VAL:HG22	1:FJ:77:THR:HG22	1.81	0.63
1:AA:89:PRO:HG2	1:AA:92:TYR:HB2	1.81	0.63
1:AM:122:ASN:HB2	1:CB:20:SER:O	1.98	0.63
1:BO:67:VAL:HG22	1:BO:77:THR:HG22	1.81	0.63
1:BY:15:ARG:NH1	1:FK:103:THR:HG21	2.14	0.63
1:CC:89:PRO:HG2	1:CC:92:TYR:HB2	1.81	0.63
1:CH:89:PRO:HG2	1:CH:92:TYR:HB2	1.81	0.63
1:CK:10:VAL:HG21	1:FW:103:THR:HG22	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:67:VAL:HG22	1:CP:77:THR:HG22	1.81	0.63
1:CQ:89:PRO:HG2	1:CQ:92:TYR:HB2	1.81	0.63
1:DB:122:ASN:HB2	1:GK:20:SER:O	1.99	0.63
1:DD:89:PRO:HG2	1:DD:92:TYR:HB2	1.81	0.63
1:EC:67:VAL:HG22	1:EC:77:THR:HG22	1.81	0.63
1:EH:89:PRO:HG2	1:EH:92:TYR:HB2	1.81	0.63
1:EY:89:PRO:HG2	1:EY:92:TYR:HB2	1.81	0.63
1:GE:67:VAL:HG22	1:GE:77:THR:HG22	1.81	0.63
1:AC:103:THR:HG21	1:DO:15:ARG:NH1	2.14	0.63
1:AK:67:VAL:HG22	1:AK:77:THR:HG22	1.81	0.63
1:AQ:124:TYR:OXT	1:FW:2:ARG:NH1	2.32	0.63
1:AV:89:PRO:HG2	1:AV:92:TYR:HB2	1.81	0.63
1:AW:10:VAL:HG21	1:FC:103:THR:HG22	1.79	0.63
1:BD:89:PRO:HG2	1:BD:92:TYR:HB2	1.81	0.63
1:BX:67:VAL:HG22	1:BX:77:THR:HG22	1.81	0.63
1:CU:89:PRO:HG2	1:CU:92:TYR:HB2	1.81	0.63
1:DS:103:THR:HG21	1:GQ:15:ARG:NH1	2.14	0.63
1:FB:89:PRO:HG2	1:FB:92:TYR:HB2	1.81	0.63
1:FH:89:PRO:HG2	1:FH:92:TYR:HB2	1.81	0.63
1:FI:89:PRO:HG2	1:FI:92:TYR:HB2	1.81	0.63
1:FK:89:PRO:HG2	1:FK:92:TYR:HB2	1.81	0.63
1:FT:89:PRO:HG2	1:FT:92:TYR:HB2	1.81	0.63
1:GM:89:PRO:HG2	1:GM:92:TYR:HB2	1.81	0.63
1:GR:89:PRO:HG2	1:GR:92:TYR:HB2	1.81	0.63
1:GS:89:PRO:HG2	1:GS:92:TYR:HB2	1.81	0.63
1:GT:67:VAL:HG22	1:GT:77:THR:HG22	1.81	0.63
1:AD:89:PRO:HG2	1:AD:92:TYR:HB2	1.81	0.63
1:AF:89:PRO:HG2	1:AF:92:TYR:HB2	1.81	0.63
1:AO:89:PRO:HG2	1:AO:92:TYR:HB2	1.81	0.63
1:BH:89:PRO:HG2	1:BH:92:TYR:HB2	1.81	0.63
1:BS:89:PRO:HG2	1:BS:92:TYR:HB2	1.81	0.63
1:CF:89:PRO:HG2	1:CF:92:TYR:HB2	1.81	0.63
1:CI:89:PRO:HG2	1:CI:92:TYR:HB2	1.81	0.63
1:CJ:67:VAL:HG22	1:CJ:77:THR:HG22	1.81	0.63
1:CP:124:TYR:C	1:DL:2:ARG:HH12	2.02	0.63
1:DF:103:THR:HG21	1:GR:15:ARG:HH11	1.62	0.63
1:EN:96:HIS:CG	1:FJ:66:VAL:HG21	2.33	0.63
1:GA:89:PRO:HG2	1:GA:92:TYR:HB2	1.81	0.63
1:GG:89:PRO:HG2	1:GG:92:TYR:HB2	1.81	0.63
1:GN:67:VAL:HG22	1:GN:77:THR:HG22	1.81	0.63
1:AR:89:PRO:HG2	1:AR:92:TYR:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:89:PRO:HG2	1:AX:92:TYR:HB2	1.81	0.62
1:CG:67:VAL:HG22	1:CG:77:THR:HG22	1.81	0.62
1:CT:91:THR:HG22	1:GF:68:VAL:HG11	1.81	0.62
1:CY:67:VAL:HG22	1:CY:77:THR:HG22	1.81	0.62
1:DF:89:PRO:HG2	1:DF:92:TYR:HB2	1.81	0.62
1:DK:67:VAL:HG22	1:DK:77:THR:HG22	1.81	0.62
1:DL:103:THR:HG21	1:GX:15:ARG:HH11	1.64	0.62
1:DS:3:LEU:HG	1:GQ:123:ASN:HB3	1.81	0.62
1:DV:103:THR:OG1	1:GE:62:LEU:HD21	1.99	0.62
1:FF:89:PRO:HG2	1:FF:92:TYR:HB2	1.81	0.62
1:FS:67:VAL:HG22	1:FS:77:THR:HG22	1.81	0.62
1:GI:89:PRO:HG2	1:GI:92:TYR:HB2	1.81	0.62
1:AT:67:VAL:HG22	1:AT:77:THR:HG22	1.81	0.62
1:BZ:10:VAL:HG21	1:DT:103:THR:HG22	1.81	0.62
1:CA:67:VAL:HG22	1:CA:77:THR:HG22	1.81	0.62
1:CD:67:VAL:HG22	1:CD:77:THR:HG22	1.81	0.62
1:CQ:103:THR:HG21	1:GC:15:ARG:HH11	1.63	0.62
1:DC:89:PRO:HG2	1:DC:92:TYR:HB2	1.81	0.62
1:EG:89:PRO:HG2	1:EG:92:TYR:HB2	1.81	0.62
1:EO:67:VAL:HG22	1:EO:77:THR:HG22	1.81	0.62
1:FU:89:PRO:HG2	1:FU:92:TYR:HB2	1.81	0.62
1:AU:89:PRO:HG2	1:AU:92:TYR:HB2	1.81	0.62
1:CJ:103:THR:HG21	1:CO:15:ARG:NH1	2.12	0.62
1:EB:89:PRO:HG2	1:EB:92:TYR:HB2	1.81	0.62
1:EH:103:THR:OG1	1:EO:62:LEU:HD21	1.99	0.62
1:EX:67:VAL:HG22	1:EX:77:THR:HG22	1.81	0.62
1:GH:67:VAL:HG22	1:GH:77:THR:HG22	1.81	0.62
1:GL:89:PRO:HG2	1:GL:92:TYR:HB2	1.81	0.62
1:GW:67:VAL:HG22	1:GW:77:THR:HG22	1.81	0.62
1:AC:91:THR:HG22	1:DO:68:VAL:HG11	1.81	0.62
1:BF:67:VAL:HG22	1:BF:77:THR:HG22	1.81	0.62
1:BR:67:VAL:HG22	1:BR:77:THR:HG22	1.81	0.62
1:CE:89:PRO:HG2	1:CE:92:TYR:HB2	1.81	0.62
1:CK:89:PRO:HG2	1:CK:92:TYR:HB2	1.81	0.62
1:CX:89:PRO:HG2	1:CX:92:TYR:HB2	1.81	0.62
1:DL:89:PRO:HG2	1:DL:92:TYR:HB2	1.81	0.62
1:EE:89:PRO:HG2	1:EE:92:TYR:HB2	1.81	0.62
1:GX:89:PRO:HG2	1:GX:92:TYR:HB2	1.81	0.62
1:AE:67:VAL:HG22	1:AE:77:THR:HG22	1.81	0.62
1:AE:103:THR:HG22	1:GA:10:VAL:HG21	1.80	0.62
1:BB:105:ILE:HG23	1:BR:105:ILE:HG23	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:89:PRO:HG2	1:DA:92:TYR:HB2	1.81	0.62
1:DM:103:THR:OG1	1:GT:62:LEU:HD21	1.99	0.62
1:EI:67:VAL:HG22	1:EI:77:THR:HG22	1.81	0.62
1:EM:89:PRO:HG2	1:EM:92:TYR:HB2	1.81	0.62
1:ET:89:PRO:HG2	1:ET:92:TYR:HB2	1.81	0.62
1:FG:67:VAL:HG22	1:FG:77:THR:HG22	1.81	0.62
1:FN:89:PRO:HG2	1:FN:92:TYR:HB2	1.81	0.62
1:FX:89:PRO:HG2	1:FX:92:TYR:HB2	1.81	0.62
1:AJ:89:PRO:HG2	1:AJ:92:TYR:HB2	1.81	0.62
1:BA:89:PRO:HG2	1:BA:92:TYR:HB2	1.81	0.62
1:BG:2:ARG:NH1	1:BL:124:TYR:OXT	2.32	0.62
1:BK:1:MET:SD	1:DW:111:GLN:HB2	2.39	0.62
1:BN:89:PRO:HG2	1:BN:92:TYR:HB2	1.81	0.62
1:BT:99:LYS:HE2	1:DN:15:ARG:HH11	1.64	0.62
1:CT:89:PRO:HG2	1:CT:92:TYR:HB2	1.81	0.62
1:CW:89:PRO:HG2	1:CW:92:TYR:HB2	1.81	0.62
1:DU:89:PRO:HG2	1:DU:92:TYR:HB2	1.81	0.62
1:EP:89:PRO:HG2	1:EP:92:TYR:HB2	1.81	0.62
1:EU:67:VAL:HG22	1:EU:77:THR:HG22	1.81	0.62
1:FP:67:VAL:HG22	1:FP:77:THR:HG22	1.81	0.62
1:AL:89:PRO:HG2	1:AL:92:TYR:HB2	1.81	0.62
1:AM:89:PRO:HG2	1:AM:92:TYR:HB2	1.81	0.62
1:AP:58:VAL:HG11	1:BU:117:VAL:HG22	1.81	0.62
1:AY:89:PRO:HG2	1:AY:92:TYR:HB2	1.81	0.62
1:CK:15:ARG:NH1	1:FW:103:THR:HG21	2.14	0.62
1:CX:103:THR:HG22	1:DK:10:VAL:HG21	1.82	0.62
1:DS:89:PRO:HG2	1:DS:92:TYR:HB2	1.81	0.62
1:DV:1:MET:SD	1:GE:111:GLN:HB2	2.40	0.62
1:DY:89:PRO:HG2	1:DY:92:TYR:HB2	1.81	0.62
1:AO:19:VAL:O	1:FR:121:LEU:HD11	1.99	0.62
1:BK:102:GLN:HB2	1:DW:10:VAL:HG13	1.80	0.62
1:CM:28:ARG:HG2	1:CM:44:SER:HB3	1.82	0.62
1:DP:89:PRO:HG2	1:DP:92:TYR:HB2	1.81	0.62
1:DR:89:PRO:HG2	1:DR:92:TYR:HB2	1.81	0.62
1:EA:89:PRO:HG2	1:EA:92:TYR:HB2	1.81	0.62
1:EK:10:VAL:HG21	1:ER:103:THR:HG22	1.82	0.62
1:EK:89:PRO:HG2	1:EK:92:TYR:HB2	1.81	0.62
1:EQ:89:PRO:HG2	1:EQ:92:TYR:HB2	1.81	0.62
1:EZ:89:PRO:HG2	1:EZ:92:TYR:HB2	1.81	0.62
1:FZ:89:PRO:HG2	1:FZ:92:TYR:HB2	1.81	0.62
1:GF:89:PRO:HG2	1:GF:92:TYR:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:10:VAL:HG21	1:EY:103:THR:HG22	1.80	0.62
1:BM:89:PRO:HG2	1:BM:92:TYR:HB2	1.81	0.62
1:BV:89:PRO:HG2	1:BV:92:TYR:HB2	1.81	0.62
1:BY:89:PRO:HG2	1:BY:92:TYR:HB2	1.81	0.62
1:CK:2:ARG:NH1	1:GH:124:TYR:OXT	2.33	0.62
1:DC:91:THR:HG22	1:GO:68:VAL:HG11	1.81	0.62
1:DF:103:THR:HG22	1:GR:10:VAL:HG21	1.81	0.62
1:DH:28:ARG:HG2	1:DH:44:SER:HB3	1.82	0.62
1:EF:67:VAL:HG22	1:EF:77:THR:HG22	1.81	0.62
1:EH:103:THR:HG21	1:EO:15:ARG:NH1	2.14	0.62
1:EL:28:ARG:HG2	1:EL:44:SER:HB3	1.82	0.62
1:FC:89:PRO:HG2	1:FC:92:TYR:HB2	1.81	0.62
1:FR:89:PRO:HG2	1:FR:92:TYR:HB2	1.81	0.62
1:FS:28:ARG:HG2	1:FS:44:SER:HB3	1.82	0.62
1:FV:28:ARG:HG2	1:FV:44:SER:HB3	1.82	0.62
1:FV:67:VAL:HG22	1:FV:77:THR:HG22	1.81	0.62
1:AH:28:ARG:HG2	1:AH:44:SER:HB3	1.82	0.62
1:AN:117:VAL:HG22	1:FR:58:VAL:HG11	1.82	0.62
1:AZ:28:ARG:HG2	1:AZ:44:SER:HB3	1.82	0.62
1:BR:28:ARG:HG2	1:BR:44:SER:HB3	1.82	0.62
1:BU:28:ARG:HG2	1:BU:44:SER:HB3	1.82	0.62
1:CD:28:ARG:HG2	1:CD:44:SER:HB3	1.82	0.62
1:CY:28:ARG:HG2	1:CY:44:SER:HB3	1.82	0.62
1:DL:103:THR:HG21	1:GX:15:ARG:NH1	2.13	0.62
1:DN:28:ARG:HG2	1:DN:44:SER:HB3	1.82	0.62
1:DT:28:ARG:HG2	1:DT:44:SER:HB3	1.82	0.62
1:EO:28:ARG:HG2	1:EO:44:SER:HB3	1.82	0.62
1:FG:28:ARG:HG2	1:FG:44:SER:HB3	1.82	0.62
1:GV:89:PRO:HG2	1:GV:92:TYR:HB2	1.81	0.62
1:AG:89:PRO:HG2	1:AG:92:TYR:HB2	1.81	0.61
1:AI:89:PRO:HG2	1:AI:92:TYR:HB2	1.81	0.61
1:CM:67:VAL:HG22	1:CM:77:THR:HG22	1.81	0.61
1:DK:28:ARG:HG2	1:DK:44:SER:HB3	1.82	0.61
1:EF:28:ARG:HG2	1:EF:44:SER:HB3	1.82	0.61
1:EJ:89:PRO:HG2	1:EJ:92:TYR:HB2	1.81	0.61
1:EX:28:ARG:HG2	1:EX:44:SER:HB3	1.82	0.61
1:GB:28:ARG:HG2	1:GB:44:SER:HB3	1.82	0.61
1:GB:67:VAL:HG22	1:GB:77:THR:HG22	1.81	0.61
1:GD:67:VAL:HG22	1:GD:77:THR:HG22	1.82	0.61
1:AN:22:GLN:HE21	1:FR:124:TYR:HA	1.63	0.61
1:AQ:67:VAL:HG22	1:AQ:77:THR:HG22	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:67:VAL:HG22	1:AW:77:THR:HG22	1.81	0.61
1:AY:58:VAL:HG11	1:EI:117:VAL:HG22	1.81	0.61
1:BN:67:VAL:HG22	1:BN:77:THR:HG22	1.83	0.61
1:BW:67:VAL:HG22	1:BW:77:THR:HG22	1.82	0.61
1:CF:67:VAL:HG22	1:CF:77:THR:HG22	1.82	0.61
1:CI:67:VAL:HG22	1:CI:77:THR:HG22	1.82	0.61
1:DB:67:VAL:HG22	1:DB:77:THR:HG22	1.81	0.61
1:DS:67:VAL:HG22	1:DS:77:THR:HG22	1.82	0.61
1:DY:67:VAL:HG22	1:DY:77:THR:HG22	1.82	0.61
1:DZ:67:VAL:HG22	1:DZ:77:THR:HG22	1.81	0.61
1:GG:67:VAL:HG22	1:GG:77:THR:HG22	1.83	0.61
1:GN:28:ARG:HG2	1:GN:44:SER:HB3	1.82	0.61
1:AE:22:GLN:HE21	1:GA:124:TYR:C	2.02	0.61
1:AG:20:SER:HB3	1:AG:30:VAL:HG23	1.82	0.61
1:AV:67:VAL:HG22	1:AV:77:THR:HG22	1.83	0.61
1:AY:20:SER:HB3	1:AY:30:VAL:HG23	1.82	0.61
1:CC:67:VAL:HG22	1:CC:77:THR:HG22	1.82	0.61
1:CL:20:SER:HB3	1:CL:30:VAL:HG23	1.83	0.61
1:CV:67:VAL:HG22	1:CV:77:THR:HG22	1.81	0.61
1:DB:15:ARG:HH11	1:GJ:99:LYS:HE2	1.65	0.61
1:FO:89:PRO:HG2	1:FO:92:TYR:HB2	1.81	0.61
1:FU:67:VAL:HG22	1:FU:77:THR:HG22	1.82	0.61
1:GU:89:PRO:HG2	1:GU:92:TYR:HB2	1.81	0.61
1:AD:28:ARG:HG2	1:AD:44:SER:HB3	1.83	0.61
1:AS:20:SER:HB3	1:AS:30:VAL:HG23	1.83	0.61
1:BE:20:SER:HB3	1:BE:30:VAL:HG23	1.83	0.61
1:BE:89:PRO:HG2	1:BE:92:TYR:HB2	1.81	0.61
1:BK:20:SER:HB3	1:BK:30:VAL:HG23	1.83	0.61
1:BW:20:SER:HB3	1:BW:30:VAL:HG23	1.83	0.61
1:CJ:15:ARG:NH1	1:CO:103:THR:HG21	2.15	0.61
1:CP:103:THR:HG21	1:DJ:15:ARG:NH1	2.14	0.61
1:EE:20:SER:HB3	1:EE:30:VAL:HG23	1.83	0.61
1:ER:67:VAL:HG22	1:ER:77:THR:HG22	1.81	0.61
1:EW:67:VAL:HG22	1:EW:77:THR:HG22	1.83	0.61
1:FL:89:PRO:HG2	1:FL:92:TYR:HB2	1.81	0.61
1:GJ:20:SER:HB3	1:GJ:30:VAL:HG23	1.83	0.61
1:AJ:28:ARG:HG2	1:AJ:44:SER:HB3	1.83	0.61
1:AW:103:THR:HG22	1:FC:10:VAL:HG21	1.83	0.61
1:BK:67:VAL:HG22	1:BK:77:THR:HG22	1.83	0.61
1:BQ:89:PRO:HG2	1:BQ:92:TYR:HB2	1.81	0.61
1:CH:98:THR:HG22	1:FT:118:ASP:CG	2.20	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:20:SER:HB3	1:CI:30:VAL:HG23	1.83	0.61
1:CR:67:VAL:HG22	1:CR:77:THR:HG22	1.83	0.61
1:CZ:89:PRO:HG2	1:CZ:92:TYR:HB2	1.81	0.61
1:DO:89:PRO:HG2	1:DO:92:TYR:HB2	1.81	0.61
1:DV:89:PRO:HG2	1:DV:92:TYR:HB2	1.81	0.61
1:EK:67:VAL:HG22	1:EK:77:THR:HG22	1.83	0.61
1:EL:67:VAL:HG22	1:EL:77:THR:HG22	1.81	0.61
1:EN:89:PRO:HG2	1:EN:92:TYR:HB2	1.81	0.61
1:FC:20:SER:HB3	1:FC:30:VAL:HG23	1.82	0.61
1:FE:89:PRO:HG2	1:FE:92:TYR:HB2	1.81	0.61
1:FF:67:VAL:HG22	1:FF:77:THR:HG22	1.82	0.61
1:FQ:89:PRO:HG2	1:FQ:92:TYR:HB2	1.81	0.61
1:GK:67:VAL:HG22	1:GK:77:THR:HG22	1.81	0.61
1:GP:89:PRO:HG2	1:GP:92:TYR:HB2	1.81	0.61
1:BD:68:VAL:HG11	1:EP:91:THR:HG22	1.81	0.61
1:BG:89:PRO:HG2	1:BG:92:TYR:HB2	1.81	0.61
1:BL:67:VAL:HG22	1:BL:77:THR:HG22	1.81	0.61
1:BT:89:PRO:HG2	1:BT:92:TYR:HB2	1.81	0.61
1:CB:68:VAL:HG11	1:FN:91:THR:CG2	2.30	0.61
1:CF:103:THR:HG22	1:GN:10:VAL:HG21	1.82	0.61
1:CL:89:PRO:HG2	1:CL:92:TYR:HB2	1.81	0.61
1:CN:89:PRO:HG2	1:CN:92:TYR:HB2	1.81	0.61
1:CX:20:SER:HB3	1:CX:30:VAL:HG23	1.83	0.61
1:DA:28:ARG:HG2	1:DA:44:SER:HB3	1.83	0.61
1:DG:20:SER:HB3	1:DG:30:VAL:HG23	1.83	0.61
1:DJ:89:PRO:HG2	1:DJ:92:TYR:HB2	1.81	0.61
1:DV:116:PRO:O	1:GE:56:ARG:NH1	2.33	0.61
1:DW:28:ARG:HG2	1:DW:44:SER:HB3	1.82	0.61
1:EH:67:VAL:HG22	1:EH:77:THR:HG22	1.83	0.61
1:EH:122:ASN:HB2	1:EP:20:SER:O	1.99	0.61
1:EN:15:ARG:NH1	1:FJ:103:THR:HG21	2.14	0.61
1:EQ:28:ARG:HG2	1:EQ:44:SER:HB3	1.83	0.61
1:EW:20:SER:HB3	1:EW:30:VAL:HG23	1.82	0.61
1:FI:67:VAL:HG22	1:FI:77:THR:HG22	1.83	0.61
1:FW:89:PRO:HG2	1:FW:92:TYR:HB2	1.81	0.61
1:GG:20:SER:HB3	1:GG:30:VAL:HG23	1.83	0.61
1:GK:28:ARG:HG2	1:GK:44:SER:HB3	1.82	0.61
1:GO:89:PRO:HG2	1:GO:92:TYR:HB2	1.81	0.61
1:GP:20:SER:HB3	1:GP:30:VAL:HG23	1.82	0.61
1:AE:15:ARG:HD3	1:GA:99:LYS:HE2	1.82	0.61
1:AR:118:ASP:CG	1:ED:98:THR:HG22	2.21	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:67:VAL:HG22	1:AS:77:THR:HG22	1.83	0.61
1:AT:28:ARG:HG2	1:AT:44:SER:HB3	1.82	0.61
1:AV:28:ARG:HG2	1:AV:44:SER:HB3	1.83	0.61
1:AY:99:LYS:HE2	1:EI:15:ARG:HD3	1.82	0.61
1:BB:28:ARG:HG2	1:BB:44:SER:HB3	1.83	0.61
1:BW:89:PRO:HG2	1:BW:92:TYR:HB2	1.81	0.61
1:CA:28:ARG:HG2	1:CA:44:SER:HB3	1.82	0.61
1:CF:20:SER:HB3	1:CF:30:VAL:HG23	1.82	0.61
1:CN:1:MET:HE2	1:CN:3:LEU:HA	1.83	0.61
1:DA:20:SER:HB3	1:DA:30:VAL:HG23	1.82	0.61
1:DG:89:PRO:HG2	1:DG:92:TYR:HB2	1.81	0.61
1:DI:89:PRO:HG2	1:DI:92:TYR:HB2	1.81	0.61
1:DX:89:PRO:HG2	1:DX:92:TYR:HB2	1.81	0.61
1:EB:20:SER:HB3	1:EB:30:VAL:HG23	1.82	0.61
1:ET:67:VAL:HG22	1:ET:77:THR:HG22	1.83	0.61
1:EV:89:PRO:HG2	1:EV:92:TYR:HB2	1.81	0.61
1:FS:124:TYR:OXT	1:GR:2:ARG:NH1	2.34	0.61
1:GM:28:ARG:HG2	1:GM:44:SER:HB3	1.83	0.61
1:GP:67:VAL:HG22	1:GP:77:THR:HG22	1.82	0.61
1:AE:28:ARG:HG2	1:AE:44:SER:HB3	1.82	0.61
1:AY:102:GLN:HB2	1:EI:10:VAL:HG13	1.83	0.61
1:BB:20:SER:HB3	1:BB:30:VAL:HG23	1.83	0.61
1:BB:89:PRO:HG2	1:BB:92:TYR:HB2	1.81	0.61
1:BE:67:VAL:HG22	1:BE:77:THR:HG22	1.83	0.61
1:BJ:89:PRO:HG2	1:BJ:92:TYR:HB2	1.81	0.61
1:BN:28:ARG:HG2	1:BN:44:SER:HB3	1.83	0.61
1:BQ:20:SER:HB3	1:BQ:30:VAL:HG23	1.83	0.61
1:BQ:28:ARG:HG2	1:BQ:44:SER:HB3	1.83	0.61
1:BV:15:ARG:NH1	1:FH:103:THR:HG21	2.15	0.61
1:CI:103:THR:HG21	1:GH:15:ARG:NH1	2.15	0.61
1:DI:91:THR:HG22	1:GU:68:VAL:HG11	1.82	0.61
1:DM:20:SER:HB3	1:DM:30:VAL:HG23	1.83	0.61
1:DV:67:VAL:HG22	1:DV:77:THR:HG22	1.83	0.61
1:EN:10:VAL:HG21	1:FJ:103:THR:HG22	1.83	0.61
1:EW:89:PRO:HG2	1:EW:92:TYR:HB2	1.81	0.61
1:GD:89:PRO:HG2	1:GD:92:TYR:HB2	1.81	0.61
1:GS:20:SER:HB3	1:GS:30:VAL:HG23	1.82	0.61
1:AA:67:VAL:HG22	1:AA:77:THR:HG22	1.83	0.61
1:AD:20:SER:HB3	1:AD:30:VAL:HG23	1.82	0.61
1:AJ:20:SER:HB3	1:AJ:30:VAL:HG23	1.83	0.61
1:AP:28:ARG:HG2	1:AP:44:SER:HB3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:67:VAL:HG22	1:BB:77:THR:HG22	1.82	0.61
1:BE:3:LEU:HG	1:BL:123:ASN:HB3	1.81	0.61
1:BE:28:ARG:HG2	1:BE:44:SER:HB3	1.83	0.61
1:BG:10:VAL:HG21	1:ES:103:THR:HG22	1.83	0.61
1:CG:28:ARG:HG2	1:CG:44:SER:HB3	1.82	0.61
1:CO:28:ARG:HG2	1:CO:44:SER:HB3	1.83	0.61
1:CP:28:ARG:HG2	1:CP:44:SER:HB3	1.82	0.61
1:CR:89:PRO:HG2	1:CR:92:TYR:HB2	1.81	0.61
1:CU:67:VAL:HG22	1:CU:77:THR:HG22	1.83	0.61
1:DD:20:SER:HB3	1:DD:30:VAL:HG23	1.83	0.61
1:DI:103:THR:HG21	1:GU:15:ARG:NH1	2.16	0.61
1:DP:20:SER:HB3	1:DP:30:VAL:HG23	1.82	0.61
1:DT:67:VAL:HG22	1:DT:77:THR:HG22	1.81	0.61
1:DY:20:SER:HB3	1:DY:30:VAL:HG23	1.82	0.61
1:ED:89:PRO:HG2	1:ED:92:TYR:HB2	1.81	0.61
1:EK:28:ARG:HG2	1:EK:44:SER:HB3	1.83	0.61
1:ES:89:PRO:HG2	1:ES:92:TYR:HB2	1.81	0.61
1:FL:28:ARG:HG2	1:FL:44:SER:HB3	1.83	0.61
1:AL:103:THR:HG21	1:DX:15:ARG:NH1	2.15	0.61
1:AM:124:TYR:C	1:CA:22:GLN:HE21	2.04	0.61
1:AP:67:VAL:HG22	1:AP:77:THR:HG22	1.83	0.61
1:BW:28:ARG:HG2	1:BW:44:SER:HB3	1.83	0.61
1:CC:28:ARG:HG2	1:CC:44:SER:HB3	1.83	0.61
1:CM:103:THR:HG22	1:DG:10:VAL:HG21	1.83	0.61
1:CX:67:VAL:HG22	1:CX:77:THR:HG22	1.83	0.61
1:DA:67:VAL:HG22	1:DA:77:THR:HG22	1.83	0.61
1:DD:28:ARG:HG2	1:DD:44:SER:HB3	1.83	0.61
1:DG:67:VAL:HG22	1:DG:77:THR:HG22	1.83	0.61
1:DJ:28:ARG:HG2	1:DJ:44:SER:HB3	1.83	0.61
1:DP:28:ARG:HG2	1:DP:44:SER:HB3	1.83	0.61
1:DS:28:ARG:HG2	1:DS:44:SER:HB3	1.83	0.61
1:EH:20:SER:HB3	1:EH:30:VAL:HG23	1.83	0.61
1:FA:28:ARG:HG2	1:FA:44:SER:HB3	1.82	0.61
1:FC:67:VAL:HG22	1:FC:77:THR:HG22	1.83	0.61
1:FR:20:SER:HB3	1:FR:30:VAL:HG23	1.82	0.61
1:FV:124:TYR:OXT	1:GU:2:ARG:NH1	2.33	0.61
1:AA:20:SER:HB3	1:AA:30:VAL:HG23	1.82	0.60
1:AI:68:VAL:HG11	1:DU:91:THR:HG22	1.82	0.60
1:AM:20:SER:HB3	1:AM:30:VAL:HG23	1.82	0.60
1:AN:28:ARG:HG2	1:AN:44:SER:HB3	1.82	0.60
1:AP:89:PRO:HG2	1:AP:92:TYR:HB2	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:28:ARG:HG2	1:AY:44:SER:HB3	1.83	0.60
1:AY:67:VAL:HG22	1:AY:77:THR:HG22	1.82	0.60
1:BM:15:ARG:NH1	1:EY:103:THR:HG21	2.14	0.60
1:BV:1:MET:HE2	1:BV:3:LEU:HA	1.83	0.60
1:BZ:99:LYS:HE2	1:DT:15:ARG:NH1	2.15	0.60
1:CO:89:PRO:HG2	1:CO:92:TYR:HB2	1.81	0.60
1:CU:20:SER:HB3	1:CU:30:VAL:HG23	1.83	0.60
1:CX:28:ARG:HG2	1:CX:44:SER:HB3	1.83	0.60
1:DE:67:VAL:HG22	1:DE:77:THR:HG22	1.81	0.60
1:DI:15:ARG:HH11	1:GU:103:THR:HG21	1.65	0.60
1:DP:67:VAL:HG22	1:DP:77:THR:HG22	1.82	0.60
1:DV:28:ARG:HG2	1:DV:44:SER:HB3	1.83	0.60
1:FF:20:SER:HB3	1:FF:30:VAL:HG23	1.83	0.60
1:FO:28:ARG:HG2	1:FO:44:SER:HB3	1.83	0.60
1:FO:67:VAL:HG22	1:FO:77:THR:HG22	1.83	0.60
1:FU:28:ARG:HG2	1:FU:44:SER:HB3	1.83	0.60
1:FX:28:ARG:HG2	1:FX:44:SER:HB3	1.83	0.60
1:FX:67:VAL:HG22	1:FX:77:THR:HG22	1.83	0.60
1:GJ:89:PRO:HG2	1:GJ:92:TYR:HB2	1.81	0.60
1:GP:28:ARG:HG2	1:GP:44:SER:HB3	1.83	0.60
1:GV:67:VAL:HG22	1:GV:77:THR:HG22	1.83	0.60
1:AG:28:ARG:HG2	1:AG:44:SER:HB3	1.83	0.60
1:AW:28:ARG:HG2	1:AW:44:SER:HB3	1.82	0.60
1:BC:28:ARG:HG2	1:BC:44:SER:HB3	1.82	0.60
1:BS:10:VAL:HG21	1:FE:103:THR:HG22	1.83	0.60
1:CI:28:ARG:HG2	1:CI:44:SER:HB3	1.83	0.60
1:CU:28:ARG:HG2	1:CU:44:SER:HB3	1.83	0.60
1:CV:15:ARG:NH1	1:GM:99:LYS:HE2	2.16	0.60
1:DC:2:ARG:HH12	1:DE:124:TYR:C	2.03	0.60
1:DF:10:VAL:HG21	1:GR:103:THR:HG22	1.82	0.60
1:DF:103:THR:HG21	1:GR:15:ARG:NH1	2.15	0.60
1:DM:15:ARG:NH1	1:GT:103:THR:HG21	2.11	0.60
1:DV:20:SER:HB3	1:DV:30:VAL:HG23	1.82	0.60
1:EH:99:LYS:HE2	1:EO:15:ARG:HH11	1.65	0.60
1:EN:28:ARG:HG2	1:EN:44:SER:HB3	1.83	0.60
1:FI:28:ARG:HG2	1:FI:44:SER:HB3	1.83	0.60
1:FR:67:VAL:HG22	1:FR:77:THR:HG22	1.83	0.60
1:AF:103:THR:HG22	1:DR:10:VAL:HG21	1.82	0.60
1:AM:28:ARG:HG2	1:AM:44:SER:HB3	1.83	0.60
1:AP:20:SER:HB3	1:AP:30:VAL:HG23	1.82	0.60
1:BP:89:PRO:HG2	1:BP:92:TYR:HB2	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:67:VAL:HG22	1:CL:77:THR:HG22	1.82	0.60
1:CR:20:SER:HB3	1:CR:30:VAL:HG23	1.82	0.60
1:DJ:67:VAL:HG22	1:DJ:77:THR:HG22	1.83	0.60
1:EK:20:SER:HB3	1:EK:30:VAL:HG23	1.83	0.60
1:GA:28:ARG:HG2	1:GA:44:SER:HB3	1.83	0.60
1:GD:28:ARG:HG2	1:GD:44:SER:HB3	1.83	0.60
1:GV:28:ARG:HG2	1:GV:44:SER:HB3	1.83	0.60
1:AB:28:ARG:HG2	1:AB:44:SER:HB3	1.82	0.60
1:AJ:67:VAL:HG22	1:AJ:77:THR:HG22	1.83	0.60
1:AO:1:MET:HE2	1:AO:3:LEU:HA	1.84	0.60
1:AZ:123:ASN:HB3	1:EW:3:LEU:HG	1.82	0.60
1:BI:28:ARG:HG2	1:BI:44:SER:HB3	1.82	0.60
1:BK:28:ARG:HG2	1:BK:44:SER:HB3	1.83	0.60
1:BL:22:GLN:HB3	1:DW:124:TYR:CB	2.32	0.60
1:BO:28:ARG:HG2	1:BO:44:SER:HB3	1.82	0.60
1:CT:15:ARG:HH11	1:GF:103:THR:HG21	1.65	0.60
1:CY:1:MET:HG2	1:GG:123:ASN:OD1	2.01	0.60
1:DL:10:VAL:HG21	1:GX:103:THR:HG22	1.84	0.60
1:DS:20:SER:HB3	1:DS:30:VAL:HG23	1.83	0.60
1:GD:20:SER:HB3	1:GD:30:VAL:HG23	1.83	0.60
1:GW:28:ARG:HG2	1:GW:44:SER:HB3	1.82	0.60
1:AE:15:ARG:HH11	1:GA:99:LYS:HE2	1.66	0.60
1:BD:2:ARG:HH12	1:BR:124:TYR:C	2.04	0.60
1:CB:103:THR:HG22	1:FN:10:VAL:HG21	1.82	0.60
1:CD:103:THR:HG22	1:CR:10:VAL:HG21	1.84	0.60
1:CY:10:VAL:HG21	1:GG:103:THR:HG22	1.83	0.60
1:DU:1:MET:HE2	1:DU:3:LEU:HA	1.83	0.60
1:DY:28:ARG:HG2	1:DY:44:SER:HB3	1.83	0.60
1:DZ:28:ARG:HG2	1:DZ:44:SER:HB3	1.82	0.60
1:EN:67:VAL:HG22	1:EN:77:THR:HG22	1.82	0.60
1:EU:28:ARG:HG2	1:EU:44:SER:HB3	1.82	0.60
1:FI:20:SER:HB3	1:FI:30:VAL:HG23	1.83	0.60
1:FX:20:SER:HB3	1:FX:30:VAL:HG23	1.82	0.60
1:GA:67:VAL:HG22	1:GA:77:THR:HG22	1.83	0.60
1:GE:28:ARG:HG2	1:GE:44:SER:HB3	1.82	0.60
1:GJ:28:ARG:HG2	1:GJ:44:SER:HB3	1.83	0.60
1:GM:20:SER:HB3	1:GM:30:VAL:HG23	1.82	0.60
1:AI:103:THR:HG21	1:DU:15:ARG:NH1	2.17	0.60
1:BH:67:VAL:HG22	1:BH:77:THR:HG22	1.83	0.60
1:BW:103:THR:HG22	1:DQ:10:VAL:HG21	1.83	0.60
1:CS:28:ARG:HG2	1:CS:44:SER:HB3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CW:68:VAL:HG11	1:GI:91:THR:HG22	1.84	0.60
1:DV:50:GLY:O	1:DV:90:LYS:NZ	2.35	0.60
1:FY:28:ARG:HG2	1:FY:44:SER:HB3	1.82	0.60
1:GJ:67:VAL:HG22	1:GJ:77:THR:HG22	1.83	0.60
1:GO:70:ASP:OD1	1:GO:71:ALA:N	2.35	0.60
1:GS:67:VAL:HG22	1:GS:77:THR:HG22	1.83	0.60
1:GV:20:SER:HB3	1:GV:30:VAL:HG23	1.82	0.60
1:AC:89:PRO:HG2	1:AC:92:TYR:HB2	1.81	0.60
1:AK:28:ARG:HG2	1:AK:44:SER:HB3	1.82	0.60
1:AM:99:LYS:HE2	1:CA:15:ARG:HD3	1.82	0.60
1:AV:50:GLY:O	1:AV:90:LYS:NZ	2.35	0.60
1:BD:70:ASP:OD1	1:BD:71:ALA:N	2.35	0.60
1:BH:28:ARG:HG2	1:BH:44:SER:HB3	1.83	0.60
1:BT:20:SER:HB3	1:BT:30:VAL:HG23	1.82	0.60
1:BT:28:ARG:HG2	1:BT:44:SER:HB3	1.83	0.60
1:CI:50:GLY:O	1:CI:90:LYS:NZ	2.35	0.60
1:CV:28:ARG:HG2	1:CV:44:SER:HB3	1.82	0.60
1:CW:15:ARG:NH1	1:GI:103:THR:HG21	2.15	0.60
1:DS:10:VAL:HG21	1:GQ:103:THR:HG22	1.82	0.60
1:EJ:1:MET:HE2	1:EJ:3:LEU:HA	1.83	0.60
1:EN:20:SER:HB3	1:EN:30:VAL:HG23	1.82	0.60
1:EN:50:GLY:O	1:EN:90:LYS:NZ	2.35	0.60
1:FL:50:GLY:O	1:FL:90:LYS:NZ	2.35	0.60
1:GC:89:PRO:HG2	1:GC:92:TYR:HB2	1.81	0.60
1:GQ:28:ARG:HG2	1:GQ:44:SER:HB3	1.82	0.60
1:GR:70:ASP:OD1	1:GR:71:ALA:N	2.35	0.60
1:AC:70:ASP:OD1	1:AC:71:ALA:N	2.35	0.60
1:AO:15:ARG:NH1	1:EA:103:THR:HG21	2.16	0.60
1:AO:70:ASP:OD1	1:AO:71:ALA:N	2.35	0.60
1:AQ:28:ARG:HG2	1:AQ:44:SER:HB3	1.82	0.60
1:BF:28:ARG:HG2	1:BF:44:SER:HB3	1.82	0.60
1:BT:10:VAL:HG21	1:DN:103:THR:HG22	1.82	0.60
1:CB:89:PRO:HG2	1:CB:92:TYR:HB2	1.81	0.60
1:CJ:28:ARG:HG2	1:CJ:44:SER:HB3	1.82	0.60
1:CL:28:ARG:HG2	1:CL:44:SER:HB3	1.83	0.60
1:CT:70:ASP:OD1	1:CT:71:ALA:N	2.35	0.60
1:DB:28:ARG:HG2	1:DB:44:SER:HB3	1.82	0.60
1:DG:50:GLY:O	1:DG:90:LYS:NZ	2.35	0.60
1:DJ:50:GLY:O	1:DJ:90:LYS:NZ	2.35	0.60
1:DM:67:VAL:HG22	1:DM:77:THR:HG22	1.83	0.60
1:DP:50:GLY:O	1:DP:90:LYS:NZ	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:70:ASP:OD1	1:EA:71:ALA:N	2.35	0.60
1:EB:67:VAL:HG22	1:EB:77:THR:HG22	1.82	0.60
1:EJ:70:ASP:OD1	1:EJ:71:ALA:N	2.35	0.60
1:EK:103:THR:HG22	1:ER:10:VAL:HG21	1.84	0.60
1:ET:20:SER:HB3	1:ET:30:VAL:HG23	1.82	0.60
1:EZ:67:VAL:HG22	1:EZ:77:THR:HG22	1.83	0.60
1:FF:50:GLY:O	1:FF:90:LYS:NZ	2.35	0.60
1:FL:67:VAL:HG22	1:FL:77:THR:HG22	1.82	0.60
1:GT:28:ARG:HG2	1:GT:44:SER:HB3	1.82	0.60
1:GU:70:ASP:OD1	1:GU:71:ALA:N	2.35	0.60
1:AA:50:GLY:O	1:AA:90:LYS:NZ	2.35	0.60
1:AV:20:SER:HB3	1:AV:30:VAL:HG23	1.83	0.60
1:BA:70:ASP:OD1	1:BA:71:ALA:N	2.35	0.60
1:BH:20:SER:HB3	1:BH:30:VAL:HG23	1.83	0.60
1:BJ:70:ASP:OD1	1:BJ:71:ALA:N	2.35	0.60
1:BQ:67:VAL:HG22	1:BQ:77:THR:HG22	1.83	0.60
1:CE:70:ASP:OD1	1:CE:71:ALA:N	2.35	0.60
1:CK:70:ASP:OD1	1:CK:71:ALA:N	2.35	0.60
1:CN:15:ARG:NH1	1:FZ:103:THR:HG21	2.16	0.60
1:CO:67:VAL:HG22	1:CO:77:THR:HG22	1.83	0.60
1:CR:50:GLY:O	1:CR:90:LYS:NZ	2.35	0.60
1:DA:50:GLY:O	1:DA:90:LYS:NZ	2.35	0.60
1:DC:70:ASP:OD1	1:DC:71:ALA:N	2.35	0.60
1:DM:50:GLY:O	1:DM:90:LYS:NZ	2.35	0.60
1:EC:28:ARG:HG2	1:EC:44:SER:HB3	1.82	0.60
1:EW:28:ARG:HG2	1:EW:44:SER:HB3	1.83	0.60
1:EZ:20:SER:HB3	1:EZ:30:VAL:HG23	1.83	0.60
1:FD:28:ARG:HG2	1:FD:44:SER:HB3	1.82	0.60
1:FF:28:ARG:HG2	1:FF:44:SER:HB3	1.83	0.60
1:FJ:28:ARG:HG2	1:FJ:44:SER:HB3	1.82	0.60
1:FL:20:SER:HB3	1:FL:30:VAL:HG23	1.82	0.60
1:FR:50:GLY:O	1:FR:90:LYS:NZ	2.35	0.60
1:FU:50:GLY:O	1:FU:90:LYS:NZ	2.35	0.60
1:AG:50:GLY:O	1:AG:90:LYS:NZ	2.35	0.60
1:AI:70:ASP:OD1	1:AI:71:ALA:N	2.35	0.60
1:AR:70:ASP:OD1	1:AR:71:ALA:N	2.35	0.60
1:AV:103:THR:HG21	1:EF:15:ARG:NH1	2.17	0.60
1:BQ:50:GLY:O	1:BQ:90:LYS:NZ	2.35	0.60
1:BT:67:VAL:HG22	1:BT:77:THR:HG22	1.82	0.60
1:CC:20:SER:HB3	1:CC:30:VAL:HG23	1.82	0.60
1:CO:20:SER:HB3	1:CO:30:VAL:HG23	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:50:GLY:O	1:CU:90:LYS:NZ	2.35	0.60
1:CW:20:SER:O	1:GM:122:ASN:HB2	2.02	0.60
1:DM:122:ASN:HB2	1:GU:20:SER:O	2.01	0.60
1:DS:50:GLY:O	1:DS:90:LYS:NZ	2.35	0.60
1:EE:67:VAL:HG22	1:EE:77:THR:HG22	1.82	0.60
1:EQ:50:GLY:O	1:EQ:90:LYS:NZ	2.35	0.60
1:ER:28:ARG:HG2	1:ER:44:SER:HB3	1.82	0.60
1:ES:70:ASP:OD1	1:ES:71:ALA:N	2.35	0.60
1:EZ:50:GLY:O	1:EZ:90:LYS:NZ	2.35	0.60
1:FE:70:ASP:OD1	1:FE:71:ALA:N	2.35	0.60
1:FM:28:ARG:HG2	1:FM:44:SER:HB3	1.82	0.60
1:GC:70:ASP:OD1	1:GC:71:ALA:N	2.35	0.60
1:GO:1:MET:HE2	1:GO:3:LEU:HA	1.84	0.60
1:GP:50:GLY:O	1:GP:90:LYS:NZ	2.35	0.60
1:AD:10:VAL:HG21	1:BC:103:THR:HG22	1.84	0.59
1:AD:67:VAL:HG22	1:AD:77:THR:HG22	1.83	0.59
1:AG:67:VAL:HG22	1:AG:77:THR:HG22	1.83	0.59
1:BG:70:ASP:OD1	1:BG:71:ALA:N	2.35	0.59
1:BK:50:GLY:O	1:BK:90:LYS:NZ	2.35	0.59
1:BT:50:GLY:O	1:BT:90:LYS:NZ	2.35	0.59
1:BY:1:MET:HE2	1:BY:3:LEU:HA	1.84	0.59
1:CT:15:ARG:NH1	1:GF:103:THR:HG21	2.16	0.59
1:DD:67:VAL:HG22	1:DD:77:THR:HG22	1.83	0.59
1:DV:99:LYS:HE2	1:GE:15:ARG:NH1	2.16	0.59
1:ED:1:MET:HE2	1:ED:3:LEU:HA	1.84	0.59
1:EI:28:ARG:HG2	1:EI:44:SER:HB3	1.82	0.59
1:EQ:67:VAL:HG22	1:EQ:77:THR:HG22	1.83	0.59
1:FR:28:ARG:HG2	1:FR:44:SER:HB3	1.83	0.59
1:FV:15:ARG:NH1	1:GS:103:THR:HG21	2.17	0.59
1:GA:20:SER:HB3	1:GA:30:VAL:HG23	1.83	0.59
1:GM:50:GLY:O	1:GM:90:LYS:NZ	2.35	0.59
1:AA:28:ARG:HG2	1:AA:44:SER:HB3	1.83	0.59
1:AD:50:GLY:O	1:AD:90:LYS:NZ	2.35	0.59
1:AS:28:ARG:HG2	1:AS:44:SER:HB3	1.83	0.59
1:AS:50:GLY:O	1:AS:90:LYS:NZ	2.35	0.59
1:BL:28:ARG:HG2	1:BL:44:SER:HB3	1.82	0.59
1:BM:1:MET:HB3	1:EY:123:ASN:OD1	2.02	0.59
1:BN:20:SER:HB3	1:BN:30:VAL:HG23	1.83	0.59
1:BP:70:ASP:OD1	1:BP:71:ALA:N	2.35	0.59
1:BQ:10:VAL:HG21	1:EC:103:THR:HG22	1.84	0.59
1:BY:70:ASP:OD1	1:BY:71:ALA:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:28:ARG:HG2	1:BZ:44:SER:HB3	1.83	0.59
1:CN:70:ASP:OD1	1:CN:71:ALA:N	2.35	0.59
1:DF:1:MET:HE2	1:DF:3:LEU:HA	1.84	0.59
1:EY:70:ASP:OD1	1:EY:71:ALA:N	2.35	0.59
1:FO:20:SER:HB3	1:FO:30:VAL:HG23	1.83	0.59
1:FP:28:ARG:HG2	1:FP:44:SER:HB3	1.82	0.59
1:GM:67:VAL:HG22	1:GM:77:THR:HG22	1.82	0.59
1:AU:70:ASP:OD1	1:AU:71:ALA:N	2.35	0.59
1:AX:70:ASP:OD1	1:AX:71:ALA:N	2.35	0.59
1:BH:50:GLY:O	1:BH:90:LYS:NZ	2.35	0.59
1:BW:50:GLY:O	1:BW:90:LYS:NZ	2.35	0.59
1:BX:28:ARG:HG2	1:BX:44:SER:HB3	1.82	0.59
1:BZ:20:SER:HB3	1:BZ:30:VAL:HG23	1.82	0.59
1:BZ:67:VAL:HG22	1:BZ:77:THR:HG22	1.83	0.59
1:CC:103:THR:HG21	1:GK:15:ARG:NH1	2.17	0.59
1:CX:50:GLY:O	1:CX:90:LYS:NZ	2.35	0.59
1:CZ:67:VAL:HG12	1:CZ:77:THR:HG22	1.85	0.59
1:DP:103:THR:HG21	1:GW:15:ARG:NH1	2.17	0.59
1:DR:70:ASP:OD1	1:DR:71:ALA:N	2.35	0.59
1:DY:50:GLY:O	1:DY:90:LYS:NZ	2.35	0.59
1:EG:67:VAL:HG12	1:EG:77:THR:HG22	1.85	0.59
1:EV:67:VAL:HG12	1:EV:77:THR:HG22	1.85	0.59
1:FB:70:ASP:OD1	1:FB:71:ALA:N	2.35	0.59
1:GG:28:ARG:HG2	1:GG:44:SER:HB3	1.83	0.59
1:GH:28:ARG:HG2	1:GH:44:SER:HB3	1.82	0.59
1:CF:50:GLY:O	1:CF:90:LYS:NZ	2.35	0.59
1:CH:70:ASP:OD1	1:CH:71:ALA:N	2.35	0.59
1:CR:28:ARG:HG2	1:CR:44:SER:HB3	1.83	0.59
1:CZ:2:ARG:NH1	1:DK:124:TYR:OXT	2.35	0.59
1:DJ:20:SER:HB3	1:DJ:30:VAL:HG23	1.83	0.59
1:EH:28:ARG:HG2	1:EH:44:SER:HB3	1.83	0.59
1:FQ:70:ASP:OD1	1:FQ:71:ALA:N	2.35	0.59
1:FW:70:ASP:OD1	1:FW:71:ALA:N	2.35	0.59
1:FZ:70:ASP:OD1	1:FZ:71:ALA:N	2.35	0.59
1:GG:50:GLY:O	1:GG:90:LYS:NZ	2.35	0.59
1:GI:67:VAL:HG12	1:GI:77:THR:HG22	1.85	0.59
1:GL:70:ASP:OD1	1:GL:71:ALA:N	2.35	0.59
1:AJ:50:GLY:O	1:AJ:90:LYS:NZ	2.35	0.59
1:AO:67:VAL:HG12	1:AO:77:THR:HG22	1.85	0.59
1:AR:67:VAL:HG12	1:AR:77:THR:HG22	1.85	0.59
1:BD:67:VAL:HG12	1:BD:77:THR:HG22	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:103:THR:HG21	1:FK:15:ARG:NH1	2.16	0.59
1:BZ:50:GLY:O	1:BZ:90:LYS:NZ	2.35	0.59
1:CW:67:VAL:HG12	1:CW:77:THR:HG22	1.85	0.59
1:CW:70:ASP:OD1	1:CW:71:ALA:N	2.35	0.59
1:DU:70:ASP:OD1	1:DU:71:ALA:N	2.35	0.59
1:DX:67:VAL:HG12	1:DX:77:THR:HG22	1.85	0.59
1:EB:50:GLY:O	1:EB:90:LYS:NZ	2.35	0.59
1:ED:67:VAL:HG12	1:ED:77:THR:HG22	1.85	0.59
