



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:18 PM EDT

PDB ID : 6YF9 / pdb_00006yf9
Title : Virus-like particle of bacteriophage AVE002
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

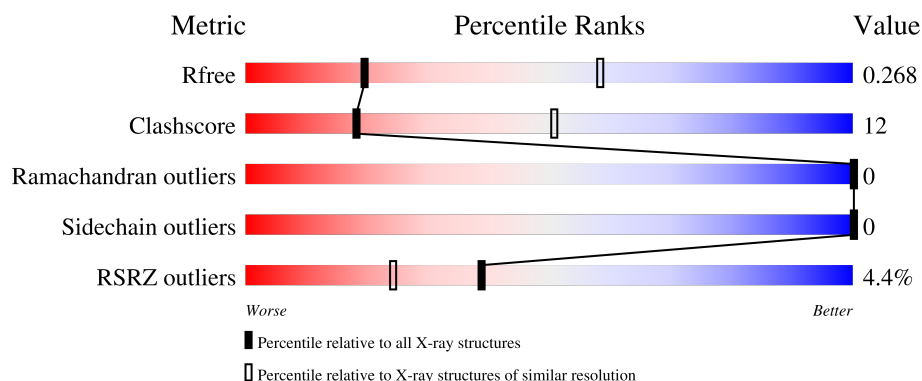
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	140	6% 75% 25%
1	AB	140	% 77% 23%
1	AC	140	% 81% 19%
1	AD	140	7% 71% 29%
1	AE	140	2% 71% 29%

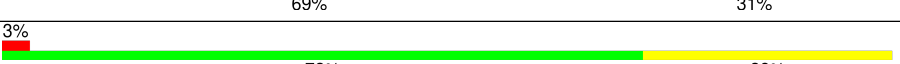
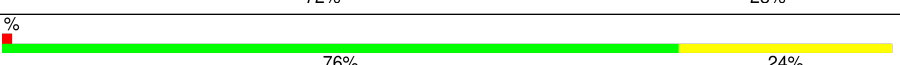
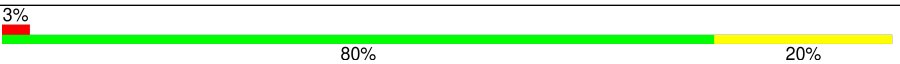
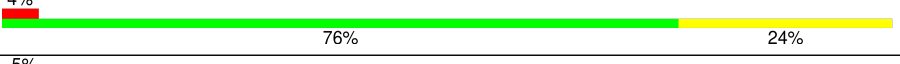
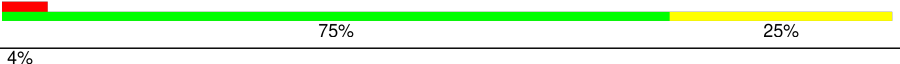
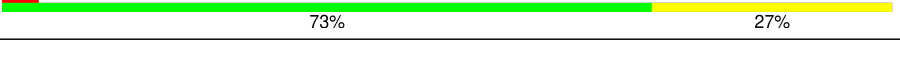
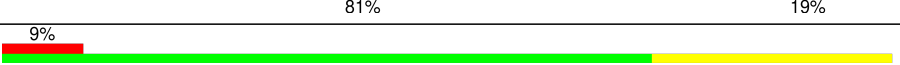
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Mol	Chain	Length	Quality of chain	
1	AF	140		
1	AG	140		
1	AH	140		
1	AI	140		
1	AJ	140		
1	AK	140		
1	AL	140		
1	AM	140		
1	AN	140		
1	AO	140		
1	AP	140		
1	AQ	140		
1	AR	140		
1	AS	140		
1	AT	140		
1	AU	140		
1	AV	140		
1	AW	140		
1	AX	140		
1	AY	140		
1	AZ	140		
1	BA	140		
1	BB	140		
1	BC	140		
1	BD	140		

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Mol	Chain	Length	Quality of chain	
1	BE	140		
1	BF	140		
1	BG	140		
1	BH	140		
1	BI	140		
1	BJ	140		
1	BK	140		
1	BL	140		
1	BM	140		
1	BN	140		
1	BO	140		
1	BP	140		
1	BQ	140		
1	BR	140		
1	BS	140		
1	BT	140		
1	BU	140		
1	BV	140		
1	BW	140		
1	BX	140		
1	BY	140		
1	BZ	140		
1	CA	140		
1	CB	140		
1	CC	140		

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Mol	Chain	Length	Quality of chain
1	CD	140	3% 74% 26%
1	CE	140	2% 77% 23%
1	CF	140	7% 71% 29%
1	CG	140	4% 71% 29%
1	CH	140	8% 74% 26%
1	CI	140	10% 71% 29%
1	CJ	140	% 73% 27%
1	CK	140	% 78% 22%
1	CL	140	9% 66% 34%
1	CM	140	4% 74% 26%
1	CN	140	7% 78% 22%
1	CO	140	7% 69% 31%
1	CP	140	3% 76% 24%
1	CQ	140	8% 72% 28%
1	CR	140	3% 71% 29%
1	CS	140	9% 69% 31%
1	CT	140	% 73% 27%
1	CU	140	11% 66% 34%
1	CV	140	% 76% 24%
1	CW	140	6% 78% 22%
1	CX	140	3% 74% 26%
1	CY	140	3% 75% 25%
1	CZ	140	4% 81% 19%
1	DA	140	8% 70% 30%
1	DB	140	% 79% 21%

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Mol	Chain	Length	Quality of chain
1	DC	140	5% 75% 25%
1	DD	140	14% 64% 36%
1	DE	140	17% 73% 27%
1	DF	140	9% 72% 28%
1	DG	140	6% 73% 27%
1	DH	140	5% 69% 31%
1	DI	140	2% 79% 21%
1	DJ	140	8% 71% 29%
1	DK	140	% 76% 24%
1	DL	140	2% 75% 25%
1	DM	140	4% 71% 29%
1	DN	140	2% 76% 24%
1	DO	140	% 80% 20%
1	DP	140	3% 72% 28%
1	DQ	140	% 75% 25%
1	DR	140	% 80% 20%
1	DS	140	4% 69% 31%
1	DT	140	7% 74% 26%
1	DU	140	2% 76% 24%
1	DV	140	3% 72% 28%
1	DW	140	% 77% 23%
1	DX	140	4% 81% 19%
1	DY	140	6% 72% 28%
1	DZ	140	% 76% 24%
1	EA	140	3% 79% 21%

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Mol	Chain	Length	Quality of chain
1	EB	140	
1	EC	140	
1	ED	140	
1	EE	140	
1	EF	140	
1	EG	140	
1	EH	140	
1	EI	140	
1	EJ	140	
1	EK	140	
1	EL	140	
1	EM	140	
1	EN	140	
1	EO	140	
1	EP	140	
1	EQ	140	
1	ER	140	
1	ES	140	
1	ET	140	
1	EU	140	
1	EV	140	
1	EW	140	
1	EX	140	
1	EY	140	
1	EZ	140	

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Mol	Chain	Length	Quality of chain	
1	FA	140	5%	73% 27%
1	FB	140	3%	74% 26%
1	FC	140	6%	72% 28%
1	FD	140	4%	73% 27%
1	FE	140	%	81% 19%
1	FF	140	4%	70% 30%
1	FG	140	2%	72% 28%
1	FH	140	4%	75% 25%
1	FI	140	4%	74% 26%
1	FJ	140	7%	69% 31%
1	FK	140	%	78% 22%
1	FL	140	5%	69% 31%
1	FM	140	4%	73% 27%
1	FN	140	8%	69% 31%
1	FO	140	6%	72% 28%
1	FP	140	3%	75% 25%
1	FQ	140	%	74% 26%
1	FR	140	5%	72% 28%
1	FS	140	%	76% 24%
1	FT	140	5%	76% 24%
1	FU	140	6%	71% 29%
1	FV	140	3%	75% 25%
1	FW	140	%	79% 21%
1	FX	140	6%	74% 26%
1	FY	140	4%	75% 25%

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Mol	Chain	Length	Quality of chain
1	FZ	140	9% 76% 24%
1	GA	140	5% 68% 32%
1	GB	140	2% 74% 26%
1	GC	140	4% 69% 31%
1	GD	140	8% 71% 29%
1	GE	140	2% 75% 25%
1	GF	140	4% 73% 27%
1	GG	140	4% 70% 30%
1	GH	140	4% 72% 28%
1	GI	140	3% 78% 22%
1	GJ	140	6% 72% 28%
1	GK	140	3% 74% 26%
1	GL	140	4% 82% 18%
1	GM	140	7% 71% 29%
1	GN	140	4% 75% 25%
1	GO	140	4% 78% 22%
1	GP	140	6% 72% 28%
1	GQ	140	% 72% 28%
1	GR	140	6% 72% 28%
1	GS	140	4% 72% 28%
1	GT	140	% 76% 24%
1	GU	140	3% 77% 23%
1	GV	140	6% 71% 29%
1	GW	140	% 76% 24%
1	GX	140	3% 76% 24%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 184320 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	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AB	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AC	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AD	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AE	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AF	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AG	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AH	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AI	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AJ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AK	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AL	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AM	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AN	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AO	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AP	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AR	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AS	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AT	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AU	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AV	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AW	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AX	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AY	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	AZ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BA	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BB	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BC	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BD	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BE	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BF	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BG	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BH	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BI	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BJ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BK	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BL	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BM	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BN	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BO	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BP	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BQ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BR	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BS	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BT	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BU	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BV	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BW	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BX	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BY	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	BZ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CA	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CB	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CC	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CD	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CE	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CF	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CG	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CH	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CI	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CJ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CK	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CL	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CM	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CN	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CO	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CP	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CQ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CR	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CS	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CT	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CU	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CV	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CW	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CX	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CY	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	CZ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DA	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DB	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DC	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DD	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DE	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DF	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DG	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DH	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DI	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DJ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DK	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DL	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DM	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DN	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DO	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DP	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DQ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DR	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DS	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DT	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DU	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DV	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DW	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DX	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DY	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	DZ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EA	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EB	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EC	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	ED	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EE	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EF	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EG	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EH	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EI	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EJ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EK	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EL	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EM	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EN	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EO	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EP	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EQ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	ER	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	ES	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	ET	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EU	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EV	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EW	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EX	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EY	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	EZ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FA	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FB	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FC	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FD	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FE	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FF	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FG	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FH	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FI	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FJ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FK	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FL	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	FM	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FN	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FO	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FP	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FQ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FR	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FS	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FT	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FU	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FV	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FW	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FX	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FY	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	FZ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GA	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GB	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GC	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GD	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GE	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GF	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GG	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			

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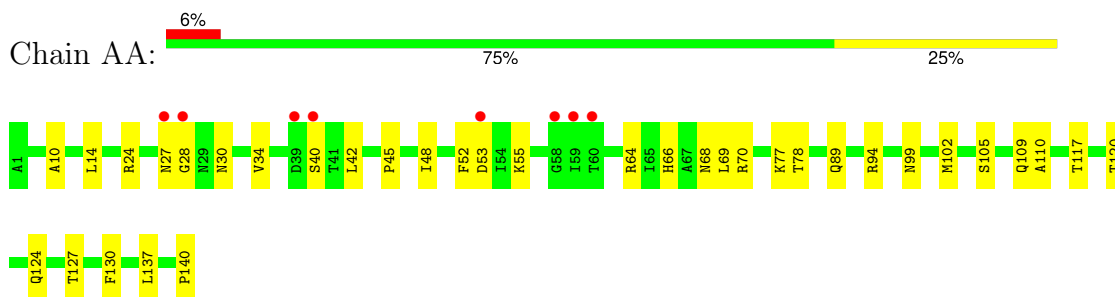
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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			1024	639	177	205	3			
1	GI	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GJ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GK	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GL	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GM	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GN	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GO	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GP	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GQ	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GR	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GS	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GT	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GU	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GV	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GW	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			
1	GX	140	Total	C	N	O	S	0	0	0
			1024	639	177	205	3			

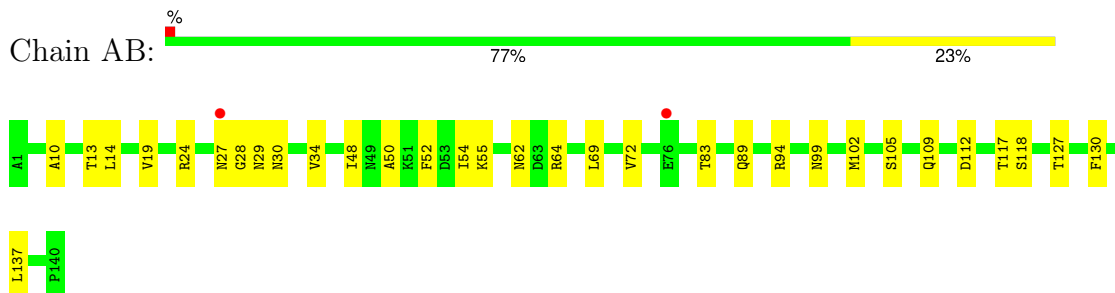
3 Residue-property plots [i](#)

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.

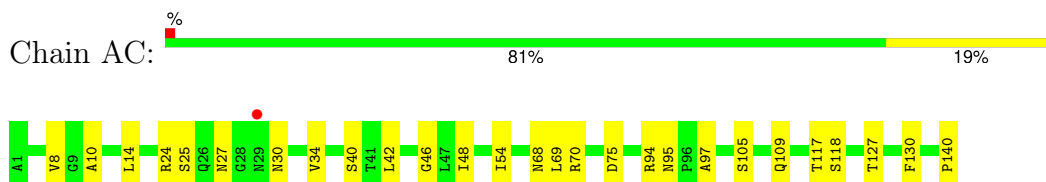
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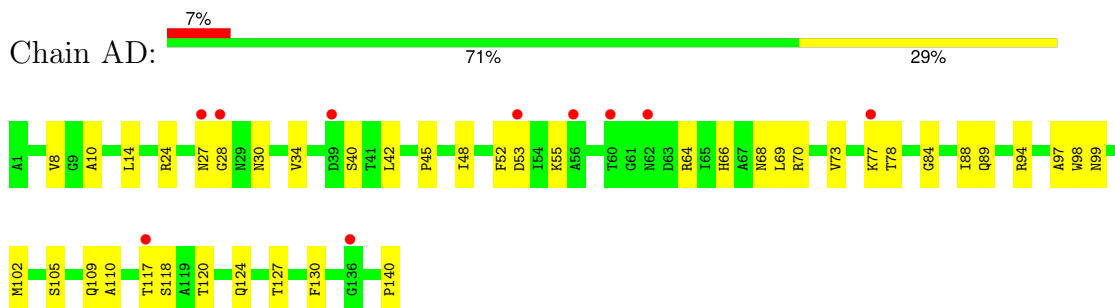
- Molecule 1: coat protein



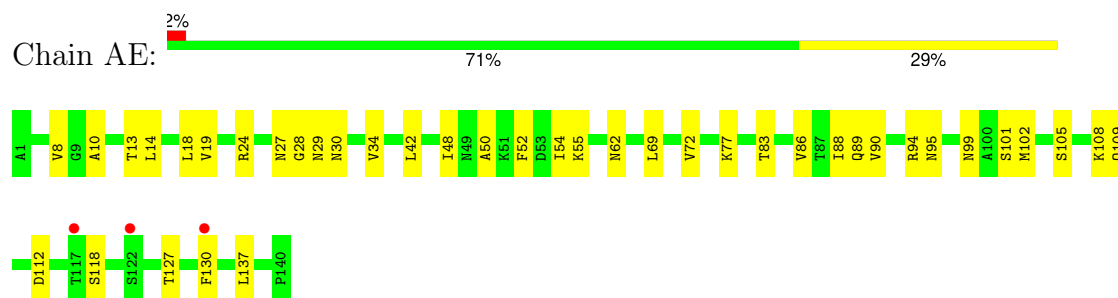
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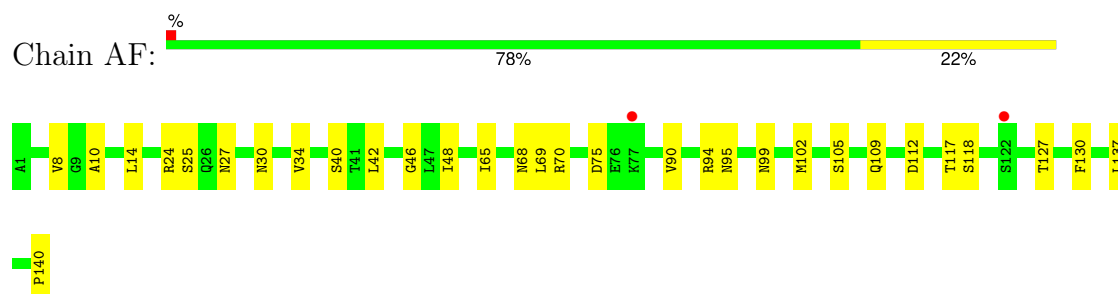
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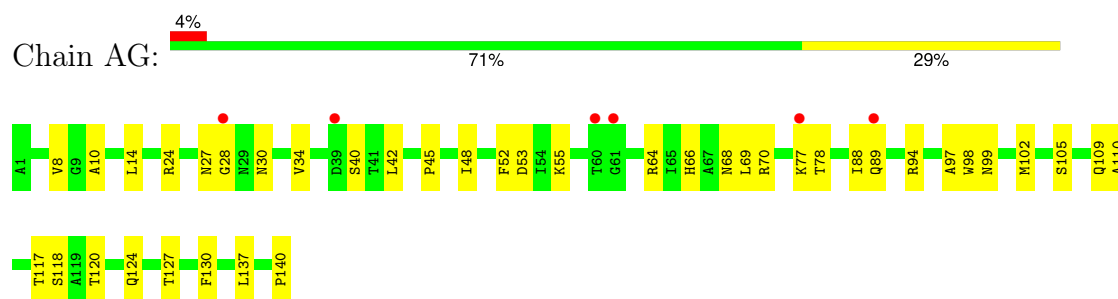
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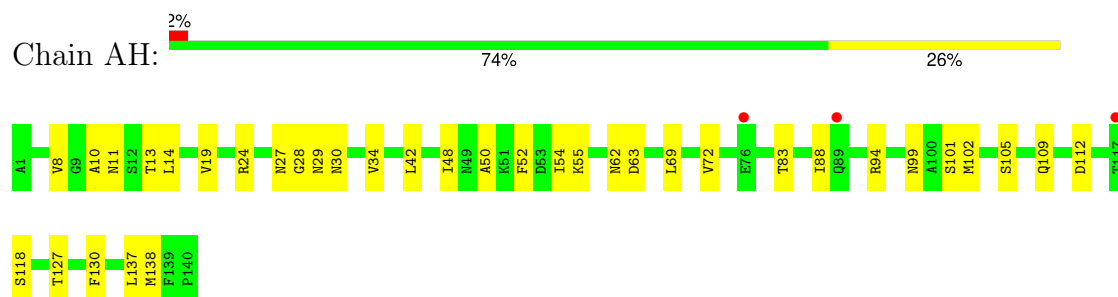
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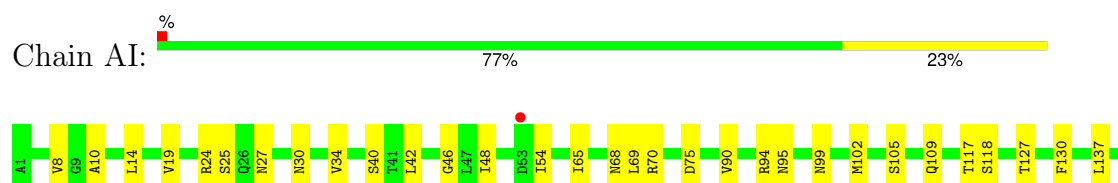
- Molecule 1: coat protein



- Molecule 1: coat protein

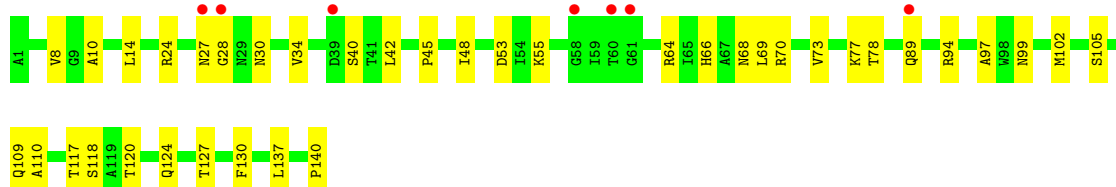
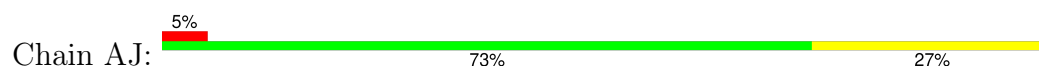


- Molecule 1: coat protein

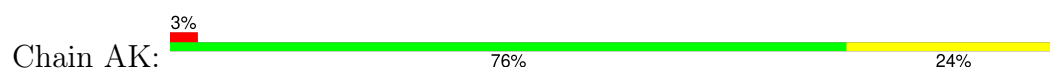


P140

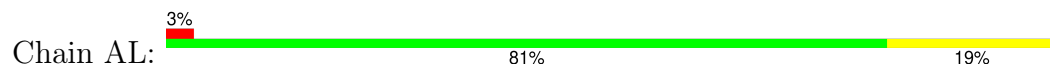
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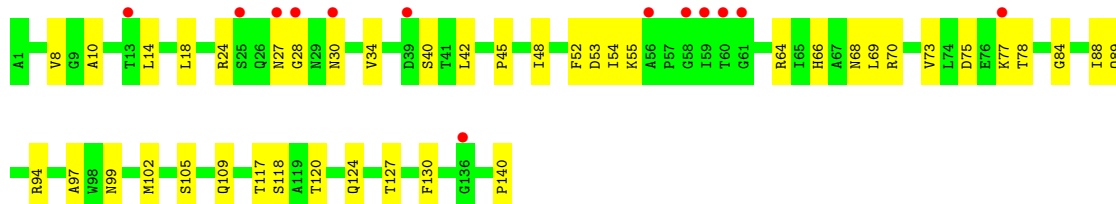
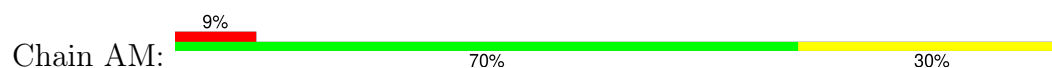
- Molecule 1: coat protein



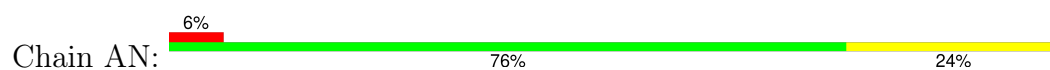
- Molecule 1: coat protein

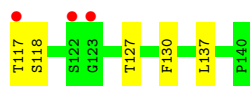


- Molecule 1: coat protein

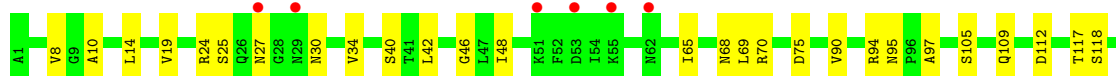
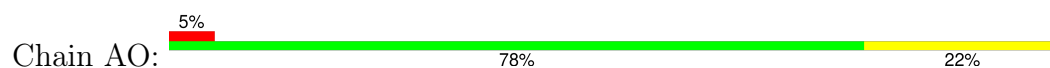


- Molecule 1: coat protein





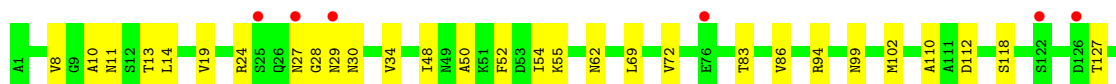
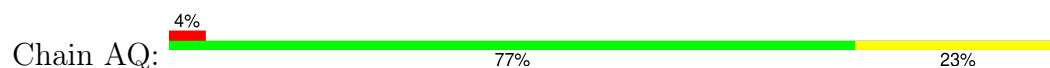
- Molecule 1: coat protein



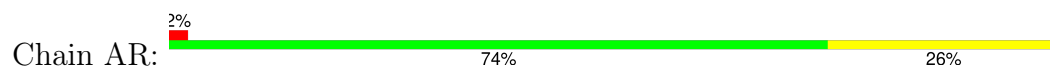
- Molecule 1: coat protein



- Molecule 1: coat protein

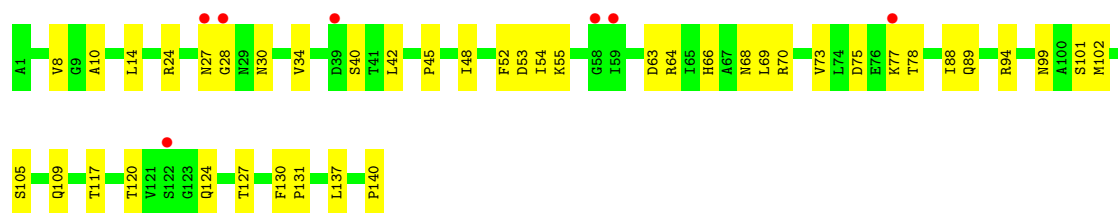


- Molecule 1: coat protein

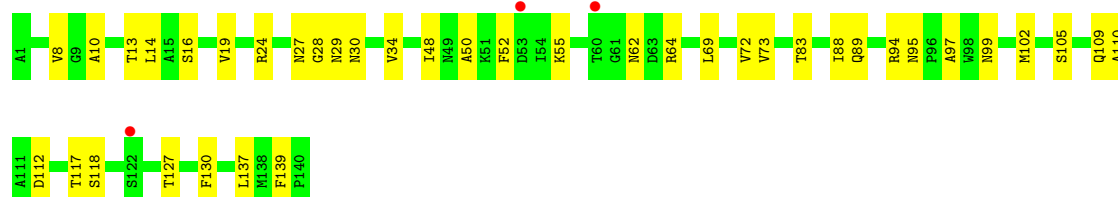
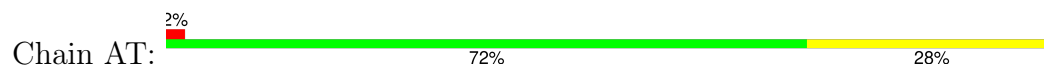


- Molecule 1: coat protein

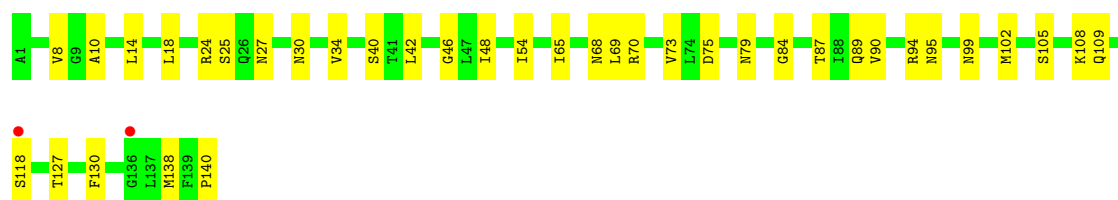
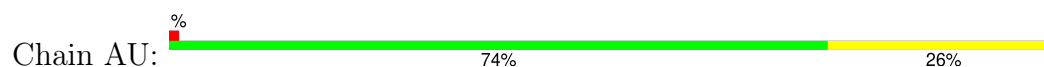




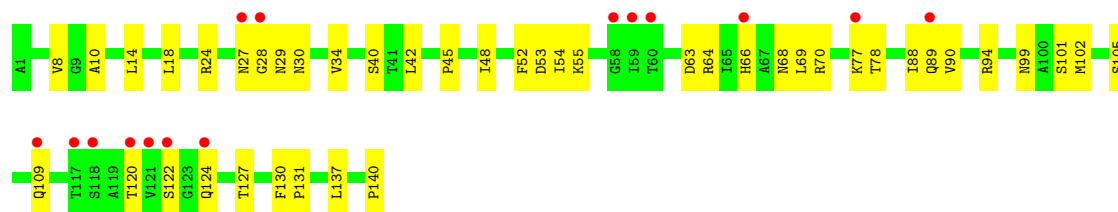
• Molecule 1: coat protein



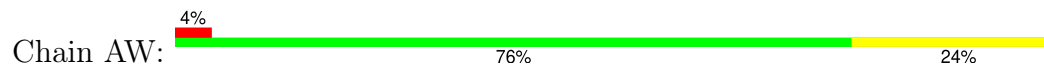
• Molecule 1: coat protein



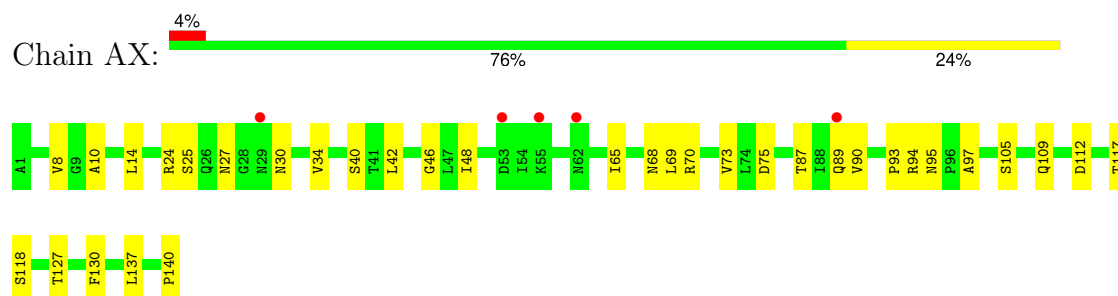
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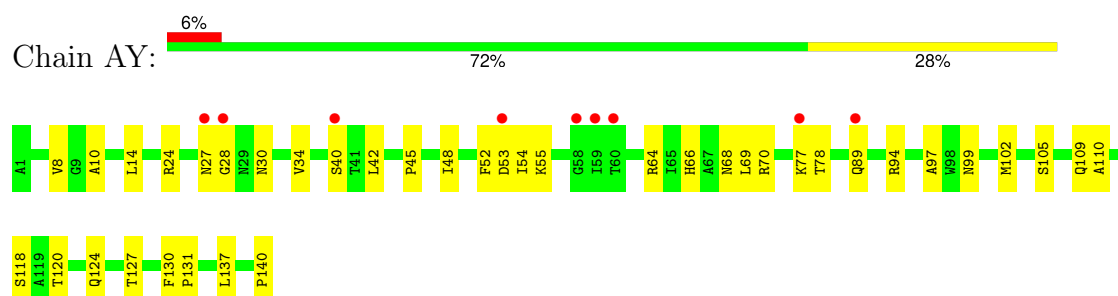
• Molecule 1: coat protein



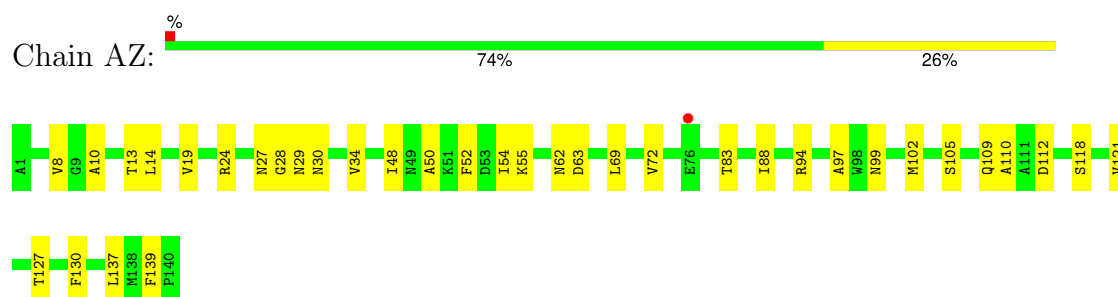
● Molecule 1: coat protein



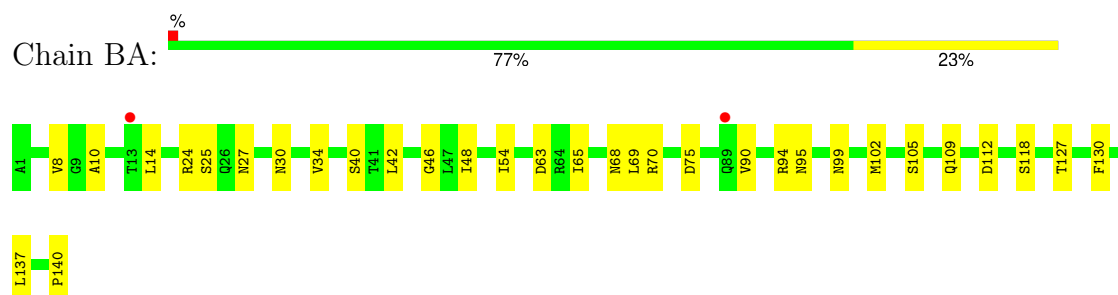
● Molecule 1: coat protein



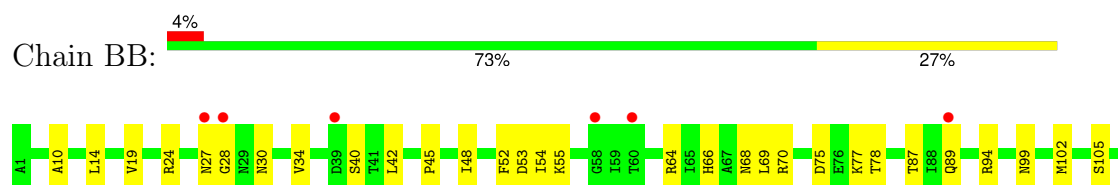
● Molecule 1: coat protein



● Molecule 1: coat protein

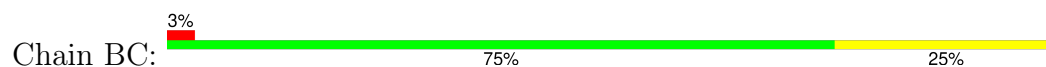


● Molecule 1: coat protein

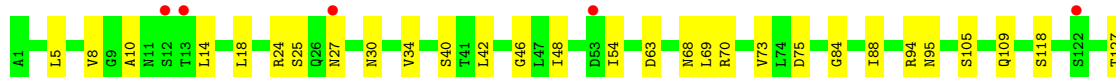
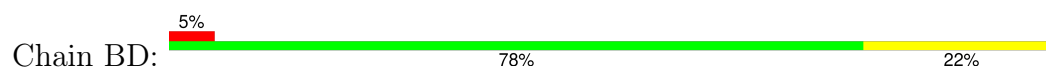




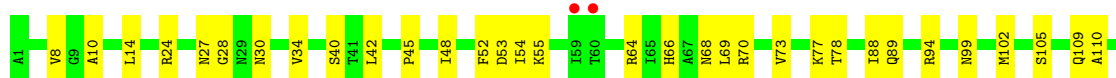
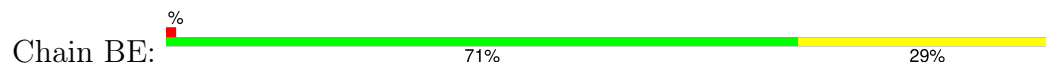
- Molecule 1: coat protein



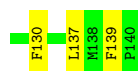
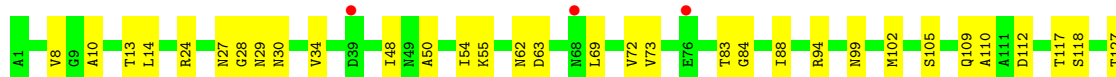
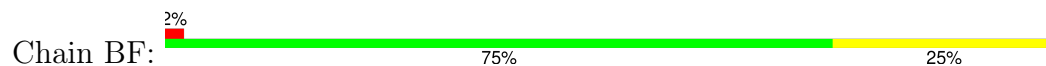
- Molecule 1: coat protein



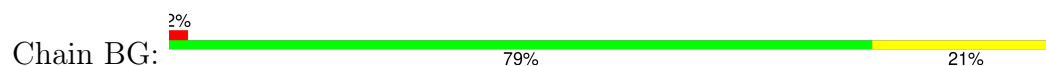
- Molecule 1: coat protein



- Molecule 1: coat protein

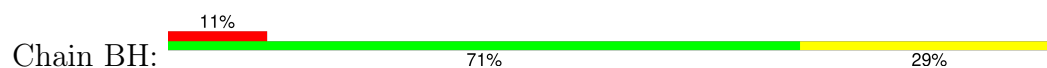


- Molecule 1: coat protein

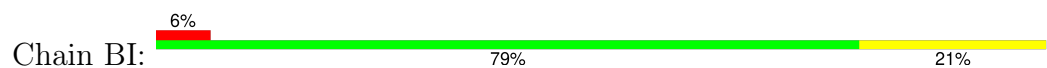




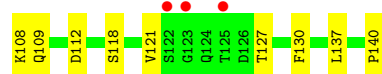
- Molecule 1: coat protein



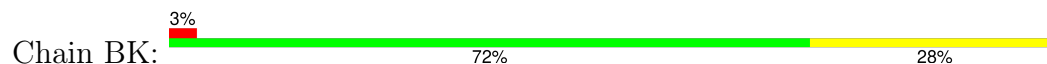
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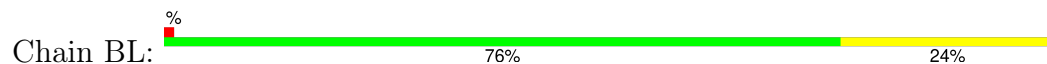
- Molecule 1: coat protein

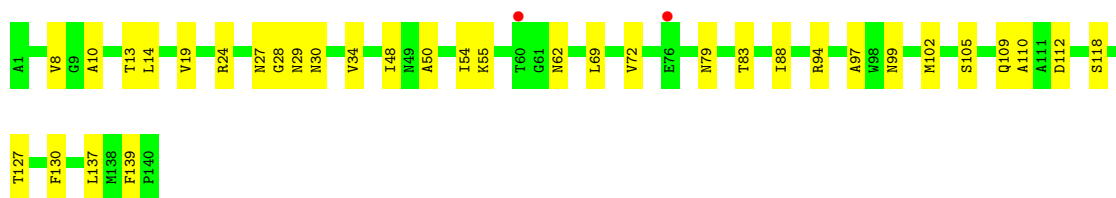


- Molecule 1: coat protein

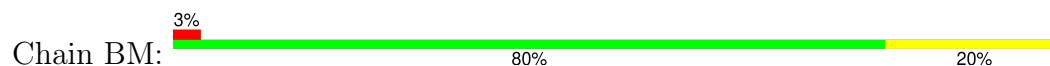


- Molecule 1: coat protein

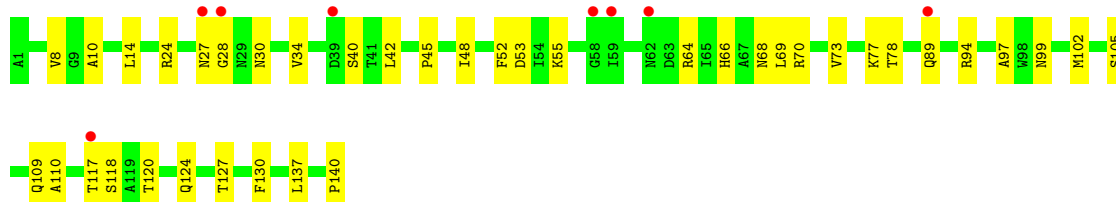
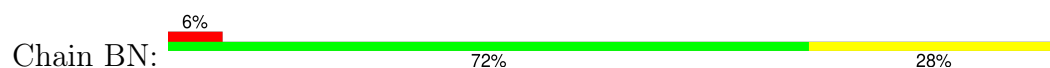




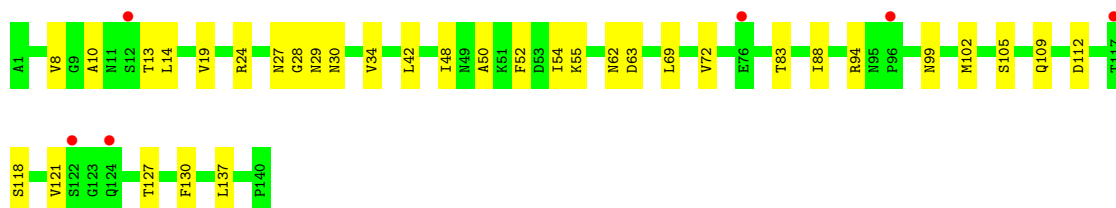
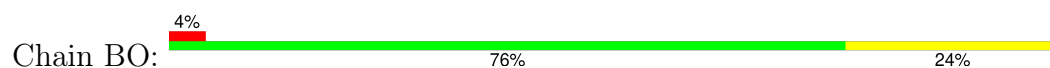
- Molecule 1: coat protein



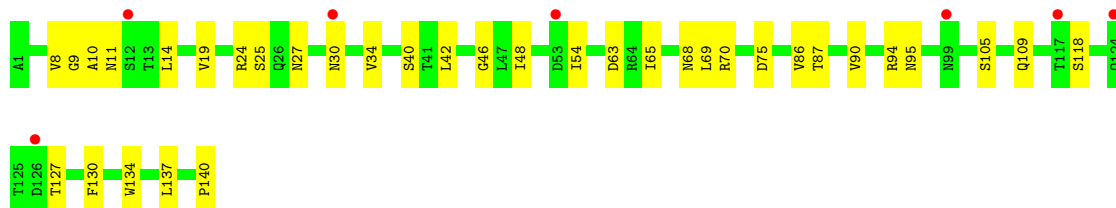
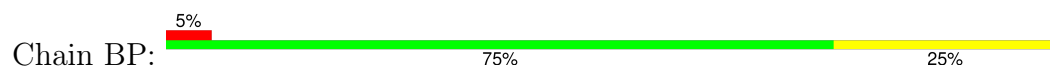
- Molecule 1: coat protein



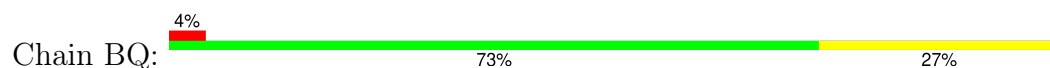
- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein





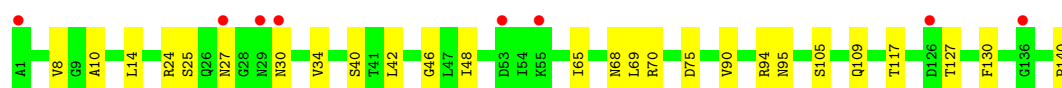
- Molecule 1: coat protein

Chain BR: 76% 24%



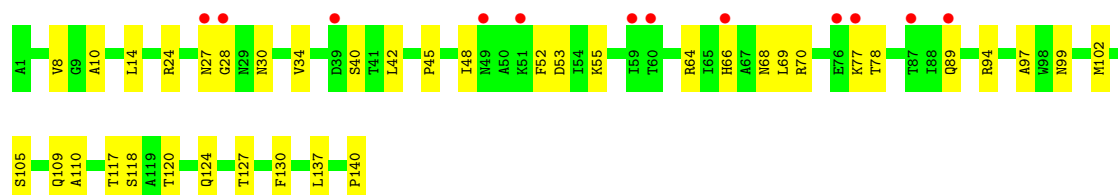
- Molecule 1: coat protein

Chain BS: 6% 81% 19%



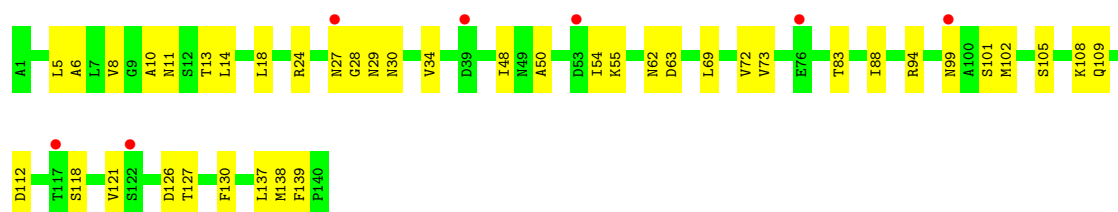
- Molecule 1: coat protein

Chain BT: 9% 73% 27%



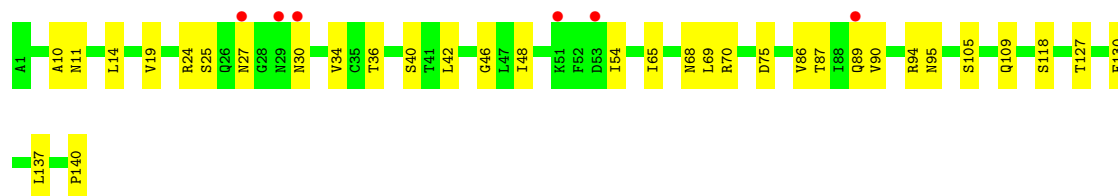
- Molecule 1: coat protein

Chain BU: 5% 71% 29%

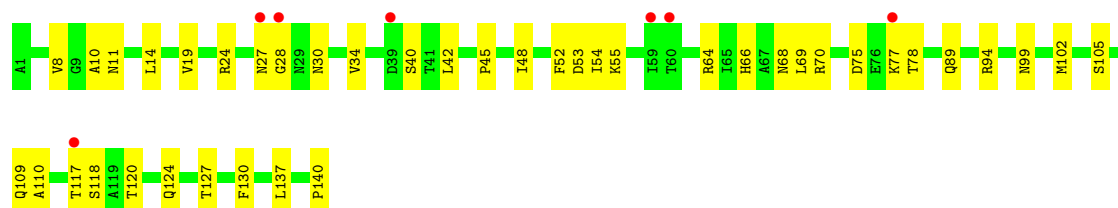
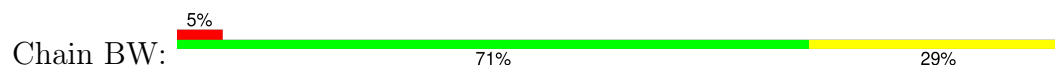


- Molecule 1: coat protein

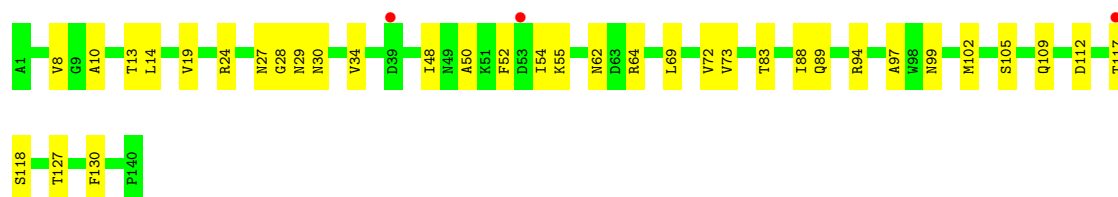
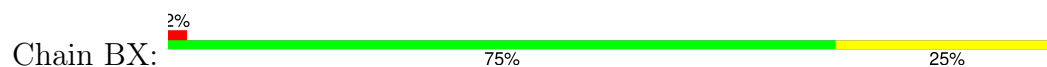
Chain BV: 4% 76% 24%



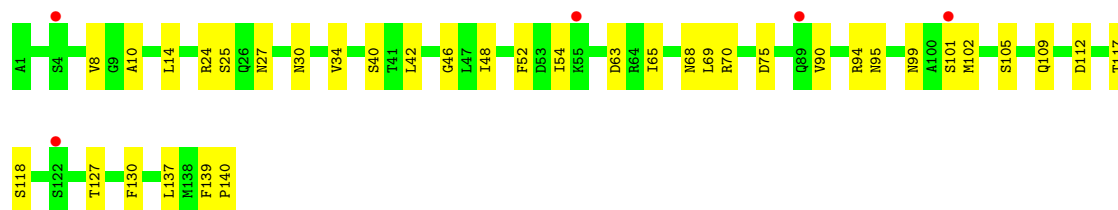
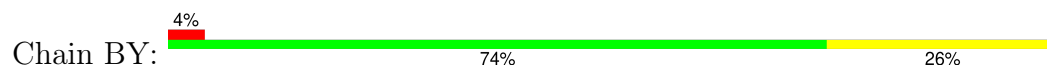
- Molecule 1: coat protein



- Molecule 1: coat protein



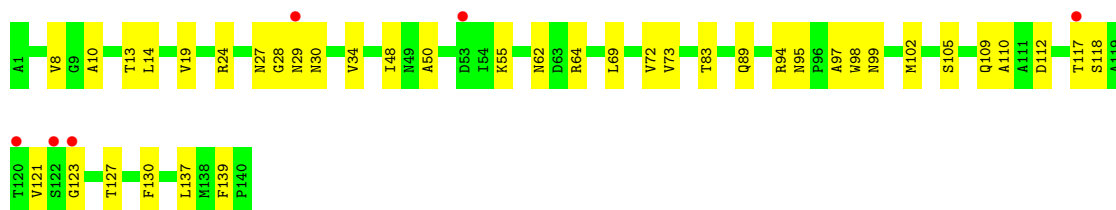
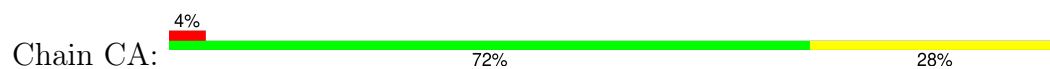
- Molecule 1: coat protein