1:ES:1:MET:HE2	1:ES:3:LEU:HA	1.85	0.59
1:FT:67:VAL:HG12	1:FT:77:THR:HG22	1.85	0.59
1:GA:50:GLY:O	1:GA:90:LYS:NZ	2.35	0.59
1:GD:50:GLY:O	1:GD:90:LYS:NZ	2.35	0.59
1:GF:70:ASP:OD1	1:GF:71:ALA:N	2.35	0.59
1:AA:103:THR:HG21	1:BI:15:ARG:NH1	2.17	0.59
1:AE:15:ARG:NH1	1:GA:103:THR:HG21	2.17	0.59
1:AM:99:LYS:HE2	1:CA:15:ARG:NH1	2.18	0.59
1:AY:50:GLY:O	1:AY:90:LYS:NZ	2.35	0.59
1:BM:67:VAL:HG12	1:BM:77:THR:HG22	1.85	0.59
1:BS:70:ASP:OD1	1:BS:71:ALA:N	2.35	0.59
1:CG:111:GLN:HB2	1:CL:1:MET:SD	2.42	0.59
1:CH:1:MET:HE2	1:CH:3:LEU:HA	1.84	0.59
1:CH:10:VAL:HG21	1:FT:103:THR:HG22	1.83	0.59
1:CP:103:THR:HG22	1:DJ:10:VAL:HG21	1.84	0.59
1:CZ:70:ASP:OD1	1:CZ:71:ALA:N	2.35	0.59
1:DI:70:ASP:OD1	1:DI:71:ALA:N	2.35	0.59
1:DO:1:MET:HE2	1:DO:3:LEU:HA	1.85	0.59
1:EG:70:ASP:OD1	1:EG:71:ALA:N	2.35	0.59
1:EH:50:GLY:O	1:EH:90:LYS:NZ	2.35	0.59
1:EK:50:GLY:O	1:EK:90:LYS:NZ	2.35	0.59
1:EK:103:THR:HG21	1:ER:15:ARG:NH1	2.17	0.59
1:FB:67:VAL:HG12	1:FB:77:THR:HG22	1.85	0.59
1:FC:28:ARG:HG2	1:FC:44:SER:HB3	1.83	0.59
1:FD:15:ARG:NH1	1:FF:103:THR:HG21	2.18	0.59
1:FN:1:MET:HE2	1:FN:3:LEU:HA	1.84	0.59
1:FT:1:MET:HE2	1:FT:3:LEU:HA	1.85	0.59
1:FT:70:ASP:OD1	1:FT:71:ALA:N	2.35	0.59
1:GV:50:GLY:O	1:GV:90:LYS:NZ	2.35	0.59
1:AC:1:MET:HE2	1:AC:3:LEU:HA	1.84	0.59
1:AM:50:GLY:O	1:AM:90:LYS:NZ	2.35	0.59
1:AM:67:VAL:HG22	1:AM:77:THR:HG22	1.83	0.59
1:AR:98:THR:HG22	1:ED:118:ASP:CG	2.22	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:1:MET:HE2	1:BA:3:LEU:HA	1.85	0.59
1:BG:1:MET:HE2	1:BG:3:LEU:HA	1.85	0.59
1:BT:106:ALA:HB1	1:DN:8:LEU:HD22	1.85	0.59
1:CB:70:ASP:OD1	1:CB:71:ALA:N	2.35	0.59
1:CT:67:VAL:HG12	1:CT:77:THR:HG22	1.85	0.59
1:DI:1:MET:HE2	1:DI:3:LEU:HA	1.85	0.59
1:DL:70:ASP:OD1	1:DL:71:ALA:N	2.35	0.59
1:EE:50:GLY:O	1:EE:90:LYS:NZ	2.35	0.59
1:EP:1:MET:HE2	1:EP:3:LEU:HA	1.84	0.59
1:EP:70:ASP:OD1	1:EP:71:ALA:N	2.35	0.59
1:ET:2:ARG:HA	1:FG:124:TYR:O	2.02	0.59
1:ET:28:ARG:HG2	1:ET:44:SER:HB3	1.83	0.59
1:EZ:28:ARG:HG2	1:EZ:44:SER:HB3	1.83	0.59
1:GF:1:MET:HE2	1:GF:3:LEU:HA	1.84	0.59
1:GJ:50:GLY:O	1:GJ:90:LYS:NZ	2.35	0.59
1:AE:10:VAL:HG13	1:GA:102:GLN:HB2	1.84	0.59
1:BD:1:MET:HE2	1:BD:3:LEU:HA	1.84	0.59
1:BJ:67:VAL:HG12	1:BJ:77:THR:HG22	1.85	0.59
1:BP:67:VAL:HG12	1:BP:77:THR:HG22	1.85	0.59
1:BS:1:MET:HE2	1:BS:3:LEU:HA	1.85	0.59
1:BY:67:VAL:HG12	1:BY:77:THR:HG22	1.85	0.59
1:CE:1:MET:HE2	1:CE:3:LEU:HA	1.85	0.59
1:CF:103:THR:HG21	1:GN:15:ARG:NH1	2.17	0.59
1:DE:28:ARG:HG2	1:DE:44:SER:HB3	1.82	0.59
1:DM:28:ARG:HG2	1:DM:44:SER:HB3	1.83	0.59
1:EE:28:ARG:HG2	1:EE:44:SER:HB3	1.83	0.59
1:EQ:20:SER:HB3	1:EQ:30:VAL:HG23	1.83	0.59
1:ES:67:VAL:HG12	1:ES:77:THR:HG22	1.85	0.59
1:EW:50:GLY:O	1:EW:90:LYS:NZ	2.35	0.59
1:FX:50:GLY:O	1:FX:90:LYS:NZ	2.35	0.59
1:GF:67:VAL:HG12	1:GF:77:THR:HG22	1.85	0.59
1:GS:50:GLY:O	1:GS:90:LYS:NZ	2.35	0.59
1:AF:70:ASP:OD1	1:AF:71:ALA:N	2.35	0.59
1:AP:50:GLY:O	1:AP:90:LYS:NZ	2.35	0.59
1:AZ:103:THR:HG22	1:EW:10:VAL:HG21	1.84	0.59
1:CO:50:GLY:O	1:CO:90:LYS:NZ	2.35	0.59
1:CQ:70:ASP:OD1	1:CQ:71:ALA:N	2.35	0.59
1:CZ:1:MET:HE2	1:CZ:3:LEU:HA	1.85	0.59
1:DO:70:ASP:OD1	1:DO:71:ALA:N	2.35	0.59
1:DR:1:MET:HE2	1:DR:3:LEU:HA	1.85	0.59
1:DV:122:ASN:HB2	1:GF:20:SER:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DX:70:ASP:OD1	1:DX:71:ALA:N	2.35	0.59
1:ED:70:ASP:OD1	1:ED:71:ALA:N	2.35	0.59
1:GC:67:VAL:HG12	1:GC:77:THR:HG22	1.85	0.59
1:GI:70:ASP:OD1	1:GI:71:ALA:N	2.35	0.59
1:AF:67:VAL:HG12	1:AF:77:THR:HG22	1.85	0.59
1:BB:50:GLY:O	1:BB:90:LYS:NZ	2.35	0.59
1:CD:103:THR:HG21	1:CR:15:ARG:NH1	2.14	0.59
1:CQ:118:ASP:CG	1:GC:98:THR:HG22	2.23	0.59
1:DQ:28:ARG:HG2	1:DQ:44:SER:HB3	1.82	0.59
1:DY:103:THR:HG22	1:FY:10:VAL:HG21	1.84	0.59
1:EB:28:ARG:HG2	1:EB:44:SER:HB3	1.83	0.59
1:FC:50:GLY:O	1:FC:90:LYS:NZ	2.35	0.59
1:FI:50:GLY:O	1:FI:90:LYS:NZ	2.35	0.59
1:FU:20:SER:HB3	1:FU:30:VAL:HG23	1.83	0.59
1:GC:1:MET:HE2	1:GC:3:LEU:HA	1.85	0.59
1:BE:50:GLY:O	1:BE:90:LYS:NZ	2.35	0.58
1:BH:103:THR:HG21	1:BO:15:ARG:NH1	2.18	0.58
1:BN:10:VAL:HG21	1:DZ:103:THR:HG22	1.85	0.58
1:BV:70:ASP:OD1	1:BV:71:ALA:N	2.35	0.58
1:CB:8:LEU:HD11	1:FN:107:TRP:CE2	2.38	0.58
1:CF:28:ARG:HG2	1:CF:44:SER:HB3	1.83	0.58
1:CW:1:MET:HE2	1:CW:3:LEU:HA	1.84	0.58
1:CW:103:THR:HG21	1:GI:15:ARG:NH1	2.18	0.58
1:DB:66:VAL:HG21	1:GJ:96:HIS:CG	2.38	0.58
1:DD:50:GLY:O	1:DD:90:LYS:NZ	2.35	0.58
1:DF:70:ASP:OD1	1:DF:71:ALA:N	2.35	0.58
1:FN:70:ASP:OD1	1:FN:71:ALA:N	2.35	0.58
1:GR:1:MET:HE2	1:GR:3:LEU:HA	1.85	0.58
1:GS:28:ARG:HG2	1:GS:44:SER:HB3	1.83	0.58
1:AL:2:ARG:HH12	1:BX:124:TYR:C	2.06	0.58
1:AL:70:ASP:OD1	1:AL:71:ALA:N	2.35	0.58
1:AN:10:VAL:HG13	1:FR:102:GLN:HB2	1.84	0.58
1:BA:67:VAL:HG12	1:BA:77:THR:HG22	1.85	0.58
1:BG:67:VAL:HG12	1:BG:77:THR:HG22	1.85	0.58
1:BN:50:GLY:O	1:BN:90:LYS:NZ	2.35	0.58
1:CC:50:GLY:O	1:CC:90:LYS:NZ	2.35	0.58
1:CG:10:VAL:HG13	1:CL:102:GLN:HB2	1.85	0.58
1:CT:118:ASP:CG	1:GF:98:THR:HG22	2.23	0.58
1:EN:103:THR:OG1	1:FJ:62:LEU:HD21	2.03	0.58
1:ET:1:MET:HB3	1:FG:123:ASN:OD1	2.03	0.58
1:EV:70:ASP:OD1	1:EV:71:ALA:N	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FH:70:ASP:OD1	1:FH:71:ALA:N	2.35	0.58
1:FK:67:VAL:HG12	1:FK:77:THR:HG22	1.85	0.58
1:FN:67:VAL:HG12	1:FN:77:THR:HG22	1.85	0.58
1:FQ:67:VAL:HG12	1:FQ:77:THR:HG22	1.85	0.58
1:FZ:67:VAL:HG12	1:FZ:77:THR:HG22	1.85	0.58
1:BM:1:MET:HE2	1:BM:3:LEU:HA	1.84	0.58
1:CL:50:GLY:O	1:CL:90:LYS:NZ	2.35	0.58
1:DG:28:ARG:HG2	1:DG:44:SER:HB3	1.83	0.58
1:DI:67:VAL:HG12	1:DI:77:THR:HG22	1.85	0.58
1:DL:1:MET:HE2	1:DL:3:LEU:HA	1.85	0.58
1:DR:67:VAL:HG12	1:DR:77:THR:HG22	1.85	0.58
1:EJ:67:VAL:HG12	1:EJ:77:THR:HG22	1.85	0.58
1:EM:70:ASP:OD1	1:EM:71:ALA:N	2.35	0.58
1:ET:50:GLY:O	1:ET:90:LYS:NZ	2.35	0.58
1:FV:103:THR:HG21	1:GS:15:ARG:NH1	2.15	0.58
1:GL:67:VAL:HG12	1:GL:77:THR:HG22	1.85	0.58
1:GU:67:VAL:HG12	1:GU:77:THR:HG22	1.85	0.58
1:GX:70:ASP:OD1	1:GX:71:ALA:N	2.35	0.58
1:AG:10:VAL:HG21	1:BF:103:THR:HG22	1.83	0.58
1:AI:1:MET:HE2	1:AI:3:LEU:HA	1.84	0.58
1:AI:8:LEU:HD11	1:DU:107:TRP:CE2	2.38	0.58
1:AX:1:MET:HE2	1:AX:3:LEU:HA	1.85	0.58
1:BB:103:THR:HG22	1:BR:10:VAL:HG21	1.86	0.58
1:BK:45:LEU:HD11	1:BK:58:VAL:HG13	1.86	0.58
1:CT:103:THR:HG21	1:GF:15:ARG:NH1	2.19	0.58
1:CU:122:ASN:HB2	1:DI:20:SER:O	2.03	0.58
1:AP:102:GLN:HB2	1:BU:10:VAL:HG13	1.85	0.58
1:BS:67:VAL:HG12	1:BS:77:THR:HG22	1.85	0.58
1:CC:45:LEU:HD11	1:CC:58:VAL:HG13	1.86	0.58
1:DP:45:LEU:HD11	1:DP:58:VAL:HG13	1.86	0.58
1:EH:96:HIS:CG	1:EO:66:VAL:HG21	2.38	0.58
1:FE:67:VAL:HG12	1:FE:77:THR:HG22	1.85	0.58
1:FK:70:ASP:OD1	1:FK:71:ALA:N	2.35	0.58
1:GR:67:VAL:HG12	1:GR:77:THR:HG22	1.85	0.58
1:GU:1:MET:HE2	1:GU:3:LEU:HA	1.85	0.58
1:AI:15:ARG:NH1	1:DU:103:THR:HG21	2.18	0.58
1:AI:20:SER:O	1:GD:122:ASN:HB2	2.02	0.58
1:AM:103:THR:OG1	1:CA:62:LEU:HD21	2.02	0.58
1:CK:67:VAL:HG12	1:CK:77:THR:HG22	1.85	0.58
1:CP:30:VAL:HG22	1:CP:42:VAL:HG12	1.86	0.58
1:EM:67:VAL:HG12	1:EM:77:THR:HG22	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EV:1:MET:HE2	1:EV:3:LEU:HA	1.85	0.58
1:FA:15:ARG:NH1	1:FL:103:THR:HG21	2.18	0.58
1:FO:50:GLY:O	1:FO:90:LYS:NZ	2.35	0.58
1:FS:30:VAL:HG22	1:FS:42:VAL:HG12	1.86	0.58
1:FW:67:VAL:HG12	1:FW:77:THR:HG22	1.85	0.58
1:AM:45:LEU:HD11	1:AM:58:VAL:HG13	1.86	0.58
1:AN:15:ARG:NH1	1:FR:103:THR:HG21	2.18	0.58
1:BN:96:HIS:CG	1:DZ:66:VAL:HG21	2.39	0.58
1:CD:22:GLN:HB3	1:GK:124:TYR:HB2	1.84	0.58
1:CY:103:THR:HG22	1:GG:10:VAL:HG21	1.83	0.58
1:DH:30:VAL:HG22	1:DH:42:VAL:HG12	1.86	0.58
1:DL:67:VAL:HG12	1:DL:77:THR:HG22	1.85	0.58
1:DV:45:LEU:HD11	1:DV:58:VAL:HG13	1.86	0.58
1:EE:45:LEU:HD11	1:EE:58:VAL:HG13	1.86	0.58
1:EF:30:VAL:HG22	1:EF:42:VAL:HG12	1.86	0.58
1:EN:45:LEU:HD11	1:EN:58:VAL:HG13	1.86	0.58
1:EU:30:VAL:HG22	1:EU:42:VAL:HG12	1.86	0.58
1:EY:1:MET:HE2	1:EY:3:LEU:HA	1.85	0.58
1:EZ:45:LEU:HD11	1:EZ:58:VAL:HG13	1.86	0.58
1:FM:30:VAL:HG22	1:FM:42:VAL:HG12	1.86	0.58
1:FO:45:LEU:HD11	1:FO:58:VAL:HG13	1.86	0.58
1:FP:105:ILE:HG23	1:GV:105:ILE:HG23	1.86	0.58
1:AJ:45:LEU:HD11	1:AJ:58:VAL:HG13	1.86	0.58
1:AK:30:VAL:HG22	1:AK:42:VAL:HG12	1.86	0.58
1:AM:1:MET:SD	1:CA:111:GLN:HB2	2.44	0.58
1:AX:67:VAL:HG12	1:AX:77:THR:HG22	1.85	0.58
1:AX:118:ASP:CG	1:EJ:98:THR:HG22	2.24	0.58
1:AY:1:MET:SD	1:EI:111:GLN:HB2	2.44	0.58
1:AZ:30:VAL:HG22	1:AZ:42:VAL:HG12	1.86	0.58
1:BL:30:VAL:HG22	1:BL:42:VAL:HG12	1.86	0.58
1:BT:1:MET:SD	1:DN:111:GLN:HB2	2.44	0.58
1:CB:67:VAL:HG12	1:CB:77:THR:HG22	1.85	0.58
1:CE:67:VAL:HG12	1:CE:77:THR:HG22	1.85	0.58
1:CG:22:GLN:NE2	1:CL:124:TYR:OXT	2.37	0.58
1:CI:45:LEU:HD11	1:CI:58:VAL:HG13	1.86	0.58
1:CX:45:LEU:HD11	1:CX:58:VAL:HG13	1.86	0.58
1:DF:67:VAL:HG12	1:DF:77:THR:HG22	1.85	0.58
1:DN:30:VAL:HG22	1:DN:42:VAL:HG12	1.86	0.58
1:EI:30:VAL:HG22	1:EI:42:VAL:HG12	1.86	0.58
1:ET:45:LEU:HD11	1:ET:58:VAL:HG13	1.86	0.58
1:GL:1:MET:HE2	1:GL:3:LEU:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GM:45:LEU:HD11	1:GM:58:VAL:HG13	1.86	0.58
1:AK:91:THR:OG1	1:FO:78:ILE:HD13	2.02	0.58
1:AM:116:PRO:O	1:CA:56:ARG:NH1	2.37	0.58
1:AQ:30:VAL:HG22	1:AQ:42:VAL:HG12	1.86	0.58
1:BC:30:VAL:HG22	1:BC:42:VAL:HG12	1.86	0.58
1:BH:45:LEU:HD11	1:BH:58:VAL:HG13	1.86	0.58
1:BM:70:ASP:OD1	1:BM:71:ALA:N	2.35	0.58
1:BT:45:LEU:HD11	1:BT:58:VAL:HG13	1.86	0.58
1:BW:45:LEU:HD11	1:BW:58:VAL:HG13	1.86	0.58
1:CB:1:MET:HE2	1:CB:3:LEU:HA	1.85	0.58
1:CQ:67:VAL:HG12	1:CQ:77:THR:HG22	1.85	0.58
1:DD:45:LEU:HD11	1:DD:58:VAL:HG13	1.86	0.58
1:FP:30:VAL:HG22	1:FP:42:VAL:HG12	1.86	0.58
1:FX:45:LEU:HD11	1:FX:58:VAL:HG13	1.86	0.58
1:GV:45:LEU:HD11	1:GV:58:VAL:HG13	1.86	0.58
1:AC:67:VAL:HG12	1:AC:77:THR:HG22	1.85	0.58
1:AG:45:LEU:HD11	1:AG:58:VAL:HG13	1.86	0.58
1:AL:67:VAL:HG12	1:AL:77:THR:HG22	1.85	0.58
1:AQ:123:ASN:HB3	1:FU:3:LEU:HG	1.84	0.58
1:AZ:124:TYR:OXT	1:EY:2:ARG:NH1	2.37	0.58
1:BH:124:TYR:C	1:BO:22:GLN:HE21	2.08	0.58
1:CK:1:MET:HE2	1:CK:3:LEU:HA	1.85	0.58
1:CO:45:LEU:HD11	1:CO:58:VAL:HG13	1.86	0.58
1:DA:10:VAL:HG21	1:DE:103:THR:HG22	1.85	0.58
1:DS:45:LEU:HD11	1:DS:58:VAL:HG13	1.86	0.58
1:EC:30:VAL:HG22	1:EC:42:VAL:HG12	1.86	0.58
1:EO:30:VAL:HG22	1:EO:42:VAL:HG12	1.86	0.58
1:ER:30:VAL:HG22	1:ER:42:VAL:HG12	1.86	0.58
1:EX:98:THR:HG22	1:FI:118:ASP:HB3	1.85	0.58
1:FH:67:VAL:HG12	1:FH:77:THR:HG22	1.85	0.58
1:FL:45:LEU:HD11	1:FL:58:VAL:HG13	1.86	0.58
1:AD:45:LEU:HD11	1:AD:58:VAL:HG13	1.86	0.57
1:AI:67:VAL:HG12	1:AI:77:THR:HG22	1.85	0.57
1:AT:103:THR:HG21	1:EZ:15:ARG:NH1	2.16	0.57
1:AU:1:MET:HE2	1:AU:3:LEU:HA	1.85	0.57
1:BV:67:VAL:HG12	1:BV:77:THR:HG22	1.85	0.57
1:CH:67:VAL:HG12	1:CH:77:THR:HG22	1.85	0.57
1:CJ:30:VAL:HG22	1:CJ:42:VAL:HG12	1.86	0.57
1:DA:103:THR:HG22	1:DE:10:VAL:HG21	1.85	0.57
1:EP:67:VAL:HG12	1:EP:77:THR:HG22	1.85	0.57
1:FA:123:ASN:HB3	1:FL:3:LEU:HG	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:1:MET:HE2	1:FB:3:LEU:HA	1.85	0.57
1:FJ:30:VAL:HG22	1:FJ:42:VAL:HG12	1.86	0.57
1:GG:45:LEU:HD11	1:GG:58:VAL:HG13	1.86	0.57
1:AB:30:VAL:HG22	1:AB:42:VAL:HG12	1.86	0.57
1:AS:45:LEU:HD11	1:AS:58:VAL:HG13	1.86	0.57
1:BB:45:LEU:HD11	1:BB:58:VAL:HG13	1.86	0.57
1:BJ:10:VAL:HG21	1:EV:103:THR:HG22	1.86	0.57
1:BQ:45:LEU:HD11	1:BQ:58:VAL:HG13	1.86	0.57
1:BR:30:VAL:HG22	1:BR:42:VAL:HG12	1.86	0.57
1:BS:103:THR:HG22	1:FE:10:VAL:HG21	1.86	0.57
1:BT:120:GLY:HA2	1:DN:47:GLN:HE22	1.69	0.57
1:CA:30:VAL:HG22	1:CA:42:VAL:HG12	1.86	0.57
1:CC:15:ARG:NH1	1:GK:103:THR:HG21	2.10	0.57
1:CN:67:VAL:HG12	1:CN:77:THR:HG22	1.85	0.57
1:DC:67:VAL:HG12	1:DC:77:THR:HG22	1.85	0.57
1:EA:67:VAL:HG12	1:EA:77:THR:HG22	1.85	0.57
1:EM:1:MET:HE2	1:EM:3:LEU:HA	1.86	0.57
1:EN:103:THR:HG21	1:FJ:15:ARG:NH1	2.18	0.57
1:EY:67:VAL:HG12	1:EY:77:THR:HG22	1.85	0.57
1:FI:45:LEU:HD11	1:FI:58:VAL:HG13	1.86	0.57
1:FU:45:LEU:HD11	1:FU:58:VAL:HG13	1.86	0.57
1:GQ:30:VAL:HG22	1:GQ:42:VAL:HG12	1.86	0.57
1:GW:30:VAL:HG22	1:GW:42:VAL:HG12	1.86	0.57
1:AF:1:MET:HE2	1:AF:3:LEU:HA	1.86	0.57
1:AM:15:ARG:NH1	1:CA:103:THR:HG21	2.12	0.57
1:AY:45:LEU:HD11	1:AY:58:VAL:HG13	1.86	0.57
1:BP:1:MET:HE2	1:BP:3:LEU:HA	1.86	0.57
1:CL:45:LEU:HD11	1:CL:58:VAL:HG13	1.86	0.57
1:CR:45:LEU:HD11	1:CR:58:VAL:HG13	1.86	0.57
1:DA:45:LEU:HD11	1:DA:58:VAL:HG13	1.86	0.57
1:EK:45:LEU:HD11	1:EK:58:VAL:HG13	1.86	0.57
1:EL:30:VAL:HG22	1:EL:42:VAL:HG12	1.86	0.57
1:EQ:45:LEU:HD11	1:EQ:58:VAL:HG13	1.86	0.57
1:EW:45:LEU:HD11	1:EW:58:VAL:HG13	1.86	0.57
1:GP:45:LEU:HD11	1:GP:58:VAL:HG13	1.86	0.57
1:AI:107:TRP:CE2	1:DU:8:LEU:HD11	2.39	0.57
1:AU:67:VAL:HG12	1:AU:77:THR:HG22	1.85	0.57
1:CN:39:ASN:HD21	1:CN:42:VAL:HG23	1.70	0.57
1:CT:1:MET:HE2	1:CT:3:LEU:HA	1.85	0.57
1:DE:30:VAL:HG22	1:DE:42:VAL:HG12	1.86	0.57
1:DJ:45:LEU:HD11	1:DJ:58:VAL:HG13	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DL:47:GLN:HG3	1:DL:58:VAL:HG22	1.87	0.57
1:DX:1:MET:HE2	1:DX:3:LEU:HA	1.87	0.57
1:DY:45:LEU:HD11	1:DY:58:VAL:HG13	1.86	0.57
1:FC:45:LEU:HD11	1:FC:58:VAL:HG13	1.86	0.57
1:FH:1:MET:HE2	1:FH:3:LEU:HA	1.86	0.57
1:FY:30:VAL:HG22	1:FY:42:VAL:HG12	1.86	0.57
1:GE:30:VAL:HG22	1:GE:42:VAL:HG12	1.86	0.57
1:GH:30:VAL:HG22	1:GH:42:VAL:HG12	1.86	0.57
1:GJ:45:LEU:HD11	1:GJ:58:VAL:HG13	1.86	0.57
1:GX:67:VAL:HG12	1:GX:77:THR:HG22	1.85	0.57
1:AD:103:THR:HG21	1:BC:15:ARG:NH1	2.19	0.57
1:AL:39:ASN:HD21	1:AL:42:VAL:HG23	1.70	0.57
1:AR:1:MET:HE2	1:AR:3:LEU:HA	1.86	0.57
1:AV:3:LEU:HG	1:EF:123:ASN:HB3	1.85	0.57
1:AX:47:GLN:HG3	1:AX:58:VAL:HG22	1.87	0.57
1:CK:47:GLN:HG3	1:CK:58:VAL:HG22	1.87	0.57
1:CS:30:VAL:HG22	1:CS:42:VAL:HG12	1.86	0.57
1:CS:124:TYR:C	1:DF:2:ARG:HH12	2.08	0.57
1:CZ:47:GLN:HG3	1:CZ:58:VAL:HG22	1.87	0.57
1:DC:1:MET:HE2	1:DC:3:LEU:HA	1.85	0.57
1:DX:47:GLN:HG3	1:DX:58:VAL:HG22	1.87	0.57
1:FK:47:GLN:HG3	1:FK:58:VAL:HG22	1.87	0.57
1:GO:67:VAL:HG12	1:GO:77:THR:HG22	1.85	0.57
1:AL:1:MET:HE2	1:AL:3:LEU:HA	1.87	0.57
1:AL:47:GLN:HG3	1:AL:58:VAL:HG22	1.87	0.57
1:BO:30:VAL:HG22	1:BO:42:VAL:HG12	1.86	0.57
1:BT:103:THR:HG21	1:DN:15:ARG:NH1	2.20	0.57
1:CE:39:ASN:HD21	1:CE:42:VAL:HG23	1.70	0.57
1:CT:10:VAL:HG21	1:GF:103:THR:HG22	1.86	0.57
1:CU:45:LEU:HD11	1:CU:58:VAL:HG13	1.86	0.57
1:DC:47:GLN:HG3	1:DC:58:VAL:HG22	1.87	0.57
1:DO:67:VAL:HG12	1:DO:77:THR:HG22	1.85	0.57
1:EB:102:GLN:HB2	1:GB:10:VAL:HG13	1.87	0.57
1:FK:1:MET:HE2	1:FK:3:LEU:HA	1.86	0.57
1:FN:47:GLN:HG3	1:FN:58:VAL:HG22	1.87	0.57
1:GB:30:VAL:HG22	1:GB:42:VAL:HG12	1.86	0.57
1:GS:45:LEU:HD11	1:GS:58:VAL:HG13	1.86	0.57
1:AF:68:VAL:HG11	1:DR:91:THR:HG22	1.85	0.57
1:AP:10:VAL:HG21	1:BU:103:THR:HG22	1.86	0.57
1:BD:47:GLN:HG3	1:BD:58:VAL:HG22	1.87	0.57
1:BF:30:VAL:HG22	1:BF:42:VAL:HG12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:39:ASN:HD21	1:BY:42:VAL:HG23	1.70	0.57
1:CE:47:GLN:HG3	1:CE:58:VAL:HG22	1.87	0.57
1:CQ:1:MET:HE2	1:CQ:3:LEU:HA	1.87	0.57
1:DU:39:ASN:HD21	1:DU:42:VAL:HG23	1.70	0.57
1:EG:47:GLN:HG3	1:EG:58:VAL:HG22	1.87	0.57
1:ES:47:GLN:HG3	1:ES:58:VAL:HG22	1.87	0.57
1:FF:45:LEU:HD11	1:FF:58:VAL:HG13	1.86	0.57
1:FG:30:VAL:HG22	1:FG:42:VAL:HG12	1.86	0.57
1:GD:45:LEU:HD11	1:GD:58:VAL:HG13	1.86	0.57
1:GF:47:GLN:HG3	1:GF:58:VAL:HG22	1.87	0.57
1:GI:39:ASN:HD21	1:GI:42:VAL:HG23	1.70	0.57
1:GK:30:VAL:HG22	1:GK:42:VAL:HG12	1.86	0.57
1:AC:47:GLN:HG3	1:AC:58:VAL:HG22	1.87	0.57
1:AK:124:TYR:O	1:FO:2:ARG:HA	2.04	0.57
1:AN:15:ARG:HD3	1:FR:99:LYS:HE2	1.87	0.57
1:AR:123:ASN:OD1	1:ED:1:MET:HB3	2.05	0.57
1:AS:85:THR:OG1	1:EL:83:SER:OG	2.22	0.57
1:BD:39:ASN:HD21	1:BD:42:VAL:HG23	1.70	0.57
1:BP:39:ASN:HD21	1:BP:42:VAL:HG23	1.70	0.57
1:CH:78:ILE:HD13	1:FT:91:THR:HB	1.86	0.57
1:CQ:39:ASN:HD21	1:CQ:42:VAL:HG23	1.70	0.57
1:CV:30:VAL:HG22	1:CV:42:VAL:HG12	1.86	0.57
1:DI:39:ASN:HD21	1:DI:42:VAL:HG23	1.70	0.57
1:EB:45:LEU:HD11	1:EB:58:VAL:HG13	1.86	0.57
1:EP:47:GLN:HG3	1:EP:58:VAL:HG22	1.87	0.57
1:FB:47:GLN:HG3	1:FB:58:VAL:HG22	1.87	0.57
1:FT:39:ASN:HD21	1:FT:42:VAL:HG23	1.70	0.57
1:FZ:1:MET:HE2	1:FZ:3:LEU:HA	1.86	0.57
1:AU:39:ASN:HD21	1:AU:42:VAL:HG23	1.70	0.57
1:BK:124:TYR:HA	1:DW:22:GLN:HE21	1.69	0.57
1:BM:47:GLN:HG3	1:BM:58:VAL:HG22	1.87	0.57
1:BQ:88:LEU:HD13	1:BQ:97:ILE:HD13	1.87	0.57
1:BS:2:ARG:NH1	1:EC:124:TYR:OXT	2.37	0.57
1:BZ:45:LEU:HD11	1:BZ:58:VAL:HG13	1.86	0.57
1:CE:124:TYR:CE2	1:FO:19:VAL:HB	2.39	0.57
1:CP:1:MET:HG2	1:DJ:123:ASN:OD1	2.05	0.57
1:CP:15:ARG:NH1	1:DJ:103:THR:HG21	2.20	0.57
1:CW:39:ASN:HD21	1:CW:42:VAL:HG23	1.70	0.57
1:DM:103:THR:HG21	1:GT:15:ARG:NH1	2.20	0.57
1:DR:39:ASN:HD21	1:DR:42:VAL:HG23	1.70	0.57
1:DR:47:GLN:HG3	1:DR:58:VAL:HG22	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EB:58:VAL:HG11	1:GB:117:VAL:HG22	1.86	0.57
1:ED:39:ASN:HD21	1:ED:42:VAL:HG23	1.70	0.57
1:EH:99:LYS:HE2	1:EO:15:ARG:NH1	2.20	0.57
1:EY:39:ASN:HD21	1:EY:42:VAL:HG23	1.70	0.57
1:FQ:47:GLN:HG3	1:FQ:58:VAL:HG22	1.87	0.57
1:GV:88:LEU:HD13	1:GV:97:ILE:HD13	1.87	0.57
1:AI:39:ASN:HD21	1:AI:42:VAL:HG23	1.70	0.57
1:AJ:88:LEU:HD13	1:AJ:97:ILE:HD13	1.87	0.57
1:AP:88:LEU:HD13	1:AP:97:ILE:HD13	1.87	0.57
1:AV:88:LEU:HD13	1:AV:97:ILE:HD13	1.87	0.57
1:AX:39:ASN:HD21	1:AX:42:VAL:HG23	1.70	0.57
1:BB:88:LEU:HD13	1:BB:97:ILE:HD13	1.87	0.57
1:BV:47:GLN:HG3	1:BV:58:VAL:HG22	1.87	0.57
1:CF:45:LEU:HD11	1:CF:58:VAL:HG13	1.86	0.57
1:CG:30:VAL:HG22	1:CG:42:VAL:HG12	1.86	0.57
1:CI:88:LEU:HD13	1:CI:97:ILE:HD13	1.87	0.57
1:DA:88:LEU:HD13	1:DA:97:ILE:HD13	1.87	0.57
1:DF:39:ASN:HD21	1:DF:42:VAL:HG23	1.70	0.57
1:DM:10:VAL:HG21	1:GT:103:THR:HG22	1.85	0.57
1:EB:10:VAL:HG21	1:GB:103:THR:HG22	1.87	0.57
1:ED:47:GLN:HG3	1:ED:58:VAL:HG22	1.87	0.57
1:FH:47:GLN:HG3	1:FH:58:VAL:HG22	1.87	0.57
1:FN:39:ASN:HD21	1:FN:42:VAL:HG23	1.70	0.57
1:FR:88:LEU:HD13	1:FR:97:ILE:HD13	1.87	0.57
1:FV:103:THR:HG22	1:GS:10:VAL:HG21	1.87	0.57
1:GA:45:LEU:HD11	1:GA:58:VAL:HG13	1.86	0.57
1:GO:47:GLN:HG3	1:GO:58:VAL:HG22	1.87	0.57
1:AG:88:LEU:HD13	1:AG:97:ILE:HD13	1.87	0.56
1:AW:30:VAL:HG22	1:AW:42:VAL:HG12	1.86	0.56
1:BK:58:VAL:HG11	1:DW:117:VAL:CG2	2.35	0.56
1:BM:98:THR:HG22	1:EY:118:ASP:CG	2.25	0.56
1:BO:20:SER:O	1:DZ:122:ASN:HB2	2.04	0.56
1:BT:116:PRO:O	1:DN:56:ARG:NH1	2.35	0.56
1:BW:88:LEU:HD13	1:BW:97:ILE:HD13	1.87	0.56
1:CZ:39:ASN:HD21	1:CZ:42:VAL:HG23	1.70	0.56
1:DA:103:THR:HG21	1:DE:15:ARG:NH1	2.20	0.56
1:DC:103:THR:HG21	1:GO:15:ARG:NH1	2.18	0.56
1:DG:45:LEU:HD11	1:DG:58:VAL:HG13	1.86	0.56
1:DI:47:GLN:HG3	1:DI:58:VAL:HG22	1.87	0.56
1:DU:47:GLN:HG3	1:DU:58:VAL:HG22	1.87	0.56
1:DW:30:VAL:HG22	1:DW:42:VAL:HG12	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FQ:1:MET:HE2	1:FQ:3:LEU:HA	1.86	0.56
1:AC:118:ASP:HB3	1:DO:98:THR:HG22	1.87	0.56
1:AD:88:LEU:HD13	1:AD:97:ILE:HD13	1.87	0.56
1:AD:99:LYS:HE2	1:BC:15:ARG:HH11	1.70	0.56
1:AK:10:VAL:HG21	1:FO:103:THR:HG22	1.87	0.56
1:AP:45:LEU:HD11	1:AP:58:VAL:HG13	1.86	0.56
1:AR:39:ASN:HD21	1:AR:42:VAL:HG23	1.70	0.56
1:AX:62:LEU:HD21	1:EJ:103:THR:OG1	2.06	0.56
1:BG:47:GLN:HG3	1:BG:58:VAL:HG22	1.87	0.56
1:BN:45:LEU:HD11	1:BN:58:VAL:HG13	1.86	0.56
1:BX:30:VAL:HG22	1:BX:42:VAL:HG12	1.86	0.56
1:CB:39:ASN:HD21	1:CB:42:VAL:HG23	1.70	0.56
1:CH:39:ASN:HD21	1:CH:42:VAL:HG23	1.70	0.56
1:CU:88:LEU:HD13	1:CU:97:ILE:HD13	1.87	0.56
1:CY:30:VAL:HG22	1:CY:42:VAL:HG12	1.86	0.56
1:DO:39:ASN:HD21	1:DO:42:VAL:HG23	1.70	0.56
1:DP:88:LEU:HD13	1:DP:97:ILE:HD13	1.87	0.56
1:DU:67:VAL:HG12	1:DU:77:THR:HG22	1.85	0.56
1:DV:99:LYS:HE2	1:GE:15:ARG:HD3	1.85	0.56
1:DY:103:THR:HG21	1:FY:15:ARG:NH1	2.21	0.56
1:EV:47:GLN:HG3	1:EV:58:VAL:HG22	1.87	0.56
1:EY:47:GLN:HG3	1:EY:58:VAL:HG22	1.87	0.56
1:FE:47:GLN:HG3	1:FE:58:VAL:HG22	1.87	0.56
1:GT:30:VAL:HG22	1:GT:42:VAL:HG12	1.86	0.56
1:AA:3:LEU:HG	1:BI:123:ASN:HB3	1.88	0.56
1:AA:45:LEU:HD11	1:AA:58:VAL:HG13	1.86	0.56
1:AE:30:VAL:HG22	1:AE:42:VAL:HG12	1.86	0.56
1:AH:15:ARG:NH1	1:GD:99:LYS:HE2	2.20	0.56
1:AH:30:VAL:HG22	1:AH:42:VAL:HG12	1.86	0.56
1:AN:30:VAL:HG22	1:AN:42:VAL:HG12	1.86	0.56
1:AO:47:GLN:HG3	1:AO:58:VAL:HG22	1.87	0.56
1:AT:30:VAL:HG22	1:AT:42:VAL:HG12	1.86	0.56
1:AY:88:LEU:HD13	1:AY:97:ILE:HD13	1.87	0.56
1:BA:39:ASN:HD21	1:BA:42:VAL:HG23	1.70	0.56
1:BE:45:LEU:HD11	1:BE:58:VAL:HG13	1.86	0.56
1:BH:88:LEU:HD13	1:BH:97:ILE:HD13	1.87	0.56
1:BJ:39:ASN:HD21	1:BJ:42:VAL:HG23	1.70	0.56
1:BN:15:ARG:NH1	1:DZ:103:THR:HG21	2.17	0.56
1:BS:47:GLN:HG3	1:BS:58:VAL:HG22	1.87	0.56
1:BU:30:VAL:HG22	1:BU:42:VAL:HG12	1.86	0.56
1:BY:47:GLN:HG3	1:BY:58:VAL:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:30:VAL:HG22	1:CD:42:VAL:HG12	1.86	0.56
1:CX:103:THR:HG21	1:DK:15:ARG:NH1	2.20	0.56
1:DB:30:VAL:HG22	1:DB:42:VAL:HG12	1.86	0.56
1:DK:30:VAL:HG22	1:DK:42:VAL:HG12	1.86	0.56
1:DL:39:ASN:HD21	1:DL:42:VAL:HG23	1.70	0.56
1:DS:88:LEU:HD13	1:DS:97:ILE:HD13	1.87	0.56
1:EE:103:THR:HG21	1:EU:15:ARG:NH1	2.20	0.56
1:EM:39:ASN:HD21	1:EM:42:VAL:HG23	1.70	0.56
1:EW:88:LEU:HD13	1:EW:97:ILE:HD13	1.87	0.56
1:FH:39:ASN:HD21	1:FH:42:VAL:HG23	1.70	0.56
1:FS:103:THR:HG21	1:GP:15:ARG:NH1	2.19	0.56
1:FS:103:THR:HG22	1:GP:10:VAL:HG21	1.87	0.56
1:FT:47:GLN:HG3	1:FT:58:VAL:HG22	1.87	0.56
1:FV:30:VAL:HG22	1:FV:42:VAL:HG12	1.86	0.56
1:FX:88:LEU:HD13	1:FX:97:ILE:HD13	1.87	0.56
1:GN:30:VAL:HG22	1:GN:42:VAL:HG12	1.86	0.56
1:GP:88:LEU:HD13	1:GP:97:ILE:HD13	1.87	0.56
1:GX:39:ASN:HD21	1:GX:42:VAL:HG23	1.70	0.56
1:AC:118:ASP:CG	1:DO:98:THR:HG22	2.26	0.56
1:AG:103:THR:HG21	1:BF:15:ARG:NH1	2.19	0.56
1:BV:39:ASN:HD21	1:BV:42:VAL:HG23	1.70	0.56
1:CM:30:VAL:HG22	1:CM:42:VAL:HG12	1.86	0.56
1:DZ:30:VAL:HG22	1:DZ:42:VAL:HG12	1.86	0.56
1:EK:88:LEU:HD13	1:EK:97:ILE:HD13	1.87	0.56
1:EV:2:ARG:HH12	1:FG:124:TYR:C	2.08	0.56
1:FA:30:VAL:HG22	1:FA:42:VAL:HG12	1.86	0.56
1:FR:45:LEU:HD11	1:FR:58:VAL:HG13	1.86	0.56
1:GJ:88:LEU:HD13	1:GJ:97:ILE:HD13	1.87	0.56
1:GX:1:MET:HE2	1:GX:3:LEU:HA	1.87	0.56
1:AO:39:ASN:HD21	1:AO:42:VAL:HG23	1.70	0.56
1:AV:78:ILE:HD13	1:EF:91:THR:OG1	2.04	0.56
1:AY:65:PRO:HB3	1:AY:79:LYS:HG2	1.88	0.56
1:CE:22:GLN:NE2	1:FQ:124:TYR:HA	2.20	0.56
1:DO:47:GLN:HG3	1:DO:58:VAL:HG22	1.87	0.56
1:EA:39:ASN:HD21	1:EA:42:VAL:HG23	1.70	0.56
1:EH:120:GLY:HA2	1:EO:47:GLN:HE22	1.71	0.56
1:EN:65:PRO:HB3	1:EN:79:LYS:HG2	1.88	0.56
1:FC:88:LEU:HD13	1:FC:97:ILE:HD13	1.87	0.56
1:FD:30:VAL:HG22	1:FD:42:VAL:HG12	1.86	0.56
1:FD:123:ASN:HB3	1:FF:3:LEU:HG	1.88	0.56
1:FF:88:LEU:HD13	1:FF:97:ILE:HD13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GC:39:ASN:HD21	1:GC:42:VAL:HG23	1.70	0.56
1:GD:88:LEU:HD13	1:GD:97:ILE:HD13	1.87	0.56
1:GL:39:ASN:HD21	1:GL:42:VAL:HG23	1.70	0.56
1:AC:39:ASN:HD21	1:AC:42:VAL:HG23	1.70	0.56
1:AV:45:LEU:HD11	1:AV:58:VAL:HG13	1.86	0.56
1:AY:103:THR:HG21	1:EI:15:ARG:NH1	2.21	0.56
1:BG:39:ASN:HD21	1:BG:42:VAL:HG23	1.70	0.56
1:BH:120:GLY:HA2	1:BO:47:GLN:HE22	1.70	0.56
1:BJ:47:GLN:HG3	1:BJ:58:VAL:HG22	1.87	0.56
1:BQ:3:LEU:HG	1:EC:123:ASN:HB3	1.86	0.56
1:BS:39:ASN:HD21	1:BS:42:VAL:HG23	1.70	0.56
1:BT:103:THR:OG1	1:DN:62:LEU:HD21	2.05	0.56
1:CN:47:GLN:HG3	1:CN:58:VAL:HG22	1.87	0.56
1:CO:65:PRO:HB3	1:CO:79:LYS:HG2	1.88	0.56
1:CT:47:GLN:HG3	1:CT:58:VAL:HG22	1.87	0.56
1:DC:39:ASN:HD21	1:DC:42:VAL:HG23	1.70	0.56
1:DM:45:LEU:HD11	1:DM:58:VAL:HG13	1.86	0.56
1:DQ:30:VAL:HG22	1:DQ:42:VAL:HG12	1.86	0.56
1:EE:88:LEU:HD13	1:EE:97:ILE:HD13	1.87	0.56
1:EM:47:GLN:HG3	1:EM:58:VAL:HG22	1.87	0.56
1:FB:39:ASN:HD21	1:FB:42:VAL:HG23	1.70	0.56
1:FL:65:PRO:HB3	1:FL:79:LYS:HG2	1.88	0.56
1:GI:47:GLN:HG3	1:GI:58:VAL:HG22	1.87	0.56
1:GR:47:GLN:HG3	1:GR:58:VAL:HG22	1.87	0.56
1:AF:2:ARG:NH1	1:BC:124:TYR:OXT	2.39	0.56
1:AF:15:ARG:NH1	1:DR:103:THR:HG21	2.21	0.56
1:AU:121:LEU:HD22	1:EE:20:SER:HA	1.88	0.56
1:BE:65:PRO:HB3	1:BE:79:LYS:HG2	1.88	0.56
1:BM:39:ASN:HD21	1:BM:42:VAL:HG23	1.70	0.56
1:BY:2:ARG:HH12	1:DQ:124:TYR:C	2.08	0.56
1:CT:39:ASN:HD21	1:CT:42:VAL:HG23	1.70	0.56
1:DA:3:LEU:HG	1:DE:123:ASN:HB3	1.87	0.56
1:DB:124:TYR:C	1:GL:2:ARG:HH12	2.09	0.56
1:DD:65:PRO:HB3	1:DD:79:LYS:HG2	1.88	0.56
1:DF:47:GLN:HG3	1:DF:58:VAL:HG22	1.87	0.56
1:EJ:39:ASN:HD21	1:EJ:42:VAL:HG23	1.70	0.56
1:EL:99:LYS:O	1:EL:103:THR:HG23	2.06	0.56
1:EW:65:PRO:HB3	1:EW:79:LYS:HG2	1.88	0.56
1:FE:39:ASN:HD21	1:FE:42:VAL:HG23	1.70	0.56
1:FR:65:PRO:HB3	1:FR:79:LYS:HG2	1.88	0.56
1:FW:1:MET:HE2	1:FW:3:LEU:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GM:65:PRO:HB3	1:GM:79:LYS:HG2	1.88	0.56
1:GO:39:ASN:HD21	1:GO:42:VAL:HG23	1.70	0.56
1:GP:65:PRO:HB3	1:GP:79:LYS:HG2	1.88	0.56
1:GU:39:ASN:HD21	1:GU:42:VAL:HG23	1.70	0.56
1:AF:39:ASN:HD21	1:AF:42:VAL:HG23	1.70	0.56
1:AF:103:THR:HG21	1:DR:15:ARG:HH11	1.70	0.56
1:AH:22:GLN:NE2	1:GD:124:TYR:OXT	2.38	0.56
1:AJ:65:PRO:HB3	1:AJ:79:LYS:HG2	1.88	0.56
1:AS:88:LEU:HD13	1:AS:97:ILE:HD13	1.87	0.56
1:AV:65:PRO:HB3	1:AV:79:LYS:HG2	1.88	0.56
1:BR:99:LYS:O	1:BR:103:THR:HG23	2.06	0.56
1:BZ:88:LEU:HD13	1:BZ:97:ILE:HD13	1.87	0.56
1:CD:99:LYS:O	1:CD:103:THR:HG23	2.06	0.56
1:CI:65:PRO:HB3	1:CI:79:LYS:HG2	1.88	0.56
1:CM:99:LYS:O	1:CM:103:THR:HG23	2.06	0.56
1:CM:124:TYR:C	1:DI:2:ARG:HH12	2.09	0.56
1:CR:88:LEU:HD13	1:CR:97:ILE:HD13	1.87	0.56
1:CV:103:THR:HG21	1:GM:15:ARG:NH1	2.17	0.56
1:DK:99:LYS:O	1:DK:103:THR:HG23	2.06	0.56
1:DN:99:LYS:O	1:DN:103:THR:HG23	2.06	0.56
1:EO:99:LYS:O	1:EO:103:THR:HG23	2.06	0.56
1:EP:39:ASN:HD21	1:EP:42:VAL:HG23	1.70	0.56
1:EU:99:LYS:O	1:EU:103:THR:HG23	2.06	0.56
1:FI:65:PRO:HB3	1:FI:79:LYS:HG2	1.88	0.56
1:GM:88:LEU:HD13	1:GM:97:ILE:HD13	1.87	0.56
1:GS:65:PRO:HB3	1:GS:79:LYS:HG2	1.88	0.56
1:GV:65:PRO:HB3	1:GV:79:LYS:HG2	1.88	0.56
1:GW:99:LYS:O	1:GW:103:THR:HG23	2.06	0.56
1:AB:15:ARG:NH1	1:FX:103:THR:HG21	2.21	0.56
1:AH:15:ARG:HH11	1:GD:99:LYS:HE2	1.69	0.56
1:AP:65:PRO:HB3	1:AP:79:LYS:HG2	1.88	0.56
1:BI:30:VAL:HG22	1:BI:42:VAL:HG12	1.86	0.56
1:CB:47:GLN:HG3	1:CB:58:VAL:HG22	1.87	0.56
1:CC:124:TYR:OXT	1:GK:22:GLN:NE2	2.39	0.56
1:CF:124:TYR:OXT	1:GN:22:GLN:NE2	2.39	0.56
1:DC:124:TYR:CE1	1:GO:2:ARG:HD2	2.41	0.56
1:DW:99:LYS:O	1:DW:103:THR:HG23	2.06	0.56
1:EA:1:MET:HE2	1:EA:3:LEU:HA	1.88	0.56
1:EG:1:MET:HE2	1:EG:3:LEU:HA	1.86	0.56
1:EH:45:LEU:HD11	1:EH:58:VAL:HG13	1.86	0.56
1:FU:88:LEU:HD13	1:FU:97:ILE:HD13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GD:65:PRO:HB3	1:GD:79:LYS:HG2	1.88	0.56
1:AA:65:PRO:HB3	1:AA:79:LYS:HG2	1.88	0.56
1:AF:47:GLN:HG3	1:AF:58:VAL:HG22	1.87	0.56
1:AG:15:ARG:NH1	1:BF:103:THR:HG21	2.18	0.56
1:AI:47:GLN:HG3	1:AI:58:VAL:HG22	1.87	0.56
1:BP:47:GLN:HG3	1:BP:58:VAL:HG22	1.87	0.56
1:CK:39:ASN:HD21	1:CK:42:VAL:HG23	1.70	0.56
1:CW:47:GLN:HG3	1:CW:58:VAL:HG22	1.87	0.56
1:DV:65:PRO:HB3	1:DV:79:LYS:HG2	1.88	0.56
1:EF:99:LYS:O	1:EF:103:THR:HG23	2.06	0.56
1:EJ:47:GLN:HG3	1:EJ:58:VAL:HG22	1.87	0.56
1:FC:65:PRO:HB3	1:FC:79:LYS:HG2	1.88	0.56
1:FO:65:PRO:HB3	1:FO:79:LYS:HG2	1.88	0.56
1:FY:99:LYS:O	1:FY:103:THR:HG23	2.06	0.56
1:GC:47:GLN:HG3	1:GC:58:VAL:HG22	1.87	0.56
1:GL:47:GLN:HG3	1:GL:58:VAL:HG22	1.87	0.56
1:GN:99:LYS:O	1:GN:103:THR:HG23	2.06	0.56
1:AA:88:LEU:HD13	1:AA:97:ILE:HD13	1.87	0.55
1:AK:15:ARG:NH1	1:FO:103:THR:HG21	2.21	0.55
1:AK:99:LYS:O	1:AK:103:THR:HG23	2.06	0.55
1:AK:122:ASN:HB2	1:FP:20:SER:O	2.06	0.55
1:AQ:99:LYS:O	1:AQ:103:THR:HG23	2.06	0.55
1:BF:99:LYS:O	1:BF:103:THR:HG23	2.06	0.55
1:BU:99:LYS:O	1:BU:103:THR:HG23	2.06	0.55
1:CH:47:GLN:HG3	1:CH:58:VAL:HG22	1.87	0.55
1:CJ:124:TYR:OXT	1:CQ:2:ARG:NH1	2.40	0.55
1:CX:65:PRO:HB3	1:CX:79:LYS:HG2	1.88	0.55
1:CX:88:LEU:HD13	1:CX:97:ILE:HD13	1.87	0.55
1:DB:99:LYS:O	1:DB:103:THR:HG23	2.06	0.55
1:DG:88:LEU:HD13	1:DG:97:ILE:HD13	1.87	0.55
1:DI:15:ARG:NH1	1:GU:103:THR:HG21	2.21	0.55
1:DM:99:LYS:HE2	1:GT:15:ARG:HH11	1.71	0.55
1:DP:65:PRO:HB3	1:DP:79:LYS:HG2	1.88	0.55
1:DU:2:ARG:HH12	1:GQ:124:TYR:C	2.10	0.55
1:DX:39:ASN:HD21	1:DX:42:VAL:HG23	1.70	0.55
1:DZ:99:LYS:O	1:DZ:103:THR:HG23	2.06	0.55
1:EA:2:ARG:HH12	1:FY:124:TYR:C	2.09	0.55
1:EA:47:GLN:HG3	1:EA:58:VAL:HG22	1.87	0.55
1:EB:88:LEU:HD13	1:EB:97:ILE:HD13	1.87	0.55
1:EI:99:LYS:O	1:EI:103:THR:HG23	2.06	0.55
1:EV:39:ASN:HD21	1:EV:42:VAL:HG23	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FL:88:LEU:HD13	1:FL:97:ILE:HD13	1.87	0.55
1:FM:99:LYS:O	1:FM:103:THR:HG23	2.06	0.55
1:FW:39:ASN:HD21	1:FW:42:VAL:HG23	1.70	0.55
1:GU:47:GLN:HG3	1:GU:58:VAL:HG22	1.87	0.55
1:AD:65:PRO:HB3	1:AD:79:LYS:HG2	1.88	0.55
1:AN:99:LYS:O	1:AN:103:THR:HG23	2.06	0.55
1:AW:124:TYR:C	1:FE:2:ARG:HH12	2.09	0.55
1:BA:47:GLN:HG3	1:BA:58:VAL:HG22	1.87	0.55
1:BE:88:LEU:HD13	1:BE:97:ILE:HD13	1.87	0.55
1:BI:99:LYS:O	1:BI:103:THR:HG23	2.06	0.55
1:BJ:1:MET:HE2	1:BJ:3:LEU:HA	1.88	0.55
1:CC:121:LEU:HD11	1:GL:19:VAL:O	2.05	0.55
1:CL:65:PRO:HB3	1:CL:79:LYS:HG2	1.88	0.55
1:CO:88:LEU:HD13	1:CO:97:ILE:HD13	1.87	0.55
1:CQ:103:THR:HG21	1:GC:15:ARG:NH1	2.21	0.55
1:DE:99:LYS:O	1:DE:103:THR:HG23	2.06	0.55
1:DS:103:THR:HG22	1:GQ:10:VAL:HG21	1.89	0.55
1:DV:120:GLY:HA2	1:GE:47:GLN:HE22	1.71	0.55
1:DY:88:LEU:HD13	1:DY:97:ILE:HD13	1.87	0.55
1:EB:1:MET:SD	1:GB:111:GLN:HB2	2.45	0.55
1:ES:39:ASN:HD21	1:ES:42:VAL:HG23	1.70	0.55
1:FK:39:ASN:HD21	1:FK:42:VAL:HG23	1.70	0.55
1:GR:39:ASN:HD21	1:GR:42:VAL:HG23	1.70	0.55
1:AH:99:LYS:O	1:AH:103:THR:HG23	2.06	0.55
1:AO:8:LEU:HD11	1:EA:107:TRP:CE2	2.42	0.55
1:AR:47:GLN:HG3	1:AR:58:VAL:HG22	1.87	0.55
1:AU:47:GLN:HG3	1:AU:58:VAL:HG22	1.87	0.55
1:BB:65:PRO:HB3	1:BB:79:LYS:HG2	1.88	0.55
1:BQ:65:PRO:HB3	1:BQ:79:LYS:HG2	1.88	0.55
1:CI:15:ARG:NH1	1:GH:103:THR:HG21	2.17	0.55
1:CQ:47:GLN:HG3	1:CQ:58:VAL:HG22	1.87	0.55
1:CR:65:PRO:HB3	1:CR:79:LYS:HG2	1.88	0.55
1:DT:30:VAL:HG22	1:DT:42:VAL:HG12	1.86	0.55
1:DV:88:LEU:HD13	1:DV:97:ILE:HD13	1.87	0.55
1:ET:88:LEU:HD13	1:ET:97:ILE:HD13	1.87	0.55
1:FD:99:LYS:O	1:FD:103:THR:HG23	2.06	0.55
1:FQ:39:ASN:HD21	1:FQ:42:VAL:HG23	1.70	0.55
1:GE:99:LYS:O	1:GE:103:THR:HG23	2.06	0.55
1:GG:65:PRO:HB3	1:GG:79:LYS:HG2	1.88	0.55
1:GT:99:LYS:O	1:GT:103:THR:HG23	2.06	0.55
1:AM:88:LEU:HD13	1:AM:97:ILE:HD13	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:65:PRO:HB3	1:AS:79:LYS:HG2	1.88	0.55
1:BN:88:LEU:HD13	1:BN:97:ILE:HD13	1.87	0.55
1:BO:99:LYS:O	1:BO:103:THR:HG23	2.06	0.55
1:CF:65:PRO:HB3	1:CF:79:LYS:HG2	1.88	0.55
1:CU:99:LYS:HE2	1:DH:15:ARG:HH11	1.71	0.55
1:DA:65:PRO:HB3	1:DA:79:LYS:HG2	1.88	0.55
1:EH:102:GLN:HB2	1:EO:10:VAL:HG13	1.88	0.55
1:EK:65:PRO:HB3	1:EK:79:LYS:HG2	1.88	0.55
1:EN:88:LEU:HD13	1:EN:97:ILE:HD13	1.87	0.55
1:FE:1:MET:HE2	1:FE:3:LEU:HA	1.87	0.55
1:FJ:99:LYS:O	1:FJ:103:THR:HG23	2.06	0.55
1:FW:47:GLN:HG3	1:FW:58:VAL:HG22	1.87	0.55
1:GK:99:LYS:O	1:GK:103:THR:HG23	2.06	0.55
1:BH:65:PRO:HB3	1:BH:79:LYS:HG2	1.88	0.55
1:BL:99:LYS:O	1:BL:103:THR:HG23	2.06	0.55
1:BN:118:ASP:HB3	1:DZ:98:THR:HG22	1.88	0.55
1:BT:88:LEU:HD13	1:BT:97:ILE:HD13	1.87	0.55
1:BX:99:LYS:O	1:BX:103:THR:HG23	2.06	0.55
1:CC:124:TYR:HA	1:GK:22:GLN:HE21	1.69	0.55
1:CV:99:LYS:O	1:CV:103:THR:HG23	2.06	0.55
1:DJ:65:PRO:HB3	1:DJ:79:LYS:HG2	1.88	0.55
1:DM:88:LEU:HD13	1:DM:97:ILE:HD13	1.87	0.55
1:DQ:99:LYS:O	1:DQ:103:THR:HG23	2.06	0.55
1:EX:30:VAL:HG22	1:EX:42:VAL:HG12	1.86	0.55
1:FO:88:LEU:HD13	1:FO:97:ILE:HD13	1.87	0.55
1:FS:99:LYS:O	1:FS:103:THR:HG23	2.06	0.55
1:AE:10:VAL:HG13	1:GA:102:GLN:CB	2.37	0.55
1:AK:123:ASN:OD1	1:FO:1:MET:HB3	2.06	0.55
1:AR:78:ILE:HD13	1:ED:91:THR:HB	1.89	0.55
1:AT:99:LYS:O	1:AT:103:THR:HG23	2.06	0.55
1:AZ:99:LYS:O	1:AZ:103:THR:HG23	2.06	0.55
1:BC:99:LYS:O	1:BC:103:THR:HG23	2.06	0.55
1:BT:65:PRO:HB3	1:BT:79:LYS:HG2	1.88	0.55
1:CP:99:LYS:O	1:CP:103:THR:HG23	2.06	0.55
1:DC:68:VAL:HG11	1:GO:91:THR:CG2	2.36	0.55
1:DG:65:PRO:HB3	1:DG:79:LYS:HG2	1.88	0.55
1:EC:99:LYS:O	1:EC:103:THR:HG23	2.06	0.55
1:EH:65:PRO:HB3	1:EH:79:LYS:HG2	1.88	0.55
1:EN:122:ASN:HB2	1:FK:20:SER:O	2.07	0.55
1:ER:99:LYS:O	1:ER:103:THR:HG23	2.06	0.55
1:FP:99:LYS:O	1:FP:103:THR:HG23	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FZ:39:ASN:HD21	1:FZ:42:VAL:HG23	1.70	0.55
1:GA:65:PRO:HB3	1:GA:79:LYS:HG2	1.88	0.55
1:GI:1:MET:HE2	1:GI:3:LEU:HA	1.88	0.55
1:AH:103:THR:HG21	1:GD:15:ARG:NH1	2.18	0.55
1:BW:65:PRO:HB3	1:BW:79:LYS:HG2	1.88	0.55
1:DM:65:PRO:HB3	1:DM:79:LYS:HG2	1.88	0.55
1:ET:65:PRO:HB3	1:ET:79:LYS:HG2	1.88	0.55
1:FZ:47:GLN:HG3	1:FZ:58:VAL:HG22	1.87	0.55
1:GF:39:ASN:HD21	1:GF:42:VAL:HG23	1.70	0.55
1:AW:99:LYS:O	1:AW:103:THR:HG23	2.06	0.55
1:CY:99:LYS:O	1:CY:103:THR:HG23	2.06	0.55
1:DJ:88:LEU:HD13	1:DJ:97:ILE:HD13	1.87	0.55
1:EE:122:ASN:HB2	1:EV:20:SER:O	2.07	0.55
1:ES:2:ARG:HH12	1:FM:124:TYR:C	2.09	0.55
1:FG:99:LYS:O	1:FG:103:THR:HG23	2.06	0.55
1:FI:88:LEU:HD13	1:FI:97:ILE:HD13	1.87	0.55
1:AC:2:ARG:HH12	1:BI:124:TYR:C	2.10	0.55
1:AL:107:TRP:CE2	1:DX:8:LEU:HD11	2.42	0.55
1:BY:91:THR:HG22	1:FK:68:VAL:HG11	1.89	0.55
1:CC:88:LEU:HD13	1:CC:97:ILE:HD13	1.87	0.55
1:CF:88:LEU:HD13	1:CF:97:ILE:HD13	1.87	0.55
1:CJ:99:LYS:O	1:CJ:103:THR:HG23	2.06	0.55
1:DB:103:THR:HG22	1:GJ:10:VAL:CG2	2.34	0.55
1:EE:15:ARG:NH1	1:EU:103:THR:HG21	2.17	0.55
1:EH:88:LEU:HD13	1:EH:97:ILE:HD13	1.87	0.55
1:EQ:88:LEU:HD13	1:EQ:97:ILE:HD13	1.87	0.55
1:EX:99:LYS:O	1:EX:103:THR:HG23	2.06	0.55
1:EZ:65:PRO:HB3	1:EZ:79:LYS:HG2	1.88	0.55
1:FV:99:LYS:O	1:FV:103:THR:HG23	2.06	0.55
1:GB:99:LYS:O	1:GB:103:THR:HG23	2.06	0.55
1:GH:99:LYS:O	1:GH:103:THR:HG23	2.06	0.55
1:GQ:99:LYS:O	1:GQ:103:THR:HG23	2.06	0.55
1:AB:99:LYS:O	1:AB:103:THR:HG23	2.06	0.55
1:AE:99:LYS:O	1:AE:103:THR:HG23	2.06	0.55
1:AP:1:MET:SD	1:BU:111:GLN:HB2	2.47	0.55
1:AU:124:TYR:HA	1:EG:22:GLN:NE2	2.21	0.55
1:BK:65:PRO:HB3	1:BK:79:LYS:HG2	1.88	0.55
1:CG:117:VAL:HG22	1:CL:58:VAL:HG11	1.89	0.55
1:CL:88:LEU:HD13	1:CL:97:ILE:HD13	1.87	0.55
1:CS:15:ARG:NH1	1:DD:103:THR:HG21	2.22	0.55
1:CU:15:ARG:NH1	1:DH:103:THR:HG21	2.17	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:91:THR:HG22	1:GL:68:VAL:HG11	1.87	0.55
1:DD:88:LEU:HD13	1:DD:97:ILE:HD13	1.87	0.55
1:EB:65:PRO:HB3	1:EB:79:LYS:HG2	1.88	0.55
1:EZ:88:LEU:HD13	1:EZ:97:ILE:HD13	1.87	0.55
1:FU:65:PRO:HB3	1:FU:79:LYS:HG2	1.88	0.55
1:AA:15:ARG:NH1	1:BI:103:THR:HG21	2.15	0.54
1:AG:65:PRO:HB3	1:AG:79:LYS:HG2	1.88	0.54
1:AQ:15:ARG:NH1	1:FU:103:THR:HG21	2.22	0.54
1:CU:65:PRO:HB3	1:CU:79:LYS:HG2	1.88	0.54
1:CV:22:GLN:HE21	1:GM:124:TYR:C	2.10	0.54
1:DI:8:LEU:HD11	1:GU:107:TRP:CE2	2.41	0.54
1:DS:65:PRO:HB3	1:DS:79:LYS:HG2	1.88	0.54
1:DY:65:PRO:HB3	1:DY:79:LYS:HG2	1.88	0.54
1:GA:88:LEU:HD13	1:GA:97:ILE:HD13	1.87	0.54
1:GG:88:LEU:HD13	1:GG:97:ILE:HD13	1.87	0.54
1:BK:88:LEU:HD13	1:BK:97:ILE:HD13	1.87	0.54
1:BM:98:THR:HG22	1:EY:118:ASP:HB3	1.89	0.54
1:BZ:65:PRO:HB3	1:BZ:79:LYS:HG2	1.88	0.54
1:CA:99:LYS:O	1:CA:103:THR:HG23	2.06	0.54
1:CC:65:PRO:HB3	1:CC:79:LYS:HG2	1.88	0.54
1:CF:20:SER:O	1:FT:122:ASN:HB2	2.07	0.54
1:CG:22:GLN:HB3	1:GN:124:TYR:HB2	1.89	0.54
1:CG:99:LYS:O	1:CG:103:THR:HG23	2.06	0.54
1:CK:103:THR:HG22	1:FW:10:VAL:HG21	1.88	0.54
1:CY:83:SER:OG	1:GG:85:THR:OG1	2.25	0.54
1:EB:124:TYR:HA	1:GB:22:GLN:HE21	1.71	0.54
1:ET:103:THR:HG22	1:FG:10:VAL:HG21	1.89	0.54
1:FP:10:VAL:HG21	1:GV:103:THR:HG22	1.88	0.54
1:GJ:65:PRO:HB3	1:GJ:79:LYS:HG2	1.88	0.54
1:CS:99:LYS:O	1:CS:103:THR:HG23	2.06	0.54
1:DO:2:ARG:NH1	1:GT:124:TYR:OXT	2.41	0.54
1:DT:99:LYS:O	1:DT:103:THR:HG23	2.06	0.54
1:DV:124:TYR:CD2	1:GF:19:VAL:HB	2.43	0.54
1:FA:99:LYS:O	1:FA:103:THR:HG23	2.06	0.54
1:FF:65:PRO:HB3	1:FF:79:LYS:HG2	1.88	0.54
1:GX:47:GLN:HG3	1:GX:58:VAL:HG22	1.87	0.54
1:AF:103:THR:HG21	1:DR:15:ARG:NH1	2.23	0.54
1:AM:65:PRO:HB3	1:AM:79:LYS:HG2	1.88	0.54
1:AW:15:ARG:NH1	1:FC:103:THR:HG21	2.23	0.54
1:BK:10:VAL:HG21	1:DW:103:THR:HG22	1.90	0.54
1:GS:88:LEU:HD13	1:GS:97:ILE:HD13	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:103:THR:HG21	1:FC:15:ARG:NH1	2.19	0.54
1:DV:103:THR:HG21	1:GE:15:ARG:NH1	2.22	0.54
1:EE:65:PRO:HB3	1:EE:79:LYS:HG2	1.88	0.54
1:AR:91:THR:HB	1:ED:78:ILE:HD13	1.90	0.54
1:AX:84:VAL:HG13	1:EJ:84:VAL:HG22	1.89	0.54
1:BN:65:PRO:HB3	1:BN:79:LYS:HG2	1.88	0.54
1:EG:39:ASN:HD21	1:EG:42:VAL:HG23	1.70	0.54
1:BP:103:THR:HG22	1:FB:10:VAL:HG21	1.90	0.54
1:CT:107:TRP:CE2	1:GF:8:LEU:HD11	2.43	0.54
1:DB:15:ARG:NH1	1:GJ:99:LYS:HE2	2.23	0.54
1:DH:99:LYS:O	1:DH:103:THR:HG23	2.06	0.54
1:EX:103:THR:HG21	1:FI:15:ARG:NH1	2.19	0.54
1:AD:99:LYS:HE2	1:BC:15:ARG:NH1	2.23	0.54
1:AN:111:GLN:HB2	1:FR:1:MET:SD	2.48	0.54
1:AR:118:ASP:HB3	1:ED:98:THR:HG22	1.89	0.54
1:AY:10:VAL:HG21	1:EI:103:THR:HG22	1.88	0.54
1:CB:121:LEU:HD22	1:FL:20:SER:HA	1.89	0.54
1:EN:99:LYS:HE2	1:FJ:15:ARG:HH11	1.73	0.54
1:EX:10:VAL:HG21	1:FI:103:THR:HG22	1.90	0.54
1:AP:124:TYR:HA	1:BU:22:GLN:HE21	1.73	0.54
1:AS:78:ILE:HD13	1:EL:91:THR:OG1	2.08	0.54
1:AY:58:VAL:HG11	1:EI:117:VAL:CG2	2.37	0.54
1:EH:8:LEU:HD22	1:EO:106:ALA:HB1	1.89	0.54
1:BK:99:LYS:HE2	1:DW:15:ARG:HD3	1.90	0.54
1:CB:91:THR:HG22	1:FN:68:VAL:HG11	1.90	0.54
1:BK:102:GLN:CB	1:DW:10:VAL:HG13	2.38	0.53
1:BK:121:LEU:HD11	1:DX:19:VAL:O	2.08	0.53
1:DL:98:THR:HG22	1:GX:118:ASP:CG	2.29	0.53
1:FX:65:PRO:HB3	1:FX:79:LYS:HG2	1.88	0.53
1:AE:62:LEU:HD21	1:GA:103:THR:OG1	2.07	0.53
1:AP:20:SER:O	1:ED:122:ASN:HB2	2.08	0.53
1:BM:91:THR:HB	1:EY:78:ILE:HD13	1.89	0.53
1:BN:122:ASN:HB2	1:EA:20:SER:O	2.09	0.53
1:AB:1:MET:HG2	1:FX:123:ASN:OD1	2.08	0.53
1:BM:118:ASP:CG	1:EY:98:THR:HG22	2.29	0.53
1:CT:118:ASP:HB3	1:GF:98:THR:HG22	1.91	0.53
1:CU:103:THR:HG21	1:DH:15:ARG:NH1	2.23	0.53
1:DB:123:ASN:OD1	1:GJ:1:MET:HB3	2.08	0.53
1:CH:84:VAL:HG22	1:FT:84:VAL:HG13	1.90	0.53
1:CI:3:LEU:HG	1:GH:123:ASN:HB3	1.90	0.53
1:EI:22:GLN:HB3	1:EO:124:TYR:CB	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EQ:65:PRO:HB3	1:EQ:79:LYS:HG2	1.88	0.53
1:AG:103:THR:HG22	1:BF:10:VAL:HG21	1.91	0.53
1:AH:15:ARG:NH1	1:GD:103:THR:HG21	2.24	0.53
1:AQ:45:LEU:HD12	1:AQ:60:MET:HG2	1.91	0.53
1:BK:62:LEU:HD21	1:DW:103:THR:OG1	2.09	0.53
1:BT:99:LYS:HE2	1:DN:15:ARG:NH1	2.23	0.53
1:EH:102:GLN:CB	1:EO:10:VAL:HG13	2.38	0.53
1:FS:45:LEU:HD12	1:FS:60:MET:HG2	1.91	0.53
1:AG:3:LEU:HG	1:BF:123:ASN:HB3	1.90	0.53
1:CN:91:THR:HB	1:FZ:78:ILE:HD13	1.91	0.53
1:CP:47:GLN:HG3	1:CP:58:VAL:HG22	1.91	0.53
1:EU:45:LEU:HD12	1:EU:60:MET:HG2	1.91	0.53
1:FD:47:GLN:HG3	1:FD:58:VAL:HG22	1.91	0.53
1:GQ:47:GLN:HG3	1:GQ:58:VAL:HG22	1.91	0.53
1:AZ:45:LEU:HD12	1:AZ:60:MET:HG2	1.91	0.53
1:CV:45:LEU:HD12	1:CV:60:MET:HG2	1.91	0.53
1:CV:123:ASN:HB3	1:GM:3:LEU:HG	1.90	0.53
1:CY:45:LEU:HD12	1:CY:60:MET:HG2	1.91	0.53
1:DH:45:LEU:HD12	1:DH:60:MET:HG2	1.91	0.53
1:DN:45:LEU:HD12	1:DN:60:MET:HG2	1.91	0.53
1:EC:47:GLN:HG3	1:EC:58:VAL:HG22	1.91	0.53
1:FP:47:GLN:HG3	1:FP:58:VAL:HG22	1.91	0.53
1:GB:45:LEU:HD12	1:GB:60:MET:HG2	1.91	0.53
1:GJ:35:THR:HG22	1:GJ:37:ALA:H	1.74	0.53
1:GW:47:GLN:HG3	1:GW:58:VAL:HG22	1.91	0.53
1:AJ:35:THR:HG22	1:AJ:37:ALA:H	1.74	0.53
1:AO:91:THR:HG22	1:EA:68:VAL:HG11	1.91	0.53
1:BA:10:VAL:HG21	1:EM:103:THR:HG22	1.91	0.53
1:BJ:22:GLN:NE2	1:EV:124:TYR:HA	2.23	0.53
1:BL:47:GLN:HG3	1:BL:58:VAL:HG22	1.91	0.53
1:CD:45:LEU:HD12	1:CD:60:MET:HG2	1.91	0.53
1:DI:107:TRP:CE2	1:GU:8:LEU:HD11	2.44	0.53
1:DK:47:GLN:HG3	1:DK:58:VAL:HG22	1.91	0.53
1:DV:96:HIS:CG	1:GE:66:VAL:HG21	2.44	0.53
1:DW:47:GLN:HG3	1:DW:58:VAL:HG22	1.91	0.53
1:GK:47:GLN:HG3	1:GK:58:VAL:HG22	1.91	0.53
1:AI:2:ARG:HH12	1:BF:124:TYR:C	2.12	0.53
1:AK:83:SER:OG	1:FO:85:THR:OG1	2.27	0.53
1:AN:47:GLN:HG3	1:AN:58:VAL:HG22	1.91	0.53
1:AR:122:ASN:HB2	1:EB:20:SER:O	2.08	0.53
1:BG:91:THR:HG22	1:ES:68:VAL:HG11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:35:THR:HG22	1:BH:37:ALA:H	1.74	0.53
1:BH:103:THR:HG22	1:BO:10:VAL:HG21	1.91	0.53
1:BK:35:THR:HG22	1:BK:37:ALA:H	1.74	0.53
1:BO:45:LEU:HD12	1:BO:60:MET:HG2	1.91	0.53
1:CA:47:GLN:HG3	1:CA:58:VAL:HG22	1.91	0.53
1:CP:45:LEU:HD12	1:CP:60:MET:HG2	1.91	0.53
1:CV:15:ARG:NH1	1:GM:103:THR:HG21	2.24	0.53
1:DW:45:LEU:HD12	1:DW:60:MET:HG2	1.91	0.53
1:EI:47:GLN:HG3	1:EI:58:VAL:HG22	1.91	0.53
1:EQ:122:ASN:HB2	1:FN:20:SER:O	2.08	0.53
1:EX:45:LEU:HD12	1:EX:60:MET:HG2	1.91	0.53
1:FI:35:THR:HG22	1:FI:37:ALA:H	1.74	0.53
1:FX:35:THR:HG22	1:FX:37:ALA:H	1.74	0.53
1:GP:35:THR:HG22	1:GP:37:ALA:H	1.74	0.53
1:GV:35:THR:HG22	1:GV:37:ALA:H	1.74	0.53
1:AM:124:TYR:CD2	1:CB:19:VAL:HB	2.44	0.53
1:AT:103:THR:HG22	1:EZ:10:VAL:HG21	1.89	0.53
1:BE:103:THR:HG21	1:BL:15:ARG:NH1	2.24	0.53
1:BF:45:LEU:HD12	1:BF:60:MET:HG2	1.91	0.53
1:BT:35:THR:HG22	1:BT:37:ALA:H	1.74	0.53
1:BW:35:THR:HG22	1:BW:37:ALA:H	1.74	0.53
1:CG:47:GLN:HG3	1:CG:58:VAL:HG22	1.91	0.53
1:CJ:123:ASN:HB3	1:CO:3:LEU:HG	1.91	0.53
1:CO:35:THR:HG22	1:CO:37:ALA:H	1.74	0.53
1:CV:56:ARG:NH1	1:GM:116:PRO:O	2.38	0.53
1:CY:47:GLN:HG3	1:CY:58:VAL:HG22	1.91	0.53
1:DB:47:GLN:HG3	1:DB:58:VAL:HG22	1.91	0.53
1:DD:35:THR:HG22	1:DD:37:ALA:H	1.74	0.53
1:DP:35:THR:HG22	1:DP:37:ALA:H	1.74	0.53
1:DV:35:THR:HG22	1:DV:37:ALA:H	1.74	0.53
1:EK:35:THR:HG22	1:EK:37:ALA:H	1.74	0.53
1:ER:47:GLN:HG3	1:ER:58:VAL:HG22	1.91	0.53
1:EX:124:TYR:OXT	1:FK:2:ARG:NH1	2.41	0.53
1:FV:45:LEU:HD12	1:FV:60:MET:HG2	1.91	0.53
1:GB:47:GLN:HG3	1:GB:58:VAL:HG22	1.91	0.53
1:GS:35:THR:HG22	1:GS:37:ALA:H	1.74	0.53
1:GT:47:GLN:HG3	1:GT:58:VAL:HG22	1.91	0.53
1:GW:45:LEU:HD12	1:GW:60:MET:HG2	1.91	0.53
1:AB:47:GLN:HG3	1:AB:58:VAL:HG22	1.91	0.52
1:AG:35:THR:HG22	1:AG:37:ALA:H	1.74	0.52
1:AP:35:THR:HG22	1:AP:37:ALA:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:124:TYR:C	1:FW:2:ARG:HH12	2.12	0.52
1:BI:45:LEU:HD12	1:BI:60:MET:HG2	1.91	0.52
1:BI:47:GLN:HG3	1:BI:58:VAL:HG22	1.91	0.52
1:BK:124:TYR:OXT	1:DW:22:GLN:NE2	2.42	0.52
1:BM:3:LEU:N	1:EY:124:TYR:O	2.33	0.52
1:CI:103:THR:HG22	1:GH:10:VAL:HG21	1.90	0.52
1:CN:98:THR:HG22	1:FZ:118:ASP:CG	2.29	0.52
1:DG:35:THR:HG22	1:DG:37:ALA:H	1.74	0.52
1:DK:45:LEU:HD12	1:DK:60:MET:HG2	1.91	0.52
1:DN:47:GLN:HG3	1:DN:58:VAL:HG22	1.91	0.52
1:DZ:45:LEU:HD12	1:DZ:60:MET:HG2	1.91	0.52
1:EL:45:LEU:HD12	1:EL:60:MET:HG2	1.91	0.52
1:EO:45:LEU:HD12	1:EO:60:MET:HG2	1.91	0.52
1:EQ:103:THR:HG22	1:FM:10:VAL:HG21	1.90	0.52
1:EU:47:GLN:HG3	1:EU:58:VAL:HG22	1.91	0.52
1:FG:47:GLN:HG3	1:FG:58:VAL:HG22	1.91	0.52
1:GH:45:LEU:HD12	1:GH:60:MET:HG2	1.91	0.52
1:AK:47:GLN:HG3	1:AK:58:VAL:HG22	1.91	0.52
1:AN:45:LEU:HD12	1:AN:60:MET:HG2	1.91	0.52
1:BC:47:GLN:HG3	1:BC:58:VAL:HG22	1.91	0.52
1:BU:45:LEU:HD12	1:BU:60:MET:HG2	1.91	0.52
1:BU:47:GLN:HG3	1:BU:58:VAL:HG22	1.91	0.52
1:BZ:35:THR:HG22	1:BZ:37:ALA:H	1.74	0.52
1:CC:35:THR:HG22	1:CC:37:ALA:H	1.74	0.52
1:CC:124:TYR:C	1:GK:22:GLN:HE21	2.13	0.52
1:CG:10:VAL:HG13	1:CL:102:GLN:CB	2.39	0.52
1:FC:35:THR:HG22	1:FC:37:ALA:H	1.74	0.52
1:GQ:45:LEU:HD12	1:GQ:60:MET:HG2	1.91	0.52
1:AB:91:THR:OG1	1:FX:78:ILE:HD13	2.10	0.52
1:AE:45:LEU:HD12	1:AE:60:MET:HG2	1.91	0.52
1:AT:47:GLN:HG3	1:AT:58:VAL:HG22	1.91	0.52
1:AZ:47:GLN:HG3	1:AZ:58:VAL:HG22	1.91	0.52
1:CA:45:LEU:HD12	1:CA:60:MET:HG2	1.91	0.52
1:CM:45:LEU:HD12	1:CM:60:MET:HG2	1.91	0.52
1:CM:47:GLN:HG3	1:CM:58:VAL:HG22	1.91	0.52
1:CU:35:THR:HG22	1:CU:37:ALA:H	1.74	0.52
1:DB:45:LEU:HD12	1:DB:60:MET:HG2	1.91	0.52
1:DT:45:LEU:HD12	1:DT:60:MET:HG2	1.91	0.52
1:EE:35:THR:HG22	1:EE:37:ALA:H	1.74	0.52
1:FJ:45:LEU:HD12	1:FJ:60:MET:HG2	1.91	0.52
1:FJ:47:GLN:HG3	1:FJ:58:VAL:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GD:35:THR:HG22	1:GD:37:ALA:H	1.74	0.52
1:AD:35:THR:HG22	1:AD:37:ALA:H	1.74	0.52
1:AR:1:MET:HB3	1:ED:123:ASN:OD1	2.09	0.52
1:AT:15:ARG:NH1	1:EZ:103:THR:HG21	2.24	0.52
1:AW:47:GLN:HG3	1:AW:58:VAL:HG22	1.91	0.52
1:BQ:103:THR:HG21	1:EC:15:ARG:NH1	2.25	0.52
1:BW:103:THR:HG21	1:DQ:15:ARG:NH1	2.24	0.52
1:CU:103:THR:OG1	1:DH:62:LEU:HD21	2.09	0.52
1:DE:47:GLN:HG3	1:DE:58:VAL:HG22	1.91	0.52
1:DS:35:THR:HG22	1:DS:37:ALA:H	1.74	0.52
1:EE:103:THR:HG22	1:EU:10:VAL:HG21	1.91	0.52
1:EN:35:THR:HG22	1:EN:37:ALA:H	1.74	0.52
1:ER:45:LEU:HD12	1:ER:60:MET:HG2	1.91	0.52
1:EW:35:THR:HG22	1:EW:37:ALA:H	1.74	0.52
1:FM:45:LEU:HD12	1:FM:60:MET:HG2	1.91	0.52
1:FM:47:GLN:HG3	1:FM:58:VAL:HG22	1.91	0.52
1:AB:45:LEU:HD12	1:AB:60:MET:HG2	1.91	0.52
1:AF:98:THR:HG22	1:DR:118:ASP:CG	2.30	0.52
1:AM:118:ASP:OD2	1:CA:98:THR:HG22	2.08	0.52
1:AR:98:THR:HG22	1:ED:118:ASP:HB3	1.91	0.52
1:AT:45:LEU:HD12	1:AT:60:MET:HG2	1.91	0.52
1:BC:45:LEU:HD12	1:BC:60:MET:HG2	1.91	0.52
1:BF:47:GLN:HG3	1:BF:58:VAL:HG22	1.91	0.52
1:BH:15:ARG:NH1	1:BO:103:THR:HG21	2.18	0.52
1:CK:2:ARG:HH12	1:GH:124:TYR:C	2.12	0.52
1:CM:103:THR:HG21	1:DG:15:ARG:NH1	2.21	0.52
1:CR:35:THR:HG22	1:CR:37:ALA:H	1.74	0.52
1:CY:123:ASN:HB3	1:GG:3:LEU:HG	1.92	0.52
1:DQ:45:LEU:HD12	1:DQ:60:MET:HG2	1.91	0.52
1:DV:102:GLN:HB2	1:GE:10:VAL:HG13	1.91	0.52
1:EI:45:LEU:HD12	1:EI:60:MET:HG2	1.91	0.52
1:EO:47:GLN:HG3	1:EO:58:VAL:HG22	1.91	0.52
1:FA:47:GLN:HG3	1:FA:58:VAL:HG22	1.91	0.52
1:FP:45:LEU:HD12	1:FP:60:MET:HG2	1.91	0.52
1:FU:35:THR:HG22	1:FU:37:ALA:H	1.74	0.52
1:AP:121:LEU:HD11	1:BV:19:VAL:O	2.09	0.52
1:AS:10:VAL:CG2	1:EL:103:THR:HG22	2.38	0.52
1:CN:118:ASP:CG	1:FZ:98:THR:HG22	2.30	0.52
1:DQ:47:GLN:HG3	1:DQ:58:VAL:HG22	1.91	0.52
1:EB:124:TYR:OXT	1:GB:22:GLN:NE2	2.42	0.52
1:FD:45:LEU:HD12	1:FD:60:MET:HG2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FS:15:ARG:NH1	1:GP:103:THR:HG21	2.25	0.52
1:GT:45:LEU:HD12	1:GT:60:MET:HG2	1.91	0.52
1:AC:107:TRP:CE2	1:DO:8:LEU:HD11	2.44	0.52
1:AE:15:ARG:NH1	1:GA:99:LYS:HE2	2.25	0.52
1:AH:47:GLN:HG3	1:AH:58:VAL:HG22	1.91	0.52
1:AJ:10:VAL:CG2	1:BX:103:THR:HG22	2.38	0.52
1:AM:102:GLN:HB2	1:CA:10:VAL:HG13	1.92	0.52
1:BB:15:ARG:NH1	1:BR:103:THR:HG21	2.17	0.52
1:BZ:118:ASP:OD2	1:DT:98:THR:HG22	2.09	0.52
1:CG:45:LEU:HD12	1:CG:60:MET:HG2	1.91	0.52
1:EZ:35:THR:HG22	1:EZ:37:ALA:H	1.74	0.52
1:FG:45:LEU:HD12	1:FG:60:MET:HG2	1.91	0.52
1:FR:35:THR:HG22	1:FR:37:ALA:H	1.74	0.52
1:FV:47:GLN:HG3	1:FV:58:VAL:HG22	1.91	0.52
1:GE:45:LEU:HD12	1:GE:60:MET:HG2	1.91	0.52
1:AB:123:ASN:HB3	1:FX:3:LEU:HG	1.92	0.52
1:AN:47:GLN:HE22	1:FR:120:GLY:HA2	1.75	0.52
1:AR:84:VAL:HG13	1:ED:84:VAL:HG22	1.90	0.52
1:AV:35:THR:HG22	1:AV:37:ALA:H	1.74	0.52
1:BE:35:THR:HG22	1:BE:37:ALA:H	1.74	0.52
1:DM:35:THR:HG22	1:DM:37:ALA:H	1.74	0.52
1:EF:45:LEU:HD12	1:EF:60:MET:HG2	1.91	0.52
1:EH:35:THR:HG22	1:EH:37:ALA:H	1.74	0.52
1:EQ:35:THR:HG22	1:EQ:37:ALA:H	1.74	0.52
1:BG:2:ARG:HH12	1:BL:124:TYR:C	2.14	0.52
1:BN:103:THR:HG21	1:DZ:15:ARG:NH1	2.24	0.52
1:CL:35:THR:HG22	1:CL:37:ALA:H	1.74	0.52
1:CS:45:LEU:HD12	1:CS:60:MET:HG2	1.91	0.52
1:CS:47:GLN:HG3	1:CS:58:VAL:HG22	1.91	0.52
1:DA:15:ARG:NH1	1:DE:103:THR:HG21	2.22	0.52
1:DA:118:ASP:HB3	1:DE:98:THR:HG22	1.91	0.52
1:DH:47:GLN:HG3	1:DH:58:VAL:HG22	1.91	0.52
1:DL:103:THR:HG22	1:GX:10:VAL:HG21	1.92	0.52
1:EH:107:TRP:HH2	1:EO:29:PHE:CG	2.27	0.52
1:GK:45:LEU:HD12	1:GK:60:MET:HG2	1.91	0.52
1:GN:47:GLN:HG3	1:GN:58:VAL:HG22	1.91	0.52
1:AK:1:MET:HG2	1:FO:123:ASN:OD1	2.09	0.52
1:AY:35:THR:HG22	1:AY:37:ALA:H	1.74	0.52
1:BD:123:ASN:OD1	1:EP:1:MET:HB3	2.10	0.52
1:BX:45:LEU:HD12	1:BX:60:MET:HG2	1.91	0.52
1:EB:35:THR:HG22	1:EB:37:ALA:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EC:45:LEU:HD12	1:EC:60:MET:HG2	1.91	0.52
1:EE:99:LYS:HE2	1:EU:15:ARG:HH11	1.75	0.52
1:EX:15:ARG:NH1	1:FI:103:THR:HG21	2.24	0.52
1:FP:123:ASN:HB3	1:GV:3:LEU:HG	1.92	0.52
1:GN:45:LEU:HD12	1:GN:60:MET:HG2	1.91	0.52
1:AW:45:LEU:HD12	1:AW:60:MET:HG2	1.91	0.51
1:AZ:20:SER:HA	1:EI:121:LEU:HD22	1.93	0.51
1:BX:47:GLN:HG3	1:BX:58:VAL:HG22	1.91	0.51
1:BY:107:TRP:CE2	1:FK:8:LEU:HD11	2.45	0.51
1:GH:47:GLN:HG3	1:GH:58:VAL:HG22	1.91	0.51
1:AH:124:TYR:OXT	1:GF:2:ARG:NH1	2.44	0.51
1:AK:45:LEU:HD12	1:AK:60:MET:HG2	1.91	0.51
1:AL:10:VAL:HG21	1:DX:103:THR:HG22	1.91	0.51
1:AM:35:THR:HG22	1:AM:37:ALA:H	1.74	0.51
1:AN:22:GLN:HE21	1:FR:124:TYR:CA	2.23	0.51
1:AO:103:THR:HG22	1:EA:10:VAL:HG21	1.92	0.51
1:BD:92:TYR:CE2	1:EP:66:VAL:HG23	2.45	0.51
1:BR:47:GLN:HG3	1:BR:58:VAL:HG22	1.91	0.51
1:CD:47:GLN:HG3	1:CD:58:VAL:HG22	1.91	0.51
1:CP:98:THR:HG22	1:DJ:118:ASP:HB3	1.92	0.51
1:DE:45:LEU:HD12	1:DE:60:MET:HG2	1.91	0.51
1:FF:35:THR:HG22	1:FF:37:ALA:H	1.74	0.51
1:AF:8:LEU:HD11	1:DR:107:TRP:CE2	2.45	0.51
1:AH:45:LEU:HD12	1:AH:60:MET:HG2	1.91	0.51
1:AQ:47:GLN:HG3	1:AQ:58:VAL:HG22	1.91	0.51
1:AR:84:VAL:HG22	1:ED:84:VAL:HG13	1.91	0.51
1:BN:1:MET:HB3	1:DZ:123:ASN:OD1	2.10	0.51
1:BQ:35:THR:HG22	1:BQ:37:ALA:H	1.74	0.51
1:BR:45:LEU:HD12	1:BR:60:MET:HG2	1.91	0.51
1:CC:120:GLY:HA2	1:GK:47:GLN:HE22	1.75	0.51
1:CJ:45:LEU:HD12	1:CJ:60:MET:HG2	1.91	0.51
1:CJ:47:GLN:HG3	1:CJ:58:VAL:HG22	1.91	0.51
1:DM:99:LYS:HE2	1:GT:15:ARG:NH1	2.25	0.51
1:AC:10:VAL:HG21	1:DO:103:THR:HG22	1.92	0.51
1:BB:35:THR:HG22	1:BB:37:ALA:H	1.74	0.51
1:BL:45:LEU:HD12	1:BL:60:MET:HG2	1.91	0.51
1:CH:103:THR:HG22	1:FT:10:VAL:HG21	1.93	0.51
1:CS:103:THR:HG21	1:DD:15:ARG:NH1	2.21	0.51
1:EN:3:LEU:HG	1:FJ:123:ASN:HB3	1.92	0.51
1:EN:124:TYR:OXT	1:FJ:22:GLN:NE2	2.44	0.51
1:FO:35:THR:HG22	1:FO:37:ALA:H	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GA:35:THR:HG22	1:GA:37:ALA:H	1.74	0.51
1:AL:68:VAL:HG11	1:DX:91:THR:HG22	1.91	0.51
1:BP:121:LEU:HD22	1:EZ:20:SER:HA	1.93	0.51
1:BZ:124:TYR:OXT	1:DT:22:GLN:NE2	2.44	0.51
1:CG:15:ARG:HD3	1:CL:99:LYS:HE2	1.92	0.51
1:EH:99:LYS:HE2	1:EO:15:ARG:HD3	1.92	0.51
1:FS:47:GLN:HG3	1:FS:58:VAL:HG22	1.91	0.51
1:FS:98:THR:HG22	1:GP:118:ASP:HB3	1.93	0.51
1:FV:123:ASN:HB3	1:GS:3:LEU:HG	1.92	0.51
1:FY:45:LEU:HD12	1:FY:60:MET:HG2	1.91	0.51
1:FY:47:GLN:HG3	1:FY:58:VAL:HG22	1.91	0.51
1:GM:35:THR:HG22	1:GM:37:ALA:H	1.74	0.51
1:AA:35:THR:HG22	1:AA:37:ALA:H	1.74	0.51
1:AS:35:THR:HG22	1:AS:37:ALA:H	1.74	0.51
1:BO:47:GLN:HG3	1:BO:58:VAL:HG22	1.91	0.51
1:BQ:15:ARG:NH1	1:EC:103:THR:HG21	2.21	0.51
1:CV:47:GLN:HG3	1:CV:58:VAL:HG22	1.91	0.51
1:DA:35:THR:HG22	1:DA:37:ALA:H	1.74	0.51
1:EH:62:LEU:HD21	1:EO:103:THR:OG1	2.11	0.51
1:EP:2:ARG:NH1	1:FJ:124:TYR:OXT	2.44	0.51
1:GE:47:GLN:HG3	1:GE:58:VAL:HG22	1.91	0.51
1:AA:107:TRP:CE2	1:BI:8:LEU:HD11	2.45	0.51
1:AS:122:ASN:HB2	1:EM:20:SER:O	2.11	0.51
1:AX:78:ILE:HD13	1:EJ:91:THR:HB	1.92	0.51
1:BA:118:ASP:CG	1:EM:98:THR:HG22	2.30	0.51
1:BT:99:LYS:HE2	1:DN:15:ARG:HD3	1.92	0.51
1:CX:3:LEU:HG	1:DK:123:ASN:HB3	1.93	0.51
1:DI:3:LEU:N	1:GU:124:TYR:O	2.37	0.51
1:DT:47:GLN:HG3	1:DT:58:VAL:HG22	1.91	0.51
1:DZ:47:GLN:HG3	1:DZ:58:VAL:HG22	1.91	0.51
1:EL:47:GLN:HG3	1:EL:58:VAL:HG22	1.91	0.51
1:BN:35:THR:HG22	1:BN:37:ALA:H	1.74	0.51
1:CI:35:THR:HG22	1:CI:37:ALA:H	1.74	0.51
1:DC:91:THR:CG2	1:GO:68:VAL:HG11	2.41	0.51
1:DJ:35:THR:HG22	1:DJ:37:ALA:H	1.74	0.51
1:DS:15:ARG:NH1	1:GQ:103:THR:HG21	2.18	0.51
1:DY:35:THR:HG22	1:DY:37:ALA:H	1.74	0.51
1:EB:121:LEU:HD11	1:GC:19:VAL:O	2.10	0.51
1:EF:47:GLN:HG3	1:EF:58:VAL:HG22	1.91	0.51
1:FA:45:LEU:HD12	1:FA:60:MET:HG2	1.91	0.51
1:GG:35:THR:HG22	1:GG:37:ALA:H	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:58:VAL:HG11	1:BU:117:VAL:CG2	2.41	0.51
1:AX:123:ASN:OD1	1:EJ:1:MET:HB3	2.10	0.51
1:BH:10:VAL:CG2	1:BO:103:THR:HG22	2.40	0.51
1:BJ:103:THR:HG22	1:EV:10:VAL:HG21	1.91	0.51
1:CH:84:VAL:HG13	1:FT:84:VAL:HG22	1.93	0.51
1:CH:118:ASP:CG	1:FT:98:THR:HG22	2.31	0.51
1:CX:35:THR:HG22	1:CX:37:ALA:H	1.74	0.51
1:ET:35:THR:HG22	1:ET:37:ALA:H	1.74	0.51
1:AZ:22:GLN:HB3	1:EI:124:TYR:CB	2.39	0.51
1:BA:91:THR:HB	1:EM:78:ILE:HD13	1.93	0.51
1:CW:107:TRP:CE2	1:GI:8:LEU:HD11	2.45	0.51
1:ET:123:ASN:OD1	1:FG:1:MET:HG2	2.11	0.51
1:AB:8:LEU:HD11	1:FX:107:TRP:CE2	2.45	0.50
1:AE:20:SER:O	1:BC:122:ASN:HB2	2.11	0.50
1:BM:8:LEU:HD11	1:EY:107:TRP:CE2	2.45	0.50
1:BT:122:ASN:HB2	1:DO:20:SER:O	2.11	0.50
1:CZ:102:GLN:HB2	1:GL:10:VAL:HG13	1.94	0.50
1:DM:3:LEU:HG	1:GT:123:ASN:HB3	1.94	0.50
1:ET:85:THR:OG1	1:FG:83:SER:OG	2.28	0.50
1:AS:103:THR:HG21	1:EL:15:ARG:NH1	2.26	0.50
1:CF:35:THR:HG22	1:CF:37:ALA:H	1.74	0.50
1:FL:35:THR:HG22	1:FL:37:ALA:H	1.74	0.50
1:AE:47:GLN:HG3	1:AE:58:VAL:HG22	1.91	0.50
1:AM:120:GLY:HA2	1:CA:47:GLN:HE22	1.77	0.50
1:CT:91:THR:HB	1:GF:78:ILE:HD13	1.93	0.50
1:ET:122:ASN:HB2	1:FH:20:SER:O	2.12	0.50
1:EX:47:GLN:HG3	1:EX:58:VAL:HG22	1.91	0.50
1:EX:123:ASN:HB3	1:FI:3:LEU:HG	1.93	0.50
1:AN:124:TYR:CB	1:FS:22:GLN:HB3	2.38	0.50
1:AK:103:THR:HG22	1:FO:10:VAL:CG2	2.40	0.50
1:AM:103:THR:HG21	1:CA:15:ARG:NH1	2.27	0.50
1:BV:8:LEU:HD11	1:FH:107:TRP:CE2	2.46	0.50
1:BZ:15:ARG:NH1	1:DT:103:THR:HG21	2.21	0.50
1:CE:118:ASP:CG	1:FQ:98:THR:HG22	2.32	0.50
1:CW:2:ARG:NH1	1:DH:124:TYR:OXT	2.44	0.50
1:EQ:99:LYS:HE2	1:FM:15:ARG:HH11	1.77	0.50
1:FS:123:ASN:HB3	1:GP:3:LEU:HG	1.92	0.50
1:AI:91:THR:CG2	1:DU:68:VAL:HG11	2.40	0.50
1:AZ:8:LEU:HD11	1:EW:107:TRP:CE2	2.47	0.50
1:BD:107:TRP:NE1	1:EP:8:LEU:HD11	2.27	0.50
1:BJ:124:TYR:CE2	1:ET:19:VAL:HB	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:122:ASN:HB2	1:GL:20:SER:O	2.12	0.50
1:AF:2:ARG:HH12	1:BC:124:TYR:C	2.15	0.50
1:AM:103:THR:HG22	1:CA:10:VAL:HG21	1.94	0.50
1:DV:118:ASP:OD2	1:GE:98:THR:HG22	2.12	0.50
1:FA:1:MET:HG2	1:FL:123:ASN:OD1	2.12	0.50
1:AM:24:GLY:HA3	1:AN:23:GLN:HG2	1.94	0.50
1:AV:15:ARG:NH1	1:EF:103:THR:HG21	2.20	0.50
1:CQ:62:LEU:HD21	1:GC:103:THR:OG1	2.12	0.50
1:DY:24:GLY:HA3	1:DZ:23:GLN:HG2	1.94	0.50
1:AC:91:THR:HB	1:DO:78:ILE:HD13	1.94	0.50
1:BD:124:TYR:O	1:EP:3:LEU:N	2.40	0.50
1:CR:24:GLY:HA3	1:CS:23:GLN:HG2	1.94	0.50
1:CU:24:GLY:HA3	1:CV:23:GLN:HG2	1.94	0.50
1:FS:124:TYR:C	1:GR:2:ARG:HH12	2.15	0.50
1:GD:24:GLY:HA3	1:GE:23:GLN:HG2	1.94	0.50
1:AP:24:GLY:HA3	1:AQ:23:GLN:HG2	1.94	0.49
1:AP:99:LYS:HE2	1:BU:15:ARG:HD3	1.93	0.49
1:CF:24:GLY:HA3	1:CG:23:GLN:HG2	1.94	0.49
1:CF:124:TYR:C	1:GN:22:GLN:HE21	2.15	0.49
1:EB:24:GLY:HA3	1:EC:23:GLN:HG2	1.94	0.49
1:FL:24:GLY:HA3	1:FM:23:GLN:HG2	1.94	0.49
1:AR:103:THR:HG22	1:ED:10:VAL:HG21	1.93	0.49
1:AS:3:LEU:HG	1:EL:123:ASN:HB3	1.94	0.49
1:BJ:91:THR:HG22	1:EV:68:VAL:HG11	1.94	0.49
1:BW:24:GLY:HA3	1:BX:23:GLN:HG2	1.94	0.49
1:BZ:24:GLY:HA3	1:CA:23:GLN:HG2	1.94	0.49
1:CC:124:TYR:CA	1:GK:22:GLN:HE21	2.25	0.49
1:CF:122:ASN:HB2	1:GO:20:SER:O	2.12	0.49
1:DG:24:GLY:HA3	1:DH:23:GLN:HG2	1.94	0.49
1:DV:24:GLY:HA3	1:DW:23:GLN:HG2	1.94	0.49
1:EQ:103:THR:HG21	1:FM:15:ARG:NH1	2.27	0.49
1:FI:24:GLY:HA3	1:FJ:23:GLN:HG2	1.94	0.49
1:FR:24:GLY:HA3	1:FS:23:GLN:HG2	1.94	0.49
1:FV:124:TYR:C	1:GU:2:ARG:HH12	2.14	0.49
1:GG:24:GLY:HA3	1:GH:23:GLN:HG2	1.94	0.49