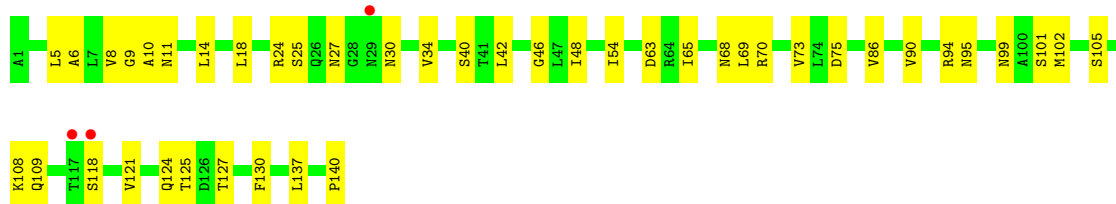
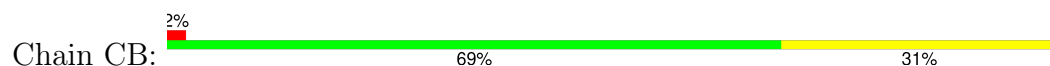
- Molecule 1: coat protein



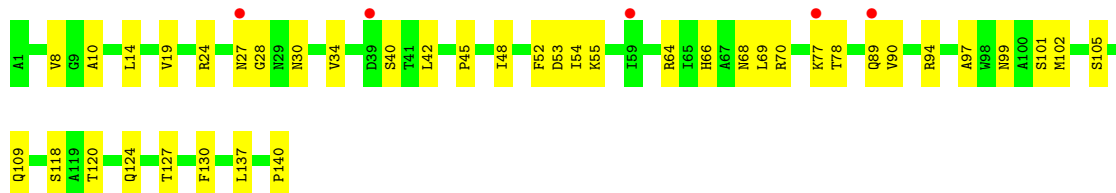
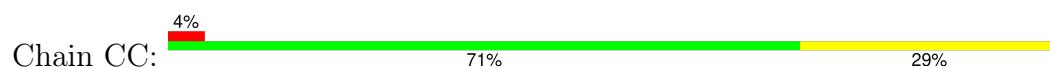
- Molecule 1: coat protein



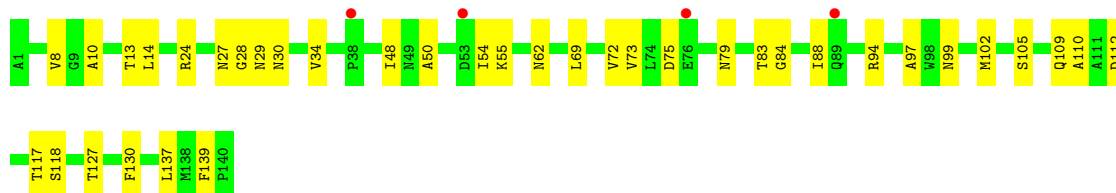
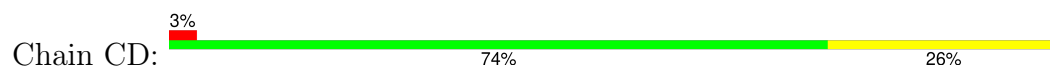
- Molecule 1: coat protein



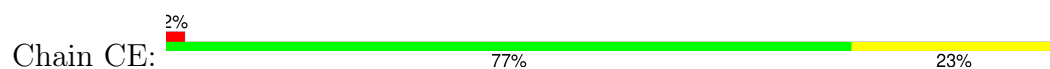
- Molecule 1: coat protein



- Molecule 1: coat protein

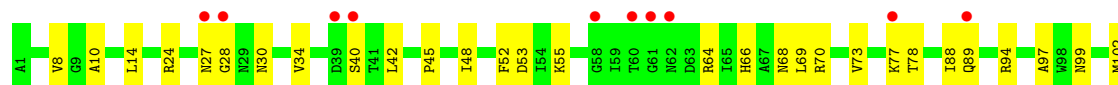
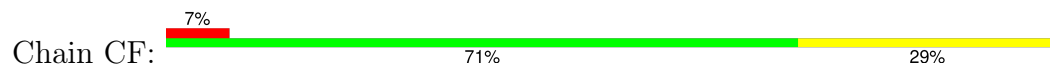


- Molecule 1: coat protein

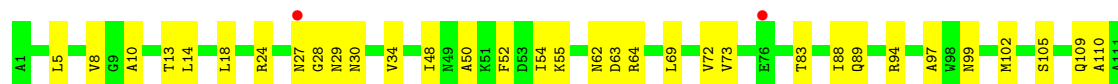
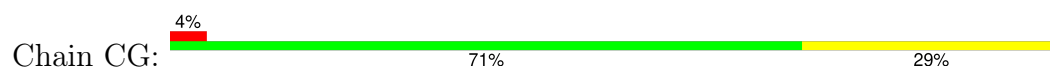




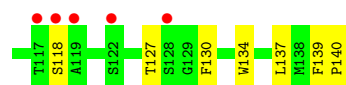
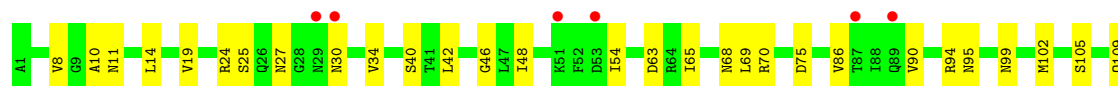
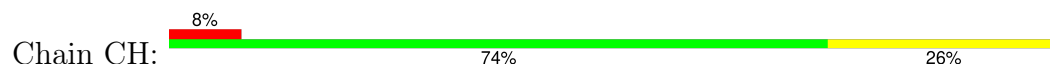
- Molecule 1: coat protein



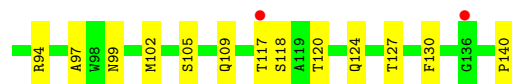
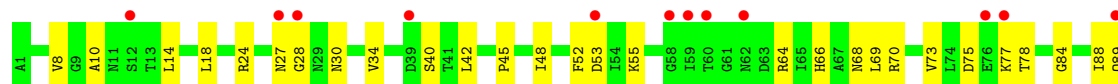
- Molecule 1: coat protein



- Molecule 1: coat protein



- Molecule 1: coat protein

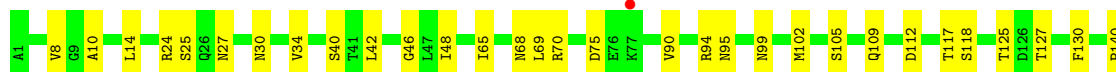
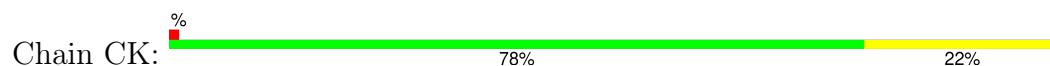


- Molecule 1: coat protein





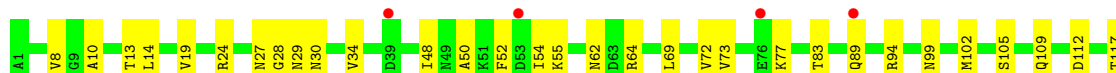
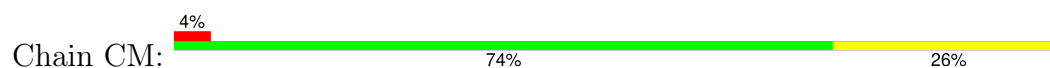
- Molecule 1: coat protein



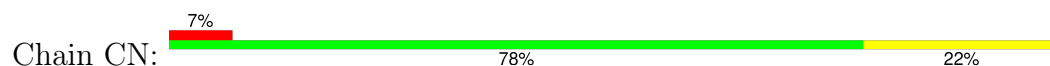
- Molecule 1: coat protein



- Molecule 1: coat protein

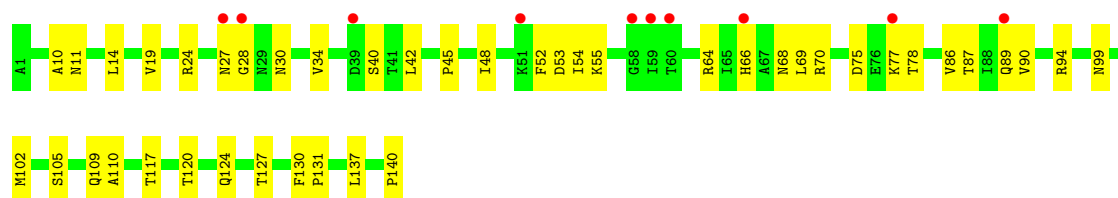


- Molecule 1: coat protein

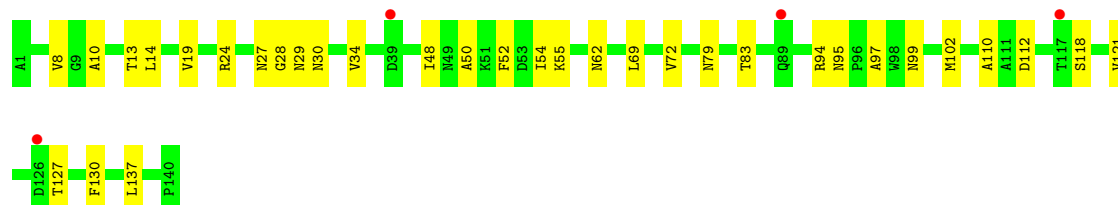
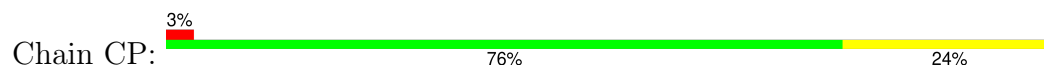


- Molecule 1: coat protein

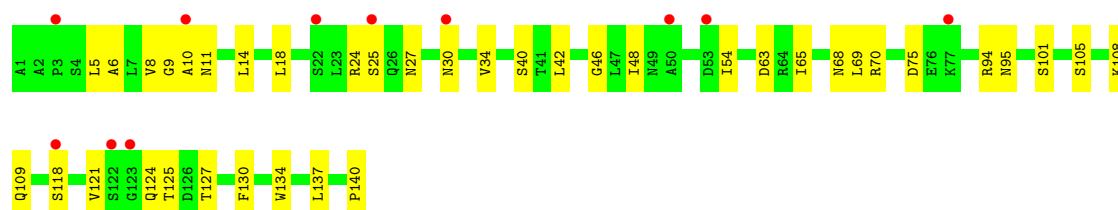
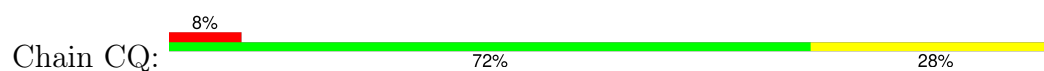




- Molecule 1: coat protein



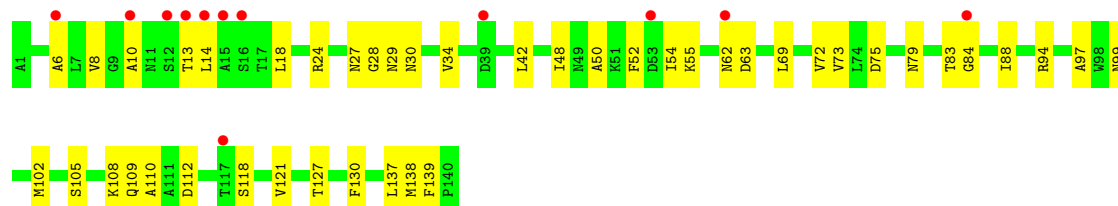
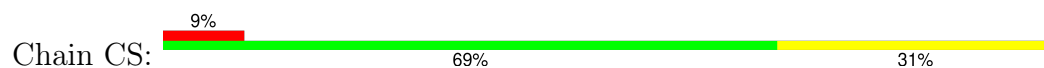
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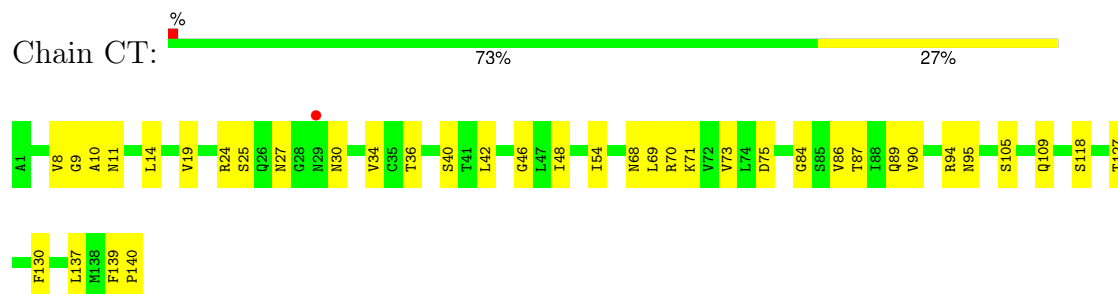
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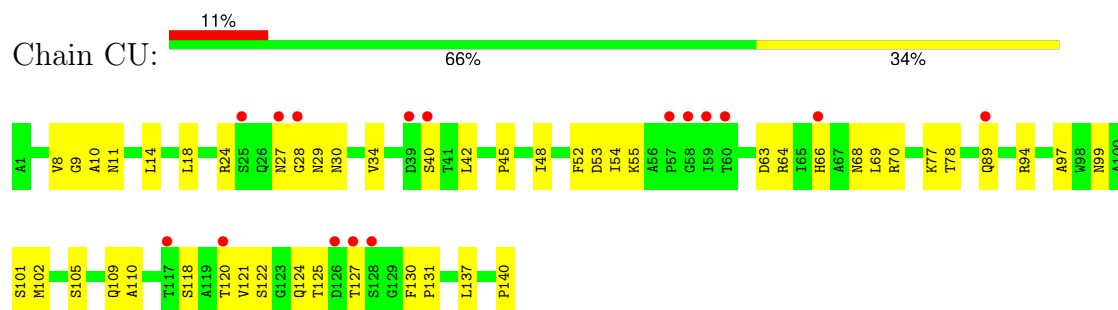
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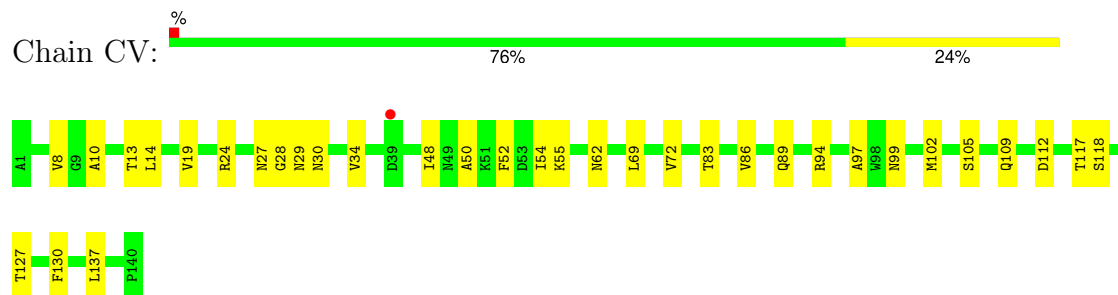
- Molecule 1: coat protein



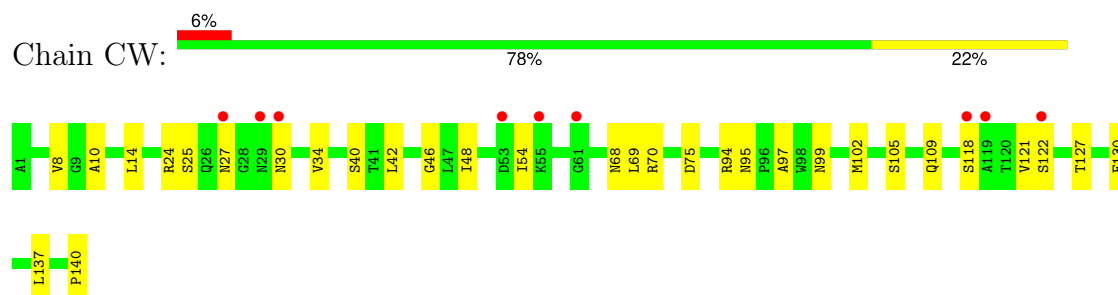
- Molecule 1: coat protein



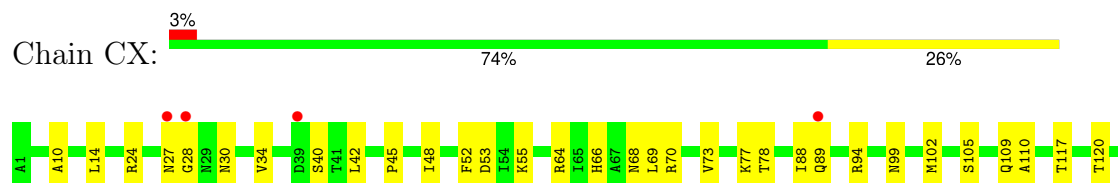
- Molecule 1: coat protein



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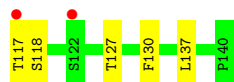
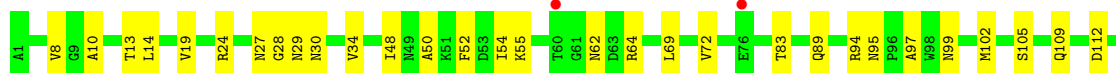
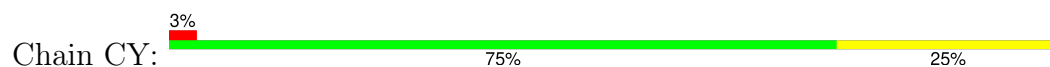


- Molecule 1: coat protein

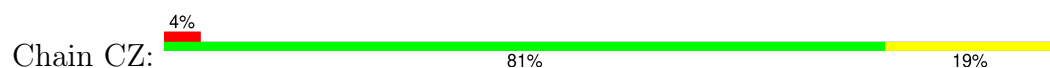




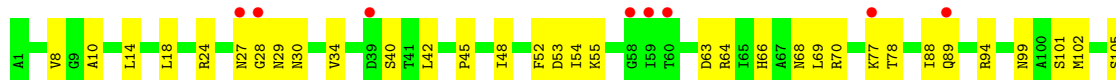
- Molecule 1: coat protein



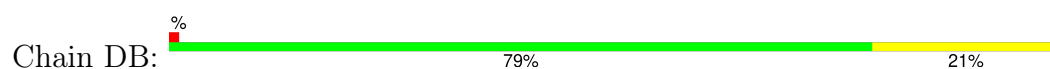
- Molecule 1: coat protein



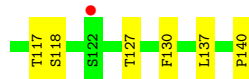
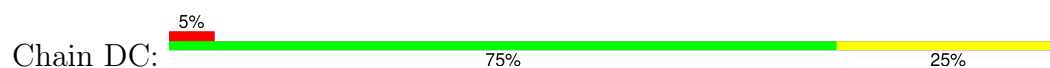
- Molecule 1: coat protein



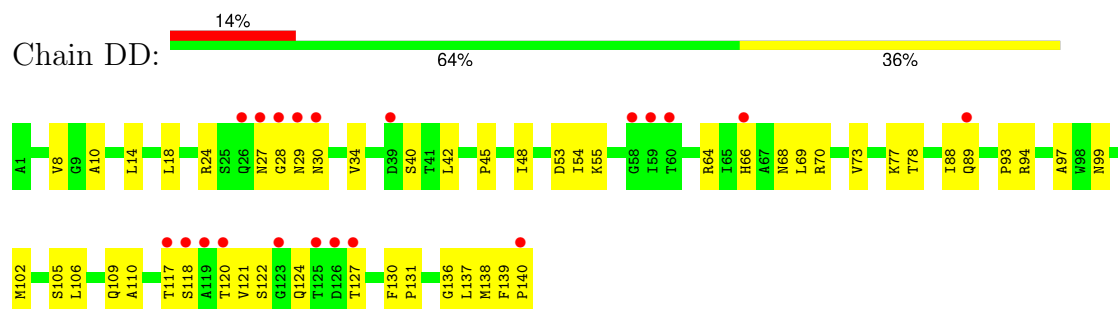
- Molecule 1: coat protein



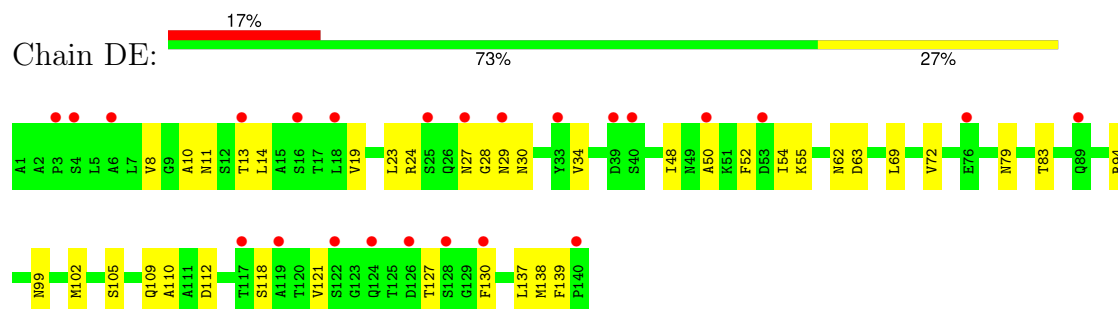
- Molecule 1: coat protein



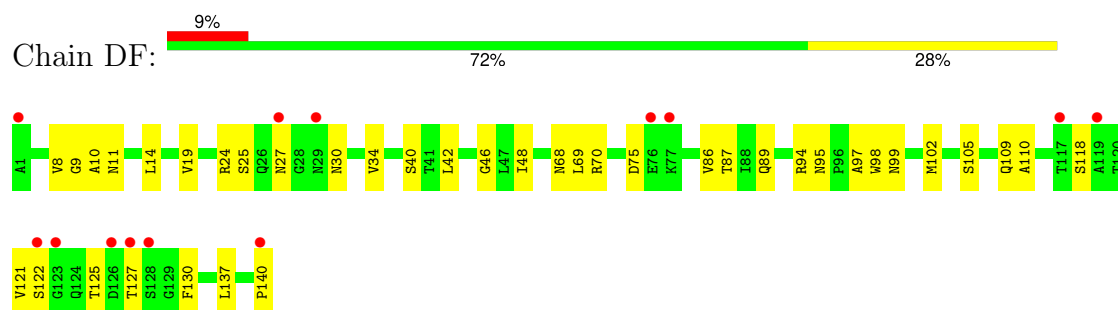
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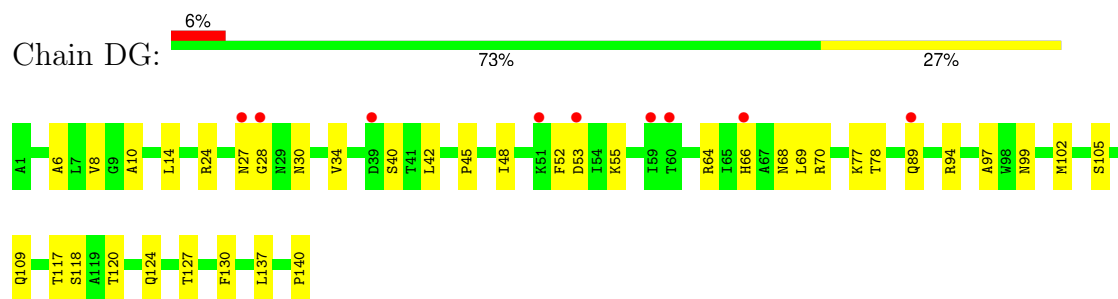
- Molecule 1: coat protein



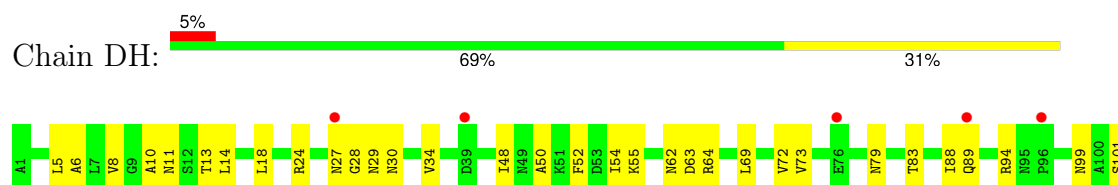
- Molecule 1: coat protein

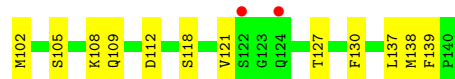


- Molecule 1: coat protein

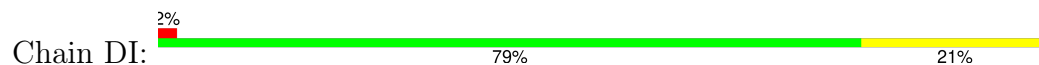


- Molecule 1: coat protein

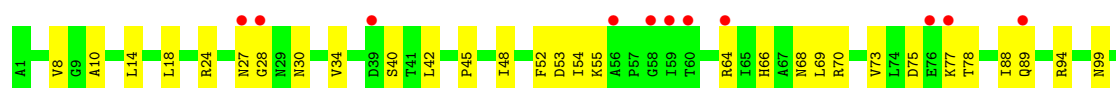
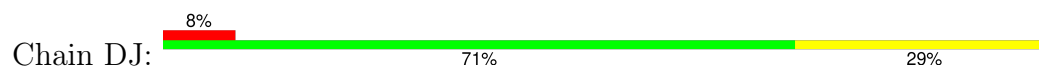




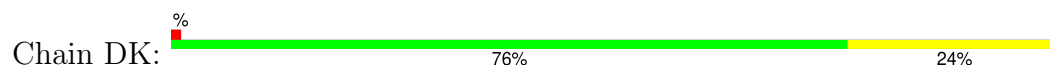
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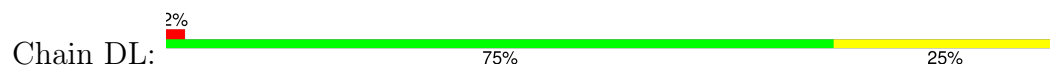
- Molecule 1: coat protein



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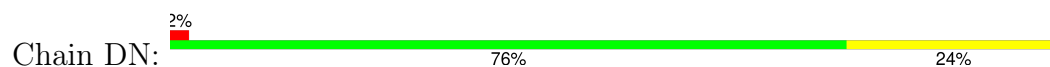


- Molecule 1: coat protein

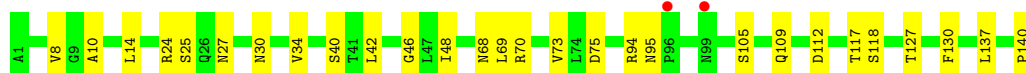
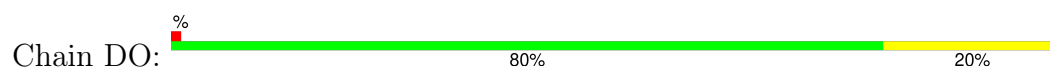




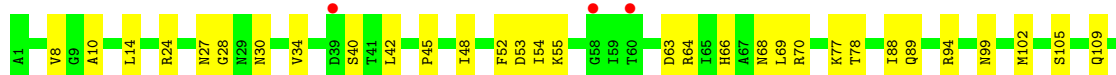
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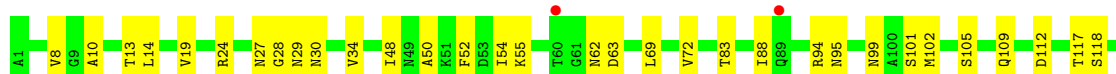
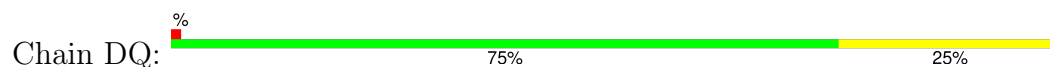
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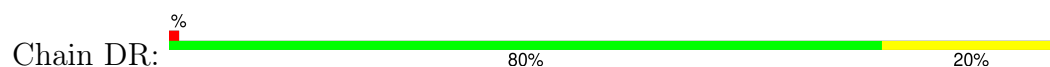
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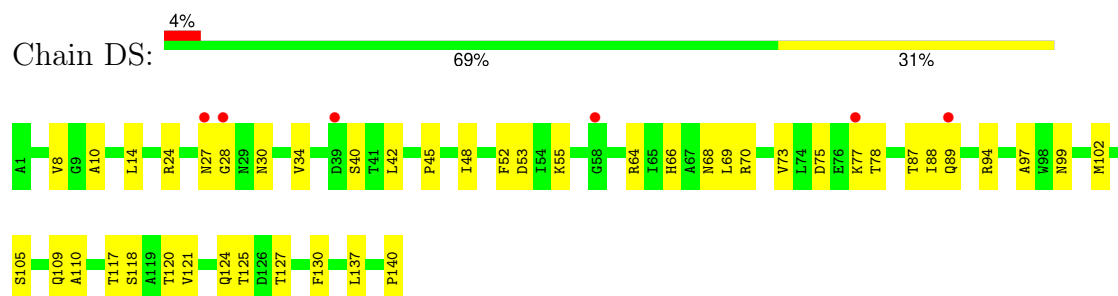
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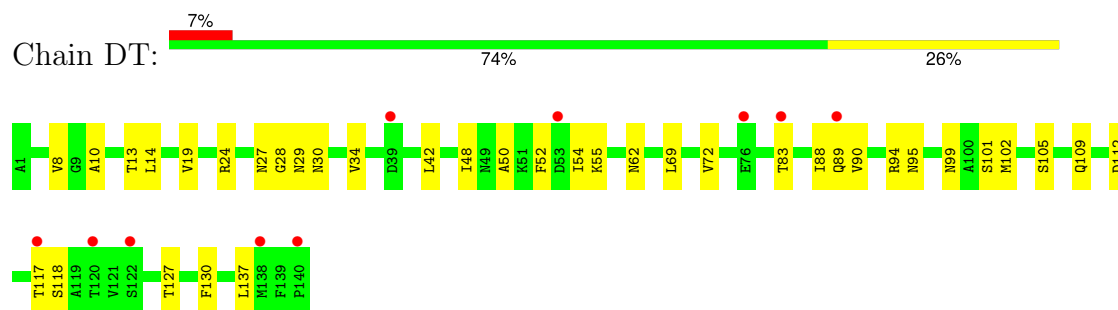
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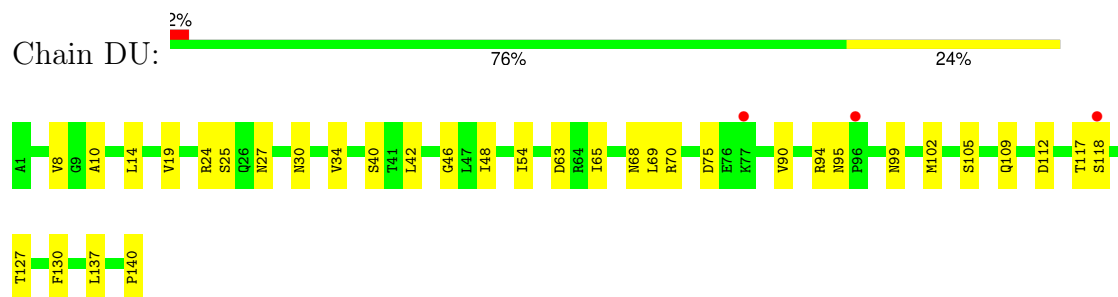
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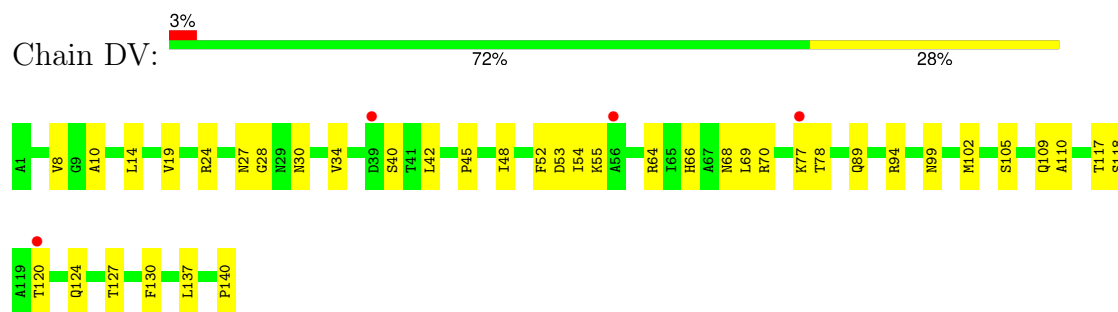
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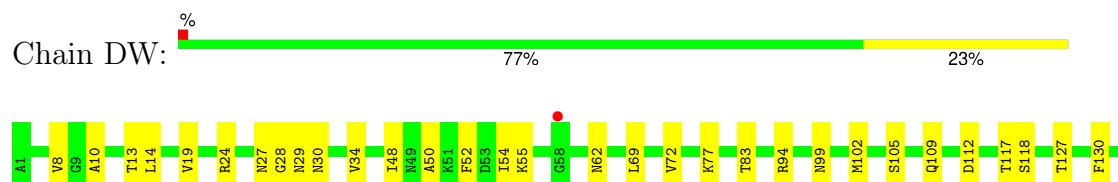
- Molecule 1: coat protein



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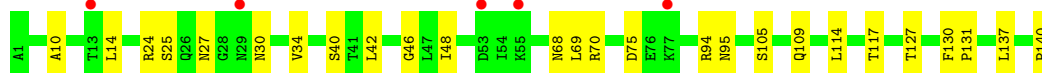
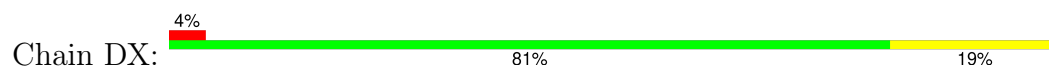


- Molecule 1: coat protein

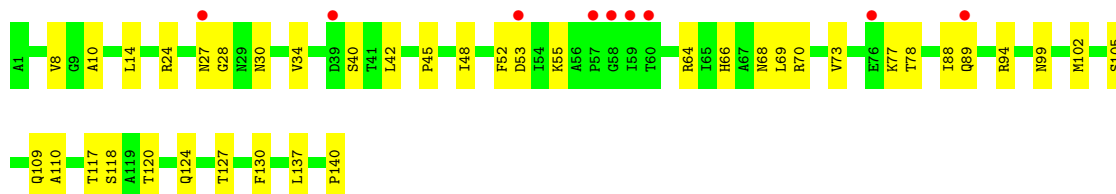
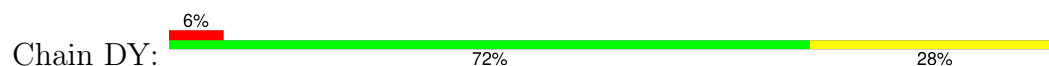




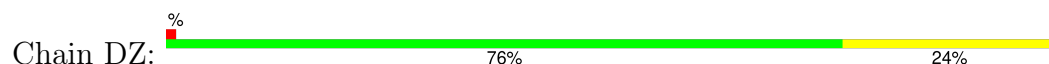
- Molecule 1: coat protein



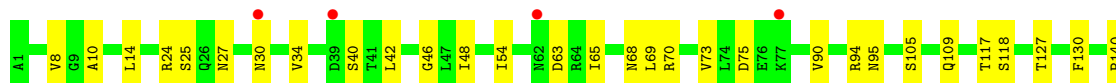
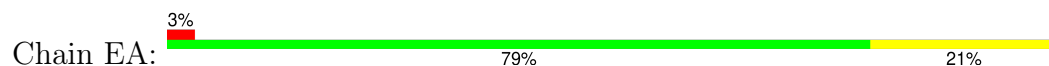
- Molecule 1: coat protein



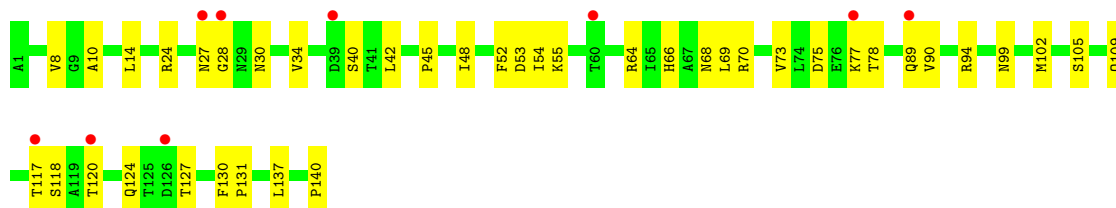
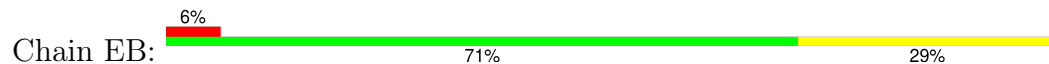
- Molecule 1: coat protein



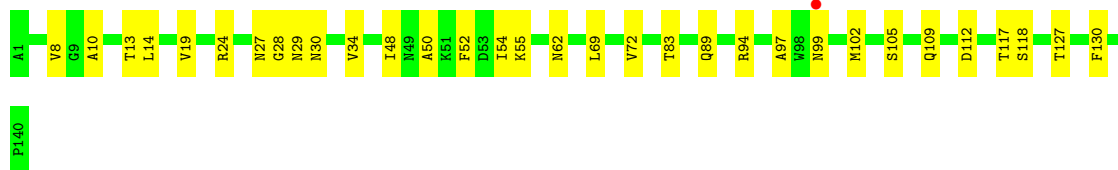
- Molecule 1: coat protein



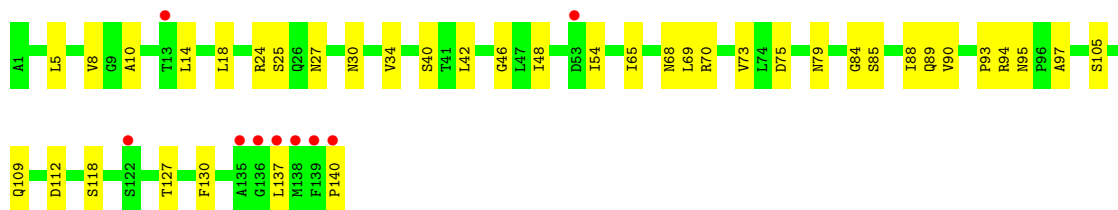
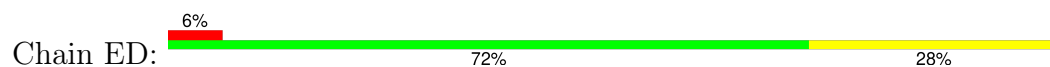
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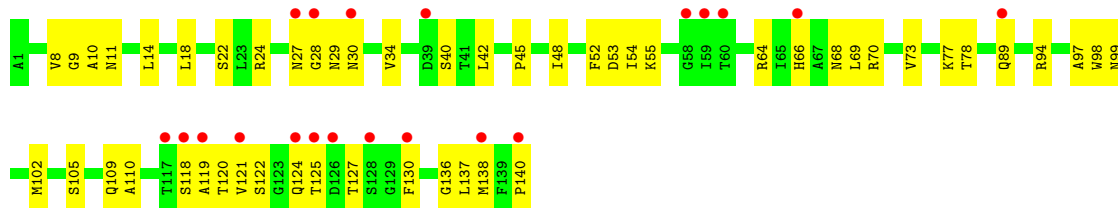
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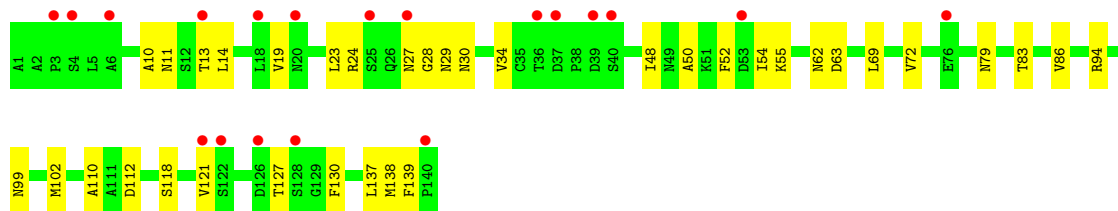
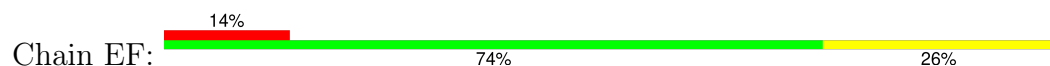
- Molecule 1: coat protein



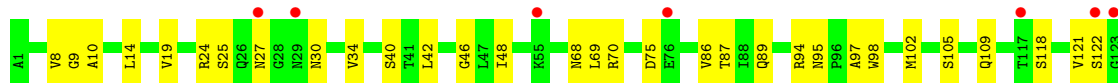
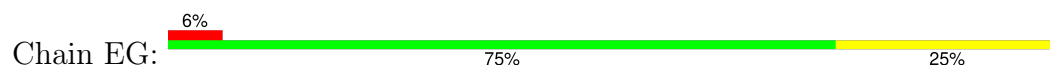
- Molecule 1: coat protein



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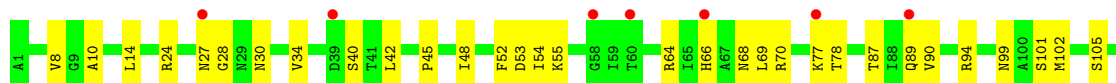
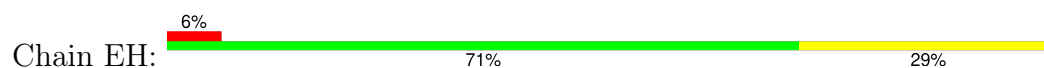


- Molecule 1: coat protein

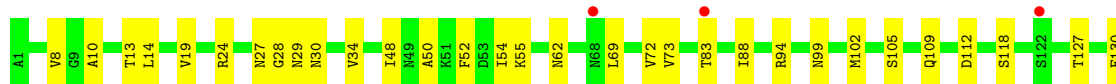
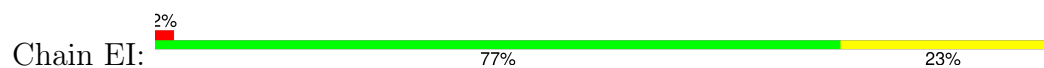




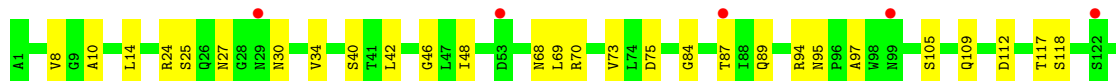
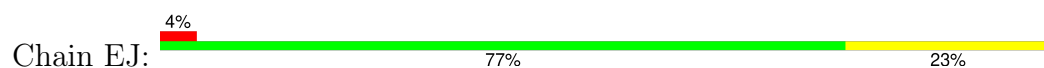
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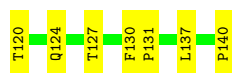
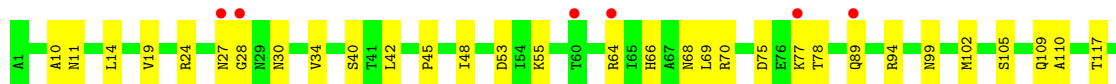
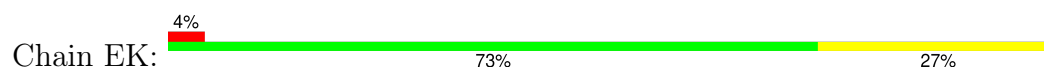
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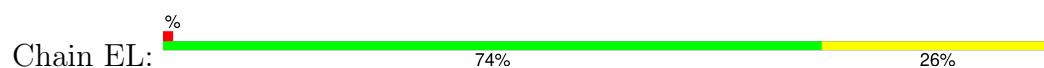
- Molecule 1: coat protein



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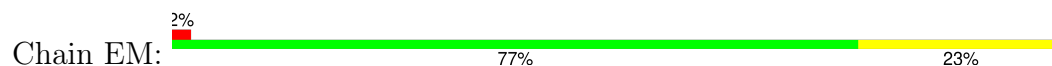