1:GS:24:GLY:HA3	1:GT:23:GLN:HG2	1.94	0.49
1:AN:117:VAL:CG2	1:FR:58:VAL:HG11	2.41	0.49
1:CG:103:THR:HG22	1:CL:10:VAL:HG21	1.95	0.49
1:CN:103:THR:OG1	1:FZ:62:LEU:HD21	2.12	0.49
1:DY:3:LEU:HG	1:FY:123:ASN:HB3	1.94	0.49
1:FA:8:LEU:HD11	1:FL:107:TRP:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FF:24:GLY:HA3	1:FG:23:GLN:HG2	1.94	0.49
1:AJ:24:GLY:HA3	1:AK:23:GLN:HG2	1.94	0.49
1:AZ:124:TYR:C	1:EY:2:ARG:HH12	2.15	0.49
1:BT:24:GLY:HA3	1:BU:23:GLN:HG2	1.94	0.49
1:CO:24:GLY:HA3	1:CP:23:GLN:HG2	1.94	0.49
1:CP:83:SER:OG	1:DJ:85:THR:OG1	2.27	0.49
1:DJ:24:GLY:HA3	1:DK:23:GLN:HG2	1.94	0.49
1:DV:119:SER:O	1:GF:36:VAL:HG13	2.13	0.49
1:GJ:24:GLY:HA3	1:GK:23:GLN:HG2	1.94	0.49
1:AD:62:LEU:HD21	1:BC:103:THR:OG1	2.12	0.49
1:AV:24:GLY:HA3	1:AW:23:GLN:HG2	1.94	0.49
1:AW:98:THR:HG22	1:FC:118:ASP:HB3	1.93	0.49
1:BH:24:GLY:HA3	1:BI:23:GLN:HG2	1.94	0.49
1:CY:91:THR:OG1	1:GG:78:ILE:HD13	2.13	0.49
1:AE:66:VAL:HG21	1:GA:96:HIS:CG	2.47	0.49
1:AE:123:ASN:HB3	1:GA:3:LEU:HG	1.93	0.49
1:AJ:103:THR:HG21	1:BX:15:ARG:NH1	2.28	0.49
1:BN:85:THR:OG1	1:DZ:83:SER:OG	2.31	0.49
1:BV:103:THR:HG22	1:FH:10:VAL:HG21	1.94	0.49
1:CG:103:THR:OG1	1:CL:62:LEU:HD21	2.13	0.49
1:FV:10:VAL:HG21	1:GS:103:THR:HG22	1.94	0.49
1:GP:24:GLY:HA3	1:GQ:23:GLN:HG2	1.94	0.49
1:GV:24:GLY:HA3	1:GW:23:GLN:HG2	1.94	0.49
1:AE:10:VAL:HG21	1:GA:103:THR:HG22	1.94	0.49
1:AP:102:GLN:CB	1:BU:10:VAL:HG13	2.42	0.49
1:AS:24:GLY:HA3	1:AT:23:GLN:HG2	1.94	0.49
1:CQ:10:VAL:HG21	1:GC:103:THR:HG22	1.95	0.49
1:CW:8:LEU:HD11	1:GI:107:TRP:CE2	2.48	0.49
1:CX:24:GLY:HA3	1:CY:23:GLN:HG2	1.94	0.49
1:AI:3:LEU:N	1:DU:124:TYR:O	2.38	0.49
1:AV:107:TRP:CD2	1:EF:8:LEU:HD11	2.47	0.49
1:BA:103:THR:HG22	1:EM:10:VAL:HG21	1.94	0.49
1:BN:103:THR:OG1	1:DZ:62:LEU:HD21	2.12	0.49
1:CC:106:ALA:HB1	1:GK:8:LEU:HD22	1.94	0.49
1:CG:22:GLN:HE21	1:CL:124:TYR:C	2.15	0.49
1:CV:98:THR:HG22	1:GM:118:ASP:OD2	2.12	0.49
1:DC:107:TRP:HZ2	1:GO:17:TYR:CG	2.30	0.49
1:EH:24:GLY:HA3	1:EI:23:GLN:HG2	1.94	0.49
1:ET:24:GLY:HA3	1:EU:23:GLN:HG2	1.94	0.49
1:ET:78:ILE:HD13	1:FG:91:THR:OG1	2.13	0.49
1:FA:103:THR:HG21	1:FL:15:ARG:NH1	2.24	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:98:THR:HG22	1:DR:118:ASP:HB3	1.93	0.49
1:AQ:103:THR:HG21	1:FU:15:ARG:NH1	2.24	0.49
1:BS:2:ARG:HH12	1:EC:124:TYR:C	2.16	0.49
1:CT:91:THR:CG2	1:GF:68:VAL:HG11	2.43	0.49
1:DD:24:GLY:HA3	1:DE:23:GLN:HG2	1.94	0.49
1:EE:24:GLY:HA3	1:EF:23:GLN:HG2	1.94	0.49
1:EQ:24:GLY:HA3	1:ER:23:GLN:HG2	1.94	0.49
1:ET:97:ILE:HG21	1:FG:117:VAL:O	2.12	0.49
1:EW:24:GLY:HA3	1:EX:23:GLN:HG2	1.94	0.49
1:CP:123:ASN:HB3	1:DJ:3:LEU:HG	1.94	0.49
1:EB:102:GLN:CB	1:GB:10:VAL:HG13	2.42	0.49
1:FO:24:GLY:HA3	1:FP:23:GLN:HG2	1.94	0.49
1:GA:24:GLY:HA3	1:GB:23:GLN:HG2	1.94	0.49
1:AE:47:GLN:HE22	1:GA:120:GLY:HA2	1.78	0.48
1:AN:106:ALA:HB1	1:FR:8:LEU:HD22	1.95	0.48
1:AR:118:ASP:CB	1:ED:98:THR:HG22	2.43	0.48
1:BK:124:TYR:C	1:DW:22:GLN:HE21	2.17	0.48
1:BM:118:ASP:HB3	1:EY:98:THR:HG22	1.95	0.48
1:CC:24:GLY:HA3	1:CD:23:GLN:HG2	1.94	0.48
1:DP:24:GLY:HA3	1:DQ:23:GLN:HG2	1.94	0.48
1:EN:99:LYS:HE2	1:FJ:15:ARG:NH1	2.28	0.48
1:AA:78:ILE:HD13	1:BI:91:THR:OG1	2.13	0.48
1:AD:24:GLY:HA3	1:AE:23:GLN:HG2	1.94	0.48
1:AY:102:GLN:CB	1:EI:10:VAL:HG13	2.44	0.48
1:BB:24:GLY:HA3	1:BC:23:GLN:HG2	1.94	0.48
1:BE:24:GLY:HA3	1:BF:23:GLN:HG2	1.94	0.48
1:BK:24:GLY:HA3	1:BL:23:GLN:HG2	1.94	0.48
1:BQ:24:GLY:HA3	1:BR:23:GLN:HG2	1.94	0.48
1:DB:98:THR:HG22	1:GJ:118:ASP:OD2	2.12	0.48
1:EH:122:ASN:ND2	1:EO:25:THR:HG22	2.28	0.48
1:EK:24:GLY:HA3	1:EL:23:GLN:HG2	1.94	0.48
1:GM:24:GLY:HA3	1:GN:23:GLN:HG2	1.94	0.48
1:BP:98:THR:HG22	1:FB:118:ASP:CG	2.34	0.48
1:BT:102:GLN:HB2	1:DN:10:VAL:HG13	1.95	0.48
1:BW:10:VAL:CG2	1:DQ:103:THR:HG22	2.41	0.48
1:CT:123:ASN:OD1	1:GF:1:MET:HB3	2.14	0.48
1:DS:24:GLY:HA3	1:DT:23:GLN:HG2	1.94	0.48
1:AC:118:ASP:CB	1:DO:98:THR:HG22	2.44	0.48
1:BK:8:LEU:HD22	1:DW:106:ALA:HB1	1.95	0.48
1:EN:24:GLY:HA3	1:EO:23:GLN:HG2	1.94	0.48
1:FC:24:GLY:HA3	1:FD:23:GLN:HG2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FU:24:GLY:HA3	1:FV:23:GLN:HG2	1.94	0.48
1:AI:124:TYR:O	1:DU:3:LEU:N	2.38	0.48
1:AS:19:VAL:HB	1:EG:124:TYR:CE2	2.48	0.48
1:BH:99:LYS:HE2	1:BO:15:ARG:HH11	1.77	0.48
1:CJ:124:TYR:C	1:CQ:2:ARG:HH12	2.17	0.48
1:CU:96:HIS:CG	1:DH:66:VAL:HG21	2.48	0.48
1:CV:8:LEU:HD22	1:GM:106:ALA:HB1	1.95	0.48
1:AA:24:GLY:HA3	1:AB:23:GLN:HG2	1.94	0.48
1:AG:24:GLY:HA3	1:AH:23:GLN:HG2	1.94	0.48
1:AR:66:VAL:HG21	1:ED:96:HIS:CG	2.49	0.48
1:AS:83:SER:OG	1:EL:85:THR:OG1	2.31	0.48
1:AY:24:GLY:HA3	1:AZ:23:GLN:HG2	1.94	0.48
1:BK:56:ARG:NH1	1:DW:116:PRO:O	2.45	0.48
1:BK:124:TYR:CA	1:DW:22:GLN:HE21	2.25	0.48
1:BN:99:LYS:HE2	1:DZ:15:ARG:HH11	1.79	0.48
1:CI:24:GLY:HA3	1:CJ:23:GLN:HG2	1.94	0.48
1:DA:24:GLY:HA3	1:DB:23:GLN:HG2	1.94	0.48
1:EB:62:LEU:HD21	1:GB:103:THR:OG1	2.14	0.48
1:FX:24:GLY:HA3	1:FY:23:GLN:HG2	1.94	0.48
1:AY:27:PHE:CE2	1:EI:123:ASN:ND2	2.82	0.48
1:BA:118:ASP:HB3	1:EM:98:THR:HG22	1.95	0.48
1:BN:24:GLY:HA3	1:BO:23:GLN:HG2	1.94	0.48
1:CE:103:THR:OG1	1:FQ:62:LEU:HD21	2.13	0.48
1:CT:103:THR:HG22	1:GF:10:VAL:CG2	2.40	0.48
1:EB:58:VAL:HG11	1:GB:117:VAL:CG2	2.44	0.48
1:ET:118:ASP:HB3	1:FG:98:THR:HG22	1.95	0.48
1:EZ:24:GLY:HA3	1:FA:23:GLN:HG2	1.94	0.48
1:FP:103:THR:OG1	1:GV:62:LEU:HD21	2.14	0.48
1:AY:124:TYR:OXT	1:EI:22:GLN:NE2	2.46	0.48
1:BB:20:SER:HA	1:EP:121:LEU:HD22	1.95	0.48
1:CD:8:LEU:HD11	1:CR:107:TRP:CD2	2.48	0.48
1:AA:123:ASN:OD1	1:BI:1:MET:HG2	2.13	0.48
1:AG:122:ASN:HB2	1:BG:20:SER:O	2.13	0.48
1:AS:123:ASN:OD1	1:EL:1:MET:HG2	2.14	0.48
1:BN:2:ARG:HA	1:DZ:124:TYR:O	2.14	0.48
1:BP:68:VAL:HG11	1:FB:91:THR:HG22	1.95	0.48
1:CL:24:GLY:HA3	1:CM:23:GLN:HG2	1.94	0.48
1:CQ:98:THR:HG22	1:GC:118:ASP:CG	2.34	0.48
1:AX:84:VAL:HG22	1:EJ:84:VAL:HG13	1.96	0.47
1:BD:103:THR:HG21	1:EP:15:ARG:NH1	2.25	0.47
1:CF:22:GLN:NE2	1:GN:124:TYR:HA	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:124:TYR:CB	1:CM:22:GLN:HB3	2.43	0.47
1:CI:122:ASN:HB2	1:GI:20:SER:O	2.14	0.47
1:CS:123:ASN:HB3	1:DD:3:LEU:HG	1.96	0.47
1:DC:83:SER:O	1:GO:84:VAL:HA	2.14	0.47
1:DM:24:GLY:HA3	1:DN:23:GLN:HG2	1.94	0.47
1:AU:10:VAL:HG21	1:EG:103:THR:HG22	1.95	0.47
1:AV:107:TRP:CZ2	1:EF:17:TYR:CD2	3.03	0.47
1:CC:99:LYS:HE2	1:GK:15:ARG:HD3	1.96	0.47
1:CQ:107:TRP:CE2	1:GC:8:LEU:HD11	2.49	0.47
1:DC:78:ILE:CD1	1:GO:91:THR:HB	2.44	0.47
1:DP:10:VAL:CG2	1:GW:103:THR:HG22	2.41	0.47
1:FD:91:THR:OG1	1:FF:78:ILE:HD13	2.14	0.47
1:FQ:19:VAL:O	1:GV:121:LEU:HD11	2.14	0.47
1:BL:19:VAL:HG11	1:DW:124:TYR:CE1	2.49	0.47
1:CB:66:VAL:HG23	1:FN:92:TYR:CE2	2.49	0.47
1:DV:102:GLN:CB	1:GE:10:VAL:HG13	2.44	0.47
1:ER:20:SER:O	1:FM:122:ASN:HB2	2.13	0.47
1:EX:15:ARG:HH11	1:FI:99:LYS:HE2	1.78	0.47
1:EY:20:SER:O	1:FI:122:ASN:HB2	2.14	0.47
1:AH:22:GLN:HE21	1:GD:124:TYR:C	2.17	0.47
1:AJ:78:ILE:HD13	1:BX:91:THR:OG1	2.15	0.47
1:CE:103:THR:HG22	1:FQ:10:VAL:HG21	1.96	0.47
1:CY:98:THR:HG22	1:GG:118:ASP:HB3	1.97	0.47
1:AE:103:THR:OG1	1:GA:62:LEU:HD21	2.14	0.47
1:AX:91:THR:HB	1:EJ:78:ILE:HD13	1.96	0.47
1:CD:17:TYR:CG	1:CR:107:TRP:HZ2	2.33	0.47
1:CT:91:THR:HB	1:GF:78:ILE:CD1	2.45	0.47
1:EB:124:TYR:CA	1:GB:22:GLN:HE21	2.26	0.47
1:EE:103:THR:OG1	1:EU:62:LEU:HD21	2.14	0.47
1:EY:18:ALA:HB2	1:EY:32:LYS:HE3	1.97	0.47
1:AN:124:TYR:CE1	1:FS:19:VAL:HG11	2.50	0.47
1:BM:2:ARG:HD2	1:EY:124:TYR:CE1	2.49	0.47
1:CU:103:THR:HG22	1:DH:10:VAL:HG21	1.95	0.47
1:EB:99:LYS:HE2	1:GB:15:ARG:HD3	1.96	0.47
1:EH:124:TYR:CA	1:EO:22:GLN:HE21	2.27	0.47
1:EJ:18:ALA:HB2	1:EJ:32:LYS:HE3	1.97	0.47
1:FV:98:THR:HG22	1:GS:118:ASP:HB3	1.96	0.47
1:GF:18:ALA:HB2	1:GF:32:LYS:HE3	1.97	0.47
1:GW:28:ARG:HG2	1:GW:44:SER:CB	2.45	0.47
1:AI:68:VAL:HG11	1:DU:91:THR:CG2	2.45	0.47
1:AJ:8:LEU:HD11	1:BX:107:TRP:CE2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:28:ARG:HG2	1:AN:44:SER:CB	2.45	0.47
1:AN:91:THR:OG1	1:FR:78:ILE:HD13	2.14	0.47
1:AR:62:LEU:HD21	1:ED:103:THR:OG1	2.15	0.47
1:AU:103:THR:HG22	1:EG:10:VAL:HG21	1.97	0.47
1:AV:107:TRP:HZ2	1:EF:17:TYR:CD2	2.32	0.47
1:AY:62:LEU:HD21	1:EI:103:THR:OG1	2.15	0.47
1:BJ:18:ALA:HB2	1:BJ:32:LYS:HE3	1.97	0.47
1:BL:28:ARG:HG2	1:BL:44:SER:CB	2.45	0.47
1:BT:122:ASN:ND2	1:DN:25:THR:HG22	2.30	0.47
1:BW:3:LEU:HG	1:DQ:123:ASN:HB3	1.97	0.47
1:BZ:92:TYR:CZ	1:DT:80:ALA:HB3	2.50	0.47
1:BZ:104:LEU:HD11	1:DT:84:VAL:HG21	1.97	0.47
1:CC:99:LYS:HE2	1:GK:15:ARG:HH11	1.80	0.47
1:CD:91:THR:OG1	1:CR:78:ILE:HD13	2.15	0.47
1:CF:99:LYS:HE2	1:GN:15:ARG:HH11	1.79	0.47
1:CG:8:LEU:HD22	1:CL:106:ALA:HB1	1.97	0.47
1:CM:28:ARG:HG2	1:CM:44:SER:CB	2.45	0.47
1:CN:1:MET:HB3	1:FZ:123:ASN:OD1	2.15	0.47
1:CN:103:THR:HG22	1:FZ:10:VAL:HG21	1.97	0.47
1:CT:118:ASP:CB	1:GF:98:THR:HG22	2.45	0.47
1:DN:28:ARG:HG2	1:DN:44:SER:CB	2.45	0.47
1:DP:107:TRP:CE2	1:GW:8:LEU:HD11	2.49	0.47
1:DV:3:LEU:HG	1:GE:123:ASN:HB3	1.96	0.47
1:DW:28:ARG:HG2	1:DW:44:SER:CB	2.45	0.47
1:DZ:28:ARG:HG2	1:DZ:44:SER:CB	2.45	0.47
1:EB:124:TYR:C	1:GB:22:GLN:HE21	2.18	0.47
1:EO:28:ARG:HG2	1:EO:44:SER:CB	2.45	0.47
1:EQ:10:VAL:CG2	1:FM:103:THR:HG22	2.44	0.47
1:FB:18:ALA:HB2	1:FB:32:LYS:HE3	1.97	0.47
1:FG:28:ARG:HG2	1:FG:44:SER:CB	2.45	0.47
1:FP:22:GLN:HE21	1:GV:124:TYR:HA	1.79	0.47
1:FP:103:THR:HG22	1:GV:10:VAL:HG21	1.96	0.47
1:FZ:18:ALA:HB2	1:FZ:32:LYS:HE3	1.97	0.47
1:AK:28:ARG:HG2	1:AK:44:SER:CB	2.45	0.47
1:AL:18:ALA:HB2	1:AL:32:LYS:HE3	1.97	0.47
1:AN:10:VAL:HG13	1:FR:102:GLN:CB	2.45	0.47
1:AR:10:VAL:HG21	1:ED:103:THR:HG22	1.97	0.47
1:BH:122:ASN:HB2	1:BP:20:SER:O	2.15	0.47
1:BP:18:ALA:HB2	1:BP:32:LYS:HE3	1.97	0.47
1:CN:8:LEU:HD11	1:FZ:107:TRP:CE2	2.49	0.47
1:CW:18:ALA:HB2	1:CW:32:LYS:HE3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DB:28:ARG:HG2	1:DB:44:SER:CB	2.45	0.47
1:DC:103:THR:HG22	1:GO:10:VAL:CG2	2.37	0.47
1:DR:18:ALA:HB2	1:DR:32:LYS:HE3	1.97	0.47
1:ES:45:LEU:HD12	1:ES:60:MET:HG2	1.97	0.47
1:EU:28:ARG:HG2	1:EU:44:SER:CB	2.45	0.47
1:FN:45:LEU:HD12	1:FN:60:MET:HG2	1.97	0.47
1:AB:103:THR:HG22	1:FX:10:VAL:CG2	2.44	0.47
1:AN:8:LEU:HD22	1:FR:106:ALA:HB1	1.97	0.47
1:AQ:28:ARG:HG2	1:AQ:44:SER:CB	2.45	0.47
1:BF:28:ARG:HG2	1:BF:44:SER:CB	2.45	0.47
1:CE:18:ALA:HB2	1:CE:32:LYS:HE3	1.97	0.47
1:CF:120:GLY:HA2	1:GN:47:GLN:HE22	1.79	0.47
1:CK:45:LEU:HD12	1:CK:60:MET:HG2	1.97	0.47
1:DI:18:ALA:HB2	1:DI:32:LYS:HE3	1.97	0.47
1:EA:18:ALA:HB2	1:EA:32:LYS:HE3	1.97	0.47
1:EC:28:ARG:HG2	1:EC:44:SER:CB	2.45	0.47
1:EP:18:ALA:HB2	1:EP:32:LYS:HE3	1.97	0.47
1:FK:18:ALA:HB2	1:FK:32:LYS:HE3	1.97	0.47
1:FP:28:ARG:HG2	1:FP:44:SER:CB	2.45	0.47
1:GK:28:ARG:HG2	1:GK:44:SER:CB	2.45	0.47
1:GL:18:ALA:HB2	1:GL:32:LYS:HE3	1.97	0.47
1:GR:45:LEU:HD12	1:GR:60:MET:HG2	1.97	0.47
1:AB:28:ARG:HG2	1:AB:44:SER:CB	2.45	0.47
1:AF:45:LEU:HD12	1:AF:60:MET:HG2	1.97	0.47
1:AO:45:LEU:HD12	1:AO:60:MET:HG2	1.97	0.47
1:AR:18:ALA:HB2	1:AR:32:LYS:HE3	1.97	0.47
1:AX:122:ASN:HB2	1:EH:20:SER:O	2.15	0.47
1:BC:28:ARG:HG2	1:BC:44:SER:CB	2.45	0.47
1:BM:98:THR:HG22	1:EY:118:ASP:CB	2.44	0.47
1:BP:45:LEU:HD12	1:BP:60:MET:HG2	1.97	0.47
1:BV:18:ALA:HB2	1:BV:32:LYS:HE3	1.97	0.47
1:BX:28:ARG:HG2	1:BX:44:SER:CB	2.45	0.47
1:CC:102:GLN:HB2	1:GK:10:VAL:HG13	1.97	0.47
1:CE:45:LEU:HD12	1:CE:60:MET:HG2	1.97	0.47
1:CP:28:ARG:HG2	1:CP:44:SER:CB	2.45	0.47
1:CW:45:LEU:HD12	1:CW:60:MET:HG2	1.97	0.47
1:CZ:2:ARG:HH12	1:DK:124:TYR:C	2.18	0.47
1:DF:18:ALA:HB2	1:DF:32:LYS:HE3	1.97	0.47
1:DO:45:LEU:HD12	1:DO:60:MET:HG2	1.97	0.47
1:ED:45:LEU:HD12	1:ED:60:MET:HG2	1.97	0.47
1:EI:28:ARG:HG2	1:EI:44:SER:CB	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EJ:45:LEU:HD12	1:EJ:60:MET:HG2	1.97	0.47
1:ES:18:ALA:HB2	1:ES:32:LYS:HE3	1.97	0.47
1:EV:18:ALA:HB2	1:EV:32:LYS:HE3	1.97	0.47
1:EV:45:LEU:HD12	1:EV:60:MET:HG2	1.97	0.47
1:GC:18:ALA:HB2	1:GC:32:LYS:HE3	1.97	0.47
1:GX:18:ALA:HB2	1:GX:32:LYS:HE3	1.97	0.47
1:AH:28:ARG:HG2	1:AH:44:SER:CB	2.45	0.46
1:AH:117:VAL:O	1:GD:97:ILE:HG21	2.16	0.46
1:AT:117:VAL:O	1:EZ:97:ILE:HG21	2.14	0.46
1:BA:45:LEU:HD12	1:BA:60:MET:HG2	1.97	0.46
1:BG:18:ALA:HB2	1:BG:32:LYS:HE3	1.97	0.46
1:BI:28:ARG:HG2	1:BI:44:SER:CB	2.45	0.46
1:CN:45:LEU:HD12	1:CN:60:MET:HG2	1.98	0.46
1:DK:28:ARG:HG2	1:DK:44:SER:CB	2.45	0.46
1:DX:18:ALA:HB2	1:DX:32:LYS:HE3	1.97	0.46
1:EA:45:LEU:HD12	1:EA:60:MET:HG2	1.97	0.46
1:EE:10:VAL:CG2	1:EU:103:THR:HG22	2.43	0.46
1:EG:18:ALA:HB2	1:EG:32:LYS:HE3	1.97	0.46
1:FD:107:TRP:CE2	1:FF:8:LEU:HD11	2.50	0.46
1:GU:45:LEU:HD12	1:GU:60:MET:HG2	1.97	0.46
1:AC:18:ALA:HB2	1:AC:32:LYS:HE3	1.97	0.46
1:AD:26:LEU:HD12	1:AD:45:LEU:O	2.16	0.46
1:AE:28:ARG:HG2	1:AE:44:SER:CB	2.45	0.46
1:AU:45:LEU:HD12	1:AU:60:MET:HG2	1.97	0.46
1:AW:1:MET:HG2	1:FC:123:ASN:OD1	2.15	0.46
1:AX:18:ALA:HB2	1:AX:32:LYS:HE3	1.97	0.46
1:BN:103:THR:HG22	1:DZ:10:VAL:HG21	1.97	0.46
1:BN:118:ASP:CG	1:DZ:98:THR:HG22	2.35	0.46
1:BZ:97:ILE:HG21	1:DT:117:VAL:O	2.15	0.46
1:CD:28:ARG:HG2	1:CD:44:SER:CB	2.45	0.46
1:CH:18:ALA:HB2	1:CH:32:LYS:HE3	1.97	0.46
1:CK:19:VAL:O	1:CO:121:LEU:HD11	2.14	0.46
1:EG:45:LEU:HD12	1:EG:60:MET:HG2	1.97	0.46
1:AI:18:ALA:HB2	1:AI:32:LYS:HE3	1.97	0.46
1:AK:107:TRP:CE2	1:FO:8:LEU:HD11	2.50	0.46
1:BD:45:LEU:HD12	1:BD:60:MET:HG2	1.97	0.46
1:BT:96:HIS:CG	1:DN:66:VAL:HG21	2.50	0.46
1:BV:45:LEU:HD12	1:BV:60:MET:HG2	1.97	0.46
1:BW:122:ASN:HB2	1:DR:20:SER:O	2.15	0.46
1:BZ:26:LEU:HD12	1:BZ:45:LEU:O	2.16	0.46
1:CD:98:THR:HG22	1:CR:118:ASP:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:10:VAL:CG2	1:DK:103:THR:HG22	2.43	0.46
1:CZ:102:GLN:CB	1:GL:10:VAL:HG13	2.46	0.46
1:FA:98:THR:HG22	1:FL:118:ASP:HB3	1.96	0.46
1:FB:45:LEU:HD12	1:FB:60:MET:HG2	1.97	0.46
1:FV:66:VAL:HG21	1:GS:96:HIS:CG	2.50	0.46
1:GT:28:ARG:HG2	1:GT:44:SER:CB	2.45	0.46
1:AC:45:LEU:HD12	1:AC:60:MET:HG2	1.97	0.46
1:AJ:26:LEU:HD12	1:AJ:45:LEU:O	2.16	0.46
1:AM:119:SER:O	1:CB:36:VAL:HG13	2.15	0.46
1:BU:28:ARG:HG2	1:BU:44:SER:CB	2.45	0.46
1:BY:8:LEU:HD11	1:FK:107:TRP:CE2	2.51	0.46
1:BY:18:ALA:HB2	1:BY:32:LYS:HE3	1.97	0.46
1:CO:26:LEU:HD12	1:CO:45:LEU:O	2.16	0.46
1:CQ:84:VAL:HG13	1:GC:84:VAL:HG22	1.97	0.46
1:CS:98:THR:HG22	1:DD:118:ASP:HB3	1.98	0.46
1:CT:18:ALA:HB2	1:CT:32:LYS:HE3	1.97	0.46
1:CZ:18:ALA:HB2	1:CZ:32:LYS:HE3	1.97	0.46
1:DB:15:ARG:NH1	1:GJ:103:THR:HG21	2.31	0.46
1:DC:45:LEU:HD12	1:DC:60:MET:HG2	1.97	0.46
1:DL:45:LEU:HD12	1:DL:60:MET:HG2	1.97	0.46
1:DU:18:ALA:HB2	1:DU:32:LYS:HE3	1.97	0.46
1:EW:26:LEU:HD12	1:EW:45:LEU:O	2.16	0.46
1:FD:103:THR:HG22	1:FF:10:VAL:CG2	2.42	0.46
1:FF:26:LEU:HD12	1:FF:45:LEU:O	2.16	0.46
1:FU:26:LEU:HD12	1:FU:45:LEU:O	2.16	0.46
1:GG:26:LEU:HD12	1:GG:45:LEU:O	2.16	0.46
1:GN:28:ARG:HG2	1:GN:44:SER:CB	2.45	0.46
1:GR:18:ALA:HB2	1:GR:32:LYS:HE3	1.97	0.46
1:AL:28:ARG:HG2	1:AL:44:SER:HB3	1.98	0.46
1:AO:18:ALA:HB2	1:AO:32:LYS:HE3	1.97	0.46
1:AO:28:ARG:HG2	1:AO:44:SER:HB3	1.98	0.46
1:AP:62:LEU:HD21	1:BU:103:THR:OG1	2.15	0.46
1:BA:28:ARG:HG2	1:BA:44:SER:HB3	1.98	0.46
1:BH:122:ASN:ND2	1:BO:25:THR:HG22	2.30	0.46
1:BJ:45:LEU:HD12	1:BJ:60:MET:HG2	1.97	0.46
1:BK:26:LEU:HD12	1:BK:45:LEU:O	2.16	0.46
1:BT:26:LEU:HD12	1:BT:45:LEU:O	2.16	0.46
1:BV:28:ARG:HG2	1:BV:44:SER:HB3	1.98	0.46
1:CA:28:ARG:HG2	1:CA:44:SER:CB	2.45	0.46
1:CB:18:ALA:HB2	1:CB:32:LYS:HE3	1.97	0.46
1:CE:28:ARG:HG2	1:CE:44:SER:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:26:LEU:HD12	1:CF:45:LEU:O	2.16	0.46
1:CY:85:THR:OG1	1:GG:83:SER:OG	2.33	0.46
1:DL:18:ALA:HB2	1:DL:32:LYS:HE3	1.97	0.46
1:DY:118:ASP:HB3	1:FY:98:THR:HG22	1.98	0.46
1:EH:116:PRO:O	1:EO:56:ARG:NH1	2.48	0.46
1:FK:45:LEU:HD12	1:FK:60:MET:HG2	1.97	0.46
1:FX:26:LEU:HD12	1:FX:45:LEU:O	2.16	0.46
1:FZ:28:ARG:HG2	1:FZ:44:SER:HB3	1.98	0.46
1:GI:18:ALA:HB2	1:GI:32:LYS:HE3	1.97	0.46
1:GL:45:LEU:HD12	1:GL:60:MET:HG2	1.97	0.46
1:AF:107:TRP:CE2	1:DR:8:LEU:HD11	2.50	0.46
1:AG:26:LEU:HD12	1:AG:45:LEU:O	2.16	0.46
1:AI:45:LEU:HD12	1:AI:60:MET:HG2	1.97	0.46
1:AR:98:THR:HG22	1:ED:118:ASP:CB	2.45	0.46
1:BM:45:LEU:HD12	1:BM:60:MET:HG2	1.97	0.46
1:BS:28:ARG:HG2	1:BS:44:SER:HB3	1.98	0.46
1:CT:28:ARG:HG2	1:CT:44:SER:HB3	1.98	0.46
1:CX:26:LEU:HD12	1:CX:45:LEU:O	2.16	0.46
1:DB:84:VAL:HG13	1:GJ:84:VAL:HG22	1.97	0.46
1:DS:26:LEU:HD12	1:DS:45:LEU:O	2.16	0.46
1:EE:26:LEU:HD12	1:EE:45:LEU:O	2.16	0.46
1:ES:28:ARG:HG2	1:ES:44:SER:HB3	1.98	0.46
1:ET:26:LEU:HD12	1:ET:45:LEU:O	2.16	0.46
1:EZ:26:LEU:HD12	1:EZ:45:LEU:O	2.16	0.46
1:FN:18:ALA:HB2	1:FN:32:LYS:HE3	1.97	0.46
1:FN:28:ARG:HG2	1:FN:44:SER:HB3	1.98	0.46
1:FQ:18:ALA:HB2	1:FQ:32:LYS:HE3	1.97	0.46
1:GC:28:ARG:HG2	1:GC:44:SER:HB3	1.98	0.46
1:GH:28:ARG:HG2	1:GH:44:SER:CB	2.45	0.46
1:GQ:28:ARG:HG2	1:GQ:44:SER:CB	2.45	0.46
1:AC:28:ARG:HG2	1:AC:44:SER:HB3	1.98	0.46
1:AE:117:VAL:HG22	1:GA:58:VAL:HG11	1.97	0.46
1:AH:94:ASN:O	1:AH:98:THR:HG23	2.16	0.46
1:AN:25:THR:HG22	1:FR:122:ASN:ND2	2.31	0.46
1:AR:45:LEU:HD12	1:AR:60:MET:HG2	1.97	0.46
1:BC:94:ASN:O	1:BC:98:THR:HG23	2.16	0.46
1:BE:26:LEU:HD12	1:BE:45:LEU:O	2.16	0.46
1:BN:26:LEU:HD12	1:BN:45:LEU:O	2.16	0.46
1:BY:68:VAL:HG11	1:FK:91:THR:HG22	1.98	0.46
1:CB:1:MET:HB3	1:FN:123:ASN:OD1	2.16	0.46
1:CG:28:ARG:HG2	1:CG:44:SER:CB	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CN:28:ARG:HG2	1:CN:44:SER:HB3	1.98	0.46
1:CQ:45:LEU:HD12	1:CQ:60:MET:HG2	1.97	0.46
1:CW:91:THR:HG22	1:GI:68:VAL:HG11	1.97	0.46
1:CY:28:ARG:HG2	1:CY:44:SER:CB	2.45	0.46
1:DA:26:LEU:HD12	1:DA:45:LEU:O	2.16	0.46
1:DC:18:ALA:HB2	1:DC:32:LYS:HE3	1.97	0.46
1:DG:26:LEU:HD12	1:DG:45:LEU:O	2.16	0.46
1:DR:28:ARG:HG2	1:DR:44:SER:HB3	1.98	0.46
1:EY:45:LEU:HD12	1:EY:60:MET:HG2	1.97	0.46
1:FD:28:ARG:HG2	1:FD:44:SER:CB	2.45	0.46
1:FY:28:ARG:HG2	1:FY:44:SER:CB	2.45	0.46
1:GB:94:ASN:O	1:GB:98:THR:HG23	2.16	0.46
1:GH:94:ASN:O	1:GH:98:THR:HG23	2.16	0.46
1:GM:26:LEU:HD12	1:GM:45:LEU:O	2.16	0.46
1:AA:20:SER:HA	1:DO:121:LEU:HD22	1.97	0.46
1:AE:94:ASN:O	1:AE:98:THR:HG23	2.16	0.46
1:AM:26:LEU:HD12	1:AM:45:LEU:O	2.16	0.46
1:BA:18:ALA:HB2	1:BA:32:LYS:HE3	1.97	0.46
1:BH:26:LEU:HD12	1:BH:45:LEU:O	2.16	0.46
1:BK:106:ALA:HB1	1:DW:8:LEU:HD22	1.98	0.46
1:BM:18:ALA:HB2	1:BM:32:LYS:HE3	1.97	0.46
1:BM:84:VAL:HG22	1:EY:84:VAL:HG13	1.98	0.46
1:BS:45:LEU:HD12	1:BS:60:MET:HG2	1.97	0.46
1:BT:118:ASP:OD2	1:DN:98:THR:HG22	2.16	0.46
1:BY:28:ARG:HG2	1:BY:44:SER:HB3	1.98	0.46
1:CI:26:LEU:HD12	1:CI:45:LEU:O	2.16	0.46
1:CM:94:ASN:O	1:CM:98:THR:HG23	2.16	0.46
1:CP:8:LEU:HD11	1:DJ:107:TRP:CE2	2.51	0.46
1:CQ:18:ALA:HB2	1:CQ:32:LYS:HE3	1.97	0.46
1:CQ:78:ILE:HD13	1:GC:91:THR:HB	1.98	0.46
1:CS:1:MET:HG2	1:DD:123:ASN:OD1	2.15	0.46
1:DK:94:ASN:O	1:DK:98:THR:HG23	2.16	0.46
1:DO:18:ALA:HB2	1:DO:32:LYS:HE3	1.97	0.46
1:EJ:10:VAL:O	1:EJ:13:GLU:HG2	2.16	0.46
1:EM:10:VAL:O	1:EM:13:GLU:HG2	2.16	0.46
1:EO:94:ASN:O	1:EO:98:THR:HG23	2.16	0.46
1:EQ:26:LEU:HD12	1:EQ:45:LEU:O	2.16	0.46
1:EQ:118:ASP:OD2	1:FM:98:THR:HG22	2.16	0.46
1:EX:103:THR:HG22	1:FI:10:VAL:HG21	1.97	0.46
1:FG:94:ASN:O	1:FG:98:THR:HG23	2.16	0.46
1:FJ:94:ASN:O	1:FJ:98:THR:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FQ:28:ARG:HG2	1:FQ:44:SER:HB3	1.98	0.46
1:FT:28:ARG:HG2	1:FT:44:SER:HB3	1.98	0.46
1:FW:45:LEU:HD12	1:FW:60:MET:HG2	1.97	0.46
1:AA:26:LEU:HD12	1:AA:45:LEU:O	2.16	0.46
1:AB:107:TRP:CE2	1:FX:8:LEU:HD11	2.50	0.46
1:AC:10:VAL:O	1:AC:13:GLU:HG2	2.16	0.46
1:AC:91:THR:CG2	1:DO:68:VAL:HG11	2.46	0.46
1:AC:123:ASN:OD1	1:DO:1:MET:HB3	2.16	0.46
1:AI:10:VAL:O	1:AI:13:GLU:HG2	2.16	0.46
1:AK:85:THR:OG1	1:FO:83:SER:OG	2.31	0.46
1:AL:10:VAL:O	1:AL:13:GLU:HG2	2.16	0.46
1:AM:96:HIS:CG	1:CA:66:VAL:HG21	2.51	0.46
1:AP:26:LEU:HD12	1:AP:45:LEU:O	2.16	0.46
1:BB:26:LEU:HD12	1:BB:45:LEU:O	2.16	0.46
1:BI:22:GLN:HB3	1:BO:124:TYR:HB2	1.98	0.46
1:BM:103:THR:HG22	1:EY:10:VAL:HG21	1.98	0.46
1:BP:28:ARG:HG2	1:BP:44:SER:HB3	1.98	0.46
1:BQ:118:ASP:OD2	1:EC:98:THR:HG22	2.16	0.46
1:BW:26:LEU:HD12	1:BW:45:LEU:O	2.16	0.46
1:CB:10:VAL:O	1:CB:13:GLU:HG2	2.16	0.46
1:CD:17:TYR:CD2	1:CR:107:TRP:CZ2	3.03	0.46
1:CH:45:LEU:HD12	1:CH:60:MET:HG2	1.97	0.46
1:CH:98:THR:HG22	1:FT:118:ASP:HB3	1.97	0.46
1:CK:18:ALA:HB2	1:CK:32:LYS:HE3	1.97	0.46
1:CN:18:ALA:HB2	1:CN:32:LYS:HE3	1.97	0.46
1:CR:26:LEU:HD12	1:CR:45:LEU:O	2.16	0.46
1:DI:118:ASP:CG	1:GU:98:THR:HG22	2.36	0.46
1:DJ:26:LEU:HD12	1:DJ:45:LEU:O	2.16	0.46
1:DP:8:LEU:HD11	1:GW:107:TRP:CE2	2.51	0.46
1:DP:26:LEU:HD12	1:DP:45:LEU:O	2.16	0.46
1:DX:10:VAL:O	1:DX:13:GLU:HG2	2.16	0.46
1:EF:28:ARG:HG2	1:EF:44:SER:CB	2.45	0.46
1:EF:94:ASN:O	1:EF:98:THR:HG23	2.16	0.46
1:EG:2:ARG:NH1	1:EU:124:TYR:OXT	2.49	0.46
1:EL:28:ARG:HG2	1:EL:44:SER:CB	2.45	0.46
1:ET:118:ASP:CG	1:FG:98:THR:HG22	2.37	0.46
1:FC:26:LEU:HD12	1:FC:45:LEU:O	2.16	0.46
1:FH:45:LEU:HD12	1:FH:60:MET:HG2	1.97	0.46
1:FI:26:LEU:HD12	1:FI:45:LEU:O	2.16	0.46
1:FL:26:LEU:HD12	1:FL:45:LEU:O	2.16	0.46
1:FM:94:ASN:O	1:FM:98:THR:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FT:18:ALA:HB2	1:FT:32:LYS:HE3	1.97	0.46
1:FW:18:ALA:HB2	1:FW:32:LYS:HE3	1.97	0.46
1:GE:28:ARG:HG2	1:GE:44:SER:CB	2.45	0.46
1:GJ:26:LEU:HD12	1:GJ:45:LEU:O	2.16	0.46
1:AF:18:ALA:HB2	1:AF:32:LYS:HE3	1.97	0.46
1:AR:28:ARG:HG2	1:AR:44:SER:HB3	1.98	0.46
1:AU:62:LEU:HD21	1:EG:103:THR:OG1	2.16	0.46
1:AX:45:LEU:HD12	1:AX:60:MET:HG2	1.97	0.46
1:AZ:94:ASN:O	1:AZ:98:THR:HG23	2.16	0.46
1:BD:18:ALA:HB2	1:BD:32:LYS:HE3	1.97	0.46
1:BH:124:TYR:HA	1:BO:22:GLN:HE21	1.80	0.46
1:CC:26:LEU:HD12	1:CC:45:LEU:O	2.16	0.46
1:CD:94:ASN:O	1:CD:98:THR:HG23	2.16	0.46
1:CJ:28:ARG:HG2	1:CJ:44:SER:CB	2.45	0.46
1:CJ:94:ASN:O	1:CJ:98:THR:HG23	2.16	0.46
1:CK:28:ARG:HG2	1:CK:44:SER:HB3	1.98	0.46
1:CV:28:ARG:HG2	1:CV:44:SER:CB	2.45	0.46
1:CZ:10:VAL:HG21	1:GL:103:THR:HG22	1.98	0.46
1:CZ:26:LEU:HD12	1:CZ:45:LEU:O	2.16	0.46
1:DB:94:ASN:O	1:DB:98:THR:HG23	2.16	0.46
1:DI:2:ARG:HD2	1:GU:124:TYR:CE1	2.51	0.46
1:DL:10:VAL:O	1:DL:13:GLU:HG2	2.16	0.46
1:DO:2:ARG:HH12	1:GT:124:TYR:C	2.18	0.46
1:DR:45:LEU:HD12	1:DR:60:MET:HG2	1.97	0.46
1:EP:28:ARG:HG2	1:EP:44:SER:HB3	1.98	0.46
1:EQ:15:ARG:NH1	1:FM:103:THR:HG21	2.26	0.46
1:ER:28:ARG:HG2	1:ER:44:SER:CB	2.45	0.46
1:ET:103:THR:HG21	1:FG:15:ARG:NH1	2.30	0.46
1:EU:94:ASN:O	1:EU:98:THR:HG23	2.16	0.46
1:FA:94:ASN:O	1:FA:98:THR:HG23	2.16	0.46
1:GA:26:LEU:HD12	1:GA:45:LEU:O	2.16	0.46
1:GI:10:VAL:O	1:GI:13:GLU:HG2	2.16	0.46
1:GI:28:ARG:HG2	1:GI:44:SER:HB3	1.98	0.46
1:GK:94:ASN:O	1:GK:98:THR:HG23	2.16	0.46
1:GL:10:VAL:O	1:GL:13:GLU:HG2	2.16	0.46
1:GQ:94:ASN:O	1:GQ:98:THR:HG23	2.16	0.46
1:GR:10:VAL:O	1:GR:13:GLU:HG2	2.16	0.46
1:GV:26:LEU:HD12	1:GV:45:LEU:O	2.16	0.46
1:AA:121:LEU:HD11	1:BJ:19:VAL:O	2.17	0.45
1:AF:26:LEU:HD12	1:AF:45:LEU:O	2.17	0.45
1:AR:80:ALA:HB3	1:ED:92:TYR:CZ	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:94:ASN:O	1:AT:98:THR:HG23	2.16	0.45
1:AV:26:LEU:HD12	1:AV:45:LEU:O	2.16	0.45
1:BD:83:SER:O	1:EP:84:VAL:HA	2.16	0.45
1:BI:94:ASN:O	1:BI:98:THR:HG23	2.16	0.45
1:BM:103:THR:OG1	1:EY:62:LEU:HD21	2.16	0.45
1:CB:26:LEU:HD12	1:CB:45:LEU:O	2.16	0.45
1:CE:10:VAL:O	1:CE:13:GLU:HG2	2.16	0.45
1:CE:26:LEU:HD12	1:CE:45:LEU:O	2.17	0.45
1:CG:123:ASN:ND2	1:CL:27:PHE:CE2	2.84	0.45
1:CH:10:VAL:O	1:CH:13:GLU:HG2	2.16	0.45
1:CP:94:ASN:O	1:CP:98:THR:HG23	2.16	0.45
1:CS:28:ARG:HG2	1:CS:44:SER:CB	2.45	0.45
1:DC:10:VAL:O	1:DC:13:GLU:HG2	2.16	0.45
1:DD:26:LEU:HD12	1:DD:45:LEU:O	2.16	0.45
1:DF:28:ARG:HG2	1:DF:44:SER:HB3	1.98	0.45
1:DI:10:VAL:O	1:DI:13:GLU:HG2	2.16	0.45
1:DR:26:LEU:HD12	1:DR:45:LEU:O	2.16	0.45
1:DU:28:ARG:HG2	1:DU:44:SER:HB3	1.98	0.45
1:EG:10:VAL:O	1:EG:13:GLU:HG2	2.16	0.45
1:EK:26:LEU:HD12	1:EK:45:LEU:O	2.16	0.45
1:EM:18:ALA:HB2	1:EM:32:LYS:HE3	1.97	0.45
1:EV:26:LEU:HD12	1:EV:45:LEU:O	2.17	0.45
1:EX:94:ASN:O	1:EX:98:THR:HG23	2.16	0.45
1:FA:107:TRP:CE2	1:FL:8:LEU:HD11	2.51	0.45
1:FK:28:ARG:HG2	1:FK:44:SER:HB3	1.98	0.45
1:FQ:10:VAL:O	1:FQ:13:GLU:HG2	2.16	0.45
1:FT:20:SER:O	1:GP:122:ASN:HB2	2.17	0.45
1:FV:94:ASN:O	1:FV:98:THR:HG23	2.16	0.45
1:FW:26:LEU:HD12	1:FW:45:LEU:O	2.17	0.45
1:GU:26:LEU:HD12	1:GU:45:LEU:O	2.17	0.45
1:GX:28:ARG:HG2	1:GX:44:SER:HB3	1.98	0.45
1:AF:10:VAL:O	1:AF:13:GLU:HG2	2.16	0.45
1:AF:19:VAL:HB	1:GA:124:TYR:CD2	2.52	0.45
1:AT:28:ARG:HG2	1:AT:44:SER:CB	2.45	0.45
1:AW:28:ARG:HG2	1:AW:44:SER:CB	2.45	0.45
1:AX:28:ARG:HG2	1:AX:44:SER:HB3	1.98	0.45
1:BM:10:VAL:O	1:BM:13:GLU:HG2	2.16	0.45
1:BQ:118:ASP:HB3	1:EC:98:THR:HG22	1.97	0.45
1:BS:18:ALA:HB2	1:BS:32:LYS:HE3	1.97	0.45
1:BT:119:SER:O	1:DO:36:VAL:HG13	2.17	0.45
1:CB:84:VAL:HA	1:FN:83:SER:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:26:LEU:HD12	1:CL:45:LEU:O	2.16	0.45
1:CQ:10:VAL:O	1:CQ:13:GLU:HG2	2.16	0.45
1:CQ:26:LEU:HD12	1:CQ:45:LEU:O	2.17	0.45
1:DE:94:ASN:O	1:DE:98:THR:HG23	2.16	0.45
1:DF:98:THR:HG22	1:GR:118:ASP:CG	2.36	0.45
1:DU:45:LEU:HD12	1:DU:60:MET:HG2	1.97	0.45
1:ED:18:ALA:HB2	1:ED:32:LYS:HE3	1.97	0.45
1:ER:94:ASN:O	1:ER:98:THR:HG23	2.16	0.45
1:ES:10:VAL:O	1:ES:13:GLU:HG2	2.16	0.45
1:FB:10:VAL:O	1:FB:13:GLU:HG2	2.16	0.45
1:FN:10:VAL:O	1:FN:13:GLU:HG2	2.16	0.45
1:FQ:45:LEU:HD12	1:FQ:60:MET:HG2	1.97	0.45
1:FT:10:VAL:O	1:FT:13:GLU:HG2	2.16	0.45
1:GF:26:LEU:HD12	1:GF:45:LEU:O	2.17	0.45
1:GO:45:LEU:HD12	1:GO:60:MET:HG2	1.97	0.45
1:GX:10:VAL:O	1:GX:13:GLU:HG2	2.16	0.45
1:AI:26:LEU:HD12	1:AI:45:LEU:O	2.16	0.45
1:AR:10:VAL:O	1:AR:13:GLU:HG2	2.16	0.45
1:AY:120:GLY:HA2	1:EI:47:GLN:HE22	1.81	0.45
1:BJ:10:VAL:O	1:BJ:13:GLU:HG2	2.16	0.45
1:BS:10:VAL:O	1:BS:13:GLU:HG2	2.16	0.45
1:BV:10:VAL:O	1:BV:13:GLU:HG2	2.16	0.45
1:BY:10:VAL:O	1:BY:13:GLU:HG2	2.16	0.45
1:CA:94:ASN:O	1:CA:98:THR:HG23	2.16	0.45
1:CF:106:ALA:HB1	1:GN:8:LEU:HD22	1.98	0.45
1:CH:1:MET:HB3	1:FT:123:ASN:OD1	2.17	0.45
1:CT:10:VAL:O	1:CT:13:GLU:HG2	2.16	0.45
1:CT:26:LEU:HD12	1:CT:45:LEU:O	2.17	0.45
1:DI:45:LEU:HD12	1:DI:60:MET:HG2	1.97	0.45
1:DM:26:LEU:HD12	1:DM:45:LEU:O	2.16	0.45
1:DR:10:VAL:O	1:DR:13:GLU:HG2	2.16	0.45
1:DT:28:ARG:HG2	1:DT:44:SER:CB	2.45	0.45
1:DY:26:LEU:HD12	1:DY:45:LEU:O	2.16	0.45
1:EC:94:ASN:O	1:EC:98:THR:HG23	2.16	0.45
1:ED:10:VAL:O	1:ED:13:GLU:HG2	2.16	0.45
1:ED:26:LEU:HD12	1:ED:45:LEU:O	2.16	0.45
1:EV:28:ARG:HG2	1:EV:44:SER:HB3	1.98	0.45
1:EX:98:THR:HG22	1:FI:118:ASP:OD2	2.16	0.45
1:FE:26:LEU:HD12	1:FE:45:LEU:O	2.17	0.45
1:FE:45:LEU:HD12	1:FE:60:MET:HG2	1.97	0.45
1:FY:94:ASN:O	1:FY:98:THR:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FZ:10:VAL:O	1:FZ:13:GLU:HG2	2.16	0.45
1:GD:26:LEU:HD12	1:GD:45:LEU:O	2.16	0.45
1:GO:18:ALA:HB2	1:GO:32:LYS:HE3	1.97	0.45
1:AH:80:ALA:HB3	1:GD:92:TYR:CZ	2.52	0.45
1:AK:94:ASN:O	1:AK:98:THR:HG23	2.16	0.45
1:AQ:94:ASN:O	1:AQ:98:THR:HG23	2.16	0.45
1:AS:26:LEU:HD12	1:AS:45:LEU:O	2.16	0.45
1:AT:98:THR:HG22	1:EZ:118:ASP:HB3	1.98	0.45
1:AV:118:ASP:HB3	1:EF:98:THR:HG22	1.99	0.45
1:CH:26:LEU:HD12	1:CH:45:LEU:O	2.16	0.45
1:CN:26:LEU:HD12	1:CN:45:LEU:O	2.17	0.45
1:CU:26:LEU:HD12	1:CU:45:LEU:O	2.16	0.45
1:DH:28:ARG:HG2	1:DH:44:SER:CB	2.45	0.45
1:DO:26:LEU:HD12	1:DO:45:LEU:O	2.17	0.45
1:DQ:28:ARG:HG2	1:DQ:44:SER:CB	2.45	0.45
1:DV:26:LEU:HD12	1:DV:45:LEU:O	2.16	0.45
1:DX:26:LEU:HD12	1:DX:45:LEU:O	2.17	0.45
1:DX:28:ARG:HG2	1:DX:44:SER:HB3	1.98	0.45
1:EB:26:LEU:HD12	1:EB:45:LEU:O	2.16	0.45
1:EJ:26:LEU:HD12	1:EJ:45:LEU:O	2.16	0.45
1:EM:26:LEU:HD12	1:EM:45:LEU:O	2.17	0.45
1:EN:26:LEU:HD12	1:EN:45:LEU:O	2.16	0.45
1:ET:99:LYS:HE2	1:FG:15:ARG:HH11	1.81	0.45
1:EX:28:ARG:HG2	1:EX:44:SER:CB	2.45	0.45
1:FB:26:LEU:HD12	1:FB:45:LEU:O	2.17	0.45
1:FJ:28:ARG:HG2	1:FJ:44:SER:CB	2.45	0.45
1:FK:26:LEU:HD12	1:FK:45:LEU:O	2.17	0.45
1:FO:26:LEU:HD12	1:FO:45:LEU:O	2.16	0.45
1:GC:26:LEU:HD12	1:GC:45:LEU:O	2.17	0.45
1:GU:18:ALA:HB2	1:GU:32:LYS:HE3	1.97	0.45
1:AB:94:ASN:O	1:AB:98:THR:HG23	2.16	0.45
1:AE:56:ARG:NH1	1:GA:116:PRO:O	2.49	0.45
1:AG:99:LYS:HE2	1:BF:15:ARG:HH11	1.81	0.45
1:AI:28:ARG:HG2	1:AI:44:SER:HB3	1.98	0.45
1:AL:26:LEU:HD12	1:AL:45:LEU:O	2.17	0.45
1:AN:116:PRO:O	1:FR:56:ARG:NH1	2.47	0.45
1:BA:10:VAL:O	1:BA:13:GLU:HG2	2.16	0.45
1:BF:94:ASN:O	1:BF:98:THR:HG23	2.16	0.45
1:BG:10:VAL:O	1:BG:13:GLU:HG2	2.16	0.45
1:BM:122:ASN:HB2	1:EW:20:SER:O	2.16	0.45
1:BN:123:ASN:OD1	1:DZ:1:MET:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:124:TYR:CD2	1:DO:19:VAL:HB	2.52	0.45
1:BX:94:ASN:O	1:BX:98:THR:HG23	2.16	0.45
1:CB:45:LEU:HD12	1:CB:60:MET:HG2	1.97	0.45
1:CZ:28:ARG:HG2	1:CZ:44:SER:HB3	1.98	0.45
1:DF:45:LEU:HD12	1:DF:60:MET:HG2	1.97	0.45
1:DT:94:ASN:O	1:DT:98:THR:HG23	2.16	0.45
1:EC:22:GLN:HB3	1:GB:124:TYR:CB	2.42	0.45
1:EP:45:LEU:HD12	1:EP:60:MET:HG2	1.97	0.45
1:FE:10:VAL:O	1:FE:13:GLU:HG2	2.16	0.45
1:FH:18:ALA:HB2	1:FH:32:LYS:HE3	1.97	0.45
1:FP:94:ASN:O	1:FP:98:THR:HG23	2.16	0.45
1:FT:45:LEU:HD12	1:FT:60:MET:HG2	1.97	0.45
1:FW:10:VAL:O	1:FW:13:GLU:HG2	2.16	0.45
1:GF:45:LEU:HD12	1:GF:60:MET:HG2	1.97	0.45
1:GI:45:LEU:HD12	1:GI:60:MET:HG2	1.97	0.45
1:GN:94:ASN:O	1:GN:98:THR:HG23	2.16	0.45
1:GP:26:LEU:HD12	1:GP:45:LEU:O	2.16	0.45
1:GS:26:LEU:HD12	1:GS:45:LEU:O	2.16	0.45
1:AC:26:LEU:HD12	1:AC:45:LEU:O	2.17	0.45
1:AN:22:GLN:NE2	1:FR:124:TYR:OXT	2.49	0.45
1:AU:18:ALA:HB2	1:AU:32:LYS:HE3	1.97	0.45
1:AW:94:ASN:O	1:AW:98:THR:HG23	2.16	0.45
1:BL:20:SER:HA	1:DW:121:LEU:HD22	1.98	0.45
1:BP:26:LEU:HD12	1:BP:45:LEU:O	2.17	0.45
1:BQ:26:LEU:HD12	1:BQ:45:LEU:O	2.16	0.45
1:BQ:99:LYS:HE2	1:EC:15:ARG:HD3	1.99	0.45
1:BY:26:LEU:HD12	1:BY:45:LEU:O	2.17	0.45
1:BZ:103:THR:HG21	1:DT:15:ARG:NH1	2.31	0.45
1:CF:124:TYR:HA	1:GN:22:GLN:HE21	1.80	0.45
1:CS:94:ASN:O	1:CS:98:THR:HG23	2.16	0.45
1:CW:26:LEU:HD12	1:CW:45:LEU:O	2.17	0.45
1:CZ:45:LEU:HD12	1:CZ:60:MET:HG2	1.97	0.45
1:CZ:47:GLN:OE1	1:GL:120:GLY:HA2	2.16	0.45
1:CZ:91:THR:CG2	1:GL:68:VAL:HG11	2.47	0.45
1:DI:26:LEU:HD12	1:DI:45:LEU:O	2.16	0.45
1:DX:45:LEU:HD12	1:DX:60:MET:HG2	1.97	0.45
1:DZ:94:ASN:O	1:DZ:98:THR:HG23	2.16	0.45
1:EH:10:VAL:HG13	1:EO:102:GLN:CB	2.47	0.45
1:EH:26:LEU:HD12	1:EH:45:LEU:O	2.16	0.45
1:EM:28:ARG:HG2	1:EM:44:SER:HB3	1.98	0.45
1:EY:10:VAL:O	1:EY:13:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FA:28:ARG:HG2	1:FA:44:SER:CB	2.45	0.45
1:FD:1:MET:HG2	1:FF:123:ASN:OD1	2.17	0.45
1:FS:94:ASN:O	1:FS:98:THR:HG23	2.16	0.45
1:FV:28:ARG:HG2	1:FV:44:SER:CB	2.45	0.45
1:GO:10:VAL:O	1:GO:13:GLU:HG2	2.16	0.45
1:GX:45:LEU:HD12	1:GX:60:MET:HG2	1.97	0.45
1:AB:83:SER:OG	1:FX:85:THR:OG1	2.31	0.45
1:AB:103:THR:HG21	1:FX:15:ARG:NH1	2.25	0.45
1:AE:30:VAL:HG13	1:AE:40:THR:HG21	1.99	0.45
1:AG:118:ASP:HB3	1:BF:98:THR:HG22	1.98	0.45
1:AN:103:THR:OG1	1:FR:62:LEU:HD21	2.17	0.45
1:AO:2:ARG:HD2	1:EA:124:TYR:CE1	2.52	0.45
1:AO:26:LEU:HD12	1:AO:45:LEU:O	2.17	0.45
1:AV:107:TRP:HZ2	1:EF:17:TYR:CG	2.34	0.45
1:BD:68:VAL:HG11	1:EP:91:THR:CG2	2.45	0.45
1:BT:103:THR:HG22	1:DN:10:VAL:HG21	1.98	0.45
1:BY:45:LEU:HD12	1:BY:60:MET:HG2	1.97	0.45
1:CC:20:SER:HA	1:FQ:121:LEU:HD22	1.99	0.45
1:CG:30:VAL:HG13	1:CG:40:THR:HG21	1.99	0.45
1:CK:10:VAL:O	1:CK:13:GLU:HG2	2.16	0.45
1:CY:94:ASN:O	1:CY:98:THR:HG23	2.16	0.45
1:DC:123:ASN:OD1	1:GO:1:MET:HB3	2.16	0.45
1:DK:30:VAL:HG13	1:DK:40:THR:HG21	1.99	0.45
1:DQ:94:ASN:O	1:DQ:98:THR:HG23	2.16	0.45
1:DZ:30:VAL:HG13	1:DZ:40:THR:HG21	1.99	0.45
1:EI:30:VAL:HG13	1:EI:40:THR:HG21	1.99	0.45
1:EM:45:LEU:HD12	1:EM:60:MET:HG2	1.97	0.45
1:EQ:103:THR:OG1	1:FM:62:LEU:HD21	2.16	0.45
1:EU:30:VAL:HG13	1:EU:40:THR:HG21	1.99	0.45
1:EV:10:VAL:O	1:EV:13:GLU:HG2	2.16	0.45
1:FE:18:ALA:HB2	1:FE:32:LYS:HE3	1.97	0.45
1:FQ:26:LEU:HD12	1:FQ:45:LEU:O	2.17	0.45
1:FT:26:LEU:HD12	1:FT:45:LEU:O	2.16	0.45
1:FZ:45:LEU:HD12	1:FZ:60:MET:HG2	1.97	0.45
1:GT:30:VAL:HG13	1:GT:40:THR:HG21	1.99	0.45
1:AB:30:VAL:HG13	1:AB:40:THR:HG21	1.99	0.45
1:AB:98:THR:HG22	1:FX:118:ASP:HB3	1.98	0.45
1:AT:30:VAL:HG13	1:AT:40:THR:HG21	1.99	0.45
1:AZ:28:ARG:HG2	1:AZ:44:SER:CB	2.45	0.45
1:BG:28:ARG:HG2	1:BG:44:SER:HB3	1.98	0.45
1:BG:45:LEU:HD12	1:BG:60:MET:HG2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:94:ASN:O	1:BO:98:THR:HG23	2.16	0.45
1:BV:26:LEU:HD12	1:BV:45:LEU:O	2.17	0.45
1:CH:103:THR:OG1	1:FT:62:LEU:HD21	2.16	0.45
1:CQ:123:ASN:OD1	1:GC:1:MET:HB3	2.17	0.45
1:CT:45:LEU:HD12	1:CT:60:MET:HG2	1.97	0.45
1:CV:94:ASN:O	1:CV:98:THR:HG23	2.16	0.45
1:CZ:10:VAL:O	1:CZ:13:GLU:HG2	2.16	0.45
1:DF:10:VAL:O	1:DF:13:GLU:HG2	2.16	0.45
1:DH:94:ASN:O	1:DH:98:THR:HG23	2.16	0.45
1:DL:26:LEU:HD12	1:DL:45:LEU:O	2.17	0.45
1:DN:30:VAL:HG13	1:DN:40:THR:HG21	1.99	0.45
1:DS:122:ASN:HB2	1:GR:20:SER:O	2.17	0.45
1:DU:10:VAL:O	1:DU:13:GLU:HG2	2.16	0.45
1:DU:26:LEU:HD12	1:DU:45:LEU:O	2.16	0.45
1:FH:10:VAL:O	1:FH:13:GLU:HG2	2.16	0.45
1:FH:26:LEU:HD12	1:FH:45:LEU:O	2.17	0.45
1:GR:26:LEU:HD12	1:GR:45:LEU:O	2.17	0.45
1:GT:94:ASN:O	1:GT:98:THR:HG23	2.16	0.45
1:GU:10:VAL:O	1:GU:13:GLU:HG2	2.16	0.45
1:GW:94:ASN:O	1:GW:98:THR:HG23	2.16	0.45
1:AC:91:THR:HB	1:DO:78:ILE:CD1	2.46	0.45
1:AD:92:TYR:CZ	1:BC:80:ALA:HB3	2.51	0.45
1:AE:106:ALA:HB1	1:GA:8:LEU:HD22	1.97	0.45
1:AL:45:LEU:HD12	1:AL:60:MET:HG2	1.97	0.45
1:AN:124:TYR:CZ	1:FS:19:VAL:HB	2.52	0.45
1:AR:85:THR:OG1	1:ED:83:SER:OG	2.35	0.45
1:AY:26:LEU:HD12	1:AY:45:LEU:O	2.16	0.45
1:BM:28:ARG:HG2	1:BM:44:SER:HB3	1.98	0.45
1:BO:30:VAL:HG13	1:BO:40:THR:HG21	1.99	0.45
1:BR:28:ARG:HG2	1:BR:44:SER:CB	2.45	0.45
1:BX:30:VAL:HG13	1:BX:40:THR:HG21	1.99	0.45
1:CB:28:ARG:HG2	1:CB:44:SER:HB3	1.98	0.45
1:CD:30:VAL:HG13	1:CD:40:THR:HG21	1.99	0.45
1:CQ:28:ARG:HG2	1:CQ:44:SER:HB3	1.98	0.45
1:DB:124:TYR:O	1:GJ:2:ARG:HA	2.17	0.45
1:DI:28:ARG:HG2	1:DI:44:SER:HB3	1.98	0.45
1:DI:118:ASP:HB3	1:GU:98:THR:HG22	1.98	0.45
1:DL:28:ARG:HG2	1:DL:44:SER:HB3	1.98	0.45
1:DP:78:ILE:HD13	1:GW:91:THR:OG1	2.17	0.45
1:DW:94:ASN:O	1:DW:98:THR:HG23	2.16	0.45
1:EA:28:ARG:HG2	1:EA:44:SER:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EH:106:ALA:HB3	1:EO:8:LEU:HD13	1.99	0.45
1:EJ:28:ARG:HG2	1:EJ:44:SER:HB3	1.98	0.45
1:ER:30:VAL:HG13	1:ER:40:THR:HG21	1.99	0.45
1:ET:83:SER:OG	1:FG:85:THR:OG1	2.33	0.45
1:FH:28:ARG:HG2	1:FH:44:SER:HB3	1.98	0.45
1:GB:28:ARG:HG2	1:GB:44:SER:CB	2.45	0.45
1:GE:30:VAL:HG13	1:GE:40:THR:HG21	1.99	0.45
1:GK:30:VAL:HG13	1:GK:40:THR:HG21	1.99	0.45
1:GO:28:ARG:HG2	1:GO:44:SER:HB3	1.98	0.45
1:AU:28:ARG:HG2	1:AU:44:SER:HB3	1.98	0.45
1:AW:123:ASN:HB3	1:FC:3:LEU:HG	1.98	0.45
1:AX:26:LEU:HD12	1:AX:45:LEU:O	2.16	0.45
1:BD:28:ARG:HG2	1:BD:44:SER:HB3	1.98	0.45
1:BG:26:LEU:HD12	1:BG:45:LEU:O	2.16	0.45
1:BJ:26:LEU:HD12	1:BJ:45:LEU:O	2.16	0.45
1:BL:94:ASN:O	1:BL:98:THR:HG23	2.16	0.45
1:BS:26:LEU:HD12	1:BS:45:LEU:O	2.17	0.45
1:BZ:116:PRO:O	1:DT:56:ARG:NH1	2.47	0.45
1:CG:94:ASN:O	1:CG:98:THR:HG23	2.16	0.45
1:CU:99:LYS:HE2	1:DH:15:ARG:NH1	2.32	0.45
1:DC:28:ARG:HG2	1:DC:44:SER:HB3	1.98	0.45
1:DO:10:VAL:O	1:DO:13:GLU:HG2	2.16	0.45
1:EL:30:VAL:HG13	1:EL:40:THR:HG21	1.99	0.45
1:EM:2:ARG:NH1	1:ER:124:TYR:OXT	2.50	0.45
1:ES:26:LEU:HD12	1:ES:45:LEU:O	2.17	0.45
1:ET:118:ASP:OD2	1:FG:98:THR:HG22	2.17	0.45
1:FD:30:VAL:HG13	1:FD:40:THR:HG21	1.99	0.45
1:FN:26:LEU:HD12	1:FN:45:LEU:O	2.17	0.45
1:FP:30:VAL:HG13	1:FP:40:THR:HG21	1.99	0.45
1:FR:26:LEU:HD12	1:FR:45:LEU:O	2.16	0.45
1:FW:28:ARG:HG2	1:FW:44:SER:HB3	1.98	0.45
1:FY:30:VAL:HG13	1:FY:40:THR:HG21	1.99	0.45
1:GF:28:ARG:HG2	1:GF:44:SER:HB3	1.98	0.45
1:AE:124:TYR:CB	1:GB:22:GLN:HB3	2.44	0.44
1:AN:30:VAL:HG13	1:AN:40:THR:HG21	1.99	0.44
1:AP:3:LEU:HG	1:BU:123:ASN:HB3	1.99	0.44
1:AR:96:HIS:CG	1:ED:66:VAL:HG21	2.53	0.44
1:BF:30:VAL:HG13	1:BF:40:THR:HG21	1.99	0.44
1:BI:30:VAL:HG13	1:BI:40:THR:HG21	1.99	0.44
1:BQ:107:TRP:CE2	1:EC:8:LEU:HD11	2.52	0.44
1:BR:30:VAL:HG13	1:BR:40:THR:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:94:ASN:O	1:BR:98:THR:HG23	2.16	0.44
1:CD:17:TYR:CD2	1:CR:107:TRP:HZ2	2.34	0.44
1:CE:62:LEU:HD21	1:FQ:103:THR:OG1	2.17	0.44
1:CJ:30:VAL:HG13	1:CJ:40:THR:HG21	1.99	0.44
1:CJ:91:THR:OG1	1:CO:78:ILE:HD13	2.17	0.44
1:DC:26:LEU:HD12	1:DC:45:LEU:O	2.17	0.44
1:DN:94:ASN:O	1:DN:98:THR:HG23	2.16	0.44
1:EB:120:GLY:HA2	1:GB:47:GLN:HE22	1.82	0.44
1:EY:28:ARG:HG2	1:EY:44:SER:HB3	1.98	0.44
1:FS:28:ARG:HG2	1:FS:44:SER:CB	2.45	0.44
1:FZ:26:LEU:HD12	1:FZ:45:LEU:O	2.16	0.44
1:GE:94:ASN:O	1:GE:98:THR:HG23	2.16	0.44
1:GI:26:LEU:HD12	1:GI:45:LEU:O	2.16	0.44
1:GL:28:ARG:HG2	1:GL:44:SER:HB3	1.98	0.44
1:AM:62:LEU:HD21	1:CA:103:THR:OG1	2.17	0.44
1:AQ:30:VAL:HG13	1:AQ:40:THR:HG21	1.99	0.44
1:AW:83:SER:OG	1:FC:85:THR:OG1	2.35	0.44
1:BD:26:LEU:HD12	1:BD:45:LEU:O	2.16	0.44
1:BE:107:TRP:CE2	1:BL:8:LEU:HD11	2.52	0.44
1:BH:103:THR:OG1	1:BO:62:LEU:HD21	2.16	0.44
1:BJ:28:ARG:HG2	1:BJ:44:SER:HB3	1.98	0.44
1:BM:26:LEU:HD12	1:BM:45:LEU:O	2.17	0.44
1:BQ:122:ASN:HB2	1:ED:20:SER:O	2.17	0.44
1:CP:30:VAL:HG13	1:CP:40:THR:HG21	1.99	0.44
1:CW:2:ARG:HH12	1:DH:124:TYR:C	2.21	0.44
1:CZ:22:GLN:CD	1:GL:124:TYR:HA	2.37	0.44
1:CZ:24:GLY:O	1:GL:122:ASN:HB3	2.17	0.44
1:DC:124:TYR:O	1:GO:3:LEU:N	2.39	0.44
1:DW:22:GLN:HB3	1:GE:124:TYR:CB	2.46	0.44
1:ED:28:ARG:HG2	1:ED:44:SER:HB3	1.98	0.44
1:EI:94:ASN:O	1:EI:98:THR:HG23	2.16	0.44
1:EP:26:LEU:HD12	1:EP:45:LEU:O	2.16	0.44
1:EX:97:ILE:HG21	1:FI:117:VAL:O	2.17	0.44
1:EY:26:LEU:HD12	1:EY:45:LEU:O	2.17	0.44
1:FB:28:ARG:HG2	1:FB:44:SER:HB3	1.98	0.44
1:GC:10:VAL:O	1:GC:13:GLU:HG2	2.16	0.44
1:GF:10:VAL:O	1:GF:13:GLU:HG2	2.16	0.44
1:GL:26:LEU:HD12	1:GL:45:LEU:O	2.16	0.44
1:GQ:30:VAL:HG13	1:GQ:40:THR:HG21	1.99	0.44
1:GR:28:ARG:HG2	1:GR:44:SER:HB3	1.98	0.44
1:AG:96:HIS:CG	1:BF:66:VAL:HG21	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:13:GLU:OE2	1:FR:99:LYS:HE3	2.18	0.44
1:AU:10:VAL:O	1:AU:13:GLU:HG2	2.16	0.44
1:AV:8:LEU:HD11	1:EF:107:TRP:CE2	2.53	0.44
1:AZ:1:MET:HG2	1:EW:123:ASN:OD1	2.18	0.44
1:AZ:117:VAL:HG22	1:EW:58:VAL:HG11	1.99	0.44
1:BA:26:LEU:HD12	1:BA:45:LEU:O	2.16	0.44
1:BD:10:VAL:O	1:BD:13:GLU:HG2	2.16	0.44
1:BM:96:HIS:CG	1:EY:66:VAL:HG21	2.53	0.44
1:BU:22:GLN:HB3	1:DN:124:TYR:CB	2.47	0.44
1:BU:94:ASN:O	1:BU:98:THR:HG23	2.16	0.44
1:CC:10:VAL:CG2	1:GK:103:THR:HG22	2.43	0.44
1:CC:78:ILE:HD13	1:GK:91:THR:OG1	2.17	0.44
1:CC:122:ASN:ND2	1:GK:25:THR:HG22	2.32	0.44
1:CM:30:VAL:HG13	1:CM:40:THR:HG21	1.99	0.44
1:CU:118:ASP:OD2	1:DH:98:THR:HG22	2.17	0.44
1:CV:124:TYR:HA	1:GM:22:GLN:NE2	2.32	0.44
1:CW:10:VAL:O	1:CW:13:GLU:HG2	2.16	0.44
1:EC:30:VAL:HG13	1:EC:40:THR:HG21	1.99	0.44
1:EG:28:ARG:HG2	1:EG:44:SER:HB3	1.98	0.44
1:FD:94:ASN:O	1:FD:98:THR:HG23	2.16	0.44
1:FM:30:VAL:HG13	1:FM:40:THR:HG21	1.99	0.44
1:GC:45:LEU:HD12	1:GC:60:MET:HG2	1.97	0.44
1:GO:26:LEU:HD12	1:GO:45:LEU:O	2.17	0.44
1:GU:28:ARG:HG2	1:GU:44:SER:HB3	1.98	0.44
1:GX:26:LEU:HD12	1:GX:45:LEU:O	2.16	0.44
1:AD:3:LEU:HG	1:BC:123:ASN:HB3	1.98	0.44
1:AF:28:ARG:HG2	1:AF:44:SER:HB3	1.98	0.44
1:AO:10:VAL:O	1:AO:13:GLU:HG2	2.16	0.44
1:AR:26:LEU:HD12	1:AR:45:LEU:O	2.17	0.44
1:AW:30:VAL:HG13	1:AW:40:THR:HG21	1.99	0.44
1:AX:107:TRP:CE2	1:EJ:8:LEU:HD11	2.52	0.44
1:BA:98:THR:HG22	1:EM:118:ASP:CG	2.37	0.44
1:BH:124:TYR:CA	1:BO:22:GLN:HE21	2.30	0.44
1:BP:10:VAL:O	1:BP:13:GLU:HG2	2.16	0.44
1:CK:98:THR:HG22	1:FW:118:ASP:CG	2.37	0.44
1:CV:30:VAL:HG13	1:CV:40:THR:HG21	1.99	0.44
1:CY:30:VAL:HG13	1:CY:40:THR:HG21	1.99	0.44
1:DC:121:LEU:HD22	1:GM:20:SER:HA	2.00	0.44
1:DE:30:VAL:HG13	1:DE:40:THR:HG21	1.99	0.44
1:DF:26:LEU:HD12	1:DF:45:LEU:O	2.17	0.44
1:DI:124:TYR:O	1:GU:3:LEU:N	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DY:97:ILE:HG21	1:FY:117:VAL:O	2.17	0.44
1:EA:10:VAL:O	1:EA:13:GLU:HG2	2.16	0.44
1:EG:26:LEU:HD12	1:EG:45:LEU:O	2.17	0.44
1:EL:94:ASN:O	1:EL:98:THR:HG23	2.16	0.44
1:EP:10:VAL:O	1:EP:13:GLU:HG2	2.16	0.44
1:FE:28:ARG:HG2	1:FE:44:SER:HB3	1.98	0.44
1:FG:30:VAL:HG13	1:FG:40:THR:HG21	1.99	0.44
1:FK:10:VAL:O	1:FK:13:GLU:HG2	2.16	0.44
1:AR:83:SER:OG	1:ED:85:THR:OG1	2.35	0.44
1:AS:45:LEU:HD11	1:AS:58:VAL:CG1	2.48	0.44
1:AX:10:VAL:O	1:AX:13:GLU:HG2	2.16	0.44
1:CH:28:ARG:HG2	1:CH:44:SER:HB3	1.98	0.44
1:CK:26:LEU:HD12	1:CK:45:LEU:O	2.17	0.44
1:CN:84:VAL:HG22	1:FZ:84:VAL:HG13	1.99	0.44
1:CY:122:ASN:HB2	1:GH:20:SER:O	2.17	0.44
1:DC:78:ILE:HD13	1:GO:91:THR:HB	2.00	0.44
1:FB:39:ASN:OD1	1:FB:40:THR:N	2.51	0.44
1:FJ:30:VAL:HG13	1:FJ:40:THR:HG21	1.99	0.44
1:FS:30:VAL:HG13	1:FS:40:THR:HG21	1.99	0.44
1:FS:98:THR:HG22	1:GP:118:ASP:OD2	2.18	0.44
1:AP:45:LEU:HD11	1:AP:58:VAL:CG1	2.48	0.44
1:AS:118:ASP:OD2	1:EL:98:THR:HG22	2.17	0.44
1:AZ:30:VAL:HG13	1:AZ:40:THR:HG21	1.99	0.44
1:BB:45:LEU:HD11	1:BB:58:VAL:CG1	2.48	0.44
1:BT:102:GLN:CB	1:DN:10:VAL:HG13	2.47	0.44
1:BZ:45:LEU:HD11	1:BZ:58:VAL:CG1	2.48	0.44
1:CN:10:VAL:O	1:CN:13:GLU:HG2	2.16	0.44
1:CS:30:VAL:HG13	1:CS:40:THR:HG21	1.99	0.44
1:CX:45:LEU:HD11	1:CX:58:VAL:CG1	2.48	0.44
1:DI:91:THR:CG2	1:GU:68:VAL:HG11	2.47	0.44
1:DO:28:ARG:HG2	1:DO:44:SER:HB3	1.98	0.44
1:EG:39:ASN:OD1	1:EG:40:THR:N	2.51	0.44
1:EP:39:ASN:OD1	1:EP:40:THR:N	2.51	0.44
1:EX:66:VAL:HG21	1:FI:96:HIS:CG	2.52	0.44
1:FA:30:VAL:HG13	1:FA:40:THR:HG21	1.99	0.44
1:FP:124:TYR:OXT	1:GX:2:ARG:NH1	2.51	0.44
1:GH:30:VAL:HG13	1:GH:40:THR:HG21	1.99	0.44
1:AE:29:PHE:CG	1:GA:107:TRP:HH2	2.36	0.44
1:BG:39:ASN:OD1	1:BG:40:THR:N	2.51	0.44
1:BN:19:VAL:HB	1:FB:124:TYR:CE2	2.53	0.44
1:CA:30:VAL:HG13	1:CA:40:THR:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:2:ARG:NH1	1:DT:124:TYR:OXT	2.51	0.44
1:CC:22:GLN:NE2	1:GK:124:TYR:HA	2.33	0.44
1:CC:45:LEU:HD12	1:CC:46:GLU:N	2.33	0.44
1:CN:122:ASN:HB2	1:FX:20:SER:O	2.18	0.44
1:CU:45:LEU:HD11	1:CU:58:VAL:CG1	2.48	0.44
1:CW:28:ARG:HG2	1:CW:44:SER:HB3	1.98	0.44
1:CX:8:LEU:HD11	1:DK:107:TRP:CE2	2.53	0.44
1:DE:28:ARG:HG2	1:DE:44:SER:CB	2.45	0.44
1:DQ:30:VAL:HG13	1:DQ:40:THR:HG21	1.99	0.44
1:EF:30:VAL:HG13	1:EF:40:THR:HG21	1.99	0.44
1:EH:45:LEU:HD12	1:EH:46:GLU:N	2.33	0.44
1:EK:3:LEU:HG	1:ER:123:ASN:HB3	2.00	0.44
1:FW:39:ASN:OD1	1:FW:40:THR:N	2.51	0.44
1:GI:39:ASN:OD1	1:GI:40:THR:N	2.51	0.44
1:AE:98:THR:HG22	1:GA:118:ASP:OD2	2.18	0.44
1:AJ:3:LEU:HG	1:BX:123:ASN:HB3	2.00	0.44
1:AX:39:ASN:OD1	1:AX:40:THR:N	2.51	0.44
1:BS:39:ASN:OD1	1:BS:40:THR:N	2.51	0.44
1:BU:30:VAL:HG13	1:BU:40:THR:HG21	1.99	0.44
1:BZ:45:LEU:HD12	1:BZ:46:GLU:N	2.33	0.44
1:BZ:119:SER:HA	1:DT:94:ASN:ND2	2.33	0.44
1:CF:99:LYS:HE2	1:GN:15:ARG:HD3	2.00	0.44
1:CH:39:ASN:OD1	1:CH:40:THR:N	2.51	0.44
1:DD:45:LEU:HD11	1:DD:58:VAL:CG1	2.48	0.44
1:DD:45:LEU:HD12	1:DD:46:GLU:N	2.33	0.44
1:DP:45:LEU:HD12	1:DP:46:GLU:N	2.33	0.44
1:DT:30:VAL:HG13	1:DT:40:THR:HG21	1.99	0.44
1:EA:26:LEU:HD12	1:EA:45:LEU:O	2.17	0.44
1:ET:45:LEU:HD12	1:ET:46:GLU:N	2.33	0.44
1:FA:83:SER:OG	1:FL:85:THR:OG1	2.36	0.44
1:FC:45:LEU:HD12	1:FC:46:GLU:N	2.33	0.44
1:FV:30:VAL:HG13	1:FV:40:THR:HG21	1.99	0.44
1:GD:45:LEU:HD11	1:GD:58:VAL:CG1	2.48	0.44
1:GD:45:LEU:HD12	1:GD:46:GLU:N	2.33	0.44
1:GJ:45:LEU:HD11	1:GJ:58:VAL:CG1	2.48	0.44
1:GS:45:LEU:HD11	1:GS:58:VAL:CG1	2.48	0.44
1:AG:45:LEU:HD12	1:AG:46:GLU:N	2.33	0.44
1:AI:39:ASN:OD1	1:AI:40:THR:N	2.51	0.44
1:AK:117:VAL:O	1:FO:97:ILE:HG21	2.18	0.44
1:AP:45:LEU:HD12	1:AP:46:GLU:N	2.33	0.44
1:AV:45:LEU:HD11	1:AV:58:VAL:CG1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:45:LEU:HD12	1:AY:46:GLU:N	2.33	0.44
1:BN:3:LEU:HG	1:DZ:123:ASN:HB3	2.00	0.44
1:BN:97:ILE:HG21	1:DZ:117:VAL:O	2.18	0.44
1:BW:45:LEU:HD11	1:BW:58:VAL:CG1	2.48	0.44
1:CG:117:VAL:CG2	1:CL:58:VAL:HG11	2.47	0.44
1:CI:45:LEU:HD11	1:CI:58:VAL:CG1	2.48	0.44
1:CO:45:LEU:HD12	1:CO:46:GLU:N	2.33	0.44
1:DH:30:VAL:HG13	1:DH:40:THR:HG21	1.99	0.44
1:DJ:45:LEU:HD12	1:DJ:46:GLU:N	2.33	0.44
1:DL:39:ASN:OD1	1:DL:40:THR:N	2.51	0.44
1:DV:45:LEU:HD12	1:DV:46:GLU:N	2.33	0.44
1:EB:45:LEU:HD12	1:EB:46:GLU:N	2.33	0.44
1:EP:2:ARG:HH12	1:FJ:124:TYR:C	2.21	0.44
1:EV:39:ASN:OD1	1:EV:40:THR:N	2.51	0.44
1:EY:39:ASN:OD1	1:EY:40:THR:N	2.51	0.44
1:EZ:45:LEU:HD12	1:EZ:46:GLU:N	2.33	0.44
1:FI:45:LEU:HD12	1:FI:46:GLU:N	2.33	0.44
1:FM:28:ARG:HG2	1:FM:44:SER:CB	2.45	0.44
1:GM:45:LEU:HD11	1:GM:58:VAL:CG1	2.48	0.44
1:GP:45:LEU:HD11	1:GP:58:VAL:CG1	2.48	0.44
1:GW:30:VAL:HG13	1:GW:40:THR:HG21	1.99	0.44
1:AD:45:LEU:HD12	1:AD:46:GLU:N	2.33	0.43
1:AJ:45:LEU:HD11	1:AJ:58:VAL:CG1	2.48	0.43
1:AL:39:ASN:OD1	1:AL:40:THR:N	2.51	0.43
1:AN:94:ASN:O	1:AN:98:THR:HG23	2.16	0.43
1:AR:39:ASN:OD1	1:AR:40:THR:N	2.51	0.43
1:AU:10:VAL:HG13	1:EG:102:GLN:CB	2.48	0.43
1:AU:26:LEU:HD12	1:AU:45:LEU:O	2.17	0.43
1:BC:30:VAL:HG13	1:BC:40:THR:HG21	1.99	0.43
1:BJ:103:THR:OG1	1:EV:62:LEU:HD21	2.18	0.43
1:BK:120:GLY:HA2	1:DW:47:GLN:HE22	1.83	0.43
1:CB:3:LEU:N	1:FN:124:TYR:O	2.43	0.43
1:CB:39:ASN:OD1	1:CB:40:THR:N	2.51	0.43
1:CO:45:LEU:HD11	1:CO:58:VAL:CG1	2.48	0.43
1:CS:83:SER:OG	1:DD:85:THR:OG1	2.36	0.43
1:CX:45:LEU:HD12	1:CX:46:GLU:N	2.33	0.43
1:DK:51:ALA:O	1:DK:90:LYS:NZ	2.50	0.43
1:DM:45:LEU:HD12	1:DM:46:GLU:N	2.33	0.43
1:DX:39:ASN:OD1	1:DX:40:THR:N	2.51	0.43
1:EB:45:LEU:HD11	1:EB:58:VAL:CG1	2.48	0.43
1:EN:45:LEU:HD12	1:EN:46:GLU:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ET:84:VAL:HG22	1:FG:84:VAL:HG13	2.00	0.43
1:EW:45:LEU:HD12	1:EW:46:GLU:N	2.33	0.43
1:GB:30:VAL:HG13	1:GB:40:THR:HG21	1.99	0.43
1:GF:39:ASN:OD1	1:GF:40:THR:N	2.51	0.43
1:GV:45:LEU:HD11	1:GV:58:VAL:CG1	2.48	0.43
1:GV:45:LEU:HD12	1:GV:46:GLU:N	2.33	0.43
1:AJ:45:LEU:HD12	1:AJ:46:GLU:N	2.33	0.43
1:AM:3:LEU:HG	1:CA:123:ASN:HB3	1.99	0.43
1:AM:102:GLN:CB	1:CA:10:VAL:HG13	2.47	0.43
1:AO:39:ASN:OD1	1:AO:40:THR:N	2.51	0.43
1:AS:45:LEU:HD12	1:AS:46:GLU:N	2.33	0.43
1:BE:45:LEU:HD12	1:BE:46:GLU:N	2.33	0.43
1:BL:30:VAL:HG13	1:BL:40:THR:HG21	1.99	0.43
1:BN:118:ASP:CB	1:DZ:98:THR:HG22	2.48	0.43
1:BO:28:ARG:HG2	1:BO:44:SER:CB	2.45	0.43
1:BW:45:LEU:HD12	1:BW:46:GLU:N	2.33	0.43
1:CI:45:LEU:HD12	1:CI:46:GLU:N	2.33	0.43
1:CN:39:ASN:OD1	1:CN:40:THR:N	2.51	0.43
1:CR:45:LEU:HD12	1:CR:46:GLU:N	2.33	0.43
1:DA:45:LEU:HD12	1:DA:46:GLU:N	2.33	0.43
1:DF:107:TRP:CE2	1:GR:8:LEU:HD11	2.52	0.43
1:DI:91:THR:HB	1:GU:78:ILE:HD13	2.00	0.43
1:DJ:19:VAL:HB	1:GX:124:TYR:CE2	2.52	0.43
1:DM:45:LEU:HD11	1:DM:58:VAL:CG1	2.48	0.43
1:EE:45:LEU:HD12	1:EE:46:GLU:N	2.33	0.43
1:EE:124:TYR:OXT	1:EU:22:GLN:NE2	2.51	0.43
1:FP:8:LEU:HB3	1:GV:106:ALA:HB1	2.00	0.43
1:FT:39:ASN:OD1	1:FT:40:THR:N	2.51	0.43
1:FU:45:LEU:HD12	1:FU:46:GLU:N	2.33	0.43
1:AF:39:ASN:OD1	1:AF:40:THR:N	2.51	0.43
1:AH:122:ASN:HB2	1:GE:20:SER:O	2.18	0.43
1:AR:103:THR:OG1	1:ED:62:LEU:HD21	2.18	0.43
1:BK:45:LEU:HD11	1:BK:58:VAL:CG1	2.48	0.43
1:BV:39:ASN:OD1	1:BV:40:THR:N	2.51	0.43
1:BY:39:ASN:OD1	1:BY:40:THR:N	2.51	0.43
1:CF:121:LEU:HD11	1:GO:19:VAL:O	2.18	0.43
1:CK:39:ASN:OD1	1:CK:40:THR:N	2.51	0.43
1:CL:45:LEU:HD11	1:CL:58:VAL:CG1	2.48	0.43
1:CS:8:LEU:HD11	1:DD:107:TRP:CE2	2.53	0.43
1:DA:122:ASN:HB2	1:DF:20:SER:O	2.18	0.43
1:DB:30:VAL:HG13	1:DB:40:THR:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EM:39:ASN:OD1	1:EM:40:THR:N	2.51	0.43
1:EO:30:VAL:HG13	1:EO:40:THR:HG21	1.99	0.43
1:EQ:45:LEU:HD12	1:EQ:46:GLU:N	2.33	0.43
1:ET:10:VAL:CG2	1:FG:103:THR:HG22	2.45	0.43
1:EX:30:VAL:HG13	1:EX:40:THR:HG21	1.99	0.43
1:FA:91:THR:OG1	1:FL:78:ILE:HD13	2.18	0.43
1:FQ:39:ASN:OD1	1:FQ:40:THR:N	2.51	0.43
1:FW:20:SER:O	1:GS:122:ASN:HB2	2.17	0.43
1:GG:45:LEU:HD11	1:GG:58:VAL:CG1	2.48	0.43
1:GR:39:ASN:OD1	1:GR:40:THR:N	2.51	0.43
1:AN:22:GLN:HE21	1:FR:124:TYR:C	2.22	0.43
1:BD:39:ASN:OD1	1:BD:40:THR:N	2.51	0.43
1:BP:39:ASN:OD1	1:BP:40:THR:N	2.51	0.43
1:CH:98:THR:HG22	1:FT:118:ASP:CB	2.48	0.43
1:DC:107:TRP:CZ2	1:GO:17:TYR:CD2	3.06	0.43
1:EA:39:ASN:OD1	1:EA:40:THR:N	2.51	0.43
1:EH:124:TYR:CD2	1:EP:19:VAL:HB	2.54	0.43
1:ES:39:ASN:OD1	1:ES:40:THR:N	2.51	0.43
1:EX:98:THR:HG22	1:FI:118:ASP:CG	2.38	0.43
1:FD:8:LEU:HD11	1:FF:107:TRP:CE2	2.54	0.43
1:FO:45:LEU:HD12	1:FO:46:GLU:N	2.33	0.43
1:GC:39:ASN:OD1	1:GC:40:THR:N	2.51	0.43
1:GJ:45:LEU:HD12	1:GJ:46:GLU:N	2.33	0.43
1:GL:39:ASN:OD1	1:GL:40:THR:N	2.51	0.43
1:GP:45:LEU:HD12	1:GP:46:GLU:N	2.33	0.43
1:AA:85:THR:OG1	1:BI:83:SER:OG	2.35	0.43
1:AG:45:LEU:HD11	1:AG:58:VAL:CG1	2.48	0.43
1:AK:30:VAL:HG13	1:AK:40:THR:HG21	1.99	0.43
1:AO:91:THR:HB	1:EA:78:ILE:HD13	2.00	0.43
1:AR:92:TYR:CZ	1:ED:80:ALA:HB3	2.53	0.43
1:AT:103:THR:OG1	1:EZ:62:LEU:HD21	2.19	0.43
1:AU:39:ASN:OD1	1:AU:40:THR:N	2.51	0.43
1:BE:20:SER:HA	1:ES:121:LEU:HD22	2.01	0.43
1:BQ:45:LEU:HD12	1:BQ:46:GLU:N	2.33	0.43
1:CE:39:ASN:OD1	1:CE:40:THR:N	2.51	0.43
1:CP:91:THR:OG1	1:DJ:78:ILE:HD13	2.18	0.43
1:CZ:39:ASN:OD1	1:CZ:40:THR:N	2.51	0.43
1:DB:83:SER:OG	1:GJ:85:THR:OG1	2.36	0.43
1:DC:39:ASN:OD1	1:DC:40:THR:N	2.51	0.43
1:DU:39:ASN:OD1	1:DU:40:THR:N	2.51	0.43
1:EE:45:LEU:HD11	1:EE:58:VAL:CG1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FE:39:ASN:OD1	1:FE:40:THR:N	2.51	0.43
1:FL:45:LEU:HD12	1:FL:46:GLU:N	2.33	0.43
1:FN:39:ASN:OD1	1:FN:40:THR:N	2.51	0.43
1:GA:45:LEU:HD11	1:GA:58:VAL:CG1	2.48	0.43
1:GG:45:LEU:HD12	1:GG:46:GLU:N	2.33	0.43
1:GX:39:ASN:OD1	1:GX:40:THR:N	2.51	0.43
1:AC:39:ASN:OD1	1:AC:40:THR:N	2.51	0.43
1:AH:30:VAL:HG13	1:AH:40:THR:HG21	1.99	0.43
1:AJ:97:ILE:HG21	1:BX:117:VAL:O	2.18	0.43
1:AM:45:LEU:HD12	1:AM:46:GLU:N	2.33	0.43
1:AQ:103:THR:HG22	1:FU:10:VAL:CG2	2.46	0.43
1:BH:45:LEU:HD12	1:BH:46:GLU:N	2.33	0.43
1:BJ:102:GLN:HB2	1:EV:10:VAL:HG13	2.00	0.43
1:BK:45:LEU:HD12	1:BK:46:GLU:N	2.33	0.43
1:CH:91:THR:HB	1:FT:78:ILE:HD13	2.00	0.43
1:CL:45:LEU:HD12	1:CL:46:GLU:N	2.33	0.43
1:CN:98:THR:HG22	1:FZ:118:ASP:HB3	2.00	0.43
1:CQ:39:ASN:OD1	1:CQ:40:THR:N	2.51	0.43
1:CU:45:LEU:HD12	1:CU:46:GLU:N	2.33	0.43
1:DB:80:ALA:HB3	1:GJ:92:TYR:CZ	2.53	0.43
1:DG:45:LEU:HD12	1:DG:46:GLU:N	2.33	0.43
1:DS:45:LEU:HD12	1:DS:46:GLU:N	2.33	0.43
1:EI:30:VAL:HG13	1:EI:40:THR:CG2	2.49	0.43
1:ER:30:VAL:HG13	1:ER:40:THR:CG2	2.49	0.43
1:FJ:30:VAL:HG13	1:FJ:40:THR:CG2	2.49	0.43
1:FV:30:VAL:HG13	1:FV:40:THR:CG2	2.49	0.43
1:AF:68:VAL:HG11	1:DR:91:THR:CG2	2.48	0.43
1:AM:45:LEU:HD11	1:AM:58:VAL:CG1	2.48	0.43
1:AN:22:GLN:HB3	1:CA:124:TYR:CB	2.48	0.43
1:AX:66:VAL:HG21	1:EJ:96:HIS:CG	2.54	0.43
1:BF:30:VAL:HG13	1:BF:40:THR:CG2	2.49	0.43
1:BJ:39:ASN:OD1	1:BJ:40:THR:N	2.51	0.43
1:BQ:45:LEU:HD11	1:BQ:58:VAL:CG1	2.48	0.43
1:BU:30:VAL:HG13	1:BU:40:THR:CG2	2.49	0.43
1:CD:83:SER:OG	1:CR:85:THR:OG1	2.34	0.43
1:CF:45:LEU:HD12	1:CF:46:GLU:N	2.33	0.43
1:CF:102:GLN:HB2	1:GN:10:VAL:HG13	2.01	0.43
1:CJ:30:VAL:HG13	1:CJ:40:THR:CG2	2.49	0.43
1:CM:103:THR:HG22	1:DG:10:VAL:HG11	2.00	0.43
1:DF:98:THR:HG22	1:GR:118:ASP:HB3	2.01	0.43
1:EH:45:LEU:HD11	1:EH:58:VAL:CG1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EH:107:TRP:CH2	1:EO:29:PHE:CD2	3.06	0.43
1:FP:66:VAL:HG21	1:GV:96:HIS:CG	2.54	0.43
1:GM:45:LEU:HD12	1:GM:46:GLU:N	2.33	0.43
1:AA:45:LEU:HD12	1:AA:46:GLU:N	2.33	0.43
1:AH:124:TYR:C	1:GF:2:ARG:HH12	2.21	0.43
1:AY:99:LYS:HE3	1:EI:13:GLU:OE2	2.18	0.43
1:AY:106:ALA:HB1	1:EI:8:LEU:HD22	2.01	0.43
1:BA:39:ASN:OD1	1:BA:40:THR:N	2.51	0.43
1:BB:45:LEU:HD12	1:BB:46:GLU:N	2.33	0.43
1:BJ:102:GLN:CB	1:EV:10:VAL:HG13	2.49	0.43
1:BT:45:LEU:HD12	1:BT:46:GLU:N	2.33	0.43
1:CH:83:SER:OG	1:FT:85:THR:OG1	2.37	0.43
1:CP:30:VAL:HG13	1:CP:40:THR:CG2	2.49	0.43
1:CW:68:VAL:HG11	1:GI:91:THR:CG2	2.47	0.43
1:DB:51:ALA:O	1:DB:90:LYS:NZ	2.50	0.43
1:DB:117:VAL:O	1:GJ:97:ILE:HG21	2.18	0.43
1:DF:39:ASN:OD1	1:DF:40:THR:N	2.51	0.43
1:DN:30:VAL:HG13	1:DN:40:THR:CG2	2.49	0.43
1:DY:8:LEU:HD11	1:FY:107:TRP:CE2	2.53	0.43
1:ED:39:ASN:OD1	1:ED:40:THR:N	2.51	0.43
1:EL:51:ALA:O	1:EL:90:LYS:NZ	2.50	0.43
1:EX:98:THR:HG22	1:FI:118:ASP:CB	2.47	0.43
1:EZ:45:LEU:HD11	1:EZ:58:VAL:CG1	2.48	0.43
1:FM:30:VAL:HG13	1:FM:40:THR:CG2	2.49	0.43
1:FX:27:PHE:CE2	1:FX:45:LEU:HD23	2.54	0.43
1:FX:45:LEU:HD11	1:FX:58:VAL:CG1	2.48	0.43
1:GA:45:LEU:HD12	1:GA:46:GLU:N	2.33	0.43
1:GN:30:VAL:HG13	1:GN:40:THR:HG21	1.99	0.43
1:AA:45:LEU:HD11	1:AA:58:VAL:CG1	2.48	0.43
1:AE:30:VAL:HG13	1:AE:40:THR:CG2	2.49	0.43
1:AS:99:LYS:HE2	1:EL:15:ARG:HH11	1.84	0.43
1:BD:85:THR:O	1:EP:82:ALA:HA	2.18	0.43
1:BE:27:PHE:CE2	1:BE:45:LEU:HD23	2.54	0.43
1:BN:62:LEU:HD21	1:DZ:103:THR:OG1	2.19	0.43
1:CA:30:VAL:HG13	1:CA:40:THR:CG2	2.49	0.43
1:CD:19:VAL:HB	1:GK:124:TYR:CZ	2.53	0.43
1:CG:123:ASN:HB3	1:CL:3:LEU:HG	2.00	0.43
1:CI:99:LYS:HE2	1:GH:15:ARG:HH11	1.84	0.43
1:CW:39:ASN:OD1	1:CW:40:THR:N	2.51	0.43
1:DB:30:VAL:HG13	1:DB:40:THR:CG2	2.49	0.43
1:DC:107:TRP:HZ2	1:GO:17:TYR:CD2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DM:124:TYR:OXT	1:GT:22:GLN:NE2	2.52	0.43
1:DR:39:ASN:OD1	1:DR:40:THR:N	2.51	0.43
1:DY:27:PHE:CE2	1:DY:45:LEU:HD23	2.54	0.43
1:EH:107:TRP:HH2	1:EO:29:PHE:CD2	2.36	0.43
1:EK:27:PHE:CE2	1:EK:45:LEU:HD23	2.54	0.43
1:EQ:27:PHE:CE2	1:EQ:45:LEU:HD23	2.54	0.43
1:EQ:45:LEU:HD11	1:EQ:58:VAL:CG1	2.48	0.43
1:EQ:96:HIS:CG	1:FM:66:VAL:HG21	2.54	0.43
1:EQ:97:ILE:HG21	1:FM:117:VAL:O	2.18	0.43
1:EX:124:TYR:C	1:FK:2:ARG:HH12	2.22	0.43
1:FI:45:LEU:HD11	1:FI:58:VAL:CG1	2.48	0.43
1:FU:45:LEU:HD11	1:FU:58:VAL:CG1	2.48	0.43
1:FZ:39:ASN:OD1	1:FZ:40:THR:N	2.51	0.43
1:GB:30:VAL:HG13	1:GB:40:THR:CG2	2.49	0.43
1:GD:27:PHE:CE2	1:GD:45:LEU:HD23	2.54	0.43
1:GH:30:VAL:HG13	1:GH:40:THR:CG2	2.49	0.43
1:AG:27:PHE:CE2	1:AG:45:LEU:HD23	2.54	0.43
1:AH:123:ASN:HB3	1:GD:3:LEU:HG	2.01	0.43
1:AM:27:PHE:CE2	1:AM:45:LEU:HD23	2.54	0.43
1:AT:30:VAL:HG13	1:AT:40:THR:CG2	2.49	0.43
1:AX:118:ASP:HB3	1:EJ:98:THR:HG22	2.01	0.43
1:AY:45:LEU:HD11	1:AY:58:VAL:CG1	2.48	0.43
1:AZ:30:VAL:HG13	1:AZ:40:THR:CG2	2.49	0.43
1:BH:45:LEU:HD11	1:BH:58:VAL:CG1	2.48	0.43
1:BH:106:ALA:HB1	1:BO:8:LEU:HD22	2.01	0.43
1:BM:39:ASN:OD1	1:BM:40:THR:N	2.51	0.43
1:BT:27:PHE:CE2	1:BT:45:LEU:HD23	2.54	0.43
1:CG:30:VAL:HG13	1:CG:40:THR:CG2	2.49	0.43
1:CS:30:VAL:HG13	1:CS:40:THR:CG2	2.49	0.43
1:DA:27:PHE:CE2	1:DA:45:LEU:HD23	2.54	0.43
1:DB:105:ILE:HG23	1:GJ:105:ILE:CG2	2.42	0.43
1:DK:30:VAL:HG13	1:DK:40:THR:CG2	2.49	0.43
1:DV:103:THR:HG22	1:GE:10:VAL:HG21	2.01	0.43
1:DW:30:VAL:HG13	1:DW:40:THR:HG21	1.99	0.43
1:EE:121:LEU:HD11	1:EV:19:VAL:O	2.19	0.43
1:EH:27:PHE:CE2	1:EH:45:LEU:HD23	2.54	0.43
1:ET:27:PHE:CE2	1:ET:45:LEU:HD23	2.54	0.43
1:FA:103:THR:HG22	1:FL:10:VAL:CG2	2.48	0.43
1:FD:30:VAL:HG13	1:FD:40:THR:CG2	2.49	0.43
1:FH:39:ASN:OD1	1:FH:40:THR:N	2.51	0.43