- Molecule 1: coat protein

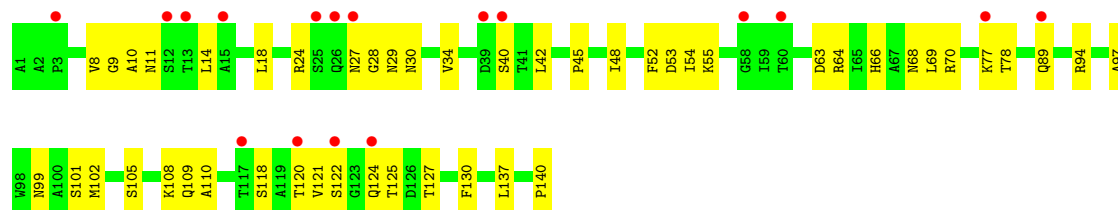




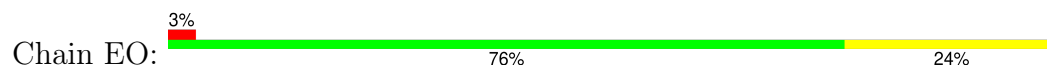
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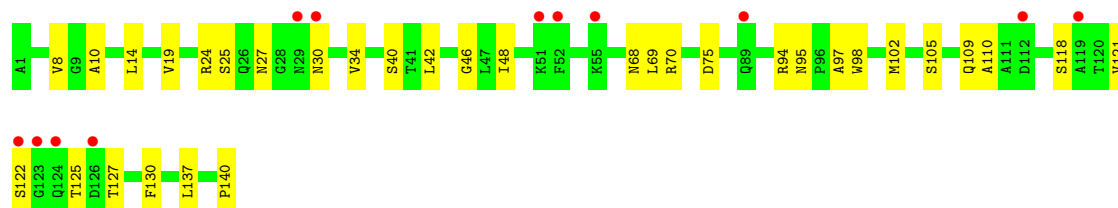
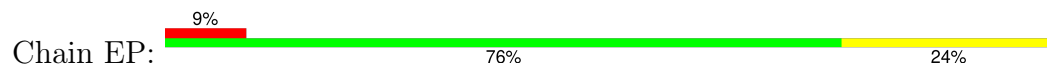
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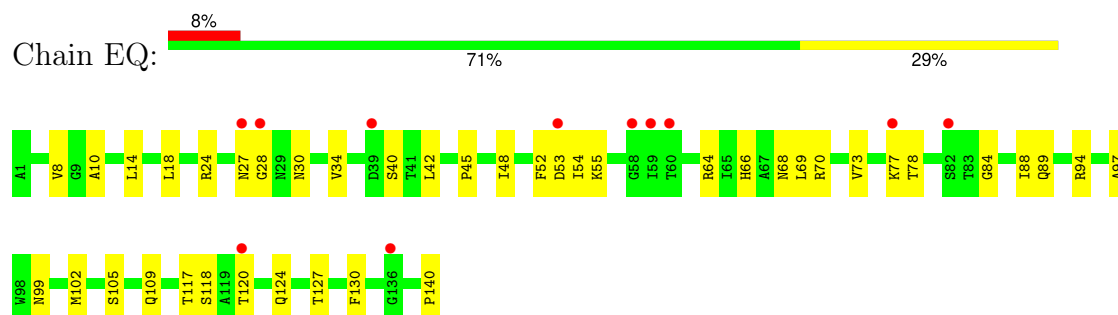
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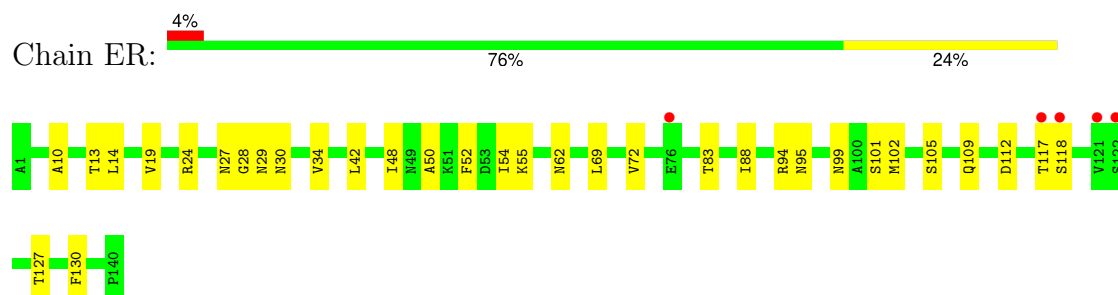
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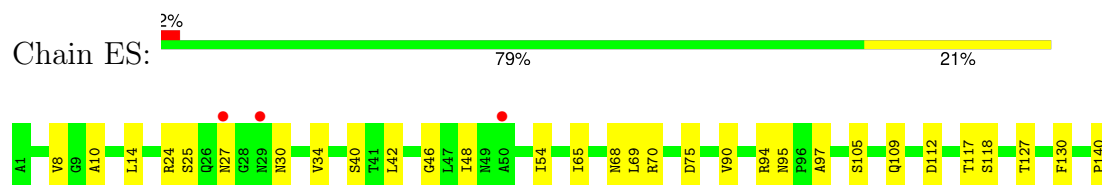
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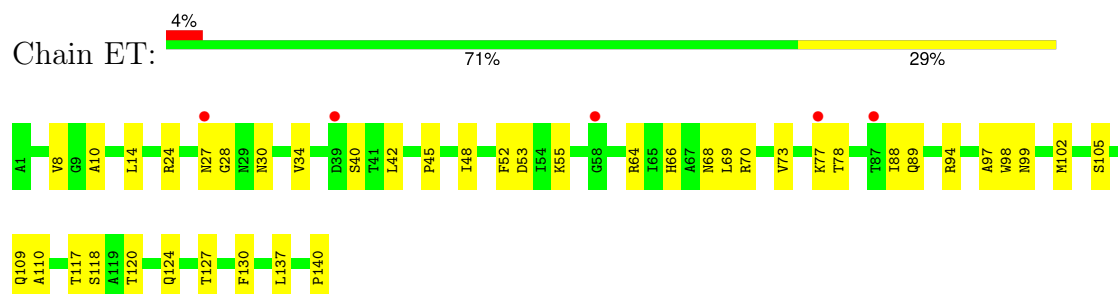
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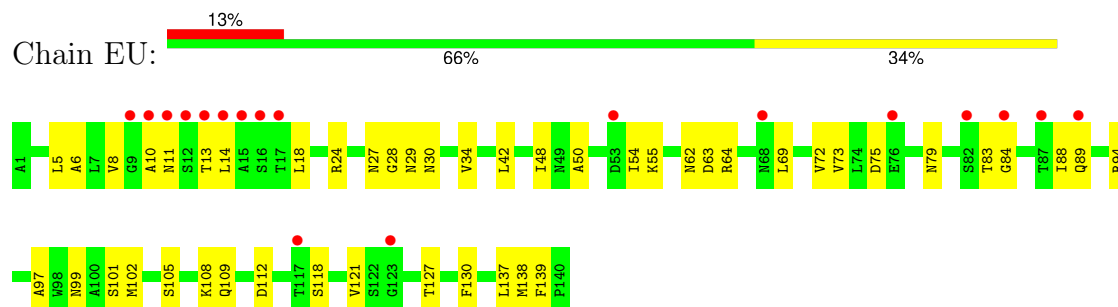
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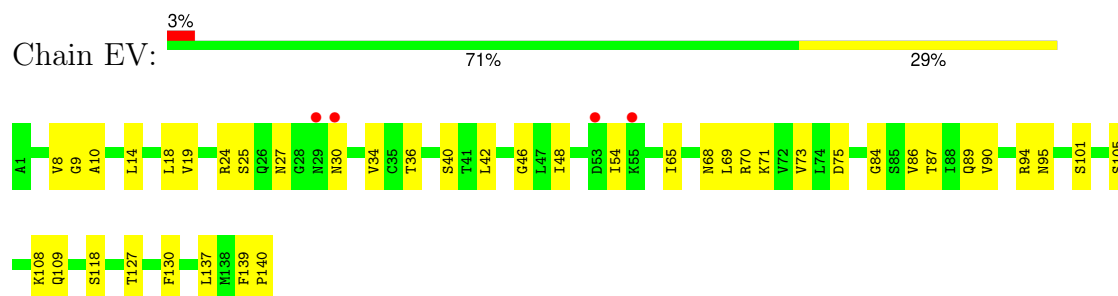
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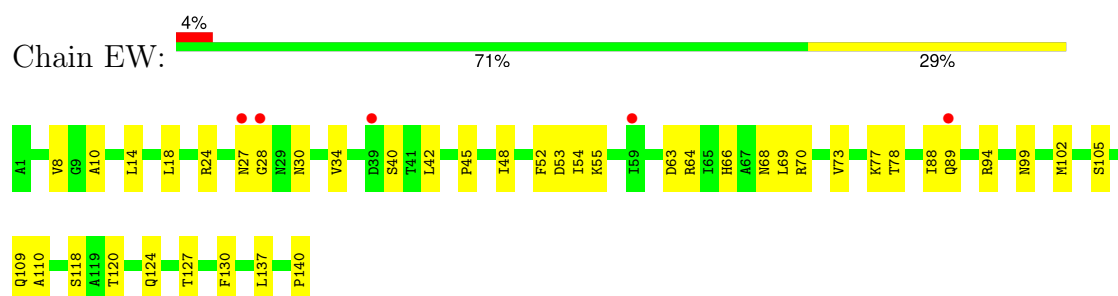
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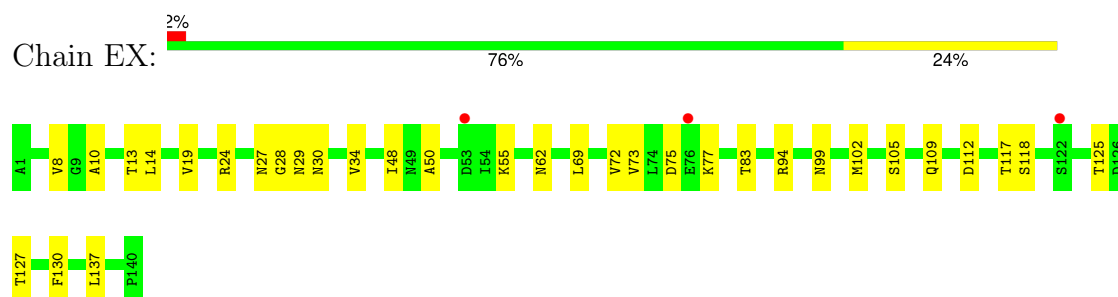
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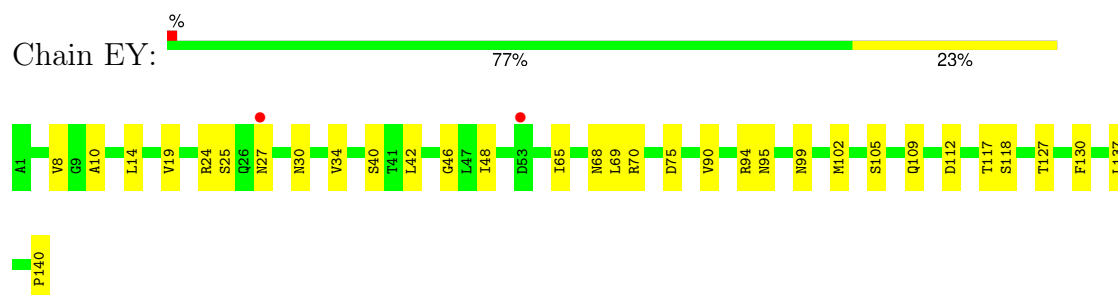
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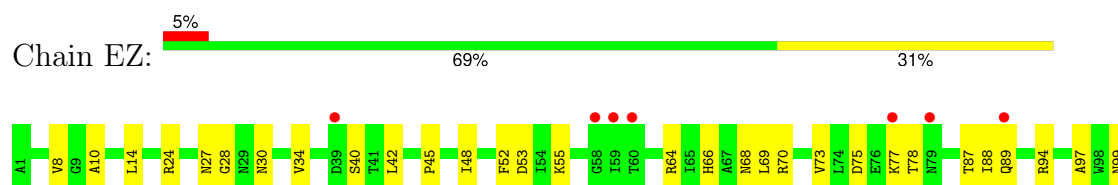
- Molecule 1: coat protein



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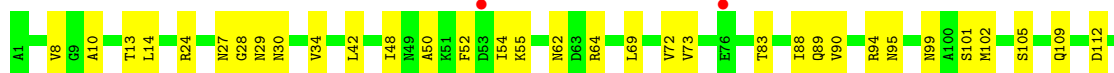
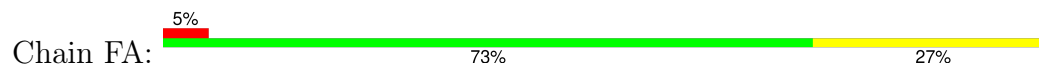


- Molecule 1: coat protein

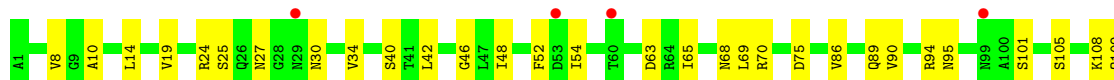
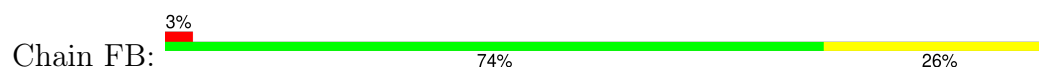




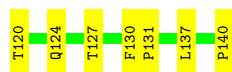
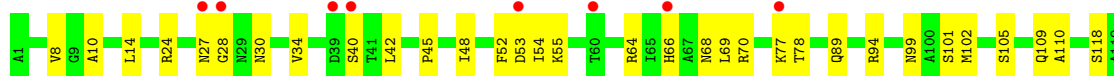
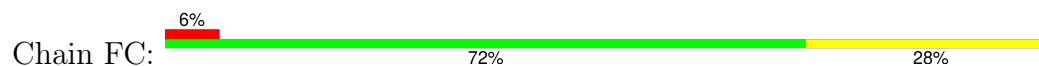
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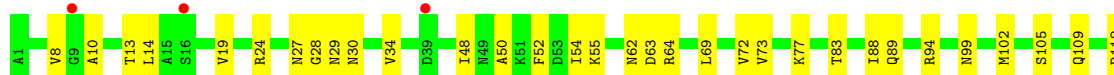
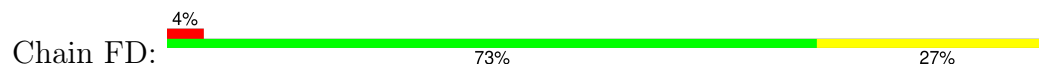
- Molecule 1: coat protein



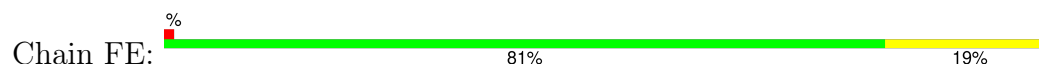
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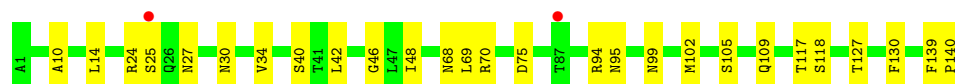


- Molecule 1: coat protein

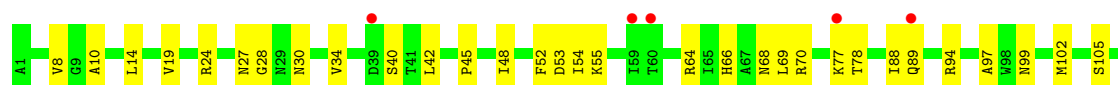


- Molecule 1: coat protein

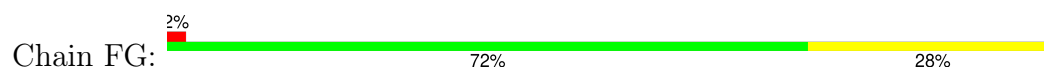




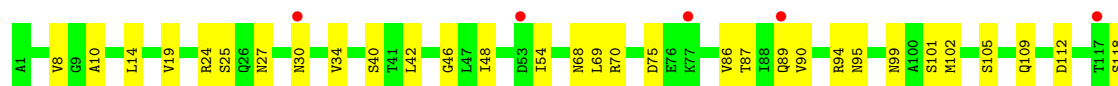
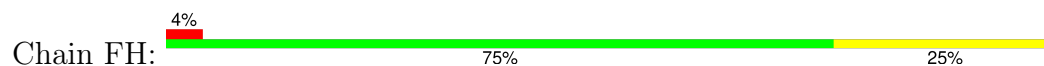
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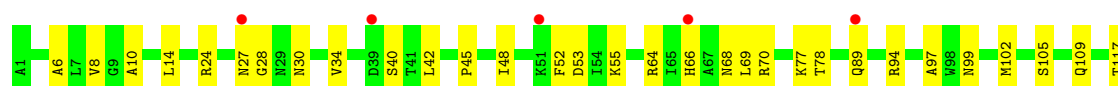
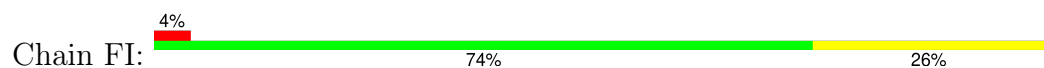
- Molecule 1: coat protein



- Molecule 1: coat protein

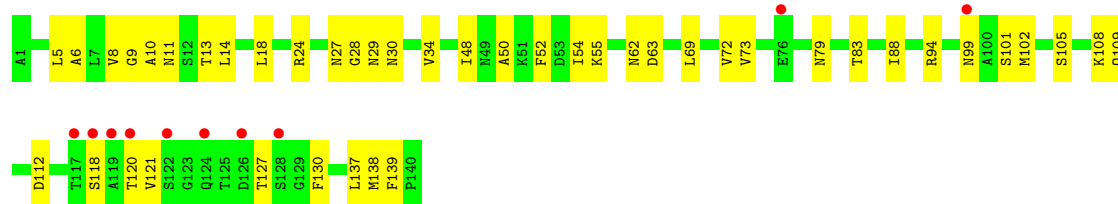


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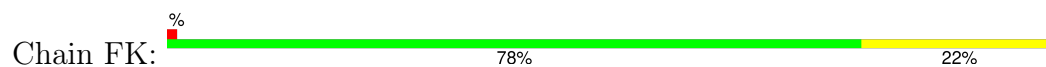


- Molecule 1: coat protein

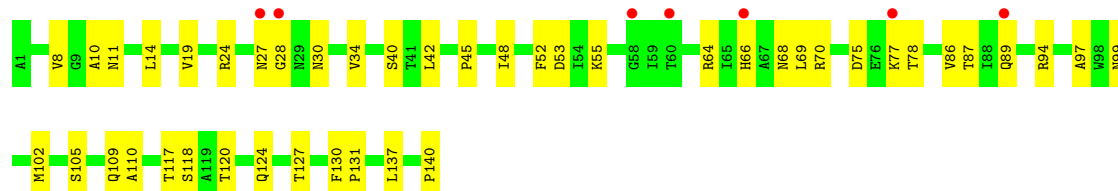




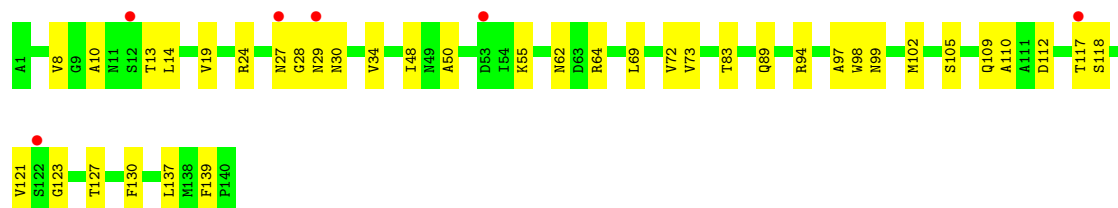
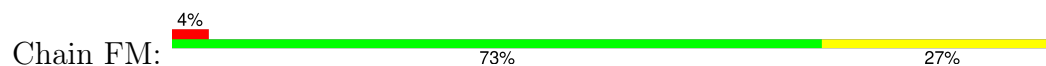
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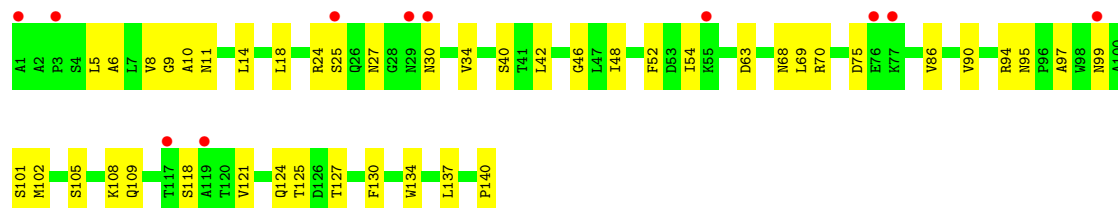
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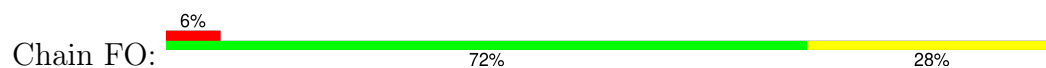
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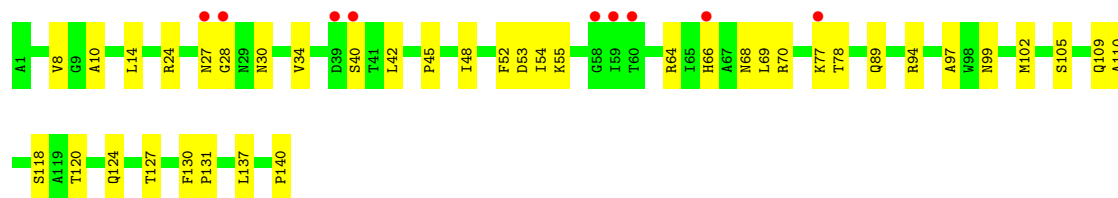


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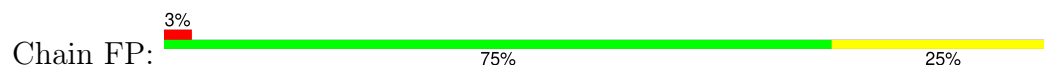


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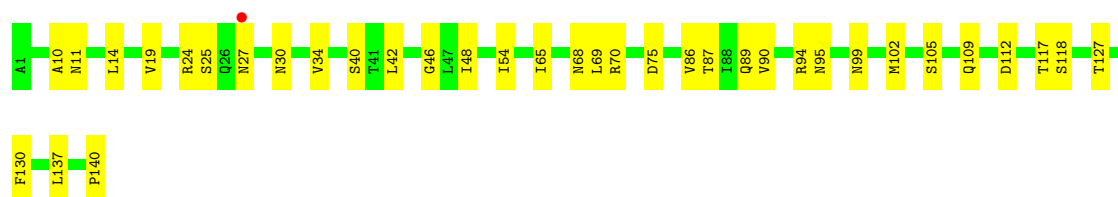
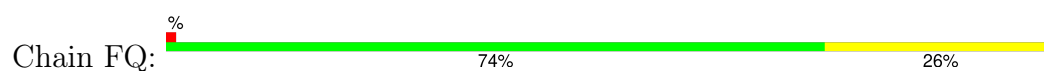




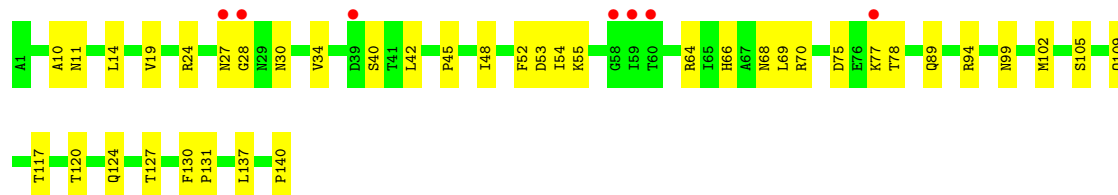
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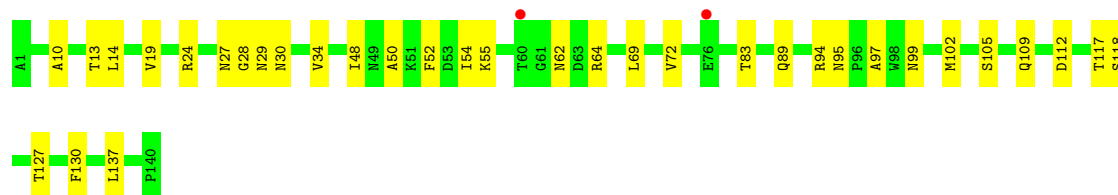
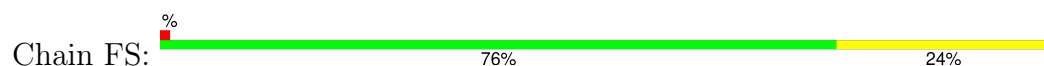
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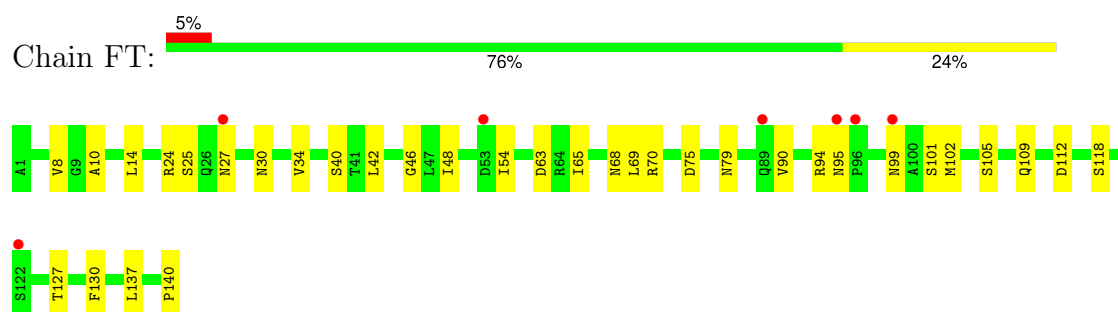
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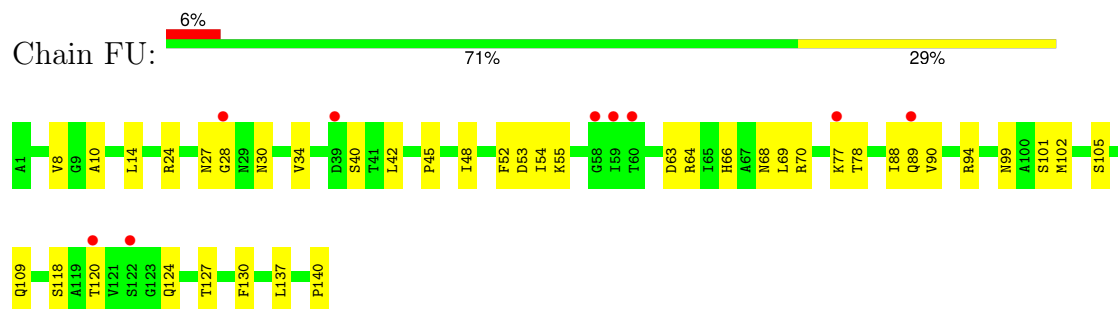
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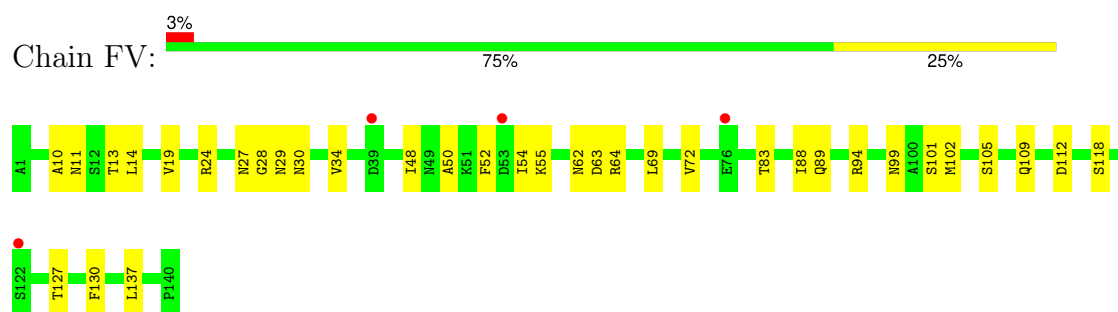
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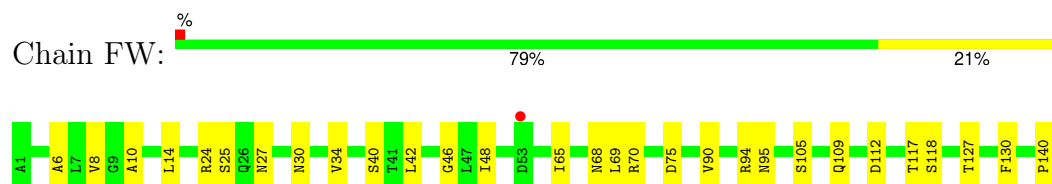
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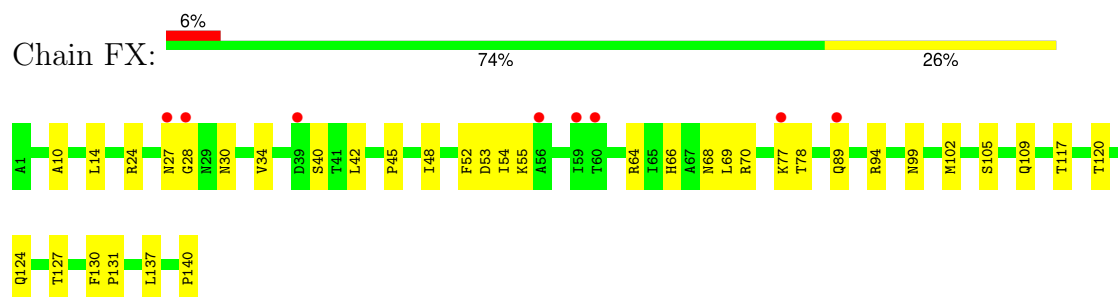
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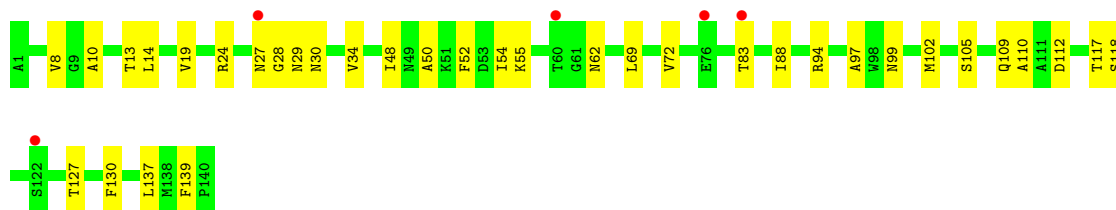
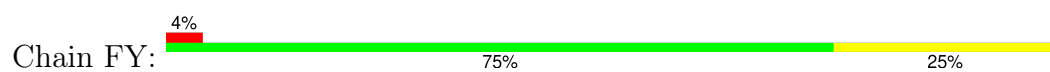
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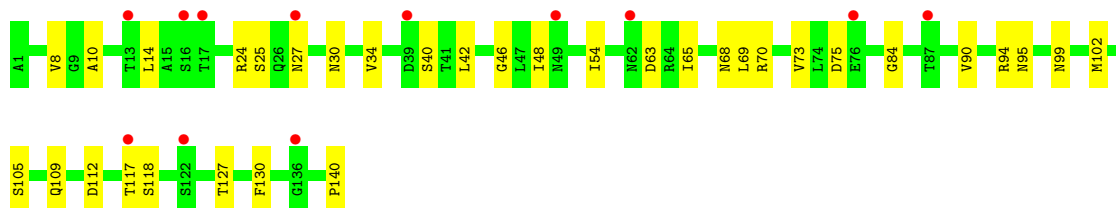
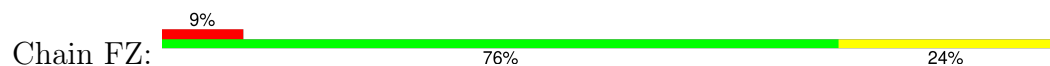
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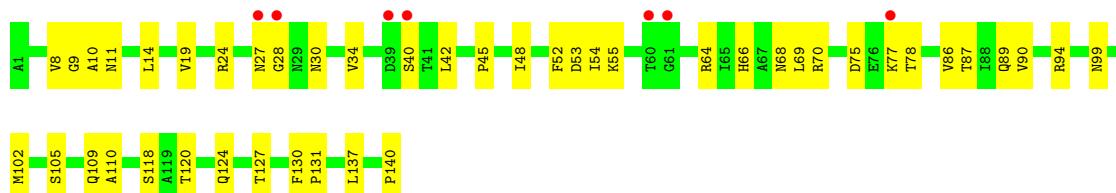
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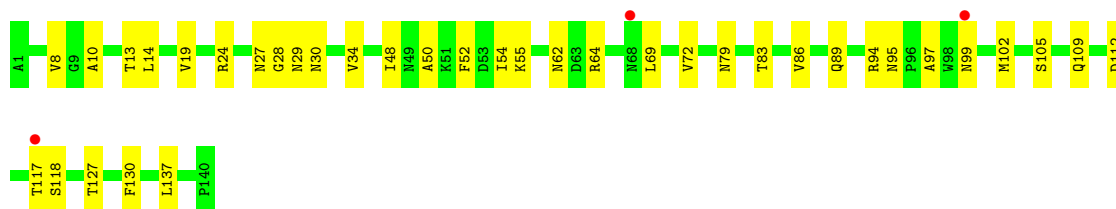
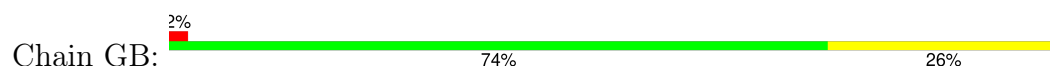
- Molecule 1: coat protein