1:FR:45:LEU:HD12	1:FR:46:GLU:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GG:27:PHE:CE2	1:GG:45:LEU:HD23	2.54	0.43
1:GW:30:VAL:HG13	1:GW:40:THR:CG2	2.49	0.43
1:AD:27:PHE:CE2	1:AD:45:LEU:HD23	2.54	0.42
1:AL:20:SER:O	1:FO:122:ASN:HB2	2.19	0.42
1:BN:45:LEU:HD12	1:BN:46:GLU:N	2.33	0.42
1:BO:30:VAL:HG13	1:BO:40:THR:CG2	2.49	0.42
1:CB:78:ILE:CD1	1:FN:91:THR:HB	2.49	0.42
1:CD:30:VAL:HG13	1:CD:40:THR:CG2	2.49	0.42
1:CF:27:PHE:CE2	1:CF:45:LEU:HD23	2.54	0.42
1:CX:27:PHE:CE2	1:CX:45:LEU:HD23	2.54	0.42
1:DD:27:PHE:CE2	1:DD:45:LEU:HD23	2.54	0.42
1:DE:30:VAL:HG13	1:DE:40:THR:CG2	2.49	0.42
1:DF:118:ASP:CG	1:GR:98:THR:HG22	2.40	0.42
1:DS:27:PHE:CE2	1:DS:45:LEU:HD23	2.54	0.42
1:EB:8:LEU:HD22	1:GB:106:ALA:HB1	2.01	0.42
1:EK:45:LEU:HD12	1:EK:46:GLU:N	2.33	0.42
1:EO:30:VAL:HG13	1:EO:40:THR:CG2	2.49	0.42
1:ET:103:THR:OG1	1:FG:62:LEU:HD21	2.18	0.42
1:FF:27:PHE:CE2	1:FF:45:LEU:HD23	2.54	0.42
1:FX:45:LEU:HD12	1:FX:46:GLU:N	2.33	0.42
1:GE:30:VAL:HG13	1:GE:40:THR:CG2	2.49	0.42
1:GM:27:PHE:CE2	1:GM:45:LEU:HD23	2.54	0.42
1:GT:30:VAL:HG13	1:GT:40:THR:CG2	2.49	0.42
1:AN:66:VAL:HG23	1:FR:92:TYR:CE2	2.54	0.42
1:BC:30:VAL:HG13	1:BC:40:THR:CG2	2.49	0.42
1:BW:8:LEU:HD11	1:DQ:107:TRP:CE2	2.54	0.42
1:CA:20:SER:O	1:DT:122:ASN:HB2	2.19	0.42
1:CC:1:MET:SD	1:GK:111:GLN:HB2	2.58	0.42
1:CE:117:VAL:O	1:FQ:97:ILE:HG21	2.20	0.42
1:CV:30:VAL:HG13	1:CV:40:THR:CG2	2.49	0.42
1:CY:30:VAL:HG13	1:CY:40:THR:CG2	2.49	0.42
1:DO:39:ASN:OD1	1:DO:40:THR:N	2.51	0.42
1:DP:123:ASN:OD1	1:GW:1:MET:HG2	2.19	0.42
1:DS:96:HIS:CG	1:GQ:66:VAL:HG21	2.54	0.42
1:DV:27:PHE:CE2	1:DV:45:LEU:HD23	2.54	0.42
1:EE:124:TYR:HA	1:EU:22:GLN:HE21	1.84	0.42
1:EF:30:VAL:HG13	1:EF:40:THR:CG2	2.49	0.42
1:EN:27:PHE:CE2	1:EN:45:LEU:HD23	2.54	0.42
1:FF:45:LEU:HD12	1:FF:46:GLU:N	2.33	0.42
1:GJ:27:PHE:CE2	1:GJ:45:LEU:HD23	2.54	0.42
1:GN:30:VAL:HG13	1:GN:40:THR:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GS:45:LEU:HD12	1:GS:46:GLU:N	2.33	0.42
1:AN:30:VAL:HG13	1:AN:40:THR:CG2	2.49	0.42
1:AY:92:TYR:CE2	1:EI:66:VAL:HG23	2.54	0.42
1:BH:27:PHE:CE2	1:BH:45:LEU:HD23	2.54	0.42
1:BT:118:ASP:HA	1:DN:97:ILE:CG2	2.49	0.42
1:BV:91:THR:HG22	1:FH:68:VAL:HG11	2.01	0.42
1:BZ:62:LEU:HD21	1:DT:103:THR:OG1	2.19	0.42
1:CE:118:ASP:HA	1:FQ:97:ILE:CG2	2.50	0.42
1:CL:27:PHE:CE2	1:CL:45:LEU:HD23	2.54	0.42
1:CO:27:PHE:CE2	1:CO:45:LEU:HD23	2.54	0.42
1:CR:45:LEU:HD11	1:CR:58:VAL:CG1	2.48	0.42
1:CT:39:ASN:OD1	1:CT:40:THR:N	2.51	0.42
1:DJ:27:PHE:CE2	1:DJ:45:LEU:HD23	2.54	0.42
1:DY:45:LEU:HD12	1:DY:46:GLU:N	2.33	0.42
1:EX:117:VAL:O	1:FI:97:ILE:HG21	2.19	0.42
1:EZ:27:PHE:CE2	1:EZ:45:LEU:HD23	2.54	0.42
1:FR:45:LEU:HD11	1:FR:58:VAL:CG1	2.48	0.42
1:GA:27:PHE:CE2	1:GA:45:LEU:HD23	2.54	0.42
1:GK:30:VAL:HG13	1:GK:40:THR:CG2	2.49	0.42
1:GO:39:ASN:OD1	1:GO:40:THR:N	2.51	0.42
1:GU:39:ASN:OD1	1:GU:40:THR:N	2.51	0.42
1:AA:99:LYS:O	1:AA:103:THR:HG23	2.20	0.42
1:AQ:30:VAL:HG13	1:AQ:40:THR:CG2	2.49	0.42
1:AV:78:ILE:HG22	1:EF:89:PRO:HG3	2.01	0.42
1:BH:3:LEU:HG	1:BO:123:ASN:HB3	2.01	0.42
1:BK:22:GLN:HE21	1:DW:124:TYR:HA	1.78	0.42
1:BL:30:VAL:HG13	1:BL:40:THR:CG2	2.49	0.42
1:BZ:27:PHE:CE2	1:BZ:45:LEU:HD23	2.54	0.42
1:CF:45:LEU:HD11	1:CF:58:VAL:CG1	2.48	0.42
1:CQ:20:SER:O	1:DJ:122:ASN:HB2	2.20	0.42
1:CR:27:PHE:CE2	1:CR:45:LEU:HD23	2.54	0.42
1:DI:39:ASN:OD1	1:DI:40:THR:N	2.51	0.42
1:DP:99:LYS:O	1:DP:103:THR:HG23	2.20	0.42
1:EE:3:LEU:HG	1:EU:123:ASN:HB3	2.01	0.42
1:EK:99:LYS:O	1:EK:103:THR:HG23	2.20	0.42
1:FD:83:SER:OG	1:FF:85:THR:OG1	2.34	0.42
1:FG:30:VAL:HG13	1:FG:40:THR:CG2	2.49	0.42
1:FK:39:ASN:OD1	1:FK:40:THR:N	2.51	0.42
1:GP:27:PHE:CE2	1:GP:45:LEU:HD23	2.54	0.42
1:GS:27:PHE:CE2	1:GS:45:LEU:HD23	2.54	0.42
1:AJ:99:LYS:O	1:AJ:103:THR:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:122:ASN:HB2	1:BY:20:SER:O	2.19	0.42
1:AL:19:VAL:O	1:FO:121:LEU:HD11	2.19	0.42
1:AV:99:LYS:O	1:AV:103:THR:HG23	2.20	0.42
1:AX:82:ALA:HB2	1:EJ:86:PHE:CE1	2.55	0.42
1:AY:27:PHE:CE2	1:AY:45:LEU:HD23	2.54	0.42
1:BI:30:VAL:HG13	1:BI:40:THR:CG2	2.49	0.42
1:BN:99:LYS:O	1:BN:103:THR:HG23	2.20	0.42
1:BU:51:ALA:O	1:BU:90:LYS:NZ	2.50	0.42
1:CC:27:PHE:CE2	1:CC:45:LEU:HD23	2.54	0.42
1:CC:45:LEU:HD11	1:CC:58:VAL:CG1	2.48	0.42
1:CG:121:LEU:HD22	1:CM:20:SER:HA	2.01	0.42
1:CJ:22:GLN:HE21	1:CO:124:TYR:HA	1.83	0.42
1:CT:122:ASN:HB2	1:GD:20:SER:O	2.19	0.42
1:CZ:1:MET:SD	1:GL:111:GLN:HB3	2.59	0.42
1:DG:27:PHE:CE2	1:DG:45:LEU:HD23	2.54	0.42
1:EB:27:PHE:CE2	1:EB:45:LEU:HD23	2.54	0.42
1:EE:27:PHE:CE2	1:EE:45:LEU:HD23	2.54	0.42
1:EN:99:LYS:O	1:EN:103:THR:HG23	2.20	0.42
1:EN:124:TYR:C	1:FJ:22:GLN:HE21	2.23	0.42
1:FA:30:VAL:HG13	1:FA:40:THR:CG2	2.49	0.42
1:FC:27:PHE:CE2	1:FC:45:LEU:HD23	2.54	0.42
1:FF:45:LEU:HD11	1:FF:58:VAL:CG1	2.48	0.42
1:FI:27:PHE:CE2	1:FI:45:LEU:HD23	2.54	0.42
1:GQ:30:VAL:HG13	1:GQ:40:THR:CG2	2.49	0.42
1:AB:30:VAL:HG13	1:AB:40:THR:CG2	2.49	0.42
1:AD:45:LEU:HD11	1:AD:58:VAL:CG1	2.48	0.42
1:AE:51:ALA:O	1:AE:90:LYS:NZ	2.50	0.42
1:AG:103:THR:OG1	1:BF:62:LEU:HD21	2.19	0.42
1:AQ:8:LEU:HD11	1:FU:107:TRP:CE2	2.53	0.42
1:AS:107:TRP:CE2	1:EL:8:LEU:HD11	2.54	0.42
1:AV:45:LEU:HD12	1:AV:46:GLU:N	2.33	0.42
1:AW:8:LEU:HD11	1:FC:107:TRP:CE2	2.54	0.42
1:BB:27:PHE:CE2	1:BB:45:LEU:HD23	2.54	0.42
1:BE:45:LEU:HD11	1:BE:58:VAL:CG1	2.48	0.42
1:BJ:99:LYS:O	1:BJ:103:THR:HG23	2.20	0.42
1:BN:16:GLU:HB3	1:BN:32:LYS:HD2	2.02	0.42
1:CC:8:LEU:HD22	1:GK:106:ALA:HB1	2.01	0.42
1:CH:62:LEU:HD21	1:FT:103:THR:OG1	2.20	0.42
1:CY:103:THR:OG1	1:GG:62:LEU:HD21	2.20	0.42
1:DU:99:LYS:O	1:DU:103:THR:HG23	2.20	0.42
1:DV:62:LEU:HD21	1:GE:103:THR:OG1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EB:99:LYS:O	1:EB:103:THR:HG23	2.20	0.42
1:EN:45:LEU:HD11	1:EN:58:VAL:CG1	2.48	0.42
1:EU:30:VAL:HG13	1:EU:40:THR:CG2	2.49	0.42
1:EW:27:PHE:CE2	1:EW:45:LEU:HD23	2.54	0.42
1:EX:30:VAL:HG13	1:EX:40:THR:CG2	2.49	0.42
1:EZ:99:LYS:O	1:EZ:103:THR:HG23	2.20	0.42
1:FC:45:LEU:HD11	1:FC:58:VAL:CG1	2.48	0.42
1:FL:45:LEU:HD11	1:FL:58:VAL:CG1	2.48	0.42
1:FN:99:LYS:O	1:FN:103:THR:HG23	2.20	0.42
1:FR:27:PHE:CE2	1:FR:45:LEU:HD23	2.54	0.42
1:GC:99:LYS:O	1:GC:103:THR:HG23	2.20	0.42
1:GG:16:GLU:HB3	1:GG:32:LYS:HD2	2.02	0.42
1:AI:2:ARG:HD2	1:DU:124:TYR:CE1	2.55	0.42
1:AK:30:VAL:HG13	1:AK:40:THR:CG2	2.49	0.42
1:AL:99:LYS:O	1:AL:103:THR:HG23	2.20	0.42
1:AO:99:LYS:O	1:AO:103:THR:HG23	2.20	0.42
1:AX:10:VAL:HG21	1:EJ:103:THR:HG22	2.02	0.42
1:AX:99:LYS:O	1:AX:103:THR:HG23	2.20	0.42
1:BA:19:VAL:O	1:EW:121:LEU:HD11	2.19	0.42
1:BD:99:LYS:O	1:BD:103:THR:HG23	2.20	0.42
1:BK:122:ASN:ND2	1:DW:25:THR:HG22	2.35	0.42
1:BL:26:LEU:HD12	1:BL:46:GLU:HB2	2.02	0.42
1:BN:45:LEU:HD11	1:BN:58:VAL:CG1	2.48	0.42
1:BN:118:ASP:OD2	1:DZ:98:THR:HG22	2.20	0.42
1:BP:99:LYS:O	1:BP:103:THR:HG23	2.20	0.42
1:BQ:27:PHE:CE2	1:BQ:45:LEU:HD23	2.54	0.42
1:BQ:99:LYS:O	1:BQ:103:THR:HG23	2.20	0.42
1:CF:99:LYS:O	1:CF:103:THR:HG23	2.20	0.42
1:CI:27:PHE:CE2	1:CI:45:LEU:HD23	2.54	0.42
1:CS:91:THR:OG1	1:DD:78:ILE:HD13	2.19	0.42
1:CU:27:PHE:CE2	1:CU:45:LEU:HD23	2.54	0.42
1:CV:97:ILE:CG2	1:GM:118:ASP:HA	2.50	0.42
1:DD:16:GLU:HB3	1:DD:32:LYS:HD2	2.02	0.42
1:DH:30:VAL:HG13	1:DH:40:THR:CG2	2.49	0.42
1:DM:118:ASP:OD2	1:GT:98:THR:HG22	2.19	0.42
1:DO:99:LYS:O	1:DO:103:THR:HG23	2.20	0.42
1:DP:15:ARG:NH1	1:GW:103:THR:HG21	2.26	0.42
1:DP:27:PHE:CE2	1:DP:45:LEU:HD23	2.54	0.42
1:DR:99:LYS:O	1:DR:103:THR:HG23	2.20	0.42
1:DZ:30:VAL:HG13	1:DZ:40:THR:CG2	2.49	0.42
1:EC:30:VAL:HG13	1:EC:40:THR:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EJ:39:ASN:OD1	1:EJ:40:THR:N	2.51	0.42
1:EN:16:GLU:HB3	1:EN:32:LYS:HD2	2.02	0.42
1:FS:30:VAL:HG13	1:FS:40:THR:CG2	2.49	0.42
1:GA:99:LYS:O	1:GA:103:THR:HG23	2.20	0.42
1:GK:51:ALA:O	1:GK:90:LYS:NZ	2.50	0.42
1:GV:16:GLU:HB3	1:GV:32:LYS:HD2	2.02	0.42
1:AB:26:LEU:HD12	1:AB:46:GLU:HB2	2.02	0.42
1:AH:30:VAL:HG13	1:AH:40:THR:CG2	2.49	0.42
1:AJ:27:PHE:CE2	1:AJ:45:LEU:HD23	2.54	0.42
1:AJ:107:TRP:CE2	1:BX:8:LEU:HD11	2.55	0.42
1:AK:26:LEU:HD12	1:AK:46:GLU:HB2	2.02	0.42
1:AM:99:LYS:O	1:AM:103:THR:HG23	2.20	0.42
1:AP:16:GLU:HB3	1:AP:32:LYS:HD2	2.02	0.42
1:AP:27:PHE:CE2	1:AP:45:LEU:HD23	2.54	0.42
1:AR:99:LYS:O	1:AR:103:THR:HG23	2.20	0.42
1:AT:20:SER:O	1:EL:122:ASN:HB2	2.20	0.42
1:AT:26:LEU:HD12	1:AT:46:GLU:HB2	2.02	0.42
1:AW:30:VAL:HG13	1:AW:40:THR:CG2	2.49	0.42
1:AY:47:GLN:OE1	1:EI:120:GLY:HA2	2.20	0.42
1:BD:118:ASP:CG	1:EP:98:THR:HG22	2.39	0.42
1:BE:16:GLU:HB3	1:BE:32:LYS:HD2	2.02	0.42
1:BH:121:LEU:HD11	1:BP:19:VAL:O	2.20	0.42
1:BK:27:PHE:CE2	1:BK:45:LEU:HD23	2.54	0.42
1:BM:53:ASN:OD1	1:BM:54:SER:N	2.53	0.42
1:BW:16:GLU:HB3	1:BW:32:LYS:HD2	2.02	0.42
1:BW:99:LYS:HE2	1:DQ:15:ARG:HH11	1.84	0.42
1:BW:118:ASP:OD2	1:DQ:98:THR:HG22	2.20	0.42
1:BY:99:LYS:O	1:BY:103:THR:HG23	2.20	0.42
1:CB:17:TYR:CG	1:FN:107:TRP:HZ2	2.38	0.42
1:CD:26:LEU:HD12	1:CD:46:GLU:HB2	2.02	0.42
1:CH:122:ASN:HB2	1:FR:20:SER:O	2.19	0.42
1:CI:99:LYS:O	1:CI:103:THR:HG23	2.20	0.42
1:CK:118:ASP:CG	1:FW:98:THR:HG22	2.40	0.42
1:CL:99:LYS:O	1:CL:103:THR:HG23	2.20	0.42
1:CU:99:LYS:O	1:CU:103:THR:HG23	2.20	0.42
1:CX:99:LYS:O	1:CX:103:THR:HG23	2.20	0.42
1:CY:66:VAL:HG21	1:GG:96:HIS:CG	2.54	0.42
1:CZ:99:LYS:O	1:CZ:103:THR:HG23	2.20	0.42
1:DF:99:LYS:O	1:DF:103:THR:HG23	2.20	0.42
1:DL:118:ASP:CG	1:GX:98:THR:HG22	2.40	0.42
1:DM:99:LYS:O	1:DM:103:THR:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:45:LEU:HD11	1:DP:58:VAL:CG1	2.48	0.42
1:DQ:26:LEU:HD12	1:DQ:46:GLU:HB2	2.02	0.42
1:DR:53:ASN:OD1	1:DR:54:SER:N	2.53	0.42
1:DV:122:ASN:ND2	1:GE:25:THR:HG22	2.35	0.42
1:DY:16:GLU:HB3	1:DY:32:LYS:HD2	2.02	0.42
1:EE:99:LYS:O	1:EE:103:THR:HG23	2.20	0.42
1:ER:26:LEU:HD12	1:ER:46:GLU:HB2	2.02	0.42
1:ET:96:HIS:CG	1:FG:66:VAL:HG21	2.55	0.42
1:FL:99:LYS:O	1:FL:103:THR:HG23	2.20	0.42
1:FP:30:VAL:HG13	1:FP:40:THR:CG2	2.49	0.42
1:FQ:99:LYS:O	1:FQ:103:THR:HG23	2.20	0.42
1:FR:99:LYS:O	1:FR:103:THR:HG23	2.20	0.42
1:FU:27:PHE:CE2	1:FU:45:LEU:HD23	2.54	0.42
1:FV:117:VAL:O	1:GS:97:ILE:HG21	2.19	0.42
1:FY:30:VAL:HG13	1:FY:40:THR:CG2	2.49	0.42
1:FZ:99:LYS:O	1:FZ:103:THR:HG23	2.20	0.42
1:GH:26:LEU:HD12	1:GH:46:GLU:HB2	2.02	0.42
1:GP:16:GLU:HB3	1:GP:32:LYS:HD2	2.02	0.42
1:GR:99:LYS:O	1:GR:103:THR:HG23	2.20	0.42
1:GU:99:LYS:O	1:GU:103:THR:HG23	2.20	0.42
1:AJ:2:ARG:HA	1:BX:124:TYR:O	2.19	0.42
1:AL:53:ASN:OD1	1:AL:54:SER:N	2.53	0.42
1:AR:53:ASN:OD1	1:AR:54:SER:N	2.53	0.42
1:AU:53:ASN:OD1	1:AU:54:SER:N	2.53	0.42
1:AV:27:PHE:CE2	1:AV:45:LEU:HD23	2.54	0.42
1:AW:26:LEU:HD12	1:AW:46:GLU:HB2	2.02	0.42
1:BB:99:LYS:O	1:BB:103:THR:HG23	2.20	0.42
1:BB:124:TYR:HA	1:BR:22:GLN:HE21	1.85	0.42
1:BD:8:LEU:HD11	1:EP:107:TRP:CE2	2.55	0.42
1:BD:53:ASN:OD1	1:BD:54:SER:N	2.53	0.42
1:BG:53:ASN:OD1	1:BG:54:SER:N	2.53	0.42
1:BH:99:LYS:O	1:BH:103:THR:HG23	2.20	0.42
1:BK:27:PHE:CE2	1:DW:123:ASN:ND2	2.88	0.42
1:BR:30:VAL:HG13	1:BR:40:THR:CG2	2.49	0.42
1:BX:30:VAL:HG13	1:BX:40:THR:CG2	2.49	0.42
1:BZ:16:GLU:HB3	1:BZ:32:LYS:HD2	2.02	0.42
1:CB:99:LYS:O	1:CB:103:THR:HG23	2.20	0.42
1:CC:16:GLU:HB3	1:CC:32:LYS:HD2	2.02	0.42
1:CM:30:VAL:HG13	1:CM:40:THR:CG2	2.49	0.42
1:CP:85:THR:OG1	1:DJ:83:SER:OG	2.37	0.42
1:CS:26:LEU:HD12	1:CS:46:GLU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CW:99:LYS:O	1:CW:103:THR:HG23	2.20	0.42
1:DG:16:GLU:HB3	1:DG:32:LYS:HD2	2.02	0.42
1:DM:27:PHE:CE2	1:DM:45:LEU:HD23	2.54	0.42
1:DS:99:LYS:O	1:DS:103:THR:HG23	2.20	0.42
1:DX:99:LYS:O	1:DX:103:THR:HG23	2.20	0.42
1:EG:53:ASN:OD1	1:EG:54:SER:N	2.53	0.42
1:EP:53:ASN:OD1	1:EP:54:SER:N	2.53	0.42
1:ET:16:GLU:HB3	1:ET:32:LYS:HD2	2.02	0.42
1:FB:53:ASN:OD1	1:FB:54:SER:N	2.53	0.42
1:FH:53:ASN:OD1	1:FH:54:SER:N	2.53	0.42
1:FK:99:LYS:O	1:FK:103:THR:HG23	2.20	0.42
1:FO:27:PHE:CE2	1:FO:45:LEU:HD23	2.54	0.42
1:FT:53:ASN:OD1	1:FT:54:SER:N	2.53	0.42
1:FU:16:GLU:HB3	1:FU:32:LYS:HD2	2.02	0.42
1:GC:53:ASN:OD1	1:GC:54:SER:N	2.53	0.42
1:GO:99:LYS:O	1:GO:103:THR:HG23	2.20	0.42
1:GX:53:ASN:OD1	1:GX:54:SER:N	2.53	0.42
1:AH:98:THR:HG22	1:GD:118:ASP:OD2	2.19	0.42
1:AP:70:ASP:OD1	1:AP:71:ALA:N	2.53	0.42
1:AS:27:PHE:CE2	1:AS:45:LEU:HD23	2.54	0.42
1:AV:70:ASP:OD1	1:AV:71:ALA:N	2.53	0.42
1:AY:99:LYS:O	1:AY:103:THR:HG23	2.20	0.42
1:BB:16:GLU:HB3	1:BB:32:LYS:HD2	2.02	0.42
1:BE:70:ASP:OD1	1:BE:71:ALA:N	2.53	0.42
1:BO:26:LEU:HD12	1:BO:46:GLU:HB2	2.02	0.42
1:BZ:99:LYS:O	1:BZ:103:THR:HG23	2.20	0.42
1:CA:26:LEU:HD12	1:CA:46:GLU:HB2	2.02	0.42
1:CH:53:ASN:OD1	1:CH:54:SER:N	2.53	0.42
1:CH:99:LYS:O	1:CH:103:THR:HG23	2.20	0.42
1:CK:99:LYS:O	1:CK:103:THR:HG23	2.20	0.42
1:CN:53:ASN:OD1	1:CN:54:SER:N	2.53	0.42
1:CO:19:VAL:HB	1:GC:124:TYR:CE2	2.55	0.42
1:CP:103:THR:OG1	1:DJ:62:LEU:HD21	2.20	0.42
1:CT:53:ASN:OD1	1:CT:54:SER:N	2.53	0.42
1:CW:53:ASN:OD1	1:CW:54:SER:N	2.53	0.42
1:CX:97:ILE:HG21	1:DK:117:VAL:O	2.20	0.42
1:DD:99:LYS:O	1:DD:103:THR:HG23	2.20	0.42
1:DI:123:ASN:OD1	1:GU:1:MET:HB3	2.20	0.42
1:DL:99:LYS:O	1:DL:103:THR:HG23	2.20	0.42
1:DN:26:LEU:HD12	1:DN:46:GLU:HB2	2.02	0.42
1:DP:16:GLU:HB3	1:DP:32:LYS:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DV:99:LYS:O	1:DV:103:THR:HG23	2.20	0.42
1:ED:99:LYS:O	1:ED:103:THR:HG23	2.20	0.42
1:EK:45:LEU:HD11	1:EK:58:VAL:CG1	2.48	0.42
1:EL:30:VAL:HG13	1:EL:40:THR:CG2	2.49	0.42
1:EN:70:ASP:OD1	1:EN:71:ALA:N	2.53	0.42
1:EP:99:LYS:O	1:EP:103:THR:HG23	2.20	0.42
1:ES:99:LYS:O	1:ES:103:THR:HG23	2.20	0.42
1:EX:62:LEU:HD21	1:FI:103:THR:OG1	2.20	0.42
1:EY:99:LYS:O	1:EY:103:THR:HG23	2.20	0.42
1:FC:99:LYS:O	1:FC:103:THR:HG23	2.20	0.42
1:FE:53:ASN:OD1	1:FE:54:SER:N	2.53	0.42
1:FF:70:ASP:OD1	1:FF:71:ALA:N	2.53	0.42
1:FH:99:LYS:O	1:FH:103:THR:HG23	2.20	0.42
1:FI:99:LYS:O	1:FI:103:THR:HG23	2.20	0.42
1:FL:27:PHE:CE2	1:FL:45:LEU:HD23	2.54	0.42
1:FW:53:ASN:OD1	1:FW:54:SER:N	2.53	0.42
1:FX:16:GLU:HB3	1:FX:32:LYS:HD2	2.02	0.42
1:GB:26:LEU:HD12	1:GB:46:GLU:HB2	2.02	0.42
1:GD:99:LYS:O	1:GD:103:THR:HG23	2.20	0.42
1:GO:53:ASN:OD1	1:GO:54:SER:N	2.53	0.42
1:GS:70:ASP:OD1	1:GS:71:ALA:N	2.53	0.42
1:GW:26:LEU:HD12	1:GW:46:GLU:HB2	2.02	0.42
1:AA:27:PHE:CE2	1:AA:45:LEU:HD23	2.54	0.41
1:AC:103:THR:HG22	1:DO:10:VAL:CG2	2.45	0.41
1:AG:16:GLU:HB3	1:AG:32:LYS:HD2	2.02	0.41
1:AP:99:LYS:O	1:AP:103:THR:HG23	2.20	0.41
1:AW:117:VAL:O	1:FC:97:ILE:HG21	2.20	0.41
1:BB:8:LEU:HD11	1:BR:107:TRP:CE2	2.55	0.41
1:BK:99:LYS:O	1:BK:103:THR:HG23	2.20	0.41
1:BM:118:ASP:CB	1:EY:98:THR:HG22	2.50	0.41
1:BR:26:LEU:HD12	1:BR:46:GLU:HB2	2.02	0.41
1:BS:8:LEU:HD11	1:FE:107:TRP:CE2	2.55	0.41
1:BS:118:ASP:HB3	1:FE:98:THR:HG22	2.02	0.41
1:CI:96:HIS:CG	1:GH:66:VAL:HG21	2.55	0.41
1:CP:122:ASN:HB2	1:DK:20:SER:O	2.19	0.41
1:CR:20:SER:HA	1:GF:121:LEU:HD22	2.01	0.41
1:CY:26:LEU:HD12	1:CY:46:GLU:HB2	2.02	0.41
1:DC:53:ASN:OD1	1:DC:54:SER:N	2.53	0.41
1:DC:99:LYS:O	1:DC:103:THR:HG23	2.20	0.41
1:DJ:99:LYS:O	1:DJ:103:THR:HG23	2.20	0.41
1:DM:62:LEU:HD21	1:GT:103:THR:OG1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DO:53:ASN:OD1	1:DO:54:SER:N	2.53	0.41
1:DP:70:ASP:OD1	1:DP:71:ALA:N	2.53	0.41
1:DV:107:TRP:HH2	1:GE:29:PHE:CG	2.38	0.41
1:DW:30:VAL:HG13	1:DW:40:THR:CG2	2.49	0.41
1:DY:70:ASP:OD1	1:DY:71:ALA:N	2.53	0.41
1:EE:16:GLU:HB3	1:EE:32:LYS:HD2	2.02	0.41
1:EE:70:ASP:OD1	1:EE:71:ALA:N	2.53	0.41
1:ET:99:LYS:O	1:ET:103:THR:HG23	2.20	0.41
1:EW:99:LYS:O	1:EW:103:THR:HG23	2.20	0.41
1:FN:53:ASN:OD1	1:FN:54:SER:N	2.53	0.41
1:FT:99:LYS:O	1:FT:103:THR:HG23	2.20	0.41
1:FX:99:LYS:O	1:FX:103:THR:HG23	2.20	0.41
1:AE:26:LEU:HD12	1:AE:46:GLU:HB2	2.02	0.41
1:AH:84:VAL:HG21	1:GD:104:LEU:HD11	2.01	0.41
1:AJ:16:GLU:HB3	1:AJ:32:LYS:HD2	2.02	0.41
1:AO:53:ASN:OD1	1:AO:54:SER:N	2.53	0.41
1:AP:99:LYS:HE3	1:BU:13:GLU:OE2	2.20	0.41
1:AR:20:SER:O	1:FU:122:ASN:HB2	2.20	0.41
1:BB:2:ARG:HH11	1:BD:2:ARG:NH1	2.19	0.41
1:BE:118:ASP:OD2	1:BL:98:THR:HG22	2.19	0.41
1:BM:99:LYS:O	1:BM:103:THR:HG23	2.20	0.41
1:BW:27:PHE:CE2	1:BW:45:LEU:HD23	2.54	0.41
1:CC:99:LYS:O	1:CC:103:THR:HG23	2.20	0.41
1:CM:51:ALA:O	1:CM:90:LYS:NZ	2.50	0.41
1:CO:16:GLU:HB3	1:CO:32:LYS:HD2	2.02	0.41
1:CQ:53:ASN:OD1	1:CQ:54:SER:N	2.53	0.41
1:CT:99:LYS:O	1:CT:103:THR:HG23	2.20	0.41
1:CV:26:LEU:HD12	1:CV:46:GLU:HB2	2.02	0.41
1:CX:16:GLU:HB3	1:CX:32:LYS:HD2	2.02	0.41
1:DJ:16:GLU:HB3	1:DJ:32:LYS:HD2	2.02	0.41
1:EC:26:LEU:HD12	1:EC:46:GLU:HB2	2.02	0.41
1:EH:99:LYS:O	1:EH:103:THR:HG23	2.20	0.41
1:EM:53:ASN:OD1	1:EM:54:SER:N	2.53	0.41
1:EO:26:LEU:HD12	1:EO:46:GLU:HB2	2.02	0.41
1:EQ:70:ASP:OD1	1:EQ:71:ALA:N	2.53	0.41
1:ET:45:LEU:HD11	1:ET:58:VAL:CG1	2.48	0.41
1:ET:70:ASP:OD1	1:ET:71:ALA:N	2.53	0.41
1:EY:53:ASN:OD1	1:EY:54:SER:N	2.53	0.41
1:FO:70:ASP:OD1	1:FO:71:ALA:N	2.53	0.41
1:FO:99:LYS:O	1:FO:103:THR:HG23	2.20	0.41
1:FP:26:LEU:HD12	1:FP:46:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FV:26:LEU:HD12	1:FV:46:GLU:HB2	2.02	0.41
1:FW:65:PRO:HB3	1:FW:79:LYS:HG2	2.03	0.41
1:GA:16:GLU:HB3	1:GA:32:LYS:HD2	2.02	0.41
1:GD:70:ASP:OD1	1:GD:71:ALA:N	2.53	0.41
1:GI:99:LYS:O	1:GI:103:THR:HG23	2.20	0.41
1:GR:53:ASN:OD1	1:GR:54:SER:N	2.53	0.41
1:GS:99:LYS:O	1:GS:103:THR:HG23	2.20	0.41
1:AA:70:ASP:OD1	1:AA:71:ALA:N	2.53	0.41
1:AD:70:ASP:OD1	1:AD:71:ALA:N	2.53	0.41
1:AD:99:LYS:O	1:AD:103:THR:HG23	2.20	0.41
1:AF:65:PRO:HB3	1:AF:79:LYS:HG2	2.03	0.41
1:AH:26:LEU:HD12	1:AH:46:GLU:HB2	2.02	0.41
1:AK:123:ASN:HB3	1:FO:3:LEU:HG	2.02	0.41
1:AP:92:TYR:CE2	1:BU:66:VAL:HG23	2.55	0.41
1:AU:22:GLN:NE2	1:EG:124:TYR:HA	2.36	0.41
1:AU:99:LYS:O	1:AU:103:THR:HG23	2.20	0.41
1:BA:53:ASN:OD1	1:BA:54:SER:N	2.53	0.41
1:BA:65:PRO:HB3	1:BA:79:LYS:HG2	2.03	0.41
1:BA:122:ASN:HB2	1:EK:20:SER:O	2.20	0.41
1:BB:70:ASP:OD1	1:BB:71:ALA:N	2.53	0.41
1:BE:99:LYS:O	1:BE:103:THR:HG23	2.20	0.41
1:BH:70:ASP:OD1	1:BH:71:ALA:N	2.53	0.41
1:BK:16:GLU:HB3	1:BK:32:LYS:HD2	2.02	0.41
1:BN:27:PHE:CE2	1:BN:45:LEU:HD23	2.54	0.41
1:BQ:16:GLU:HB3	1:BQ:32:LYS:HD2	2.02	0.41
1:BS:53:ASN:OD1	1:BS:54:SER:N	2.53	0.41
1:BV:53:ASN:OD1	1:BV:54:SER:N	2.53	0.41
1:CB:82:ALA:HA	1:FN:85:THR:O	2.21	0.41
1:CC:62:LEU:HD21	1:GK:103:THR:OG1	2.20	0.41
1:CE:99:LYS:O	1:CE:103:THR:HG23	2.20	0.41
1:CF:124:TYR:CA	1:GN:22:GLN:HE21	2.33	0.41
1:CO:2:ARG:HH11	1:CQ:2:ARG:NH1	2.19	0.41
1:CO:70:ASP:OD1	1:CO:71:ALA:N	2.53	0.41
1:CR:99:LYS:O	1:CR:103:THR:HG23	2.20	0.41
1:CY:8:LEU:HD11	1:GG:107:TRP:CE2	2.56	0.41
1:DA:16:GLU:HB3	1:DA:32:LYS:HD2	2.02	0.41
1:DG:45:LEU:HD11	1:DG:58:VAL:CG1	2.48	0.41
1:DQ:30:VAL:HG13	1:DQ:40:THR:CG2	2.49	0.41
1:DT:30:VAL:HG13	1:DT:40:THR:CG2	2.49	0.41
1:DU:65:PRO:HB3	1:DU:79:LYS:HG2	2.03	0.41
1:DX:53:ASN:OD1	1:DX:54:SER:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:53:ASN:OD1	1:EA:54:SER:N	2.53	0.41
1:ED:65:PRO:HB3	1:ED:79:LYS:HG2	2.03	0.41
1:EH:70:ASP:OD1	1:EH:71:ALA:N	2.53	0.41
1:EK:70:ASP:OD1	1:EK:71:ALA:N	2.53	0.41
1:EM:99:LYS:O	1:EM:103:THR:HG23	2.20	0.41
1:EQ:3:LEU:HG	1:FM:123:ASN:HB3	2.01	0.41
1:EQ:118:ASP:HB3	1:FM:98:THR:HG22	2.01	0.41
1:FC:2:ARG:HH11	1:FE:2:ARG:NH1	2.19	0.41
1:FI:16:GLU:HB3	1:FI:32:LYS:HD2	2.02	0.41
1:FK:53:ASN:OD1	1:FK:54:SER:N	2.53	0.41
1:FO:2:ARG:HH11	1:FQ:2:ARG:NH1	2.19	0.41
1:FQ:53:ASN:OD1	1:FQ:54:SER:N	2.53	0.41
1:GJ:99:LYS:O	1:GJ:103:THR:HG23	2.20	0.41
1:GL:53:ASN:OD1	1:GL:54:SER:N	2.53	0.41
1:AD:84:VAL:HG22	1:BC:84:VAL:HG13	2.01	0.41
1:AG:2:ARG:HH11	1:AI:2:ARG:NH1	2.19	0.41
1:AL:91:THR:HG22	1:DX:68:VAL:HG11	2.02	0.41
1:AQ:51:ALA:O	1:AQ:90:LYS:NZ	2.50	0.41
1:AV:2:ARG:HH11	1:AX:2:ARG:NH1	2.19	0.41
1:AV:121:LEU:HD11	1:EG:19:VAL:O	2.19	0.41
1:AX:98:THR:HG22	1:EJ:118:ASP:CG	2.40	0.41
1:BF:26:LEU:HD12	1:BF:46:GLU:HB2	2.02	0.41
1:BT:45:LEU:HD11	1:BT:58:VAL:CG1	2.48	0.41
1:BW:97:ILE:HG21	1:DQ:117:VAL:O	2.21	0.41
1:BZ:2:ARG:HH11	1:CB:2:ARG:NH1	2.19	0.41
1:BZ:104:LEU:HD11	1:DT:84:VAL:CG2	2.51	0.41
1:BZ:124:TYR:C	1:DT:22:GLN:HE21	2.24	0.41
1:CB:107:TRP:HZ2	1:FN:17:TYR:CG	2.39	0.41
1:CC:70:ASP:OD1	1:CC:71:ALA:N	2.53	0.41
1:CG:22:GLN:HE21	1:CL:124:TYR:HA	1.86	0.41
1:CL:70:ASP:OD1	1:CL:71:ALA:N	2.53	0.41
1:CQ:99:LYS:O	1:CQ:103:THR:HG23	2.20	0.41
1:CQ:118:ASP:HB3	1:GC:98:THR:HG22	2.01	0.41
1:CR:16:GLU:HB3	1:CR:32:LYS:HD2	2.02	0.41
1:CU:62:LEU:HD21	1:DH:103:THR:OG1	2.21	0.41
1:CZ:65:PRO:HB3	1:CZ:79:LYS:HG2	2.03	0.41
1:DA:45:LEU:HD11	1:DA:58:VAL:CG1	2.48	0.41
1:DA:70:ASP:OD1	1:DA:71:ALA:N	2.53	0.41
1:DB:26:LEU:HD12	1:DB:46:GLU:HB2	2.02	0.41
1:DU:53:ASN:OD1	1:DU:54:SER:N	2.53	0.41
1:DV:16:GLU:HB3	1:DV:32:LYS:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EQ:16:GLU:HB3	1:EQ:32:LYS:HD2	2.02	0.41
1:EW:70:ASP:OD1	1:EW:71:ALA:N	2.53	0.41
1:FC:16:GLU:HB3	1:FC:32:LYS:HD2	2.02	0.41
1:FD:26:LEU:HD12	1:FD:46:GLU:HB2	2.02	0.41
1:FF:16:GLU:HB3	1:FF:32:LYS:HD2	2.02	0.41
1:FJ:26:LEU:HD12	1:FJ:46:GLU:HB2	2.02	0.41
1:FS:8:LEU:HD11	1:GP:107:TRP:CE2	2.55	0.41
1:FS:98:THR:HG22	1:GP:118:ASP:CG	2.41	0.41
1:FZ:53:ASN:OD1	1:FZ:54:SER:N	2.53	0.41
1:GD:16:GLU:HB3	1:GD:32:LYS:HD2	2.02	0.41
1:GG:2:ARG:HH11	1:GI:2:ARG:NH1	2.19	0.41
1:GI:65:PRO:HB3	1:GI:79:LYS:HG2	2.03	0.41
1:GN:26:LEU:HD12	1:GN:46:GLU:HB2	2.02	0.41
1:GT:51:ALA:O	1:GT:90:LYS:NZ	2.50	0.41
1:AC:53:ASN:OD1	1:AC:54:SER:N	2.53	0.41
1:AJ:1:MET:HB3	1:BX:123:ASN:OD1	2.20	0.41
1:AJ:118:ASP:OD2	1:BX:98:THR:HG22	2.19	0.41
1:AO:65:PRO:HB3	1:AO:79:LYS:HG2	2.03	0.41
1:AS:2:ARG:HH11	1:AU:2:ARG:NH1	2.19	0.41
1:AX:65:PRO:HB3	1:AX:79:LYS:HG2	2.03	0.41
1:AY:2:ARG:HH11	1:BA:2:ARG:NH1	2.19	0.41
1:BA:103:THR:OG1	1:EM:62:LEU:HD21	2.20	0.41
1:BA:118:ASP:CB	1:EM:98:THR:HG22	2.51	0.41
1:BP:53:ASN:OD1	1:BP:54:SER:N	2.53	0.41
1:BS:99:LYS:O	1:BS:103:THR:HG23	2.20	0.41
1:BV:99:LYS:O	1:BV:103:THR:HG23	2.20	0.41
1:BW:2:ARG:HH11	1:BY:2:ARG:NH1	2.19	0.41
1:BW:99:LYS:O	1:BW:103:THR:HG23	2.20	0.41
1:BZ:70:ASP:OD1	1:BZ:71:ALA:N	2.53	0.41
1:CB:53:ASN:OD1	1:CB:54:SER:N	2.53	0.41
1:CB:107:TRP:CE2	1:FN:8:LEU:HD11	2.56	0.41
1:CH:20:SER:O	1:CL:122:ASN:HB2	2.19	0.41
1:CI:70:ASP:OD1	1:CI:71:ALA:N	2.53	0.41
1:CI:103:THR:OG1	1:GH:62:LEU:HD21	2.21	0.41
1:CQ:84:VAL:HG22	1:GC:84:VAL:HG13	2.02	0.41
1:CU:2:ARG:HH11	1:CW:2:ARG:NH1	2.19	0.41
1:CU:3:LEU:HG	1:DH:123:ASN:HB3	2.01	0.41
1:CU:16:GLU:HB3	1:CU:32:LYS:HD2	2.02	0.41
1:CW:65:PRO:HB3	1:CW:79:LYS:HG2	2.03	0.41
1:CZ:53:ASN:OD1	1:CZ:54:SER:N	2.53	0.41
1:DF:53:ASN:OD1	1:DF:54:SER:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DV:45:LEU:HD11	1:DV:58:VAL:CG1	2.48	0.41
1:DV:70:ASP:OD1	1:DV:71:ALA:N	2.53	0.41
1:EA:99:LYS:O	1:EA:103:THR:HG23	2.20	0.41
1:EB:2:ARG:HH11	1:ED:2:ARG:NH1	2.19	0.41
1:EB:16:GLU:HB3	1:EB:32:LYS:HD2	2.02	0.41
1:EB:70:ASP:OD1	1:EB:71:ALA:N	2.53	0.41
1:EG:99:LYS:O	1:EG:103:THR:HG23	2.20	0.41
1:EK:16:GLU:HB3	1:EK:32:LYS:HD2	2.02	0.41
1:EO:51:ALA:O	1:EO:90:LYS:NZ	2.50	0.41
1:EQ:1:MET:HB3	1:FM:123:ASN:OD1	2.21	0.41
1:ES:53:ASN:OD1	1:ES:54:SER:N	2.53	0.41
1:ET:79:LYS:O	1:FG:89:PRO:HG3	2.20	0.41
1:EW:16:GLU:HB3	1:EW:32:LYS:HD2	2.02	0.41
1:EZ:2:ARG:HH11	1:FB:2:ARG:NH1	2.19	0.41
1:EZ:70:ASP:OD1	1:EZ:71:ALA:N	2.53	0.41
1:FE:65:PRO:HB3	1:FE:79:LYS:HG2	2.03	0.41
1:FK:65:PRO:HB3	1:FK:79:LYS:HG2	2.03	0.41
1:FU:2:ARG:HH11	1:FW:2:ARG:NH1	2.19	0.41
1:FU:99:LYS:O	1:FU:103:THR:HG23	2.20	0.41
1:FW:99:LYS:O	1:FW:103:THR:HG23	2.20	0.41
1:GK:26:LEU:HD12	1:GK:46:GLU:HB2	2.02	0.41
1:GM:99:LYS:O	1:GM:103:THR:HG23	2.20	0.41
1:GV:99:LYS:O	1:GV:103:THR:HG23	2.20	0.41
1:AF:98:THR:HG22	1:DR:118:ASP:CB	2.50	0.41
1:AS:16:GLU:HB3	1:AS:32:LYS:HD2	2.02	0.41
1:AU:10:VAL:HG13	1:EG:102:GLN:HB2	2.01	0.41
1:AX:20:SER:O	1:FC:122:ASN:HB2	2.20	0.41
1:AY:16:GLU:HB3	1:AY:32:LYS:HD2	2.02	0.41
1:BC:26:LEU:HD12	1:BC:46:GLU:HB2	2.02	0.41
1:BK:70:ASP:OD1	1:BK:71:ALA:N	2.53	0.41
1:BL:51:ALA:O	1:BL:90:LYS:NZ	2.50	0.41
1:BV:91:THR:HB	1:FH:78:ILE:HD13	2.03	0.41
1:BW:70:ASP:OD1	1:BW:71:ALA:N	2.53	0.41
1:BY:65:PRO:HB3	1:BY:79:LYS:HG2	2.03	0.41
1:CE:65:PRO:HB3	1:CE:79:LYS:HG2	2.03	0.41
1:CF:1:MET:SD	1:GN:111:GLN:HB2	2.60	0.41
1:CI:2:ARG:HH11	1:CK:2:ARG:NH1	2.19	0.41
1:CS:51:ALA:O	1:CS:90:LYS:NZ	2.50	0.41
1:DC:92:TYR:CE2	1:GO:66:VAL:HG23	2.55	0.41
1:DD:2:ARG:HH11	1:DF:2:ARG:NH1	2.19	0.41
1:DG:70:ASP:OD1	1:DG:71:ALA:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DI:53:ASN:OD1	1:DI:54:SER:N	2.53	0.41
1:EG:65:PRO:HB3	1:EG:79:LYS:HG2	2.03	0.41
1:EK:122:ASN:HB2	1:ES:20:SER:O	2.20	0.41
1:EL:26:LEU:HD12	1:EL:46:GLU:HB2	2.02	0.41
1:EP:65:PRO:HB3	1:EP:79:LYS:HG2	2.03	0.41
1:ET:62:LEU:HD21	1:FG:103:THR:OG1	2.21	0.41
1:EV:99:LYS:O	1:EV:103:THR:HG23	2.20	0.41
1:EW:45:LEU:HD11	1:EW:58:VAL:CG1	2.48	0.41
1:FB:99:LYS:O	1:FB:103:THR:HG23	2.20	0.41
1:FE:99:LYS:O	1:FE:103:THR:HG23	2.20	0.41
1:FR:70:ASP:OD1	1:FR:71:ALA:N	2.53	0.41
1:FU:70:ASP:OD1	1:FU:71:ALA:N	2.53	0.41
1:GF:65:PRO:HB3	1:GF:79:LYS:HG2	2.03	0.41
1:GJ:2:ARG:HH11	1:GL:2:ARG:NH1	2.19	0.41
1:GJ:70:ASP:OD1	1:GJ:71:ALA:N	2.53	0.41
1:GL:65:PRO:HB3	1:GL:79:LYS:HG2	2.03	0.41
1:GP:99:LYS:O	1:GP:103:THR:HG23	2.20	0.41
1:GR:65:PRO:HB3	1:GR:79:LYS:HG2	2.03	0.41
1:GV:27:PHE:CE2	1:GV:45:LEU:HD23	2.54	0.41
1:AD:16:GLU:HB3	1:AD:32:LYS:HD2	2.02	0.41
1:AF:99:LYS:O	1:AF:103:THR:HG23	2.20	0.41
1:AG:70:ASP:OD1	1:AG:71:ALA:N	2.53	0.41
1:AI:53:ASN:OD1	1:AI:54:SER:N	2.53	0.41
1:AM:70:ASP:OD1	1:AM:71:ALA:N	2.53	0.41
1:AS:99:LYS:O	1:AS:103:THR:HG23	2.20	0.41
1:AU:106:ALA:HB1	1:EG:8:LEU:HB3	2.02	0.41
1:AY:56:ARG:NH1	1:EI:116:PRO:O	2.47	0.41
1:BK:99:LYS:HE3	1:DW:13:GLU:OE2	2.21	0.41
1:BM:84:VAL:HG13	1:EY:84:VAL:HG22	2.01	0.41
1:BQ:2:ARG:HH11	1:BS:2:ARG:NH1	2.19	0.41
1:BT:3:LEU:HG	1:DN:123:ASN:HB3	2.02	0.41
1:CL:16:GLU:HB3	1:CL:32:LYS:HD2	2.02	0.41
1:CR:70:ASP:OD1	1:CR:71:ALA:N	2.53	0.41
1:CV:47:GLN:HE22	1:GM:120:GLY:HA2	1.85	0.41
1:DC:107:TRP:NE1	1:GO:8:LEU:HD11	2.36	0.41
1:DR:65:PRO:HB3	1:DR:79:LYS:HG2	2.03	0.41
1:DS:2:ARG:HH11	1:DU:2:ARG:NH1	2.19	0.41
1:DS:99:LYS:HE2	1:GQ:15:ARG:HH11	1.86	0.41
1:DY:45:LEU:HD11	1:DY:58:VAL:CG1	2.48	0.41
1:DZ:26:LEU:HD12	1:DZ:46:GLU:HB2	2.02	0.41
1:EB:56:ARG:NH1	1:GB:116:PRO:O	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EH:16:GLU:HB3	1:EH:32:LYS:HD2	2.02	0.41
1:EQ:99:LYS:O	1:EQ:103:THR:HG23	2.20	0.41
1:FG:26:LEU:HD12	1:FG:46:GLU:HB2	2.02	0.41
1:FG:51:ALA:O	1:FG:90:LYS:NZ	2.50	0.41
1:FI:70:ASP:OD1	1:FI:71:ALA:N	2.53	0.41
1:FL:2:ARG:HH11	1:FN:2:ARG:NH1	2.19	0.41
1:FR:16:GLU:HB3	1:FR:32:LYS:HD2	2.02	0.41
1:GG:99:LYS:O	1:GG:103:THR:HG23	2.20	0.41
1:GO:65:PRO:HB3	1:GO:79:LYS:HG2	2.03	0.41
1:GV:70:ASP:OD1	1:GV:71:ALA:N	2.53	0.41
1:GX:99:LYS:O	1:GX:103:THR:HG23	2.20	0.41
1:AB:124:TYR:O	1:FX:2:ARG:HA	2.20	0.41
1:AF:53:ASN:OD1	1:AF:54:SER:N	2.53	0.41
1:AI:1:MET:HB3	1:DU:123:ASN:OD1	2.20	0.41
1:AT:17:TYR:HB3	1:AT:29:PHE:HB3	2.03	0.41
1:AU:111:GLN:HB3	1:EG:1:MET:SD	2.60	0.41
1:BD:65:PRO:HB3	1:BD:79:LYS:HG2	2.03	0.41
1:BE:10:VAL:HG11	1:BL:103:THR:HG22	2.03	0.41
1:BG:107:TRP:CE2	1:ES:8:LEU:HD11	2.56	0.41
1:BT:62:LEU:HD21	1:DN:103:THR:OG1	2.20	0.41
1:BT:99:LYS:O	1:BT:103:THR:HG23	2.20	0.41
1:BX:26:LEU:HD12	1:BX:46:GLU:HB2	2.02	0.41