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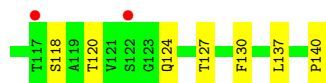
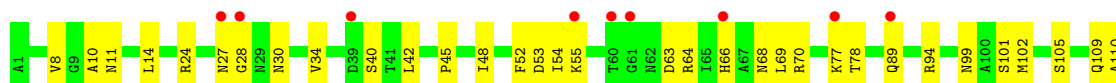
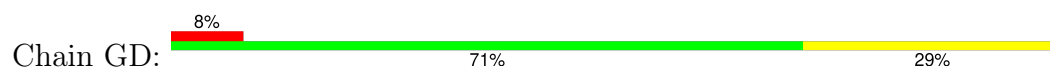


- Molecule 1: coat protein

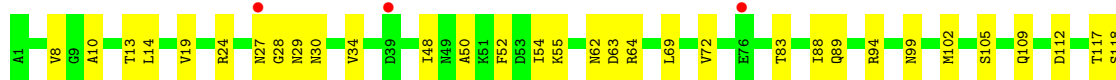
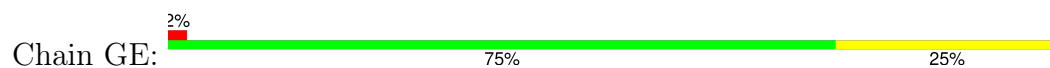




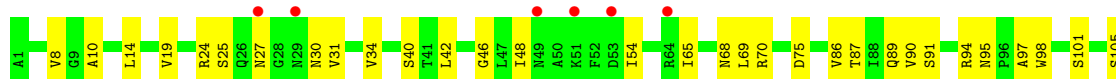
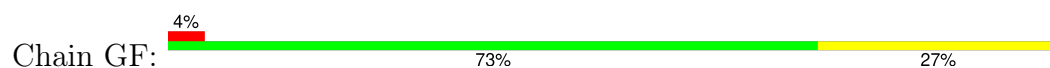
- Molecule 1: coat protein



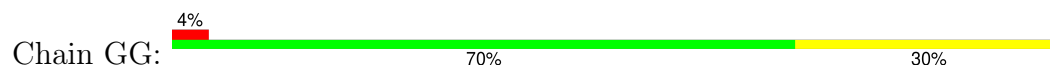
- Molecule 1: coat protein



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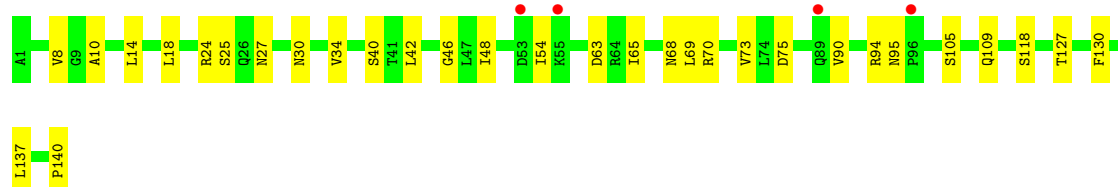
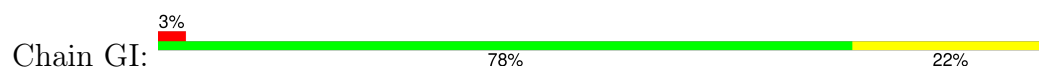


- Molecule 1: coat protein

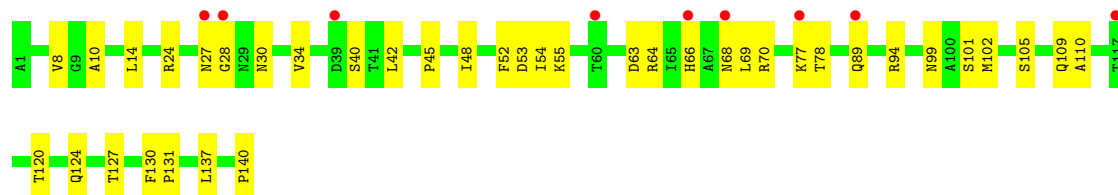
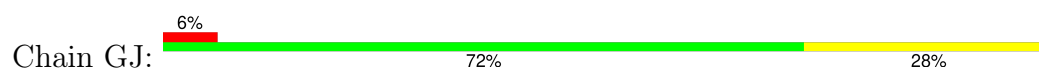




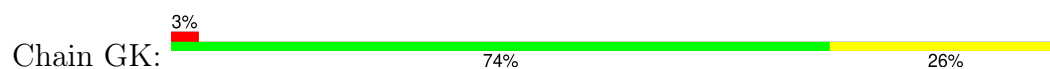
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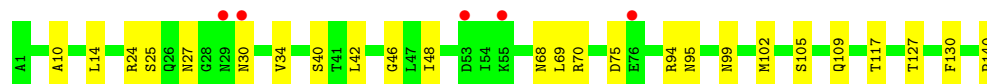
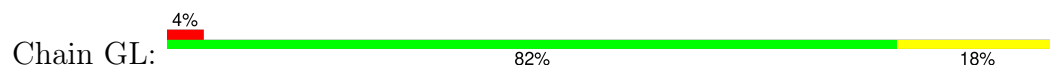
- Molecule 1: coat protein



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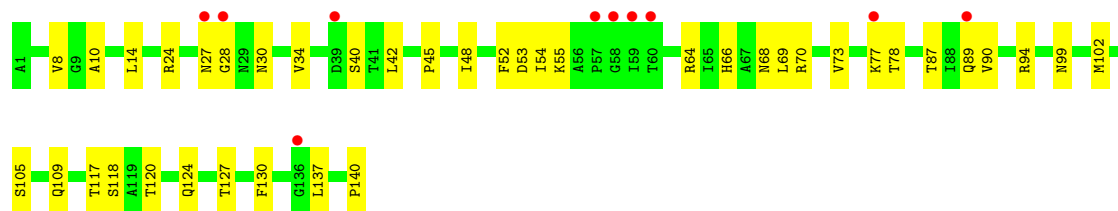


- Molecule 1: coat protein

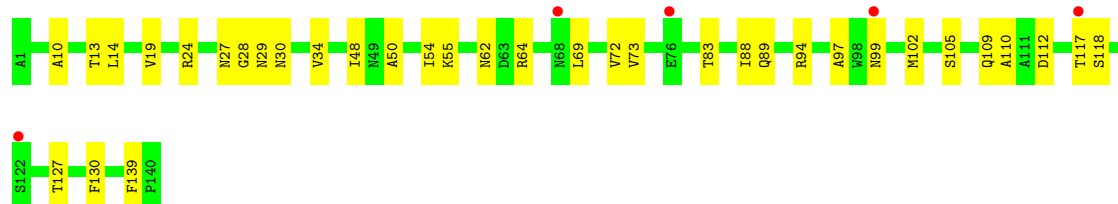
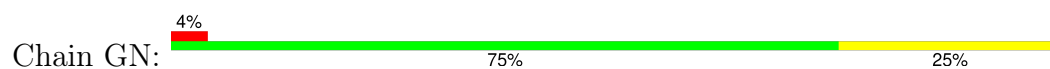


- Molecule 1: coat protein

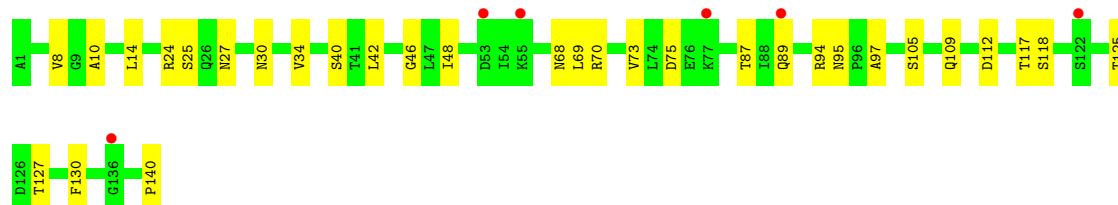
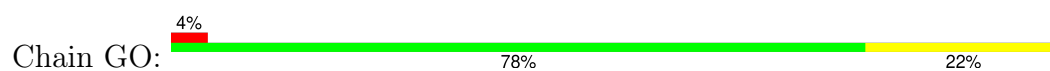




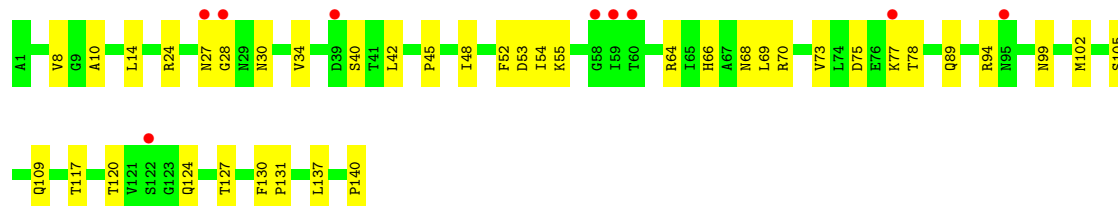
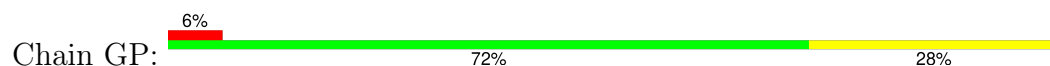
- Molecule 1: coat protein



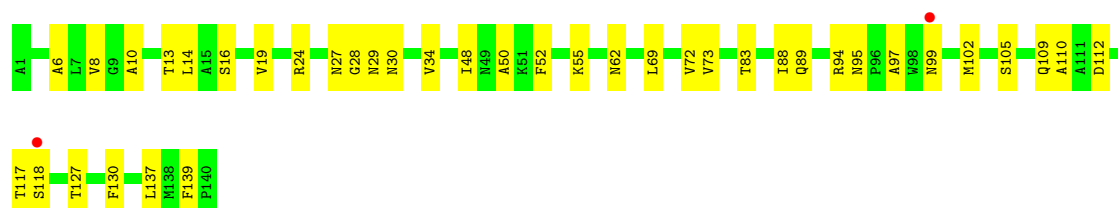
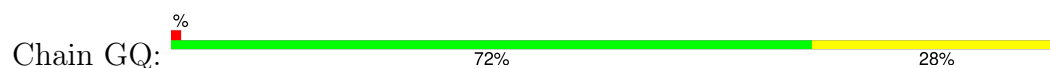
- Molecule 1: coat protein



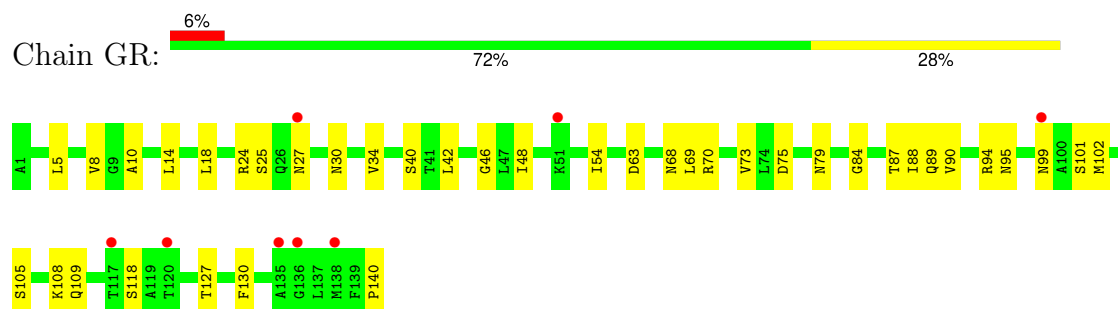
- Molecule 1: coat protein



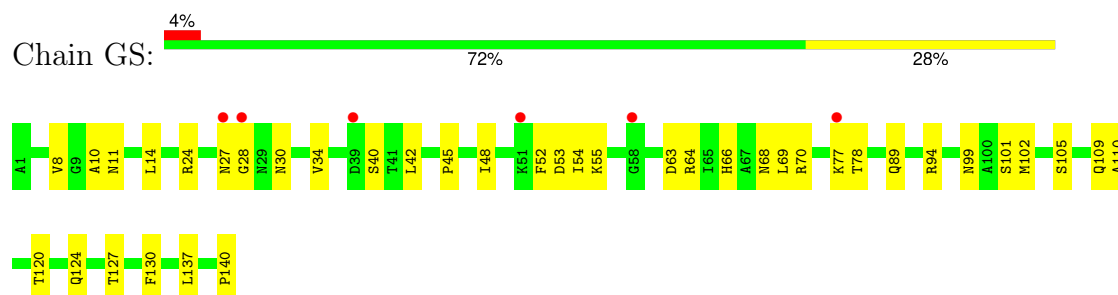
- Molecule 1: coat protein



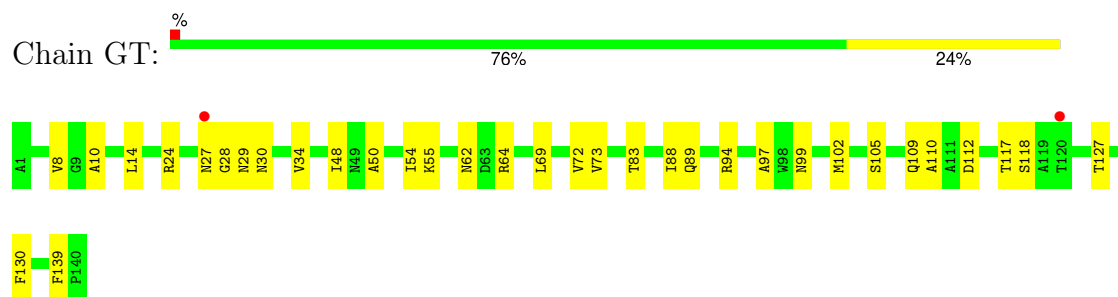
- Molecule 1: coat protein



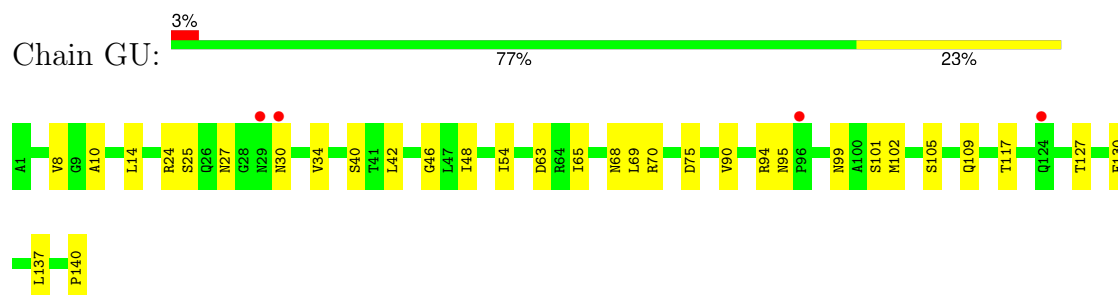
- Molecule 1: coat protein



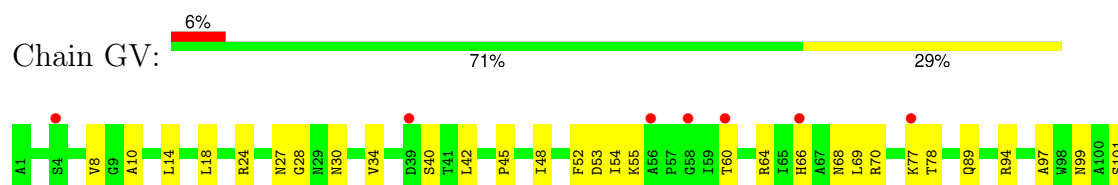
- Molecule 1: coat protein



- Molecule 1: coat protein

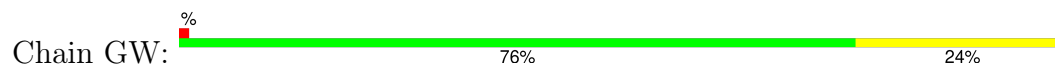


- Molecule 1: coat protein

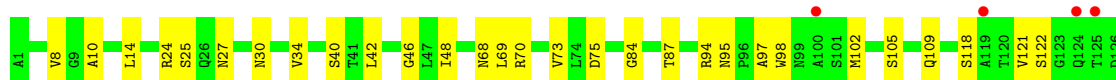
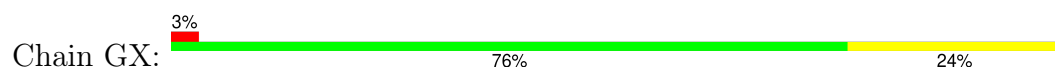




- Molecule 1: coat protein



- Molecule 1: coat protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	278.09Å 390.21Å 554.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	62.20 – 3.20 62.20 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.6 (62.20-3.20) 98.7 (62.20-3.20)	Depositor EDS
R_{merge}	0.67	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.261 , 0.266 0.263 , 0.268	Depositor DCC
R_{free} test set	6526 reflections (0.67%)	wwPDB-VP
Wilson B-factor (Å ²)	37.7	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 17.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	184320	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.24	0/1043	0.50	0/1426
1	AB	0.22	0/1043	0.49	0/1426
1	AC	0.22	0/1043	0.50	0/1426
1	AD	0.24	0/1043	0.50	0/1426
1	AE	0.23	0/1043	0.49	0/1426
1	AF	0.23	0/1043	0.51	0/1426
1	AG	0.24	0/1043	0.50	0/1426
1	AH	0.23	0/1043	0.49	0/1426
1	AI	0.22	0/1043	0.51	0/1426
1	AJ	0.24	0/1043	0.50	0/1426
1	AK	0.23	0/1043	0.49	0/1426
1	AL	0.23	0/1043	0.50	0/1426
1	AM	0.24	0/1043	0.50	0/1426
1	AN	0.23	0/1043	0.49	0/1426
1	AO	0.23	0/1043	0.51	0/1426
1	AP	0.24	0/1043	0.50	0/1426
1	AQ	0.23	0/1043	0.49	0/1426
1	AR	0.22	0/1043	0.51	0/1426
1	AS	0.24	0/1043	0.50	0/1426
1	AT	0.23	0/1043	0.49	0/1426
1	AU	0.22	0/1043	0.51	0/1426
1	AV	0.24	0/1043	0.50	0/1426
1	AW	0.23	0/1043	0.49	0/1426
1	AX	0.23	0/1043	0.50	0/1426
1	AY	0.24	0/1043	0.50	0/1426
1	AZ	0.23	0/1043	0.49	0/1426
1	BA	0.23	0/1043	0.51	0/1426
1	BB	0.24	0/1043	0.50	0/1426
1	BC	0.23	0/1043	0.49	0/1426
1	BD	0.22	0/1043	0.50	0/1426
1	BE	0.24	0/1043	0.50	0/1426
1	BF	0.23	0/1043	0.49	0/1426
1	BG	0.23	0/1043	0.50	0/1426
1	BH	0.24	0/1043	0.50	0/1426

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.23	0/1043	0.49	0/1426
1	BJ	0.23	0/1043	0.51	0/1426
1	BK	0.24	0/1043	0.50	0/1426
1	BL	0.23	0/1043	0.49	0/1426
1	BM	0.23	0/1043	0.50	0/1426
1	BN	0.24	0/1043	0.50	0/1426
1	BO	0.23	0/1043	0.49	0/1426
1	BP	0.23	0/1043	0.50	0/1426
1	BQ	0.24	0/1043	0.50	0/1426
1	BR	0.23	0/1043	0.49	0/1426
1	BS	0.23	0/1043	0.51	0/1426
1	BT	0.24	0/1043	0.50	0/1426
1	BU	0.23	0/1043	0.49	0/1426
1	BV	0.23	0/1043	0.51	0/1426
1	BW	0.24	0/1043	0.50	0/1426
1	BX	0.23	0/1043	0.49	0/1426
1	BY	0.23	0/1043	0.51	0/1426
1	BZ	0.24	0/1043	0.50	0/1426
1	CA	0.23	0/1043	0.49	0/1426
1	CB	0.23	0/1043	0.50	0/1426
1	CC	0.24	0/1043	0.50	0/1426
1	CD	0.23	0/1043	0.49	0/1426
1	CE	0.23	0/1043	0.51	0/1426
1	CF	0.24	0/1043	0.50	0/1426
1	CG	0.23	0/1043	0.49	0/1426
1	CH	0.23	0/1043	0.51	0/1426
1	CI	0.24	0/1043	0.50	0/1426
1	CJ	0.23	0/1043	0.49	0/1426
1	CK	0.23	0/1043	0.51	0/1426
1	CL	0.24	0/1043	0.50	0/1426
1	CM	0.23	0/1043	0.49	0/1426
1	CN	0.23	0/1043	0.51	0/1426
1	CO	0.24	0/1043	0.50	0/1426
1	CP	0.23	0/1043	0.49	0/1426
1	CQ	0.22	0/1043	0.51	0/1426
1	CR	0.24	0/1043	0.50	0/1426
1	CS	0.23	0/1043	0.49	0/1426
1	CT	0.22	0/1043	0.51	0/1426
1	CU	0.24	0/1043	0.50	0/1426
1	CV	0.23	0/1043	0.49	0/1426
1	CW	0.23	0/1043	0.50	0/1426
1	CX	0.24	0/1043	0.50	0/1426
1	CY	0.23	0/1043	0.49	0/1426

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CZ	0.23	0/1043	0.51	0/1426
1	DA	0.24	0/1043	0.50	0/1426
1	DB	0.23	0/1043	0.49	0/1426
1	DC	0.23	0/1043	0.51	0/1426
1	DD	0.24	0/1043	0.50	0/1426
1	DE	0.23	0/1043	0.49	0/1426
1	DF	0.23	0/1043	0.51	0/1426
1	DG	0.24	0/1043	0.50	0/1426
1	DH	0.23	0/1043	0.49	0/1426
1	DI	0.22	0/1043	0.51	0/1426
1	DJ	0.24	0/1043	0.50	0/1426
1	DK	0.23	0/1043	0.49	0/1426
1	DL	0.23	0/1043	0.50	0/1426
1	DM	0.24	0/1043	0.50	0/1426
1	DN	0.23	0/1043	0.49	0/1426
1	DO	0.22	0/1043	0.50	0/1426
1	DP	0.24	0/1043	0.50	0/1426
1	DQ	0.23	0/1043	0.49	0/1426
1	DR	0.23	0/1043	0.51	0/1426
1	DS	0.24	0/1043	0.50	0/1426
1	DT	0.23	0/1043	0.49	0/1426
1	DU	0.23	0/1043	0.51	0/1426
1	DV	0.24	0/1043	0.50	0/1426
1	DW	0.23	0/1043	0.49	0/1426
1	DX	0.23	0/1043	0.50	0/1426
1	DY	0.24	0/1043	0.50	0/1426
1	DZ	0.23	0/1043	0.49	0/1426
1	EA	0.23	0/1043	0.50	0/1426
1	EB	0.24	0/1043	0.50	0/1426
1	EC	0.23	0/1043	0.49	0/1426
1	ED	0.23	0/1043	0.51	0/1426
1	EE	0.24	0/1043	0.50	0/1426
1	EF	0.23	0/1043	0.49	0/1426
1	EG	0.22	0/1043	0.51	0/1426
1	EH	0.24	0/1043	0.50	0/1426
1	EI	0.23	0/1043	0.49	0/1426
1	EJ	0.23	0/1043	0.50	0/1426
1	EK	0.24	0/1043	0.50	0/1426
1	EL	0.23	0/1043	0.49	0/1426
1	EM	0.22	0/1043	0.50	0/1426
1	EN	0.24	0/1043	0.50	0/1426
1	EO	0.23	0/1043	0.49	0/1426
1	EP	0.23	0/1043	0.50	0/1426

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	EQ	0.24	0/1043	0.50	0/1426
1	ER	0.23	0/1043	0.49	0/1426
1	ES	0.23	0/1043	0.50	0/1426
1	ET	0.24	0/1043	0.50	0/1426
1	EU	0.23	0/1043	0.49	0/1426
1	EV	0.22	0/1043	0.50	0/1426
1	EW	0.24	0/1043	0.50	0/1426
1	EX	0.23	0/1043	0.49	0/1426
1	EY	0.23	0/1043	0.50	0/1426
1	EZ	0.24	0/1043	0.50	0/1426
1	FA	0.23	0/1043	0.49	0/1426
1	FB	0.23	0/1043	0.51	0/1426
1	FC	0.24	0/1043	0.50	0/1426
1	FD	0.23	0/1043	0.49	0/1426
1	FE	0.22	0/1043	0.50	0/1426
1	FF	0.24	0/1043	0.50	0/1426
1	FG	0.23	0/1043	0.49	0/1426
1	FH	0.22	0/1043	0.51	0/1426
1	FI	0.24	0/1043	0.50	0/1426
1	FJ	0.23	0/1043	0.49	0/1426
1	FK	0.22	0/1043	0.51	0/1426
1	FL	0.24	0/1043	0.50	0/1426
1	FM	0.23	0/1043	0.49	0/1426
1	FN	0.23	0/1043	0.50	0/1426
1	FO	0.24	0/1043	0.50	0/1426
1	FP	0.23	0/1043	0.49	0/1426
1	FQ	0.23	0/1043	0.50	0/1426
1	FR	0.24	0/1043	0.50	0/1426
1	FS	0.23	0/1043	0.49	0/1426
1	FT	0.23	0/1043	0.50	0/1426
1	FU	0.24	0/1043	0.50	0/1426
1	FV	0.23	0/1043	0.49	0/1426
1	FW	0.22	0/1043	0.51	0/1426
1	FX	0.24	0/1043	0.50	0/1426
1	FY	0.23	0/1043	0.49	0/1426
1	FZ	0.23	0/1043	0.51	0/1426
1	GA	0.24	0/1043	0.50	0/1426
1	GB	0.23	0/1043	0.49	0/1426
1	GC	0.23	0/1043	0.50	0/1426
1	GD	0.24	0/1043	0.50	0/1426
1	GE	0.23	0/1043	0.49	0/1426
1	GF	0.22	0/1043	0.51	0/1426
1	GG	0.24	0/1043	0.50	0/1426

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GH	0.23	0/1043	0.49	0/1426
1	GI	0.23	0/1043	0.50	0/1426
1	GJ	0.24	0/1043	0.50	0/1426
1	GK	0.23	0/1043	0.49	0/1426
1	GL	0.23	0/1043	0.50	0/1426
1	GM	0.24	0/1043	0.50	0/1426
1	GN	0.23	0/1043	0.49	0/1426
1	GO	0.23	0/1043	0.51	0/1426
1	GP	0.24	0/1043	0.50	0/1426
1	GQ	0.23	0/1043	0.49	0/1426
1	GR	0.23	0/1043	0.51	0/1426
1	GS	0.24	0/1043	0.50	0/1426
1	GT	0.23	0/1043	0.49	0/1426
1	GU	0.23	0/1043	0.50	0/1426
1	GV	0.24	0/1043	0.50	0/1426
1	GW	0.23	0/1043	0.49	0/1426
1	GX	0.22	0/1043	0.51	0/1426
All	All	0.23	0/187740	0.50	0/256680

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1024	0	1026	23	0
1	AB	1024	0	1026	31	0
1	AC	1024	0	1026	23	0
1	AD	1024	0	1026	36	0
1	AE	1024	0	1026	46	0
1	AF	1024	0	1026	24	0
1	AG	1024	0	1026	30	0
1	AH	1024	0	1026	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AI	1024	0	1026	29	0
1	AJ	1024	0	1026	30	0
1	AK	1024	0	1026	37	0
1	AL	1024	0	1026	22	0
1	AM	1024	0	1026	40	0
1	AN	1024	0	1026	39	0
1	AO	1024	0	1026	25	0
1	AP	1024	0	1026	42	0
1	AQ	1024	0	1026	38	0
1	AR	1024	0	1026	38	0
1	AS	1024	0	1026	35	0
1	AT	1024	0	1026	41	0
1	AU	1024	0	1026	39	0
1	AV	1024	0	1026	39	1
1	AW	1024	0	1026	37	0
1	AX	1024	0	1026	32	0
1	AY	1024	0	1026	31	0
1	AZ	1024	0	1026	38	0
1	BA	1024	0	1026	25	0
1	BB	1024	0	1026	27	0
1	BC	1024	0	1026	40	0
1	BD	1024	0	1026	31	0
1	BE	1024	0	1026	29	0
1	BF	1024	0	1026	34	0
1	BG	1024	0	1026	23	0
1	BH	1024	0	1026	35	1
1	BI	1024	0	1026	27	0
1	BJ	1024	0	1026	49	0
1	BK	1024	0	1026	31	0
1	BL	1024	0	1026	32	0
1	BM	1024	0	1026	24	0
1	BN	1024	0	1026	29	0
1	BO	1024	0	1026	39	0
1	BP	1024	0	1026	36	0
1	BQ	1024	0	1026	29	0
1	BR	1024	0	1026	32	0
1	BS	1024	0	1026	22	0
1	BT	1024	0	1026	30	0
1	BU	1024	0	1026	43	1
1	BV	1024	0	1026	34	0
1	BW	1024	0	1026	36	0
1	BX	1024	0	1026	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BY	1024	0	1026	36	0
1	BZ	1024	0	1026	36	0
1	CA	1024	0	1026	47	0
1	CB	1024	0	1026	45	0
1	CC	1024	0	1026	33	0
1	CD	1024	0	1026	37	0
1	CE	1024	0	1026	32	0
1	CF	1024	0	1026	28	0
1	CG	1024	0	1026	45	0
1	CH	1024	0	1026	30	0
1	CI	1024	0	1026	40	0
1	CJ	1024	0	1026	43	0
1	CK	1024	0	1026	25	0
1	CL	1024	0	1026	43	1
1	CM	1024	0	1026	36	0
1	CN	1024	0	1026	26	0
1	CO	1024	0	1026	38	0
1	CP	1024	0	1026	36	0
1	CQ	1024	0	1026	41	0
1	CR	1024	0	1026	31	0
1	CS	1024	0	1026	58	1
1	CT	1024	0	1026	42	0
1	CU	1024	0	1026	45	0
1	CV	1024	0	1026	36	0
1	CW	1024	0	1026	29	0
1	CX	1024	0	1026	28	0
1	CY	1024	0	1026	36	0
1	CZ	1024	0	1026	21	0
1	DA	1024	0	1026	40	2
1	DB	1024	0	1026	35	0
1	DC	1024	0	1026	35	0
1	DD	1024	0	1026	51	0
1	DE	1024	0	1026	50	0
1	DF	1024	0	1026	43	0
1	DG	1024	0	1026	30	0
1	DH	1024	0	1026	52	0
1	DI	1024	0	1026	26	0
1	DJ	1024	0	1026	34	0
1	DK	1024	0	1026	32	0
1	DL	1024	0	1026	35	0
1	DM	1024	0	1026	29	0
1	DN	1024	0	1026	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DO	1024	0	1026	24	0
1	DP	1024	0	1026	33	0
1	DQ	1024	0	1026	40	0
1	DR	1024	0	1026	22	0
1	DS	1024	0	1026	39	0
1	DT	1024	0	1026	40	0
1	DU	1024	0	1026	30	0
1	DV	1024	0	1026	30	0
1	DW	1024	0	1026	34	0
1	DX	1024	0	1026	22	0
1	DY	1024	0	1026	31	0
1	DZ	1024	0	1026	32	0
1	EA	1024	0	1026	24	0
1	EB	1024	0	1026	38	0
1	EC	1024	0	1026	31	0
1	ED	1024	0	1026	42	0
1	EE	1024	0	1026	57	0
1	EF	1024	0	1026	45	0
1	EG	1024	0	1026	34	0
1	EH	1024	0	1026	32	1
1	EI	1024	0	1026	34	0
1	EJ	1024	0	1026	31	0
1	EK	1024	0	1026	29	0
1	EL	1024	0	1026	40	0
1	EM	1024	0	1026	25	0
1	EN	1024	0	1026	52	0
1	EO	1024	0	1026	37	0
1	EP	1024	0	1026	31	0
1	EQ	1024	0	1026	33	0
1	ER	1024	0	1026	33	0
1	ES	1024	0	1026	24	0
1	ET	1024	0	1026	31	0
1	EU	1024	0	1026	65	2
1	EV	1024	0	1026	52	0
1	EW	1024	0	1026	34	0
1	EX	1024	0	1026	33	0
1	EY	1024	0	1026	26	0
1	EZ	1024	0	1026	36	0
1	FA	1024	0	1026	39	0
1	FB	1024	0	1026	37	0
1	FC	1024	0	1026	32	0
1	FD	1024	0	1026	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	FE	1024	0	1026	23	0
1	FF	1024	0	1026	35	0
1	FG	1024	0	1026	39	0
1	FH	1024	0	1026	34	0
1	FI	1024	0	1026	28	0
1	FJ	1024	0	1026	59	1
1	FK	1024	0	1026	32	0
1	FL	1024	0	1026	37	0
1	FM	1024	0	1026	39	0
1	FN	1024	0	1026	44	0
1	FO	1024	0	1026	33	0
1	FP	1024	0	1026	37	0
1	FQ	1024	0	1026	34	0
1	FR	1024	0	1026	34	0
1	FS	1024	0	1026	36	0
1	FT	1024	0	1026	31	0
1	FU	1024	0	1026	33	1
1	FV	1024	0	1026	38	0
1	FW	1024	0	1026	24	0
1	FX	1024	0	1026	27	0
1	FY	1024	0	1026	35	0
1	FZ	1024	0	1026	28	0
1	GA	1024	0	1026	40	0
1	GB	1024	0	1026	39	0
1	GC	1024	0	1026	44	0
1	GD	1024	0	1026	34	0
1	GE	1024	0	1026	36	0
1	GF	1024	0	1026	39	0
1	GG	1024	0	1026	31	0
1	GH	1024	0	1026	46	0
1	GI	1024	0	1026	29	0
1	GJ	1024	0	1026	32	0
1	GK	1024	0	1026	39	0
1	GL	1024	0	1026	20	0
1	GM	1024	0	1026	33	0
1	GN	1024	0	1026	30	0
1	GO	1024	0	1026	33	0
1	GP	1024	0	1026	34	0
1	GQ	1024	0	1026	42	0
1	GR	1024	0	1026	44	0
1	GS	1024	0	1026	32	0
1	GT	1024	0	1026	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GU	1024	0	1026	27	0
1	GV	1024	0	1026	36	0
1	GW	1024	0	1026	37	0
1	GX	1024	0	1026	32	0
All	All	184320	0	184680	4464	6

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 12.