1:BY:53:ASN:OD1	1:BY:54:SER:N	2.53	0.41
1:CB:124:TYR:CE1	1:FN:2:ARG:HD2	2.56	0.41
1:CF:2:ARG:HH11	1:CH:2:ARG:NH1	2.19	0.41
1:CK:53:ASN:OD1	1:CK:54:SER:N	2.53	0.41
1:CO:99:LYS:O	1:CO:103:THR:HG23	2.20	0.41
1:CT:65:PRO:HB3	1:CT:79:LYS:HG2	2.03	0.41
1:CV:124:TYR:OXT	1:GO:2:ARG:NH1	2.54	0.41
1:CX:10:VAL:HG11	1:DK:103:THR:HG22	2.03	0.41
1:CX:70:ASP:OD1	1:CX:71:ALA:N	2.53	0.41
1:DF:8:LEU:HD11	1:GR:107:TRP:CE2	2.56	0.41
1:DG:99:LYS:O	1:DG:103:THR:HG23	2.20	0.41
1:DI:99:LYS:O	1:DI:103:THR:HG23	2.20	0.41
1:DS:45:LEU:HD11	1:DS:58:VAL:CG1	2.48	0.41
1:DT:26:LEU:HD12	1:DT:46:GLU:HB2	2.02	0.41
1:DX:65:PRO:HB3	1:DX:79:LYS:HG2	2.03	0.41
1:EB:106:ALA:HB1	1:GB:8:LEU:HD22	2.01	0.41
1:EC:51:ALA:O	1:EC:90:LYS:NZ	2.50	0.41
1:EI:17:TYR:HB3	1:EI:29:PHE:HB3	2.03	0.41
1:EI:26:LEU:HD12	1:EI:46:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EU:21:GLU:OE1	1:EU:28:ARG:HD2	2.21	0.41
1:EW:2:ARG:HH11	1:EY:2:ARG:NH1	2.19	0.41
1:EX:26:LEU:HD12	1:EX:46:GLU:HB2	2.02	0.41
1:FA:26:LEU:HD12	1:FA:46:GLU:HB2	2.02	0.41
1:FC:70:ASP:OD1	1:FC:71:ALA:N	2.53	0.41
1:FI:2:ARG:HH11	1:FK:2:ARG:NH1	2.19	0.41
1:GF:99:LYS:O	1:GF:103:THR:HG23	2.20	0.41
1:GM:70:ASP:OD1	1:GM:71:ALA:N	2.53	0.41
1:GT:26:LEU:HD12	1:GT:46:GLU:HB2	2.02	0.41
1:GU:65:PRO:HB3	1:GU:79:LYS:HG2	2.03	0.41
1:AG:99:LYS:O	1:AG:103:THR:HG23	2.20	0.41
1:AI:123:ASN:OD1	1:DU:1:MET:HB3	2.20	0.41
1:AJ:70:ASP:OD1	1:AJ:71:ALA:N	2.53	0.41
1:AJ:85:THR:OG1	1:BX:83:SER:OG	2.36	0.41
1:AQ:26:LEU:HD12	1:AQ:46:GLU:HB2	2.02	0.41
1:AR:94:ASN:O	1:AR:98:THR:HG23	2.21	0.41
1:AS:70:ASP:OD1	1:AS:71:ALA:N	2.53	0.41
1:AW:21:GLU:OE1	1:AW:28:ARG:HD2	2.21	0.41
1:AW:51:ALA:O	1:AW:90:LYS:NZ	2.50	0.41
1:AW:122:ASN:HB2	1:FD:20:SER:O	2.21	0.41
1:AY:124:TYR:C	1:EI:22:GLN:HE21	2.24	0.41
1:BA:98:THR:HG22	1:EM:118:ASP:HB3	2.02	0.41
1:BA:99:LYS:O	1:BA:103:THR:HG23	2.20	0.41
1:BE:2:ARG:HH11	1:BG:2:ARG:NH1	2.19	0.41
1:BF:17:TYR:HB3	1:BF:29:PHE:HB3	2.03	0.41
1:BG:99:LYS:O	1:BG:103:THR:HG23	2.20	0.41
1:BI:36:VAL:H	1:BI:39:ASN:HB3	1.86	0.41
1:BK:45:LEU:CD2	1:DW:113:VAL:HA	2.50	0.41
1:BM:65:PRO:HB3	1:BM:79:LYS:HG2	2.03	0.41
1:BO:21:GLU:OE1	1:BO:28:ARG:HD2	2.21	0.41
1:CA:17:TYR:HB3	1:CA:29:PHE:HB3	2.03	0.41
1:CB:10:VAL:CG2	1:FN:103:THR:HG22	2.41	0.41
1:CF:62:LEU:HD21	1:GN:103:THR:OG1	2.20	0.41
1:CG:26:LEU:HD12	1:CG:46:GLU:HB2	2.02	0.41
1:CJ:8:LEU:HD11	1:CO:107:TRP:CE2	2.56	0.41
1:CJ:17:TYR:HB3	1:CJ:29:PHE:HB3	2.03	0.41
1:CN:99:LYS:O	1:CN:103:THR:HG23	2.20	0.41
1:CW:19:VAL:HB	1:GM:124:TYR:CD2	2.56	0.41
1:CX:2:ARG:HH11	1:CZ:2:ARG:NH1	2.19	0.41
1:CZ:25:THR:HG22	1:GL:122:ASN:ND2	2.35	0.41
1:DI:65:PRO:HB3	1:DI:79:LYS:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DJ:2:ARG:HH11	1:DL:2:ARG:NH1	2.19	0.41
1:DJ:70:ASP:OD1	1:DJ:71:ALA:N	2.53	0.41
1:DK:17:TYR:HB3	1:DK:29:PHE:HB3	2.03	0.41
1:DL:98:THR:HG22	1:GX:118:ASP:HB3	2.03	0.41
1:DM:16:GLU:HB3	1:DM:32:LYS:HD2	2.02	0.41
1:DM:70:ASP:OD1	1:DM:71:ALA:N	2.53	0.41
1:DS:16:GLU:HB3	1:DS:32:LYS:HD2	2.02	0.41
1:DV:8:LEU:HD22	1:GE:106:ALA:HB1	2.03	0.41
1:DV:118:ASP:HA	1:GE:97:ILE:CG2	2.51	0.41
1:DW:51:ALA:O	1:DW:90:LYS:NZ	2.50	0.41
1:DY:2:ARG:HH11	1:EA:2:ARG:NH1	2.19	0.41
1:DY:15:ARG:NH1	1:FY:103:THR:HG21	2.25	0.41
1:DY:99:LYS:O	1:DY:103:THR:HG23	2.20	0.41
1:EJ:53:ASN:OD1	1:EJ:54:SER:N	2.53	0.41
1:EJ:99:LYS:O	1:EJ:103:THR:HG23	2.20	0.41
1:EK:2:ARG:HH11	1:EM:2:ARG:NH1	2.19	0.41
1:EL:17:TYR:HB3	1:EL:29:PHE:HB3	2.03	0.41
1:EN:2:ARG:HH11	1:EP:2:ARG:NH1	2.19	0.41
1:EP:94:ASN:O	1:EP:98:THR:HG23	2.21	0.41
1:ER:17:TYR:HB3	1:ER:29:PHE:HB3	2.03	0.41
1:ER:36:VAL:H	1:ER:39:ASN:HB3	1.86	0.41
1:ET:2:ARG:HH11	1:EV:2:ARG:NH1	2.19	0.41
1:FA:21:GLU:OE1	1:FA:28:ARG:HD2	2.21	0.41
1:FA:36:VAL:H	1:FA:39:ASN:HB3	1.86	0.41
1:FF:2:ARG:HH11	1:FH:2:ARG:NH1	2.19	0.41
1:FF:99:LYS:O	1:FF:103:THR:HG23	2.20	0.41
1:FG:36:VAL:H	1:FG:39:ASN:HB3	1.86	0.41
1:FJ:21:GLU:OE1	1:FJ:28:ARG:HD2	2.21	0.41
1:FL:70:ASP:OD1	1:FL:71:ALA:N	2.53	0.41
1:FT:65:PRO:HB3	1:FT:79:LYS:HG2	2.03	0.41
1:FV:21:GLU:OE1	1:FV:28:ARG:HD2	2.21	0.41
1:FX:70:ASP:OD1	1:FX:71:ALA:N	2.53	0.41
1:FY:26:LEU:HD12	1:FY:46:GLU:HB2	2.02	0.41
1:GA:70:ASP:OD1	1:GA:71:ALA:N	2.53	0.41
1:GE:26:LEU:HD12	1:GE:46:GLU:HB2	2.02	0.41
1:GF:53:ASN:OD1	1:GF:54:SER:N	2.53	0.41
1:GI:53:ASN:OD1	1:GI:54:SER:N	2.53	0.41
1:GM:16:GLU:HB3	1:GM:32:LYS:HD2	2.02	0.41
1:GU:53:ASN:OD1	1:GU:54:SER:N	2.53	0.41
1:GW:17:TYR:HB3	1:GW:29:PHE:HB3	2.03	0.41
1:GX:65:PRO:HB3	1:GX:79:LYS:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:21:GLU:OE1	1:AB:28:ARG:HD2	2.21	0.41
1:AC:99:LYS:O	1:AC:103:THR:HG23	2.20	0.41
1:AD:2:ARG:HH11	1:AF:2:ARG:NH1	2.19	0.41
1:AL:65:PRO:HB3	1:AL:79:LYS:HG2	2.03	0.41
1:AL:124:TYR:CE1	1:DX:2:ARG:HD2	2.55	0.41
1:AM:8:LEU:HD22	1:CA:106:ALA:HB1	2.03	0.41
1:AP:2:ARG:HH11	1:AR:2:ARG:NH1	2.19	0.41
1:AS:8:LEU:HD11	1:EL:107:TRP:CE2	2.55	0.41
1:AU:65:PRO:HB3	1:AU:79:LYS:HG2	2.03	0.41
1:AY:70:ASP:OD1	1:AY:71:ALA:N	2.53	0.41
1:BG:65:PRO:HB3	1:BG:79:LYS:HG2	2.03	0.41
1:BI:17:TYR:HB3	1:BI:29:PHE:HB3	2.03	0.41
1:BN:70:ASP:OD1	1:BN:71:ALA:N	2.53	0.41
1:BR:21:GLU:OE1	1:BR:28:ARG:HD2	2.21	0.41
1:BT:16:GLU:HB3	1:BT:32:LYS:HD2	2.02	0.41
1:CB:94:ASN:O	1:CB:98:THR:HG23	2.21	0.41
1:CE:53:ASN:OD1	1:CE:54:SER:N	2.53	0.41
1:CP:17:TYR:HB3	1:CP:29:PHE:HB3	2.03	0.41
1:DA:2:ARG:HH11	1:DC:2:ARG:NH1	2.19	0.41
1:DF:65:PRO:HB3	1:DF:79:LYS:HG2	2.03	0.41
1:DH:36:VAL:H	1:DH:39:ASN:HB3	1.86	0.41
1:DI:91:THR:HB	1:GU:78:ILE:CD1	2.50	0.41
1:DK:26:LEU:HD12	1:DK:46:GLU:HB2	2.02	0.41
1:DL:53:ASN:OD1	1:DL:54:SER:N	2.53	0.41
1:DP:2:ARG:HH11	1:DR:2:ARG:NH1	2.19	0.41
1:DW:26:LEU:HD12	1:DW:46:GLU:HB2	2.02	0.41
1:DZ:17:TYR:HB3	1:DZ:29:PHE:HB3	2.03	0.41
1:DZ:21:GLU:OE1	1:DZ:28:ARG:HD2	2.21	0.41
1:EL:36:VAL:H	1:EL:39:ASN:HB3	1.86	0.41
1:EV:65:PRO:HB3	1:EV:79:LYS:HG2	2.03	0.41
1:FD:36:VAL:H	1:FD:39:ASN:HB3	1.86	0.41
1:FG:21:GLU:OE1	1:FG:28:ARG:HD2	2.21	0.41
1:FM:26:LEU:HD12	1:FM:46:GLU:HB2	2.02	0.41
1:FP:17:TYR:HB3	1:FP:29:PHE:HB3	2.03	0.41
1:FP:21:GLU:OE1	1:FP:28:ARG:HD2	2.21	0.41
1:FQ:65:PRO:HB3	1:FQ:79:LYS:HG2	2.03	0.41
1:FY:17:TYR:HB3	1:FY:29:PHE:HB3	2.03	0.41
1:GD:2:ARG:HH11	1:GF:2:ARG:NH1	2.19	0.41
1:GK:21:GLU:OE1	1:GK:28:ARG:HD2	2.21	0.41
1:GM:2:ARG:HH11	1:GO:2:ARG:NH1	2.19	0.41
1:AA:16:GLU:HB3	1:AA:32:LYS:HD2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:51:ALA:O	1:AB:90:LYS:NZ	2.50	0.40
1:AF:94:ASN:O	1:AF:98:THR:HG23	2.21	0.40
1:AI:99:LYS:O	1:AI:103:THR:HG23	2.20	0.40
1:AJ:2:ARG:HH11	1:AL:2:ARG:NH1	2.19	0.40
1:AM:2:ARG:HH11	1:AO:2:ARG:NH1	2.19	0.40
1:AN:17:TYR:HB3	1:AN:29:PHE:HB3	2.03	0.40
1:AO:94:ASN:O	1:AO:98:THR:HG23	2.21	0.40
1:BN:2:ARG:HH11	1:BP:2:ARG:NH1	2.19	0.40
1:BN:84:VAL:HG22	1:DZ:84:VAL:HG13	2.03	0.40
1:BO:36:VAL:H	1:BO:39:ASN:HB3	1.86	0.40
1:BS:118:ASP:CG	1:FE:98:THR:HG22	2.41	0.40
1:CA:21:GLU:OE1	1:CA:28:ARG:HD2	2.21	0.40
1:CI:16:GLU:HB3	1:CI:32:LYS:HD2	2.02	0.40
1:CS:21:GLU:OE1	1:CS:28:ARG:HD2	2.21	0.40
1:CU:70:ASP:OD1	1:CU:71:ALA:N	2.53	0.40
1:CY:17:TYR:HB3	1:CY:29:PHE:HB3	2.03	0.40
1:CZ:25:THR:HA	1:GL:122:ASN:OD1	2.21	0.40
1:DB:21:GLU:OE1	1:DB:28:ARG:HD2	2.21	0.40
1:DD:70:ASP:OD1	1:DD:71:ALA:N	2.53	0.40
1:DG:2:ARG:HH11	1:DI:2:ARG:NH1	2.19	0.40
1:DM:2:ARG:HH11	1:DO:2:ARG:NH1	2.19	0.40
1:DN:17:TYR:HB3	1:DN:29:PHE:HB3	2.03	0.40
1:DO:65:PRO:HB3	1:DO:79:LYS:HG2	2.03	0.40
1:DO:94:ASN:O	1:DO:98:THR:HG23	2.22	0.40
1:DV:2:ARG:HH11	1:DX:2:ARG:NH1	2.19	0.40
1:DV:107:TRP:HH2	1:GE:29:PHE:CD2	2.39	0.40
1:ED:53:ASN:OD1	1:ED:54:SER:N	2.53	0.40
1:EJ:65:PRO:HB3	1:EJ:79:LYS:HG2	2.03	0.40
1:EL:21:GLU:OE1	1:EL:28:ARG:HD2	2.21	0.40
1:EQ:2:ARG:HH11	1:ES:2:ARG:NH1	2.19	0.40
1:ET:8:LEU:HD11	1:FG:107:TRP:CE2	2.56	0.40
1:ET:84:VAL:HG13	1:FG:84:VAL:HG22	2.03	0.40
1:EV:53:ASN:OD1	1:EV:54:SER:N	2.53	0.40
1:EV:94:ASN:O	1:EV:98:THR:HG23	2.22	0.40
1:EY:94:ASN:O	1:EY:98:THR:HG23	2.21	0.40
1:FK:94:ASN:O	1:FK:98:THR:HG23	2.21	0.40
1:FL:16:GLU:HB3	1:FL:32:LYS:HD2	2.02	0.40
1:FQ:94:ASN:O	1:FQ:98:THR:HG23	2.21	0.40
1:FY:36:VAL:H	1:FY:39:ASN:HB3	1.86	0.40
1:GB:17:TYR:HB3	1:GB:29:PHE:HB3	2.03	0.40
1:GN:21:GLU:OE1	1:GN:28:ARG:HD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GP:70:ASP:OD1	1:GP:71:ALA:N	2.53	0.40
1:GS:16:GLU:HB3	1:GS:32:LYS:HD2	2.02	0.40
1:AC:2:ARG:HD2	1:DO:124:TYR:CE1	2.56	0.40
1:AC:65:PRO:HB3	1:AC:79:LYS:HG2	2.03	0.40
1:AE:36:VAL:H	1:AE:39:ASN:HB3	1.86	0.40
1:AI:94:ASN:O	1:AI:98:THR:HG23	2.21	0.40
1:AK:36:VAL:H	1:AK:39:ASN:HB3	1.86	0.40
1:AN:36:VAL:H	1:AN:39:ASN:HB3	1.87	0.40
1:AO:20:SER:HA	1:FR:121:LEU:CD1	2.51	0.40
1:AQ:15:ARG:HD3	1:FU:99:LYS:HE2	2.03	0.40
1:AQ:20:SER:HA	1:BU:121:LEU:HD22	2.03	0.40
1:AQ:22:GLN:HB3	1:BU:124:TYR:CB	2.45	0.40
1:BJ:124:TYR:HA	1:EV:22:GLN:NE2	2.37	0.40
1:BM:78:ILE:HD13	1:EY:91:THR:HB	2.03	0.40
1:BM:94:ASN:O	1:BM:98:THR:HG23	2.21	0.40
1:BS:94:ASN:O	1:BS:98:THR:HG23	2.21	0.40
1:BT:70:ASP:OD1	1:BT:71:ALA:N	2.53	0.40
1:BV:65:PRO:HB3	1:BV:79:LYS:HG2	2.03	0.40
1:CB:65:PRO:HB3	1:CB:79:LYS:HG2	2.03	0.40
1:CF:70:ASP:OD1	1:CF:71:ALA:N	2.53	0.40
1:CK:8:LEU:HD11	1:FW:107:TRP:CE2	2.57	0.40
1:CM:21:GLU:OE1	1:CM:28:ARG:HD2	2.21	0.40
1:CP:26:LEU:HD12	1:CP:46:GLU:HB2	2.02	0.40
1:CZ:94:ASN:O	1:CZ:98:THR:HG23	2.21	0.40
1:DA:96:HIS:CG	1:DE:66:VAL:HG21	2.56	0.40
1:DA:99:LYS:O	1:DA:103:THR:HG23	2.20	0.40
1:DN:21:GLU:OE1	1:DN:28:ARG:HD2	2.21	0.40
1:DQ:21:GLU:OE1	1:DQ:28:ARG:HD2	2.21	0.40
1:DT:21:GLU:OE1	1:DT:28:ARG:HD2	2.21	0.40
1:DT:36:VAL:H	1:DT:39:ASN:HB3	1.86	0.40
1:DW:36:VAL:H	1:DW:39:ASN:HB3	1.86	0.40
1:EH:2:ARG:HH11	1:EJ:2:ARG:NH1	2.19	0.40
1:ES:65:PRO:HB3	1:ES:79:LYS:HG2	2.03	0.40
1:ES:94:ASN:O	1:ES:98:THR:HG23	2.21	0.40
1:EX:17:TYR:HB3	1:EX:29:PHE:HB3	2.03	0.40
1:EX:36:VAL:H	1:EX:39:ASN:HB3	1.86	0.40
1:FO:16:GLU:HB3	1:FO:32:LYS:HD2	2.02	0.40
1:FO:45:LEU:HD11	1:FO:58:VAL:CG1	2.48	0.40
1:FP:36:VAL:H	1:FP:39:ASN:HB3	1.86	0.40
1:FT:94:ASN:O	1:FT:98:THR:HG23	2.21	0.40
1:GA:2:ARG:HH11	1:GC:2:ARG:NH1	2.19	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GG:70:ASP:OD1	1:GG:71:ALA:N	2.53	0.40
1:GH:36:VAL:H	1:GH:39:ASN:HB3	1.86	0.40
1:GJ:16:GLU:HB3	1:GJ:32:LYS:HD2	2.02	0.40
1:GN:17:TYR:HB3	1:GN:29:PHE:HB3	2.03	0.40
1:GQ:17:TYR:HB3	1:GQ:29:PHE:HB3	2.03	0.40
1:GT:21:GLU:OE1	1:GT:28:ARG:HD2	2.21	0.40
1:GT:36:VAL:H	1:GT:39:ASN:HB3	1.86	0.40
1:AG:118:ASP:OD2	1:BF:98:THR:HG22	2.21	0.40
1:AH:84:VAL:CG2	1:GD:104:LEU:HD11	2.52	0.40
1:AK:20:SER:O	1:BX:122:ASN:HB2	2.20	0.40
1:AK:21:GLU:OE1	1:AK:28:ARG:HD2	2.21	0.40
1:AM:16:GLU:HB3	1:AM:32:LYS:HD2	2.02	0.40
1:AN:26:LEU:HD12	1:AN:46:GLU:HB2	2.02	0.40
1:AP:107:TRP:CE2	1:BU:8:LEU:HD11	2.56	0.40
1:AQ:36:VAL:H	1:AQ:39:ASN:HB3	1.86	0.40
1:AS:1:MET:HB3	1:EL:123:ASN:OD1	2.21	0.40
1:AV:16:GLU:HB3	1:AV:32:LYS:HD2	2.02	0.40
1:AX:53:ASN:OD1	1:AX:54:SER:N	2.53	0.40
1:BC:21:GLU:OE1	1:BC:28:ARG:HD2	2.21	0.40
1:BG:94:ASN:O	1:BG:98:THR:HG23	2.21	0.40
1:BI:21:GLU:OE1	1:BI:28:ARG:HD2	2.21	0.40
1:BJ:53:ASN:OD1	1:BJ:54:SER:N	2.53	0.40
1:BS:65:PRO:HB3	1:BS:79:LYS:HG2	2.03	0.40
1:BT:2:ARG:HH11	1:BV:2:ARG:NH1	2.19	0.40
1:BV:98:THR:HG22	1:FH:118:ASP:CG	2.41	0.40
1:BX:21:GLU:OE1	1:BX:28:ARG:HD2	2.21	0.40
1:BY:94:ASN:O	1:BY:98:THR:HG23	2.21	0.40
1:CC:2:ARG:HH11	1:CE:2:ARG:NH1	2.19	0.40
1:CD:84:VAL:HA	1:CR:83:SER:O	2.21	0.40
1:CJ:21:GLU:OE1	1:CJ:28:ARG:HD2	2.21	0.40
1:CK:94:ASN:O	1:CK:98:THR:HG23	2.21	0.40
1:CN:84:VAL:HG13	1:FZ:84:VAL:HG22	2.03	0.40
1:CQ:65:PRO:HB3	1:CQ:79:LYS:HG2	2.03	0.40
1:CT:94:ASN:O	1:CT:98:THR:HG23	2.21	0.40
1:CY:21:GLU:OE1	1:CY:28:ARG:HD2	2.21	0.40
1:DI:94:ASN:O	1:DI:98:THR:HG23	2.21	0.40
1:DL:94:ASN:O	1:DL:98:THR:HG23	2.21	0.40
1:DR:94:ASN:O	1:DR:98:THR:HG23	2.21	0.40
1:DU:94:ASN:O	1:DU:98:THR:HG23	2.21	0.40
1:DW:17:TYR:HB3	1:DW:29:PHE:HB3	2.03	0.40
1:EB:27:PHE:CE2	1:GB:123:ASN:ND2	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EC:36:VAL:H	1:EC:39:ASN:HB3	1.86	0.40
1:EU:17:TYR:HB3	1:EU:29:PHE:HB3	2.03	0.40
1:EX:21:GLU:OE1	1:EX:28:ARG:HD2	2.21	0.40
1:FB:94:ASN:O	1:FB:98:THR:HG23	2.21	0.40
1:FG:17:TYR:HB3	1:FG:29:PHE:HB3	2.03	0.40
1:FV:15:ARG:HH11	1:GS:99:LYS:HE2	1.86	0.40
1:FX:2:ARG:HH11	1:FZ:2:ARG:NH1	2.19	0.40
1:FY:21:GLU:OE1	1:FY:28:ARG:HD2	2.21	0.40
1:GL:99:LYS:O	1:GL:103:THR:HG23	2.20	0.40
1:GP:2:ARG:HH11	1:GR:2:ARG:NH1	2.19	0.40
1:GQ:21:GLU:OE1	1:GQ:28:ARG:HD2	2.21	0.40
1:GQ:88:LEU:HD13	1:GQ:97:ILE:HD13	2.04	0.40
1:GX:94:ASN:O	1:GX:98:THR:HG23	2.21	0.40
1:AC:94:ASN:O	1:AC:98:THR:HG23	2.21	0.40
1:AL:78:ILE:HD13	1:DX:91:THR:HB	2.04	0.40
1:AN:103:THR:HG22	1:FR:10:VAL:CG2	2.48	0.40
1:AW:17:TYR:HB3	1:AW:29:PHE:HB3	2.03	0.40
1:AY:122:ASN:HB2	1:EJ:20:SER:O	2.21	0.40
1:AZ:26:LEU:HD12	1:AZ:46:GLU:HB2	2.02	0.40
1:BE:10:VAL:CG2	1:BL:103:THR:HG22	2.45	0.40
1:BF:36:VAL:H	1:BF:39:ASN:HB3	1.86	0.40
1:BI:88:LEU:HD13	1:BI:97:ILE:HD13	2.04	0.40
1:BK:2:ARG:HH11	1:BM:2:ARG:NH1	2.19	0.40
1:BK:20:SER:O	1:EY:122:ASN:HB2	2.22	0.40
1:BL:17:TYR:HB3	1:BL:29:PHE:HB3	2.03	0.40
1:BU:36:VAL:H	1:BU:39:ASN:HB3	1.86	0.40
1:BV:103:THR:OG1	1:FH:62:LEU:HD21	2.21	0.40
1:CG:21:GLU:OE1	1:CG:28:ARG:HD2	2.21	0.40
1:CH:94:ASN:O	1:CH:98:THR:HG23	2.21	0.40
1:CL:2:ARG:HH11	1:CN:2:ARG:NH1	2.19	0.40
1:CP:36:VAL:H	1:CP:39:ASN:HB3	1.86	0.40
1:CP:88:LEU:HD13	1:CP:97:ILE:HD13	2.04	0.40
1:DB:84:VAL:HG21	1:GJ:104:LEU:HD11	2.03	0.40
1:DE:21:GLU:OE1	1:DE:28:ARG:HD2	2.21	0.40
1:DE:26:LEU:HD12	1:DE:46:GLU:HB2	2.02	0.40
1:DK:36:VAL:H	1:DK:39:ASN:HB3	1.86	0.40
1:DK:88:LEU:HD13	1:DK:97:ILE:HD13	2.04	0.40
1:DQ:51:ALA:O	1:DQ:90:LYS:NZ	2.50	0.40
1:DW:21:GLU:OE1	1:DW:28:ARG:HD2	2.21	0.40
1:EC:17:TYR:HB3	1:EC:29:PHE:HB3	2.03	0.40
1:EF:17:TYR:HB3	1:EF:29:PHE:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EF:36:VAL:H	1:EF:39:ASN:HB3	1.86	0.40
1:EG:94:ASN:O	1:EG:98:THR:HG23	2.21	0.40
1:EI:88:LEU:HD13	1:EI:97:ILE:HD13	2.04	0.40
1:EQ:85:THR:OG1	1:FM:83:SER:OG	2.36	0.40
1:EZ:16:GLU:HB3	1:EZ:32:LYS:HD2	2.02	0.40
1:FH:65:PRO:HB3	1:FH:79:LYS:HG2	2.03	0.40
1:GC:94:ASN:O	1:GC:98:THR:HG23	2.21	0.40
1:GE:17:TYR:HB3	1:GE:29:PHE:HB3	2.03	0.40
1:GE:21:GLU:OE1	1:GE:28:ARG:HD2	2.21	0.40
1:GE:88:LEU:HD13	1:GE:97:ILE:HD13	2.04	0.40
1:GF:94:ASN:O	1:GF:98:THR:HG23	2.21	0.40
1:GK:17:TYR:HB3	1:GK:29:PHE:HB3	2.03	0.40
1:GK:36:VAL:H	1:GK:39:ASN:HB3	1.86	0.40
1:GO:94:ASN:O	1:GO:98:THR:HG23	2.21	0.40
1:GQ:26:LEU:HD12	1:GQ:46:GLU:HB2	2.02	0.40
1:AB:17:TYR:HB3	1:AB:29:PHE:HB3	2.03	0.40
1:AB:36:VAL:H	1:AB:39:ASN:HB3	1.86	0.40
1:AE:88:LEU:HD13	1:AE:97:ILE:HD13	2.04	0.40
1:AQ:21:GLU:OE1	1:AQ:28:ARG:HD2	2.21	0.40
1:AY:22:GLN:HE21	1:EI:124:TYR:HA	1.77	0.40
1:BA:94:ASN:O	1:BA:98:THR:HG23	2.21	0.40
1:BJ:65:PRO:HB3	1:BJ:79:LYS:HG2	2.03	0.40
1:BL:21:GLU:OE1	1:BL:28:ARG:HD2	2.21	0.40
1:BX:88:LEU:HD13	1:BX:97:ILE:HD13	2.04	0.40
1:CE:94:ASN:O	1:CE:98:THR:HG23	2.21	0.40
1:CG:47:GLN:HE22	1:CL:120:GLY:HA2	1.86	0.40
1:CJ:26:LEU:HD12	1:CJ:46:GLU:HB2	2.02	0.40
1:CK:65:PRO:HB3	1:CK:79:LYS:HG2	2.03	0.40
1:CM:8:LEU:HD11	1:DG:107:TRP:CE2	2.56	0.40
1:CN:94:ASN:O	1:CN:98:THR:HG23	2.21	0.40
1:CP:21:GLU:OE1	1:CP:28:ARG:HD2	2.21	0.40
1:CP:98:THR:HG22	1:DJ:118:ASP:CG	2.42	0.40
1:DB:36:VAL:H	1:DB:39:ASN:HB3	1.86	0.40
1:DE:17:TYR:HB3	1:DE:29:PHE:HB3	2.03	0.40
1:DH:21:GLU:OE1	1:DH:28:ARG:HD2	2.21	0.40
1:DL:65:PRO:HB3	1:DL:79:LYS:HG2	2.03	0.40
1:DQ:36:VAL:H	1:DQ:39:ASN:HB3	1.86	0.40
1:DS:70:ASP:OD1	1:DS:71:ALA:N	2.53	0.40
1:ED:94:ASN:O	1:ED:98:THR:HG23	2.21	0.40
1:EO:21:GLU:OE1	1:EO:28:ARG:HD2	2.21	0.40
1:ER:21:GLU:OE1	1:ER:28:ARG:HD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ER:88:LEU:HD13	1:ER:97:ILE:HD13	2.04	0.40
1:ET:15:ARG:NH1	1:FG:103:THR:HG21	2.26	0.40
1:EU:26:LEU:HD12	1:EU:46:GLU:HB2	2.02	0.40
1:EY:65:PRO:HB3	1:EY:79:LYS:HG2	2.03	0.40
1:FJ:17:TYR:HB3	1:FJ:29:PHE:HB3	2.03	0.40
1:FM:17:TYR:HB3	1:FM:29:PHE:HB3	2.03	0.40
1:FM:21:GLU:OE1	1:FM:28:ARG:HD2	2.21	0.40
1:FS:26:LEU:HD12	1:FS:46:GLU:HB2	2.02	0.40
1:GH:17:TYR:HB3	1:GH:29:PHE:HB3	2.03	0.40
1:GI:94:ASN:O	1:GI:98:THR:HG23	2.21	0.40
1:GK:88:LEU:HD13	1:GK:97:ILE:HD13	2.04	0.40
1:GN:36:VAL:H	1:GN:39:ASN:HB3	1.86	0.40
1:GQ:36:VAL:H	1:GQ:39:ASN:HB3	1.86	0.40
1:GU:94:ASN:O	1:GU:98:THR:HG23	2.21	0.40

All (24) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:32:LYS:NZ	1:GB:16:GLU:OE2[1_666]	1.39	0.81
1:BU:32:LYS:NZ	1:DW:16:GLU:OE2[1_554]	1.50	0.70
1:BH:12:GLU:O	1:GK:5:ASP:O[1_655]	1.55	0.65
1:EI:35:THR:CG2	1:GN:12:GLU:OE1[1_545]	1.55	0.65
1:BH:12:GLU:OE1	1:GK:7:ASP:OD1[1_655]	1.57	0.63
1:EG:95:GLU:OE2	1:FQ:13:GLU:O[1_655]	1.63	0.57
1:EI:35:THR:CB	1:GN:12:GLU:OE1[1_545]	1.82	0.38
1:CJ:7:ASP:OD2	1:EK:12:GLU:CB[1_454]	1.84	0.36
1:CJ:16:GLU:OE2	1:EK:12:GLU:OE1[1_454]	1.84	0.36
1:CJ:16:GLU:CD	1:EK:12:GLU:OE1[1_454]	1.89	0.31
1:DN:12:GLU:O	1:DV:96:HIS:NE2[1_554]	1.95	0.25
1:EH:95:GLU:OE1	1:GN:13:GLU:OE1[1_545]	1.96	0.24
1:FJ:12:GLU:OE2	1:GM:4:THR:OG1[1_545]	1.97	0.23
1:CI:7:ASP:CB	1:ER:16:GLU:OE2[1_454]	1.99	0.21
1:BJ:9:THR:OG1	1:GL:12:GLU:OE2[1_655]	2.00	0.20
1:BT:96:HIS:CD2	1:GE:12:GLU:OE1[1_554]	2.00	0.20
1:EG:95:GLU:OE1	1:FQ:11:GLY:O[1_655]	2.01	0.19
1:EO:7:ASP:OD2	1:GM:95:GLU:OE2[1_545]	2.08	0.12
1:AN:16:GLU:OE2	1:GB:32:LYS:NZ[1_666]	2.12	0.08
1:EG:95:GLU:OE2	1:FQ:10:VAL:N[1_655]	2.12	0.08
1:CG:16:GLU:OE1	1:EI:7:ASP:CG[1_565]	2.13	0.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EV:12:GLU:OE1	1:GL:40:THR:CG2[1_655]	2.16	0.04
1:FJ:12:GLU:OE1	1:GM:4:THR:CG2[1_545]	2.16	0.04
1:CA:12:GLU:O	1:GA:96:HIS:NE2[1_666]	2.18	0.02

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	AB	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	AC	122/124 (98%)	122 (100%)	0	0	100	100
1	AD	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	AE	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	AF	122/124 (98%)	122 (100%)	0	0	100	100
1	AG	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	AH	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	AI	122/124 (98%)	122 (100%)	0	0	100	100
1	AJ	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	AK	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	AL	122/124 (98%)	122 (100%)	0	0	100	100
1	AM	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	AN	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	AO	122/124 (98%)	122 (100%)	0	0	100	100
1	AP	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	AQ	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	AR	122/124 (98%)	122 (100%)	0	0	100	100
1	AS	122/124 (98%)	121 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AT	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	AU	122/124 (98%)	122 (100%)	0	0	100	100
1	AV	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	AW	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	AX	122/124 (98%)	122 (100%)	0	0	100	100
1	AY	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	AZ	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	BA	122/124 (98%)	122 (100%)	0	0	100	100
1	BB	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	BC	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	BD	122/124 (98%)	122 (100%)	0	0	100	100
1	BE	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	BF	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	BG	122/124 (98%)	122 (100%)	0	0	100	100
1	BH	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	BI	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	BJ	122/124 (98%)	122 (100%)	0	0	100	100
1	BK	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	BL	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	BM	122/124 (98%)	122 (100%)	0	0	100	100
1	BN	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	BO	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	BP	122/124 (98%)	122 (100%)	0	0	100	100
1	BQ	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	BR	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	BS	122/124 (98%)	122 (100%)	0	0	100	100
1	BT	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	BU	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	BV	122/124 (98%)	122 (100%)	0	0	100	100
1	BW	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	BX	113/124 (91%)	110 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BY	122/124 (98%)	122 (100%)	0	0	100	100
1	BZ	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	CA	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	CB	122/124 (98%)	122 (100%)	0	0	100	100
1	CC	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	CD	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	CE	122/124 (98%)	122 (100%)	0	0	100	100
1	CF	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	CG	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	CH	122/124 (98%)	122 (100%)	0	0	100	100
1	CI	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	CJ	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	CK	122/124 (98%)	122 (100%)	0	0	100	100
1	CL	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	CM	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	CN	122/124 (98%)	122 (100%)	0	0	100	100
1	CO	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	CP	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	CQ	122/124 (98%)	122 (100%)	0	0	100	100
1	CR	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	CS	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	CT	122/124 (98%)	122 (100%)	0	0	100	100
1	CU	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	CV	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	CW	122/124 (98%)	122 (100%)	0	0	100	100
1	CX	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	CY	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	CZ	122/124 (98%)	122 (100%)	0	0	100	100
1	DA	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	DB	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	DC	122/124 (98%)	122 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DD	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	DE	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	DF	122/124 (98%)	122 (100%)	0	0	100	100
1	DG	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	DH	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	DI	122/124 (98%)	122 (100%)	0	0	100	100
1	DJ	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	DK	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	DL	122/124 (98%)	122 (100%)	0	0	100	100
1	DM	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	DN	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	DO	122/124 (98%)	122 (100%)	0	0	100	100
1	DP	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	DQ	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	DR	122/124 (98%)	122 (100%)	0	0	100	100
1	DS	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	DT	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	DU	122/124 (98%)	122 (100%)	0	0	100	100
1	DV	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	DW	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	DX	122/124 (98%)	122 (100%)	0	0	100	100
1	DY	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	DZ	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	EA	122/124 (98%)	122 (100%)	0	0	100	100
1	EB	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	EC	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	ED	122/124 (98%)	122 (100%)	0	0	100	100
1	EE	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	EF	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	EG	122/124 (98%)	122 (100%)	0	0	100	100
1	EH	122/124 (98%)	121 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EI	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	EJ	122/124 (98%)	122 (100%)	0	0	100	100
1	EK	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	EL	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	EM	122/124 (98%)	122 (100%)	0	0	100	100
1	EN	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	EO	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	EP	122/124 (98%)	122 (100%)	0	0	100	100
1	EQ	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	ER	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	ES	122/124 (98%)	122 (100%)	0	0	100	100
1	ET	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	EU	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	EV	122/124 (98%)	122 (100%)	0	0	100	100
1	EW	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	EX	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	EY	122/124 (98%)	122 (100%)	0	0	100	100
1	EZ	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	FA	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	FB	122/124 (98%)	122 (100%)	0	0	100	100
1	FC	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	FD	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	FE	122/124 (98%)	122 (100%)	0	0	100	100
1	FF	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	FG	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	FH	122/124 (98%)	122 (100%)	0	0	100	100
1	FI	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	FJ	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	FK	122/124 (98%)	122 (100%)	0	0	100	100
1	FL	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	FM	113/124 (91%)	110 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	FN	122/124 (98%)	122 (100%)	0	0	100	100
1	FO	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	FP	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	FQ	122/124 (98%)	122 (100%)	0	0	100	100
1	FR	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	FS	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	FT	122/124 (98%)	122 (100%)	0	0	100	100
1	FU	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	FV	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	FW	122/124 (98%)	122 (100%)	0	0	100	100
1	FX	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	FY	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	FZ	122/124 (98%)	122 (100%)	0	0	100	100
1	GA	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	GB	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	GC	122/124 (98%)	122 (100%)	0	0	100	100
1	GD	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	GE	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	GF	122/124 (98%)	122 (100%)	0	0	100	100
1	GG	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	GH	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	GI	122/124 (98%)	122 (100%)	0	0	100	100
1	GJ	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	GK	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	GL	122/124 (98%)	122 (100%)	0	0	100	100
1	GM	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	GN	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	GO	122/124 (98%)	122 (100%)	0	0	100	100
1	GP	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	GQ	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	GR	122/124 (98%)	122 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GS	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	GT	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	GU	122/124 (98%)	122 (100%)	0	0	100	100
1	GV	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
1	GW	113/124 (91%)	110 (97%)	3 (3%)	0	100	100
1	GX	122/124 (98%)	122 (100%)	0	0	100	100
All	All	21420/22320 (96%)	21180 (99%)	240 (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	107/107 (100%)	107 (100%)	0	100	100
1	AB	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	AC	107/107 (100%)	107 (100%)	0	100	100
1	AD	107/107 (100%)	107 (100%)	0	100	100
1	AE	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	AF	107/107 (100%)	107 (100%)	0	100	100
1	AG	107/107 (100%)	107 (100%)	0	100	100
1	AH	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	AI	107/107 (100%)	107 (100%)	0	100	100
1	AJ	107/107 (100%)	107 (100%)	0	100	100
1	AK	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	AL	107/107 (100%)	107 (100%)	0	100	100
1	AM	107/107 (100%)	107 (100%)	0	100	100
1	AN	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	AO	107/107 (100%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AP	107/107 (100%)	107 (100%)	0	100	100
1	AQ	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	AR	107/107 (100%)	107 (100%)	0	100	100
1	AS	107/107 (100%)	107 (100%)	0	100	100
1	AT	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	AU	107/107 (100%)	107 (100%)	0	100	100
1	AV	107/107 (100%)	107 (100%)	0	100	100
1	AW	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	AX	107/107 (100%)	107 (100%)	0	100	100
1	AY	107/107 (100%)	107 (100%)	0	100	100
1	AZ	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	BA	107/107 (100%)	107 (100%)	0	100	100
1	BB	107/107 (100%)	107 (100%)	0	100	100
1	BC	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	BD	107/107 (100%)	107 (100%)	0	100	100
1	BE	107/107 (100%)	107 (100%)	0	100	100
1	BF	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	BG	107/107 (100%)	107 (100%)	0	100	100
1	BH	107/107 (100%)	107 (100%)	0	100	100
1	BI	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	BJ	107/107 (100%)	107 (100%)	0	100	100
1	BK	107/107 (100%)	107 (100%)	0	100	100
1	BL	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	BM	107/107 (100%)	107 (100%)	0	100	100
1	BN	107/107 (100%)	107 (100%)	0	100	100
1	BO	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	BP	107/107 (100%)	107 (100%)	0	100	100
1	BQ	107/107 (100%)	107 (100%)	0	100	100
1	BR	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	BS	107/107 (100%)	107 (100%)	0	100	100
1	BT	107/107 (100%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BU	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	BV	107/107 (100%)	107 (100%)	0	100	100
1	BW	107/107 (100%)	107 (100%)	0	100	100
1	BX	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	BY	107/107 (100%)	107 (100%)	0	100	100
1	BZ	107/107 (100%)	107 (100%)	0	100	100
1	CA	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	CB	107/107 (100%)	107 (100%)	0	100	100
1	CC	107/107 (100%)	107 (100%)	0	100	100
1	CD	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	CE	107/107 (100%)	107 (100%)	0	100	100
1	CF	107/107 (100%)	107 (100%)	0	100	100
1	CG	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	CH	107/107 (100%)	107 (100%)	0	100	100
1	CI	107/107 (100%)	107 (100%)	0	100	100
1	CJ	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	CK	107/107 (100%)	107 (100%)	0	100	100
1	CL	107/107 (100%)	107 (100%)	0	100	100
1	CM	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	CN	107/107 (100%)	107 (100%)	0	100	100
1	CO	107/107 (100%)	107 (100%)	0	100	100
1	CP	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	CQ	107/107 (100%)	107 (100%)	0	100	100
1	CR	107/107 (100%)	107 (100%)	0	100	100
1	CS	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	CT	107/107 (100%)	107 (100%)	0	100	100
1	CU	107/107 (100%)	107 (100%)	0	100	100
1	CV	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	CW	107/107 (100%)	107 (100%)	0	100	100
1	CX	107/107 (100%)	107 (100%)	0	100	100
1	CY	103/107 (96%)	102 (99%)	1 (1%)	76	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CZ	107/107 (100%)	107 (100%)	0	100	100
1	DA	107/107 (100%)	107 (100%)	0	100	100
1	DB	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	DC	107/107 (100%)	107 (100%)	0	100	100
1	DD	107/107 (100%)	107 (100%)	0	100	100
1	DE	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	DF	107/107 (100%)	107 (100%)	0	100	100
1	DG	107/107 (100%)	107 (100%)	0	100	100
1	DH	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	DI	107/107 (100%)	107 (100%)	0	100	100
1	DJ	107/107 (100%)	107 (100%)	0	100	100
1	DK	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	DL	107/107 (100%)	107 (100%)	0	100	100
1	DM	107/107 (100%)	107 (100%)	0	100	100
1	DN	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	DO	107/107 (100%)	107 (100%)	0	100	100
1	DP	107/107 (100%)	107 (100%)	0	100	100
1	DQ	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	DR	107/107 (100%)	107 (100%)	0	100	100
1	DS	107/107 (100%)	107 (100%)	0	100	100
1	DT	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	DU	107/107 (100%)	107 (100%)	0	100	100
1	DV	107/107 (100%)	107 (100%)	0	100	100
1	DW	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	DX	107/107 (100%)	107 (100%)	0	100	100
1	DY	107/107 (100%)	107 (100%)	0	100	100
1	DZ	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	EA	107/107 (100%)	107 (100%)	0	100	100
1	EB	107/107 (100%)	107 (100%)	0	100	100
1	EC	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	ED	107/107 (100%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	EE	107/107 (100%)	107 (100%)	0	100	100
1	EF	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	EG	107/107 (100%)	107 (100%)	0	100	100
1	EH	107/107 (100%)	107 (100%)	0	100	100
1	EI	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	EJ	107/107 (100%)	107 (100%)	0	100	100
1	EK	107/107 (100%)	107 (100%)	0	100	100
1	EL	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	EM	107/107 (100%)	107 (100%)	0	100	100
1	EN	107/107 (100%)	107 (100%)	0	100	100
1	EO	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	EP	107/107 (100%)	107 (100%)	0	100	100
1	EQ	107/107 (100%)	107 (100%)	0	100	100
1	ER	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	ES	107/107 (100%)	107 (100%)	0	100	100
1	ET	107/107 (100%)	107 (100%)	0	100	100
1	EU	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	EV	107/107 (100%)	107 (100%)	0	100	100
1	EW	107/107 (100%)	107 (100%)	0	100	100
1	EX	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	EY	107/107 (100%)	107 (100%)	0	100	100
1	EZ	107/107 (100%)	107 (100%)	0	100	100
1	FA	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	FB	107/107 (100%)	107 (100%)	0	100	100
1	FC	107/107 (100%)	107 (100%)	0	100	100
1	FD	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	FE	107/107 (100%)	107 (100%)	0	100	100
1	FF	107/107 (100%)	107 (100%)	0	100	100
1	FG	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	FH	107/107 (100%)	107 (100%)	0	100	100
1	FI	107/107 (100%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	FJ	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	FK	107/107 (100%)	107 (100%)	0	100	100
1	FL	107/107 (100%)	107 (100%)	0	100	100
1	FM	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	FN	107/107 (100%)	107 (100%)	0	100	100
1	FO	107/107 (100%)	107 (100%)	0	100	100
1	FP	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	FQ	107/107 (100%)	107 (100%)	0	100	100
1	FR	107/107 (100%)	107 (100%)	0	100	100
1	FS	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	FT	107/107 (100%)	107 (100%)	0	100	100
1	FU	107/107 (100%)	107 (100%)	0	100	100
1	FV	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	FW	107/107 (100%)	107 (100%)	0	100	100
1	FX	107/107 (100%)	107 (100%)	0	100	100
1	FY	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	FZ	107/107 (100%)	107 (100%)	0	100	100
1	GA	107/107 (100%)	107 (100%)	0	100	100
1	GB	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	GC	107/107 (100%)	107 (100%)	0	100	100
1	GD	107/107 (100%)	107 (100%)	0	100	100
1	GE	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	GF	107/107 (100%)	107 (100%)	0	100	100
1	GG	107/107 (100%)	107 (100%)	0	100	100
1	GH	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	GI	107/107 (100%)	107 (100%)	0	100	100
1	GJ	107/107 (100%)	107 (100%)	0	100	100
1	GK	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	GL	107/107 (100%)	107 (100%)	0	100	100
1	GM	107/107 (100%)	107 (100%)	0	100	100
1	GN	103/107 (96%)	102 (99%)	1 (1%)	76	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	GO	107/107 (100%)	107 (100%)	0	100	100
1	GP	107/107 (100%)	107 (100%)	0	100	100
1	GQ	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	GR	107/107 (100%)	107 (100%)	0	100	100
1	GS	107/107 (100%)	107 (100%)	0	100	100
1	GT	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	GU	107/107 (100%)	107 (100%)	0	100	100
1	GV	107/107 (100%)	107 (100%)	0	100	100
1	GW	103/107 (96%)	102 (99%)	1 (1%)	76	88
1	GX	107/107 (100%)	107 (100%)	0	100	100
All	All	19020/19260 (99%)	18960 (100%)	60 (0%)	92	96

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AB	22	GLN
1	AE	22	GLN
1	AH	22	GLN
1	AK	22	GLN
1	AN	22	GLN
1	AQ	22	GLN
1	AT	22	GLN
1	AW	22	GLN
1	AZ	22	GLN
1	BC	22	GLN
1	BF	22	GLN
1	BI	22	GLN
1	BL	22	GLN
1	BO	22	GLN
1	BR	22	GLN
1	BU	22	GLN
1	BX	22	GLN
1	CA	22	GLN
1	CD	22	GLN
1	CG	22	GLN
1	CJ	22	GLN
1	CM	22	GLN
1	CP	22	GLN

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Mol	Chain	Res	Type
1	CS	22	GLN
1	CV	22	GLN
1	CY	22	GLN
1	DB	22	GLN
1	DE	22	GLN
1	DH	22	GLN
1	DK	22	GLN
1	DN	22	GLN
1	DQ	22	GLN
1	DT	22	GLN
1	DW	22	GLN
1	DZ	22	GLN
1	EC	22	GLN
1	EF	22	GLN
1	EI	22	GLN
1	EL	22	GLN
1	EO	22	GLN
1	ER	22	GLN
1	EU	22	GLN
1	EX	22	GLN
1	FA	22	GLN
1	FD	22	GLN
1	FG	22	GLN
1	FJ	22	GLN
1	FM	22	GLN
1	FP	22	GLN
1	FS	22	GLN
1	FV	22	GLN
1	FY	22	GLN
1	GB	22	GLN
1	GE	22	GLN
1	GH	22	GLN
1	GK	22	GLN
1	GN	22	GLN
1	GQ	22	GLN
1	GT	22	GLN
1	GW	22	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (72) such sidechains are listed below:

Mol	Chain	Res	Type
1	AE	22	GLN

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Mol	Chain	Res	Type
1	AE	47	GLN
1	AH	22	GLN
1	AH	47	GLN
1	AN	22	GLN
1	AN	47	GLN
1	AQ	47	GLN
1	AT	47	GLN
1	AZ	47	GLN
1	BC	22	GLN
1	BC	47	GLN
1	BF	47	GLN
1	BI	47	GLN
1	BL	47	GLN
1	BO	22	GLN
1	BO	47	GLN
1	BR	22	GLN
1	BR	47	GLN
1	BU	22	GLN
1	BU	47	GLN
1	CA	22	GLN
1	CA	47	GLN
1	CG	22	GLN
1	CG	47	GLN
1	CJ	47	GLN
1	CM	47	GLN
1	CV	22	GLN
1	CV	47	GLN
1	DB	47	GLN
1	DH	22	GLN
1	DH	47	GLN
1	DK	47	GLN
1	DN	22	GLN
1	DN	47	GLN
1	DQ	47	GLN
1	DT	47	GLN
1	DW	22	GLN
1	DW	47	GLN
1	EC	47	GLN
1	EI	22	GLN
1	EI	47	GLN
1	EO	22	GLN
1	EO	47	GLN

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Mol	Chain	Res	Type
1	ER	22	GLN
1	ER	47	GLN
1	EU	22	GLN
1	EU	47	GLN
1	EX	47	GLN
1	FD	47	GLN
1	FJ	22	GLN
1	FJ	47	GLN
1	FM	47	GLN
1	FP	22	GLN
1	FP	47	GLN
1	FR	122	ASN
1	FS	47	GLN
1	FV	47	GLN
1	FY	47	GLN
1	GB	22	GLN
1	GB	47	GLN
1	GE	22	GLN
1	GE	47	GLN
1	GF	47	GLN
1	GH	22	GLN
1	GH	47	GLN
1	GK	22	GLN
1	GK	47	GLN
1	GN	22	GLN
1	GN	47	GLN
1	GQ	47	GLN
1	GT	47	GLN
1	GW	47	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 60 ligands modelled in this entry, 60 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	124/124 (100%)	-0.42	0 100 100	66, 92, 154, 183	0
1	AB	117/124 (94%)	-0.41	2 (1%) 70 60	67, 92, 140, 186	0
1	AC	124/124 (100%)	-0.49	0 100 100	63, 92, 150, 173	0
1	AD	124/124 (100%)	-0.45	1 (0%) 86 80	66, 92, 154, 183	0
1	AE	117/124 (94%)	-0.31	2 (1%) 70 60	67, 92, 140, 186	0
1	AF	124/124 (100%)	-0.43	0 100 100	63, 92, 150, 173	0
1	AG	124/124 (100%)	-0.41	0 100 100	66, 92, 154, 183	0
1	AH	117/124 (94%)	-0.30	1 (0%) 84 78	67, 92, 140, 186	0
1	AI	124/124 (100%)	-0.56	0 100 100	63, 92, 150, 173	0
1	AJ	124/124 (100%)	-0.61	0 100 100	66, 92, 154, 183	0
1	AK	117/124 (94%)	-0.43	1 (0%) 84 78	67, 92, 140, 186	0
1	AL	124/124 (100%)	-0.53	0 100 100	63, 92, 150, 173	0
1	AM	124/124 (100%)	-0.36	0 100 100	66, 92, 154, 183	0
1	AN	117/124 (94%)	-0.27	0 100 100	67, 92, 140, 186	0
1	AO	124/124 (100%)	-0.40	0 100 100	63, 92, 150, 173	0
1	AP	124/124 (100%)	-0.41	0 100 100	66, 92, 154, 183	0
1	AQ	117/124 (94%)	-0.39	1 (0%) 84 78	67, 92, 140, 186	0
1	AR	124/124 (100%)	-0.47	0 100 100	63, 92, 150, 173	0
1	AS	124/124 (100%)	-0.40	0 100 100	66, 92, 154, 183	0
1	AT	117/124 (94%)	-0.41	1 (0%) 84 78	67, 92, 140, 186	0
1	AU	124/124 (100%)	-0.40	0 100 100	63, 92, 150, 173	0
1	AV	124/124 (100%)	-0.34	1 (0%) 86 80	66, 92, 154, 183	0
1	AW	117/124 (94%)	-0.34	2 (1%) 70 60	67, 92, 140, 186	0
1	AX	124/124 (100%)	-0.36	0 100 100	63, 92, 150, 173	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	124/124 (100%)	-0.33	0 100 100	66, 92, 154, 183	0
1	AZ	117/124 (94%)	-0.24	1 (0%) 84 78	67, 92, 140, 186	0
1	BA	124/124 (100%)	-0.45	0 100 100	63, 92, 150, 173	0
1	BB	124/124 (100%)	-0.54	0 100 100	66, 92, 154, 183	0
1	BC	117/124 (94%)	-0.36	0 100 100	67, 92, 140, 186	0
1	BD	124/124 (100%)	-0.52	0 100 100	63, 92, 150, 173	0
1	BE	124/124 (100%)	-0.50	0 100 100	66, 92, 154, 183	0
1	BF	117/124 (94%)	-0.32	1 (0%) 84 78	67, 92, 140, 186	0
1	BG	124/124 (100%)	-0.44	0 100 100	63, 92, 150, 173	0
1	BH	124/124 (100%)	-0.36	0 100 100	66, 92, 154, 183	0
1	BI	117/124 (94%)	-0.35	1 (0%) 84 78	67, 92, 140, 186	0
1	BJ	124/124 (100%)	-0.40	0 100 100	63, 92, 150, 173	0
1	BK	124/124 (100%)	-0.34	2 (1%) 72 63	66, 92, 154, 183	0
1	BL	117/124 (94%)	-0.29	1 (0%) 84 78	67, 92, 140, 186	0
1	BM	124/124 (100%)	-0.49	0 100 100	63, 92, 150, 173	0
1	BN	124/124 (100%)	-0.56	1 (0%) 86 80	66, 92, 154, 183	0
1	BO	117/124 (94%)	-0.33	1 (0%) 84 78	67, 92, 140, 186	0
1	BP	124/124 (100%)	-0.44	0 100 100	63, 92, 150, 173	0
1	BQ	124/124 (100%)	-0.58	0 100 100	66, 92, 154, 183	0
1	BR	117/124 (94%)	-0.40	1 (0%) 84 78	67, 92, 140, 186	0
1	BS	124/124 (100%)	-0.52	0 100 100	63, 92, 150, 173	0
1	BT	124/124 (100%)	-0.28	0 100 100	66, 92, 154, 183	0
1	BU	117/124 (94%)	-0.23	0 100 100	67, 92, 140, 186	0
1	BV	124/124 (100%)	-0.36	0 100 100	63, 92, 150, 173	0
1	BW	124/124 (100%)	-0.54	0 100 100	66, 92, 154, 183	0
1	BX	117/124 (94%)	-0.29	1 (0%) 84 78	67, 92, 140, 186	0
1	BY	124/124 (100%)	-0.61	0 100 100	63, 92, 150, 173	0
1	BZ	124/124 (100%)	-0.38	0 100 100	66, 92, 154, 183	0
1	CA	117/124 (94%)	-0.28	1 (0%) 84 78	67, 92, 140, 186	0
1	CB	124/124 (100%)	-0.37	0 100 100	63, 92, 150, 173	0
1	CC	124/124 (100%)	-0.42	0 100 100	66, 92, 154, 183	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	CD	117/124 (94%)	-0.36	1 (0%) 84 78	67, 92, 140, 186	0
1	CE	124/124 (100%)	-0.39	1 (0%) 86 80	63, 92, 150, 173	0
1	CF	124/124 (100%)	-0.39	1 (0%) 86 80	66, 92, 154, 183	0
1	CG	117/124 (94%)	-0.28	3 (2%) 56 44	67, 92, 140, 186	0
1	CH	124/124 (100%)	-0.48	0 100 100	63, 92, 150, 173	0
1	CI	124/124 (100%)	-0.31	0 100 100	66, 92, 154, 183	0
1	CJ	117/124 (94%)	-0.27	1 (0%) 84 78	67, 92, 140, 186	0
1	CK	124/124 (100%)	-0.37	0 100 100	63, 92, 150, 173	0
1	CL	124/124 (100%)	-0.45	0 100 100	66, 92, 154, 183	0
1	CM	117/124 (94%)	-0.41	4 (3%) 45 33	67, 92, 140, 186	0
1	CN	124/124 (100%)	-0.53	0 100 100	63, 92, 150, 173	0
1	CO	124/124 (100%)	-0.50	0 100 100	66, 92, 154, 183	0
1	CP	117/124 (94%)	-0.43	1 (0%) 84 78	67, 92, 140, 186	0
1	CQ	124/124 (100%)	-0.54	0 100 100	63, 92, 150, 173	0
1	CR	124/124 (100%)	-0.37	0 100 100	66, 92, 154, 183	0
1	CS	117/124 (94%)	-0.42	1 (0%) 84 78	67, 92, 140, 186	0
1	CT	124/124 (100%)	-0.44	0 100 100	63, 92, 150, 173	0
1	CU	124/124 (100%)	-0.41	0 100 100	66, 92, 154, 183	0
1	CV	117/124 (94%)	-0.28	2 (1%) 70 60	67, 92, 140, 186	0
1	CW	124/124 (100%)	-0.54	0 100 100	63, 92, 150, 173	0
1	CX	124/124 (100%)	-0.47	0 100 100	66, 92, 154, 183	0
1	CY	117/124 (94%)	-0.38	1 (0%) 84 78	67, 92, 140, 186	0
1	CZ	124/124 (100%)	-0.36	0 100 100	63, 92, 150, 173	0
1	DA	124/124 (100%)	-0.45	0 100 100	66, 92, 154, 183	0
1	DB	117/124 (94%)	-0.32	1 (0%) 84 78	67, 92, 140, 186	0
1	DC	124/124 (100%)	-0.40	1 (0%) 86 80	63, 92, 150, 173	0
1	DD	124/124 (100%)	-0.48	0 100 100	66, 92, 154, 183	0
1	DE	117/124 (94%)	-0.38	1 (0%) 84 78	67, 92, 140, 186	0
1	DF	124/124 (100%)	-0.52	0 100 100	63, 92, 150, 173	0
1	DG	124/124 (100%)	-0.49	0 100 100	66, 92, 154, 183	0
1	DH	117/124 (94%)	-0.36	0 100 100	67, 92, 140, 186	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	DI	124/124 (100%)	-0.50	0 100 100	63, 92, 150, 173	0
1	DJ	124/124 (100%)	-0.52	0 100 100	66, 92, 154, 183	0
1	DK	117/124 (94%)	-0.42	1 (0%) 84 78	67, 92, 140, 186	0
1	DL	124/124 (100%)	-0.57	0 100 100	63, 92, 150, 173	0
1	DM	124/124 (100%)	-0.38	1 (0%) 86 80	66, 92, 154, 183	0
1	DN	117/124 (94%)	-0.25	1 (0%) 84 78	67, 92, 140, 186	0
1	DO	124/124 (100%)	-0.49	0 100 100	63, 92, 150, 173	0
1	DP	124/124 (100%)	-0.44	0 100 100	66, 92, 154, 183	0
1	DQ	117/124 (94%)	-0.52	2 (1%) 70 60	67, 92, 140, 186	0
1	DR	124/124 (100%)	-0.48	0 100 100	63, 92, 150, 173	0
1	DS	124/124 (100%)	-0.48	0 100 100	66, 92, 154, 183	0
1	DT	117/124 (94%)	-0.26	1 (0%) 84 78	67, 92, 140, 186	0
1	DU	124/124 (100%)	-0.56	0 100 100	63, 92, 150, 173	0
1	DV	124/124 (100%)	-0.32	0 100 100	66, 92, 154, 183	0
1	DW	117/124 (94%)	-0.17	0 100 100	67, 92, 140, 186	0
1	DX	124/124 (100%)	-0.34	0 100 100	63, 92, 150, 173	0
1	DY	124/124 (100%)	-0.60	0 100 100	66, 92, 154, 183	0
1	DZ	117/124 (94%)	-0.37	1 (0%) 84 78	67, 92, 140, 186	0
1	EA	124/124 (100%)	-0.46	0 100 100	63, 92, 150, 173	0
1	EB	124/124 (100%)	-0.41	0 100 100	66, 92, 154, 183	0
1	EC	117/124 (94%)	-0.38	1 (0%) 84 78	67, 92, 140, 186	0
1	ED	124/124 (100%)	-0.53	0 100 100	63, 92, 150, 173	0
1	EE	124/124 (100%)	-0.33	0 100 100	66, 92, 154, 183	0
1	EF	117/124 (94%)	-0.35	1 (0%) 84 78	67, 92, 140, 186	0
1	EG	124/124 (100%)	-0.28	0 100 100	63, 92, 150, 173	0
1	EH	124/124 (100%)	-0.41	0 100 100	66, 92, 154, 183	0
1	EI	117/124 (94%)	-0.15	1 (0%) 84 78	67, 92, 140, 186	0
1	EJ	124/124 (100%)	-0.46	0 100 100	63, 92, 150, 173	0
1	EK	124/124 (100%)	-0.38	0 100 100	66, 92, 154, 183	0
1	EL	117/124 (94%)	-0.35	1 (0%) 84 78	67, 92, 140, 186	0
1	EM	124/124 (100%)	-0.50	0 100 100	63, 92, 150, 173	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	EN	124/124 (100%)	-0.32	1 (0%) 86 80	66, 92, 154, 183	0
1	EO	117/124 (94%)	-0.34	0 100 100	67, 92, 140, 186	0
1	EP	124/124 (100%)	-0.54	0 100 100	63, 92, 150, 173	0
1	EQ	124/124 (100%)	-0.46	0 100 100	66, 92, 154, 183	0
1	ER	117/124 (94%)	-0.11	3 (2%) 56 44	67, 92, 140, 186	0
1	ES	124/124 (100%)	-0.32	0 100 100	63, 92, 150, 173	0
1	ET	124/124 (100%)	-0.38	0 100 100	66, 92, 154, 183	0
1	EU	117/124 (94%)	-0.30	1 (0%) 84 78	67, 92, 140, 186	0
1	EV	124/124 (100%)	-0.37	0 100 100	63, 92, 150, 173	0
1	EW	124/124 (100%)	-0.44	0 100 100	66, 92, 154, 183	0
1	EX	117/124 (94%)	-0.44	2 (1%) 70 60	67, 92, 140, 186	0
1	EY	124/124 (100%)	-0.48	0 100 100	63, 92, 150, 173	0
1	EZ	124/124 (100%)	-0.48	0 100 100	66, 92, 154, 183	0
1	FA	117/124 (94%)	-0.37	1 (0%) 84 78	67, 92, 140, 186	0
1	FB	124/124 (100%)	-0.47	0 100 100	63, 92, 150, 173	0
1	FC	124/124 (100%)	-0.49	1 (0%) 86 80	66, 92, 154, 183	0
1	FD	117/124 (94%)	-0.34	0 100 100	67, 92, 140, 186	0
1	FE	124/124 (100%)	-0.53	0 100 100	63, 92, 150, 173	0
1	FF	124/124 (100%)	-0.51	0 100 100	66, 92, 154, 183	0
1	FG	117/124 (94%)	-0.32	1 (0%) 84 78	67, 92, 140, 186	0
1	FH	124/124 (100%)	-0.46	0 100 100	63, 92, 150, 173	0
1	FI	124/124 (100%)	-0.51	0 100 100	66, 92, 154, 183	0
1	FJ	117/124 (94%)	-0.36	1 (0%) 84 78	67, 92, 140, 186	0
1	FK	124/124 (100%)	-0.56	0 100 100	63, 92, 150, 173	0
1	FL	124/124 (100%)	-0.50	0 100 100	66, 92, 154, 183	0
1	FM	117/124 (94%)	-0.40	0 100 100	67, 92, 140, 186	0
1	FN	124/124 (100%)	-0.51	0 100 100	63, 92, 150, 173	0
1	FO	124/124 (100%)	-0.48	0 100 100	66, 92, 154, 183	0
1	FP	117/124 (94%)	-0.39	0 100 100	67, 92, 140, 186	0
1	FQ	124/124 (100%)	-0.29	0 100 100	63, 92, 150, 173	0
1	FR	124/124 (100%)	-0.38	0 100 100	66, 92, 154, 183	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	FS	117/124 (94%)	-0.49	1 (0%) 84 78	67, 92, 140, 186	0
1	FT	124/124 (100%)	-0.52	0 100 100	63, 92, 150, 173	0
1	FU	124/124 (100%)	-0.47	1 (0%) 86 80	66, 92, 154, 183	0
1	FV	117/124 (94%)	-0.34	5 (4%) 35 25	67, 92, 140, 186	0
1	FW	124/124 (100%)	-0.50	0 100 100	63, 92, 150, 173	0
1	FX	124/124 (100%)	-0.52	0 100 100	66, 92, 154, 183	0
1	FY	117/124 (94%)	-0.45	1 (0%) 84 78	67, 92, 140, 186	0
1	FZ	124/124 (100%)	-0.55	0 100 100	63, 92, 150, 173	0
1	GA	124/124 (100%)	-0.31	0 100 100	66, 92, 154, 183	0
1	GB	117/124 (94%)	-0.29	0 100 100	67, 92, 140, 186	0
1	GC	124/124 (100%)	-0.40	0 100 100	63, 92, 150, 173	0
1	GD	124/124 (100%)	-0.39	0 100 100	66, 92, 154, 183	0
1	GE	117/124 (94%)	-0.22	1 (0%) 84 78	67, 92, 140, 186	0
1	GF	124/124 (100%)	-0.38	0 100 100	63, 92, 150, 173	0
1	GG	124/124 (100%)	-0.49	0 100 100	66, 92, 154, 183	0
1	GH	117/124 (94%)	-0.14	5 (4%) 35 25	67, 92, 140, 186	0
1	GI	124/124 (100%)	-0.51	0 100 100	63, 92, 150, 173	0
1	GJ	124/124 (100%)	-0.40	0 100 100	66, 92, 154, 183	0
1	GK	117/124 (94%)	-0.40	0 100 100	67, 92, 140, 186	0
1	GL	124/124 (100%)	-0.26	0 100 100	63, 92, 150, 173	0
1	GM	124/124 (100%)	-0.30	1 (0%) 86 80	66, 92, 154, 183	0
1	GN	117/124 (94%)	-0.29	0 100 100	67, 92, 140, 186	0
1	GO	124/124 (100%)	-0.46	0 100 100	63, 92, 150, 173	0
1	GP	124/124 (100%)	-0.52	0 100 100	66, 92, 154, 183	0
1	GQ	117/124 (94%)	-0.34	3 (2%) 56 44	67, 92, 140, 186	0
1	GR	124/124 (100%)	-0.50	0 100 100	63, 92, 150, 173	0
1	GS	124/124 (100%)	-0.41	0 100 100	66, 92, 154, 183	0
1	GT	117/124 (94%)	-0.23	1 (0%) 84 78	67, 92, 140, 186	0
1	GU	124/124 (100%)	-0.38	0 100 100	63, 92, 150, 173	0
1	GV	124/124 (100%)	-0.45	0 100 100	66, 92, 154, 183	0
1	GW	117/124 (94%)	-0.46	0 100 100	67, 92, 140, 186	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	GX	124/124 (100%)	-0.50	0 100 100	63, 92, 150, 173	0
All	All	21900/22320 (98%)	-0.41	83 (0%) 92 90	63, 92, 152, 186	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	FG	68	VAL	6.2
1	AE	68	VAL	5.3
1	GQ	68	VAL	5.3
1	GH	68	VAL	5.2
1	EF	68	VAL	5.1
1	EX	68	VAL	5.0
1	AW	68	VAL	5.0
1	CA	68	VAL	4.8
1	BF	68	VAL	4.5
1	DE	68	VAL	4.1
1	FV	68	VAL	4.1
1	BR	68	VAL	4.0
1	CY	68	VAL	3.9
1	EC	68	VAL	3.9
1	BL	68	VAL	3.7
1	DZ	68	VAL	3.6
1	DC	71	ALA	3.6
1	CV	68	VAL	3.6
1	BI	68	VAL	3.5
1	FJ	68	VAL	3.4
1	ER	68	VAL	3.4
1	GH	78	ILE	3.4
1	GH	76	MET	3.3
1	FY	68	VAL	3.2
1	FV	77	THR	3.2
1	GE	68	VAL	3.2
1	CG	68	VAL	3.1
1	CV	67	VAL	3.1
1	FS	68	VAL	3.0
1	GH	67	VAL	3.0
1	CM	68	VAL	3.0
1	GT	68	VAL	2.9
1	AK	68	VAL	2.9
1	DT	68	VAL	2.9
1	AE	67	VAL	2.8
1	AZ	68	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	AB	68	VAL	2.7
1	CD	68	VAL	2.7
1	EU	68	VAL	2.7
1	DQ	53	ASN	2.7
1	ER	77	THR	2.7
1	BN	53	ASN	2.7
1	AV	71	ALA	2.7
1	DQ	68	VAL	2.6
1	FV	78	ILE	2.6
1	CS	68	VAL	2.6
1	EI	68	VAL	2.6
1	GQ	77	THR	2.5
1	BO	68	VAL	2.5
1	DB	68	VAL	2.5
1	EN	53	ASN	2.5
1	BX	68	VAL	2.5
1	AH	68	VAL	2.4
1	ER	53	ASN	2.4
1	FV	79	LYS	2.4
1	GM	52	ALA	2.4
1	BK	71	ALA	2.4
1	CM	66	VAL	2.3
1	FA	68	VAL	2.3
1	CM	67	VAL	2.3
1	AB	53	ASN	2.3
1	CF	53	ASN	2.3
1	CG	77	THR	2.3
1	FU	53	ASN	2.3
1	GH	77	THR	2.3
1	AT	68	VAL	2.3
1	CM	76	MET	2.3
1	CG	76	MET	2.2
1	AQ	68	VAL	2.2
1	DN	68	VAL	2.2
1	CE	49	PHE	2.1
1	CJ	68	VAL	2.1
1	CP	53	ASN	2.1
1	DM	53	ASN	2.1
1	AW	67	VAL	2.1
1	EX	77	THR	2.1
1	BK	53	ASN	2.1
1	FV	76	MET	2.1

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Mol	Chain	Res	Type	RSRZ
1	GQ	78	ILE	2.0
1	AD	53	ASN	2.0
1	FC	53	ASN	2.0
1	DK	68	VAL	2.0
1	EL	68	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CA	GA	201	1/1	0.71	0.14	64,64,64,64	0
2	CA	BT	201	1/1	0.81	0.13	64,64,64,64	0
2	CA	BE	201	1/1	0.86	0.14	64,64,64,64	0
2	CA	EH	201	1/1	0.87	0.10	64,64,64,64	0
2	CA	EN	201	1/1	0.88	0.09	64,64,64,64	0
2	CA	DG	201	1/1	0.88	0.17	64,64,64,64	0
2	CA	BK	201	1/1	0.90	0.07	64,64,64,64	0
2	CA	AG	201	1/1	0.90	0.18	64,64,64,64	0
2	CA	FO	201	1/1	0.91	0.14	64,64,64,64	0
2	CA	DM	201	1/1	0.91	0.15	64,64,64,64	0
2	CA	EQ	201	1/1	0.92	0.14	64,64,64,64	0
2	CA	AV	201	1/1	0.92	0.20	64,64,64,64	0
2	CA	AD	201	1/1	0.92	0.11	64,64,64,64	0
2	CA	GM	201	1/1	0.92	0.06	64,64,64,64	0
2	CA	FX	201	1/1	0.93	0.18	64,64,64,64	0
2	CA	DJ	201	1/1	0.93	0.12	64,64,64,64	0
2	CA	GD	201	1/1	0.93	0.18	64,64,64,64	0
2	CA	EE	201	1/1	0.93	0.09	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CA	CI	201	1/1	0.94	0.15	64,64,64,64	0
2	CA	DD	201	1/1	0.94	0.16	64,64,64,64	0
2	CA	AY	201	1/1	0.94	0.12	64,64,64,64	0
2	CA	FC	201	1/1	0.94	0.18	64,64,64,64	0
2	CA	FI	201	1/1	0.94	0.10	64,64,64,64	0
2	CA	ET	201	1/1	0.95	0.12	64,64,64,64	0
2	CA	AP	201	1/1	0.95	0.09	64,64,64,64	0
2	CA	BZ	201	1/1	0.95	0.14	64,64,64,64	0
2	CA	BH	201	1/1	0.95	0.10	64,64,64,64	0
2	CA	CL	201	1/1	0.95	0.14	64,64,64,64	0
2	CA	EK	201	1/1	0.95	0.11	64,64,64,64	0
2	CA	AS	201	1/1	0.95	0.15	64,64,64,64	0
2	CA	GG	201	1/1	0.95	0.13	64,64,64,64	0
2	CA	BN	201	1/1	0.95	0.14	64,64,64,64	0
2	CA	GS	201	1/1	0.95	0.15	64,64,64,64	0
2	CA	DY	201	1/1	0.96	0.15	64,64,64,64	0
2	CA	CO	201	1/1	0.96	0.12	64,64,64,64	0
2	CA	CX	201	1/1	0.96	0.13	64,64,64,64	0
2	CA	DS	201	1/1	0.96	0.15	64,64,64,64	0
2	CA	FR	201	1/1	0.97	0.11	64,64,64,64	0
2	CA	AJ	201	1/1	0.97	0.17	64,64,64,64	0
2	CA	EW	201	1/1	0.97	0.10	64,64,64,64	0
2	CA	EZ	201	1/1	0.97	0.12	64,64,64,64	0
2	CA	BW	201	1/1	0.97	0.08	64,64,64,64	0
2	CA	GJ	201	1/1	0.97	0.11	64,64,64,64	0
2	CA	AM	201	1/1	0.97	0.07	64,64,64,64	0
2	CA	CR	201	1/1	0.97	0.20	64,64,64,64	0
2	CA	GV	201	1/1	0.97	0.13	64,64,64,64	0
2	CA	FU	201	1/1	0.98	0.14	64,64,64,64	0
2	CA	BB	201	1/1	0.98	0.12	64,64,64,64	0
2	CA	DA	201	1/1	0.98	0.20	64,64,64,64	0
2	CA	DP	201	1/1	0.98	0.14	64,64,64,64	0
2	CA	FF	201	1/1	0.98	0.21	64,64,64,64	0
2	CA	CC	201	1/1	0.98	0.11	64,64,64,64	0
2	CA	FL	201	1/1	0.98	0.18	64,64,64,64	0
2	CA	GP	201	1/1	0.98	0.14	64,64,64,64	0
2	CA	DV	201	1/1	0.98	0.11	64,64,64,64	0
2	CA	BQ	201	1/1	0.98	0.12	64,64,64,64	0
2	CA	CF	201	1/1	0.99	0.05	64,64,64,64	0
2	CA	CU	201	1/1	0.99	0.14	64,64,64,64	0
2	CA	AA	201	1/1	0.99	0.11	64,64,64,64	0
2	CA	EB	201	1/1	0.99	0.10	64,64,64,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.