All (4464) 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:AE:54:ILE:HG12	1:GA:137:LEU:HD13	1.36	1.06
1:CU:137:LEU:HD13	1:DH:54:ILE:HG12	1.40	1.04
1:FA:54:ILE:HG12	1:FL:137:LEU:HD13	1.42	1.02
1:BJ:95:ASN:HD21	1:EV:75:ASP:HA	1.24	0.99
1:EN:137:LEU:HD13	1:FJ:54:ILE:HG12	1.45	0.99
1:EE:121:VAL:HG11	1:EU:18:LEU:HG	1.43	0.99
1:AP:137:LEU:HD13	1:BU:54:ILE:HG12	1.44	0.97
1:CT:75:ASP:HA	1:GF:95:ASN:HD21	1.29	0.96
1:AV:54:ILE:HG12	1:EF:137:LEU:HD13	1.49	0.94
1:CJ:54:ILE:HG12	1:CO:137:LEU:HD13	1.48	0.94
1:BP:137:LEU:HD13	1:FB:54:ILE:HG12	1.48	0.94
1:BW:137:LEU:HD13	1:DQ:54:ILE:HG12	1.51	0.92
1:DA:54:ILE:HG12	1:DE:137:LEU:HD13	1.52	0.91
1:CS:73:VAL:HG11	1:DD:97:ALA:O	1.71	0.91
1:CB:18:LEU:HG	1:FN:121:VAL:HG11	1.53	0.91
1:EE:137:LEU:HD13	1:EU:54:ILE:HG12	1.53	0.90
1:EE:97:ALA:O	1:EU:73:VAL:HG11	1.71	0.89
1:AH:54:ILE:HG12	1:GD:137:LEU:HD13	1.54	0.89
1:CE:75:ASP:HA	1:FQ:95:ASN:HD21	1.38	0.88
1:EE:121:VAL:CG1	1:EU:18:LEU:HG	2.03	0.88
1:CB:137:LEU:HD13	1:FN:54:ILE:HG12	1.55	0.87
1:EE:18:LEU:HG	1:EU:121:VAL:HG11	1.56	0.87
1:EN:18:LEU:HG	1:FJ:121:VAL:HG11	1.56	0.87
1:EN:121:VAL:HG11	1:FJ:18:LEU:HG	1.58	0.86
1:CB:54:ILE:HG12	1:FN:137:LEU:HD13	1.57	0.86
1:CQ:18:LEU:HG	1:GC:121:VAL:HG11	1.57	0.85
1:DF:95:ASN:HD21	1:GR:75:ASP:HA	1.40	0.85
1:AN:54:ILE:HG12	1:FR:137:LEU:HD13	1.58	0.85
1:AM:73:VAL:HG11	1:CA:97:ALA:O	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BV:95:ASN:HD21	1:FH:75:ASP:HA	1.39	0.84
1:CS:121:VAL:HG11	1:DD:18:LEU:HG	1.59	0.84
1:CS:18:LEU:HG	1:DD:121:VAL:HG11	1.58	0.84
1:BG:75:ASP:HA	1:ES:95:ASN:HD21	1.43	0.84
1:DC:95:ASN:HD21	1:GO:75:ASP:HA	1.42	0.83
1:CB:121:VAL:HG11	1:FN:18:LEU:HG	1.61	0.83
1:EK:137:LEU:HD13	1:ER:54:ILE:HG12	1.59	0.83
1:BZ:137:LEU:HD13	1:DT:54:ILE:HG12	1.60	0.82
1:BH:137:LEU:HD13	1:BO:54:ILE:HG12	1.60	0.82
1:DB:24:ARG:HA	1:DE:138:MET:HE3	1.62	0.82
1:BP:95:ASN:HD21	1:FB:75:ASP:HA	1.43	0.82
1:DF:118:SER:HB2	1:GR:8:VAL:HB	1.60	0.82
1:DF:137:LEU:HD13	1:GR:54:ILE:HG12	1.62	0.82
1:BY:54:ILE:HG12	1:FK:137:LEU:HD13	1.62	0.81
1:AR:118:SER:HB2	1:ED:8:VAL:HB	1.62	0.81
1:CT:137:LEU:HD13	1:GF:54:ILE:HG12	1.63	0.81
1:FD:54:ILE:HG12	1:FF:137:LEU:HD13	1.61	0.81
1:AU:73:VAL:HG11	1:EG:97:ALA:O	1.80	0.81
1:FV:54:ILE:HG12	1:GS:137:LEU:HD13	1.63	0.80
1:AI:95:ASN:HD21	1:DU:75:ASP:HA	1.46	0.80
1:CQ:121:VAL:HG11	1:GC:18:LEU:HG	1.63	0.80
1:DF:97:ALA:O	1:GR:73:VAL:HG11	1.82	0.80
1:AM:8:VAL:HB	1:CA:118:SER:HB2	1.64	0.80
1:CI:73:VAL:HG11	1:GH:97:ALA:O	1.83	0.79
1:AU:8:VAL:HB	1:EG:118:SER:HB2	1.64	0.79
1:CH:137:LEU:HD13	1:FT:54:ILE:HG12	1.63	0.79
1:CQ:63:ASP:HB3	1:GC:137:LEU:HD11	1.63	0.78
1:AU:75:ASP:HA	1:EG:95:ASN:HD21	1.46	0.78
1:CT:95:ASN:HD21	1:GF:75:ASP:HA	1.49	0.78
1:CG:54:ILE:HG12	1:CL:137:LEU:HD13	1.65	0.78
1:CC:137:LEU:HD13	1:GK:54:ILE:HG12	1.63	0.78
1:BM:95:ASN:HD21	1:EY:75:ASP:HA	1.47	0.77
1:CI:8:VAL:HB	1:GH:118:SER:HB2	1.66	0.77
1:AR:97:ALA:O	1:ED:73:VAL:HG11	1.84	0.77
1:FP:54:ILE:HG12	1:GV:137:LEU:HD13	1.66	0.77
1:AO:95:ASN:HD21	1:EA:75:ASP:HA	1.48	0.77
1:CK:75:ASP:HA	1:FW:95:ASN:HD21	1.50	0.77
1:BJ:95:ASN:ND2	1:EV:75:ASP:HA	2.01	0.76
1:CS:54:ILE:HG12	1:DD:137:LEU:HD13	1.67	0.76
1:EN:121:VAL:CG1	1:FJ:18:LEU:HG	2.14	0.76
1:AD:73:VAL:HG11	1:BC:97:ALA:O	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:52:PHE:CE1	1:EF:137:LEU:HA	2.21	0.76
1:BV:137:LEU:HD13	1:FH:54:ILE:HG12	1.66	0.76
1:AC:95:ASN:HD21	1:DO:75:ASP:HA	1.49	0.76
1:AX:95:ASN:HD21	1:EJ:75:ASP:HA	1.49	0.76
1:AW:24:ARG:HA	1:EF:138:MET:HE3	1.68	0.76
1:FY:27:ASN:OD1	1:FY:28:GLY:N	2.19	0.75
1:CP:118:SER:HB2	1:DJ:8:VAL:HB	1.67	0.75
1:DS:73:VAL:HG11	1:GQ:97:ALA:O	1.86	0.75
1:CQ:54:ILE:HG12	1:GC:137:LEU:HD13	1.69	0.75
1:EN:8:VAL:HB	1:FJ:118:SER:HB2	1.67	0.75
1:AV:52:PHE:HE1	1:EF:137:LEU:HA	1.51	0.75
1:FP:27:ASN:OD1	1:FP:28:GLY:N	2.19	0.75
1:AF:75:ASP:HA	1:DR:95:ASN:HD21	1.52	0.75
1:BV:75:ASP:HA	1:FH:95:ASN:HD21	1.50	0.75
1:AV:137:LEU:HD13	1:EF:54:ILE:HG12	1.68	0.74
1:CM:27:ASN:OD1	1:CM:28:GLY:N	2.19	0.74
1:CQ:137:LEU:HD13	1:GC:54:ILE:HG12	1.69	0.74
1:DH:27:ASN:OD1	1:DH:28:GLY:N	2.19	0.74
1:DC:97:ALA:O	1:GO:73:VAL:HG11	1.86	0.74
1:BJ:54:ILE:HG12	1:EV:137:LEU:HD13	1.68	0.74
1:CY:27:ASN:OD1	1:CY:28:GLY:N	2.19	0.74
1:AT:27:ASN:OD1	1:AT:28:GLY:N	2.19	0.74
1:BM:75:ASP:HA	1:EY:95:ASN:HD21	1.50	0.74
1:DZ:27:ASN:OD1	1:DZ:28:GLY:N	2.19	0.74
1:GK:27:ASN:OD1	1:GK:28:GLY:N	2.19	0.74
1:EE:8:VAL:HB	1:EU:118:SER:HB2	1.69	0.74
1:GN:27:ASN:OD1	1:GN:28:GLY:N	2.19	0.74
1:AQ:137:LEU:HD13	1:FU:54:ILE:HG12	1.69	0.74
1:DE:27:ASN:OD1	1:DE:28:GLY:N	2.19	0.74
1:EC:27:ASN:OD1	1:EC:28:GLY:N	2.19	0.74
1:CG:118:SER:HB2	1:CL:8:VAL:HB	1.69	0.74
1:FV:27:ASN:OD1	1:FV:28:GLY:N	2.19	0.74
1:AB:27:ASN:OD1	1:AB:28:GLY:N	2.19	0.74
1:AX:75:ASP:HA	1:EJ:95:ASN:HD21	1.53	0.74
1:CB:75:ASP:HA	1:FN:95:ASN:HD21	1.52	0.74
1:DK:27:ASN:OD1	1:DK:28:GLY:N	2.19	0.73
1:GW:27:ASN:OD1	1:GW:28:GLY:N	2.19	0.73
1:AK:27:ASN:OD1	1:AK:28:GLY:N	2.19	0.73
1:DL:8:VAL:HB	1:GX:118:SER:HB2	1.70	0.73
1:EO:24:ARG:HA	1:FJ:138:MET:HE3	1.70	0.73
1:FA:27:ASN:OD1	1:FA:28:GLY:N	2.19	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:27:ASN:OD1	1:BC:28:GLY:N	2.19	0.73
1:CQ:137:LEU:HD11	1:GC:63:ASP:HB3	1.69	0.73
1:CV:27:ASN:OD1	1:CV:28:GLY:N	2.19	0.73
1:EF:27:ASN:OD1	1:EF:28:GLY:N	2.19	0.73
1:EU:27:ASN:OD1	1:EU:28:GLY:N	2.19	0.73
1:BD:8:VAL:HB	1:EP:118:SER:HB2	1.69	0.73
1:DA:52:PHE:HE1	1:DE:137:LEU:HA	1.54	0.73
1:GB:27:ASN:OD1	1:GB:28:GLY:N	2.19	0.73
1:AW:27:ASN:OD1	1:AW:28:GLY:N	2.19	0.73
1:CT:75:ASP:HA	1:GF:95:ASN:ND2	2.02	0.73
1:EU:28:GLY:HA2	1:EV:25:SER:HB2	1.71	0.73
1:GT:27:ASN:OD1	1:GT:28:GLY:N	2.19	0.73
1:BU:28:GLY:HA2	1:BV:25:SER:HB2	1.71	0.73
1:CJ:28:GLY:HA2	1:CK:25:SER:HB2	1.71	0.73
1:CV:28:GLY:HA2	1:CW:25:SER:HB2	1.71	0.73
1:FJ:28:GLY:HA2	1:FK:25:SER:HB2	1.71	0.73
1:GW:28:GLY:HA2	1:GX:25:SER:HB2	1.71	0.73
1:AE:52:PHE:CD1	1:GA:137:LEU:HD22	2.24	0.73
1:DA:52:PHE:CE1	1:DE:137:LEU:HA	2.24	0.73
1:DZ:28:GLY:HA2	1:EA:25:SER:HB2	1.71	0.73
1:EL:28:GLY:HA2	1:EM:25:SER:HB2	1.71	0.73
1:FP:28:GLY:HA2	1:FQ:25:SER:HB2	1.71	0.73
1:AK:28:GLY:HA2	1:AL:25:SER:HB2	1.71	0.73
1:AQ:27:ASN:OD1	1:AQ:28:GLY:N	2.19	0.73
1:BA:95:ASN:HD21	1:EM:75:ASP:HA	1.54	0.73
1:CE:54:ILE:HG12	1:FQ:137:LEU:HD13	1.70	0.73
1:CU:54:ILE:HG12	1:DH:137:LEU:HD13	1.70	0.73
1:CY:28:GLY:HA2	1:CZ:25:SER:HB2	1.71	0.73
1:DN:28:GLY:HA2	1:DO:25:SER:HB2	1.71	0.73
1:EL:27:ASN:OD1	1:EL:28:GLY:N	2.19	0.73
1:EQ:73:VAL:HG11	1:FM:97:ALA:O	1.89	0.73
1:GQ:28:GLY:HA2	1:GR:25:SER:HB2	1.71	0.73
1:BR:27:ASN:OD1	1:BR:28:GLY:N	2.19	0.72
1:CG:121:VAL:HG11	1:CL:18:LEU:HG	1.71	0.72
1:CP:97:ALA:O	1:DJ:73:VAL:HG11	1.89	0.72
1:CS:28:GLY:HA2	1:CT:25:SER:HB2	1.71	0.72
1:DW:27:ASN:OD1	1:DW:28:GLY:N	2.19	0.72
1:EO:28:GLY:HA2	1:EP:25:SER:HB2	1.71	0.72
1:AB:28:GLY:HA2	1:AC:25:SER:HB2	1.71	0.72
1:AE:28:GLY:HA2	1:AF:25:SER:HB2	1.71	0.72
1:CB:63:ASP:HB3	1:FN:137:LEU:HD11	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:8:VAL:HB	1:GC:118:SER:HB2	1.70	0.72
1:DC:75:ASP:HA	1:GO:95:ASN:HD21	1.51	0.72
1:DH:28:GLY:HA2	1:DI:25:SER:HB2	1.71	0.72
1:GH:28:GLY:HA2	1:GI:25:SER:HB2	1.71	0.72
1:AQ:28:GLY:HA2	1:AR:25:SER:HB2	1.71	0.72
1:CD:28:GLY:HA2	1:CE:25:SER:HB2	1.71	0.72
1:CS:73:VAL:HG12	1:DD:97:ALA:HB1	1.71	0.72
1:CY:54:ILE:HG12	1:GG:137:LEU:HD13	1.70	0.72
1:DW:28:GLY:HA2	1:DX:25:SER:HB2	1.71	0.72
1:ER:27:ASN:OD1	1:ER:28:GLY:N	2.19	0.72
1:GE:27:ASN:OD1	1:GE:28:GLY:N	2.19	0.72
1:GK:28:GLY:HA2	1:GL:25:SER:HB2	1.71	0.72
1:AV:101:SER:HB2	1:EF:11:ASN:O	1.89	0.72
1:BR:28:GLY:HA2	1:BS:25:SER:HB2	1.71	0.72
1:CH:75:ASP:HA	1:FT:95:ASN:HD21	1.54	0.72
1:EF:28:GLY:HA2	1:EG:25:SER:HB2	1.71	0.72
1:AK:118:SER:HB2	1:FO:8:VAL:HB	1.71	0.72
1:AT:28:GLY:HA2	1:AU:25:SER:HB2	1.71	0.72
1:BC:28:GLY:HA2	1:BD:25:SER:HB2	1.71	0.72
1:BI:28:GLY:HA2	1:BJ:25:SER:HB2	1.71	0.72
1:CM:28:GLY:HA2	1:CN:25:SER:HB2	1.71	0.72
1:ER:28:GLY:HA2	1:ES:25:SER:HB2	1.71	0.72
1:AH:27:ASN:OD1	1:AH:28:GLY:N	2.19	0.72
1:BI:27:ASN:OD1	1:BI:28:GLY:N	2.19	0.72
1:GB:28:GLY:HA2	1:GC:25:SER:HB2	1.71	0.72
1:FS:27:ASN:OD1	1:FS:28:GLY:N	2.19	0.72
1:FS:28:GLY:HA2	1:FT:25:SER:HB2	1.71	0.72
1:GT:28:GLY:HA2	1:GU:25:SER:HB2	1.71	0.72
1:BF:28:GLY:HA2	1:BG:25:SER:HB2	1.71	0.72
1:AH:28:GLY:HA2	1:AI:25:SER:HB2	1.71	0.72
1:AT:97:ALA:O	1:EZ:73:VAL:HG11	1.89	0.72
1:AY:137:LEU:HD13	1:EI:54:ILE:HG12	1.71	0.72
1:BF:27:ASN:OD1	1:BF:28:GLY:N	2.19	0.72
1:BT:8:VAL:HB	1:DN:118:SER:HB2	1.72	0.72
1:CG:28:GLY:HA2	1:CH:25:SER:HB2	1.71	0.72
1:BJ:137:LEU:HD13	1:EV:54:ILE:HG12	1.71	0.72
1:DE:28:GLY:HA2	1:DF:25:SER:HB2	1.71	0.72
1:DQ:28:GLY:HA2	1:DR:25:SER:HB2	1.71	0.72
1:GE:28:GLY:HA2	1:GF:25:SER:HB2	1.71	0.72
1:AZ:27:ASN:OD1	1:AZ:28:GLY:N	2.19	0.71
1:CQ:118:SER:HB2	1:GC:8:VAL:HB	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EE:124:GLN:HA	1:EU:6:ALA:HB3	1.72	0.71
1:EO:27:ASN:OD1	1:EO:28:GLY:N	2.19	0.71
1:FC:42:LEU:O	1:FE:94:ARG:NH1	2.23	0.71
1:AE:54:ILE:HG12	1:GA:137:LEU:CD1	2.15	0.71
1:BZ:42:LEU:O	1:CB:94:ARG:NH1	2.24	0.71
1:DI:95:ASN:HD21	1:GU:75:ASP:HA	1.55	0.71
1:EN:42:LEU:O	1:EP:94:ARG:NH1	2.23	0.71
1:EN:54:ILE:HG12	1:FJ:137:LEU:HD13	1.72	0.71
1:FO:42:LEU:O	1:FQ:94:ARG:NH1	2.24	0.71
1:GS:42:LEU:O	1:GU:94:ARG:NH1	2.24	0.71
1:AW:28:GLY:HA2	1:AX:25:SER:HB2	1.71	0.71
1:AZ:28:GLY:HA2	1:BA:25:SER:HB2	1.71	0.71
1:BL:28:GLY:HA2	1:BM:25:SER:HB2	1.71	0.71
1:CO:42:LEU:O	1:CQ:94:ARG:NH1	2.24	0.71
1:CW:95:ASN:HD21	1:GI:75:ASP:HA	1.55	0.71
1:EC:28:GLY:HA2	1:ED:25:SER:HB2	1.71	0.71
1:EE:42:LEU:O	1:EG:94:ARG:NH1	2.24	0.71
1:EH:42:LEU:O	1:EJ:94:ARG:NH1	2.24	0.71
1:EI:27:ASN:OD1	1:EI:28:GLY:N	2.19	0.71
1:EW:42:LEU:O	1:EY:94:ARG:NH1	2.23	0.71
1:FD:28:GLY:HA2	1:FE:25:SER:HB2	1.71	0.71
1:FM:28:GLY:HA2	1:FN:25:SER:HB2	1.71	0.71
1:FX:42:LEU:O	1:FZ:94:ARG:NH1	2.24	0.71
1:GJ:42:LEU:O	1:GL:94:ARG:NH1	2.24	0.71
1:AV:42:LEU:O	1:AX:94:ARG:NH1	2.24	0.71
1:BO:28:GLY:HA2	1:BP:25:SER:HB2	1.71	0.71
1:BX:28:GLY:HA2	1:BY:25:SER:HB2	1.71	0.71
1:DD:42:LEU:O	1:DF:94:ARG:NH1	2.24	0.71
1:EX:28:GLY:HA2	1:EY:25:SER:HB2	1.71	0.71
1:FG:28:GLY:HA2	1:FH:25:SER:HB2	1.71	0.71
1:FY:28:GLY:HA2	1:FZ:25:SER:HB2	1.71	0.71
1:AJ:42:LEU:O	1:AL:94:ARG:NH1	2.24	0.71
1:AN:27:ASN:OD1	1:AN:28:GLY:N	2.19	0.71
1:AN:28:GLY:HA2	1:AO:25:SER:HB2	1.71	0.71
1:BH:42:LEU:O	1:BJ:94:ARG:NH1	2.24	0.71
1:BJ:75:ASP:HA	1:EV:95:ASN:HD21	1.54	0.71
1:BL:27:ASN:OD1	1:BL:28:GLY:N	2.19	0.71
1:DF:75:ASP:HA	1:GR:95:ASN:HD21	1.55	0.71
1:EF:72:VAL:HG22	1:EF:83:THR:HG22	1.73	0.71
1:EI:72:VAL:HG22	1:EI:83:THR:HG22	1.73	0.71
1:FD:72:VAL:HG22	1:FD:83:THR:HG22	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FL:42:LEU:O	1:FN:94:ARG:NH1	2.24	0.71
1:BX:27:ASN:OD1	1:BX:28:GLY:N	2.19	0.71
1:CA:28:GLY:HA2	1:CB:25:SER:HB2	1.71	0.71
1:CF:42:LEU:O	1:CH:94:ARG:NH1	2.24	0.71
1:CP:72:VAL:HG22	1:CP:83:THR:HG22	1.73	0.71
1:CU:42:LEU:O	1:CW:94:ARG:NH1	2.24	0.71
1:DB:72:VAL:HG22	1:DB:83:THR:HG22	1.73	0.71
1:DQ:72:VAL:HG22	1:DQ:83:THR:HG22	1.73	0.71
1:DT:28:GLY:HA2	1:DU:25:SER:HB2	1.71	0.71
1:EC:72:VAL:HG22	1:EC:83:THR:HG22	1.73	0.71
1:EO:72:VAL:HG22	1:EO:83:THR:HG22	1.73	0.71
1:FF:42:LEU:O	1:FH:94:ARG:NH1	2.24	0.71
1:GA:42:LEU:O	1:GC:94:ARG:NH1	2.24	0.71
1:GQ:27:ASN:OD1	1:GQ:28:GLY:N	2.19	0.71
1:AQ:72:VAL:HG22	1:AQ:83:THR:HG22	1.73	0.71
1:AS:42:LEU:O	1:AU:94:ARG:NH1	2.24	0.71
1:AW:72:VAL:HG22	1:AW:83:THR:HG22	1.73	0.71
1:BI:72:VAL:HG22	1:BI:83:THR:HG22	1.73	0.71
1:CD:72:VAL:HG22	1:CD:83:THR:HG22	1.73	0.71
1:CG:72:VAL:HG22	1:CG:83:THR:HG22	1.73	0.71
1:CP:28:GLY:HA2	1:CQ:25:SER:HB2	1.71	0.71
1:DA:42:LEU:O	1:DC:94:ARG:NH1	2.24	0.71
1:DP:42:LEU:O	1:DR:94:ARG:NH1	2.24	0.71
1:DV:137:LEU:HD13	1:GE:54:ILE:HG12	1.72	0.71
1:ER:72:VAL:HG22	1:ER:83:THR:HG22	1.73	0.71
1:FG:72:VAL:HG22	1:FG:83:THR:HG22	1.73	0.71
1:FR:42:LEU:O	1:FT:94:ARG:NH1	2.23	0.71
1:GN:72:VAL:HG22	1:GN:83:THR:HG22	1.73	0.71
1:GP:42:LEU:O	1:GR:94:ARG:NH1	2.24	0.71
1:GW:72:VAL:HG22	1:GW:83:THR:HG22	1.73	0.71
1:AE:72:VAL:HG22	1:AE:83:THR:HG22	1.73	0.71
1:AN:72:VAL:HG22	1:AN:83:THR:HG22	1.73	0.71
1:AY:42:LEU:O	1:BA:94:ARG:NH1	2.24	0.71
1:AZ:72:VAL:HG22	1:AZ:83:THR:HG22	1.73	0.71
1:BO:72:VAL:HG22	1:BO:83:THR:HG22	1.73	0.71
1:CJ:72:VAL:HG22	1:CJ:83:THR:HG22	1.73	0.71
1:CM:72:VAL:HG22	1:CM:83:THR:HG22	1.73	0.71
1:DN:27:ASN:OD1	1:DN:28:GLY:N	2.19	0.71
1:DT:27:ASN:OD1	1:DT:28:GLY:N	2.19	0.71
1:FP:72:VAL:HG22	1:FP:83:THR:HG22	1.73	0.71
1:FV:28:GLY:HA2	1:FW:25:SER:HB2	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FV:72:VAL:HG22	1:FV:83:THR:HG22	1.73	0.71
1:GD:42:LEU:O	1:GF:94:ARG:NH1	2.24	0.71
1:GE:72:VAL:HG22	1:GE:83:THR:HG22	1.73	0.71
1:GT:72:VAL:HG22	1:GT:83:THR:HG22	1.73	0.71
1:AA:42:LEU:O	1:AC:94:ARG:NH1	2.24	0.71
1:BB:42:LEU:O	1:BD:94:ARG:NH1	2.24	0.71
1:BK:42:LEU:O	1:BM:94:ARG:NH1	2.24	0.71
1:CA:72:VAL:HG22	1:CA:83:THR:HG22	1.73	0.71
1:DN:72:VAL:HG22	1:DN:83:THR:HG22	1.73	0.71
1:EK:42:LEU:O	1:EM:94:ARG:NH1	2.24	0.71
1:EX:72:VAL:HG22	1:EX:83:THR:HG22	1.73	0.71
1:FI:42:LEU:O	1:FK:94:ARG:NH1	2.24	0.71
1:FM:72:VAL:HG22	1:FM:83:THR:HG22	1.73	0.71
1:AE:101:SER:HB2	1:GA:11:ASN:O	1.90	0.71
1:AH:72:VAL:HG22	1:AH:83:THR:HG22	1.73	0.71
1:DA:137:LEU:HD13	1:DE:54:ILE:HG12	1.70	0.71
1:DB:28:GLY:HA2	1:DC:25:SER:HB2	1.71	0.71
1:DE:72:VAL:HG22	1:DE:83:THR:HG22	1.73	0.71
1:DH:72:VAL:HG22	1:DH:83:THR:HG22	1.73	0.71
1:DK:28:GLY:HA2	1:DL:25:SER:HB2	1.71	0.71
1:DZ:72:VAL:HG22	1:DZ:83:THR:HG22	1.73	0.71
1:EO:94:ARG:NH1	1:EP:42:LEU:O	2.24	0.71
1:FA:28:GLY:HA2	1:FB:25:SER:HB2	1.71	0.71
1:FG:27:ASN:OD1	1:FG:28:GLY:N	2.19	0.71
1:GB:72:VAL:HG22	1:GB:83:THR:HG22	1.73	0.71
1:GG:42:LEU:O	1:GI:94:ARG:NH1	2.24	0.71
1:GK:72:VAL:HG22	1:GK:83:THR:HG22	1.73	0.71
1:GM:42:LEU:O	1:GO:94:ARG:NH1	2.24	0.71
1:AA:137:LEU:HD13	1:BI:54:ILE:HG12	1.72	0.70
1:BF:94:ARG:NH1	1:BG:42:LEU:O	2.24	0.70
1:BX:72:VAL:HG22	1:BX:83:THR:HG22	1.73	0.70
1:AB:94:ARG:NH1	1:AC:42:LEU:O	2.24	0.70
1:AK:72:VAL:HG22	1:AK:83:THR:HG22	1.73	0.70
1:BI:94:ARG:NH1	1:BJ:42:LEU:O	2.24	0.70
1:BN:42:LEU:O	1:BP:94:ARG:NH1	2.24	0.70
1:BP:11:ASN:O	1:FB:101:SER:HB2	1.90	0.70
1:BR:72:VAL:HG22	1:BR:83:THR:HG22	1.73	0.70
1:BR:94:ARG:NH1	1:BS:42:LEU:O	2.24	0.70
1:CI:42:LEU:O	1:CK:94:ARG:NH1	2.24	0.70
1:CS:72:VAL:HG22	1:CS:83:THR:HG22	1.73	0.70
1:CV:72:VAL:HG22	1:CV:83:THR:HG22	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:63:ASP:HB3	1:DE:137:LEU:HD11	1.73	0.70
1:DE:94:ARG:NH1	1:DF:42:LEU:O	2.24	0.70
1:DK:72:VAL:HG22	1:DK:83:THR:HG22	1.73	0.70
1:DW:94:ARG:NH1	1:DX:42:LEU:O	2.24	0.70
1:EZ:42:LEU:O	1:FB:94:ARG:NH1	2.24	0.70
1:FD:27:ASN:OD1	1:FD:28:GLY:N	2.19	0.70
1:FP:94:ARG:NH1	1:FQ:42:LEU:O	2.24	0.70
1:FY:94:ARG:NH1	1:FZ:42:LEU:O	2.24	0.70
1:GW:94:ARG:NH1	1:GX:42:LEU:O	2.24	0.70
1:AP:42:LEU:O	1:AR:94:ARG:NH1	2.24	0.70
1:BF:72:VAL:HG22	1:BF:83:THR:HG22	1.73	0.70
1:EF:94:ARG:NH1	1:EG:42:LEU:O	2.24	0.70
1:FM:27:ASN:OD1	1:FM:28:GLY:N	2.19	0.70
1:FV:94:ARG:NH1	1:FW:42:LEU:O	2.24	0.70
1:GH:94:ARG:NH1	1:GI:42:LEU:O	2.24	0.70
1:AK:94:ARG:NH1	1:AL:42:LEU:O	2.24	0.70
1:BU:72:VAL:HG22	1:BU:83:THR:HG22	1.73	0.70
1:BY:75:ASP:HA	1:FK:95:ASN:HD21	1.56	0.70
1:CC:42:LEU:O	1:CE:94:ARG:NH1	2.24	0.70
1:GE:94:ARG:NH1	1:GF:42:LEU:O	2.24	0.70
1:GQ:72:VAL:HG22	1:GQ:83:THR:HG22	1.73	0.70
1:AN:94:ARG:NH1	1:AO:42:LEU:O	2.24	0.70
1:BC:72:VAL:HG22	1:BC:83:THR:HG22	1.73	0.70
1:CL:42:LEU:O	1:CN:94:ARG:NH1	2.24	0.70
1:DV:42:LEU:O	1:DX:94:ARG:NH1	2.24	0.70
1:EI:28:GLY:HA2	1:EJ:25:SER:HB2	1.71	0.70
1:EL:72:VAL:HG22	1:EL:83:THR:HG22	1.73	0.70
1:EU:94:ARG:NH1	1:EV:42:LEU:O	2.24	0.70
1:FG:94:ARG:NH1	1:FH:42:LEU:O	2.24	0.70
1:FU:42:LEU:O	1:FW:94:ARG:NH1	2.24	0.70
1:AD:42:LEU:O	1:AF:94:ARG:NH1	2.24	0.70
1:BE:42:LEU:O	1:BG:94:ARG:NH1	2.24	0.70
1:BQ:42:LEU:O	1:BS:94:ARG:NH1	2.24	0.70
1:BU:94:ARG:NH1	1:BV:42:LEU:O	2.24	0.70
1:CM:94:ARG:NH1	1:CN:42:LEU:O	2.24	0.70
1:CY:72:VAL:HG22	1:CY:83:THR:HG22	1.73	0.70
1:DN:94:ARG:NH1	1:DO:42:LEU:O	2.24	0.70
1:EX:27:ASN:OD1	1:EX:28:GLY:N	2.19	0.70
1:GV:42:LEU:O	1:GX:94:ARG:NH1	2.23	0.70
1:AB:72:VAL:HG22	1:AB:83:THR:HG22	1.73	0.70
1:AG:42:LEU:O	1:AI:94:ARG:NH1	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:94:ARG:NH1	1:AI:42:LEU:O	2.24	0.70
1:BT:42:LEU:O	1:BV:94:ARG:NH1	2.24	0.70
1:CG:27:ASN:OD1	1:CG:28:GLY:N	2.19	0.70
1:DY:42:LEU:O	1:EA:94:ARG:NH1	2.24	0.70
1:ET:42:LEU:O	1:EV:94:ARG:NH1	2.24	0.70
1:FS:94:ARG:NH1	1:FT:42:LEU:O	2.24	0.70
1:GK:94:ARG:NH1	1:GL:42:LEU:O	2.24	0.70
1:GN:28:GLY:HA2	1:GO:25:SER:HB2	1.71	0.70
1:BL:94:ARG:NH1	1:BM:42:LEU:O	2.24	0.70
1:BW:42:LEU:O	1:BY:94:ARG:NH1	2.24	0.70
1:DC:118:SER:HB2	1:GO:8:VAL:HB	1.74	0.70
1:DH:94:ARG:NH1	1:DI:42:LEU:O	2.24	0.70
1:ER:94:ARG:NH1	1:ES:42:LEU:O	2.24	0.70
1:CR:42:LEU:O	1:CT:94:ARG:NH1	2.24	0.70
1:DW:72:VAL:HG22	1:DW:83:THR:HG22	1.73	0.70
1:EL:94:ARG:NH1	1:EM:42:LEU:O	2.24	0.70
1:FD:94:ARG:NH1	1:FE:42:LEU:O	2.24	0.70
1:AM:42:LEU:O	1:AO:94:ARG:NH1	2.24	0.70
1:BO:94:ARG:NH1	1:BP:42:LEU:O	2.24	0.70
1:CG:94:ARG:NH1	1:CH:42:LEU:O	2.24	0.70
1:CP:94:ARG:NH1	1:CQ:42:LEU:O	2.24	0.70
1:DK:94:ARG:NH1	1:DL:42:LEU:O	2.24	0.70
1:DM:42:LEU:O	1:DO:94:ARG:NH1	2.23	0.70
1:EQ:42:LEU:O	1:ES:94:ARG:NH1	2.24	0.70
1:FA:94:ARG:NH1	1:FB:42:LEU:O	2.24	0.70
1:AQ:94:ARG:NH1	1:AR:42:LEU:O	2.24	0.69
1:BL:72:VAL:HG22	1:BL:83:THR:HG22	1.73	0.69
1:BX:94:ARG:NH1	1:BY:42:LEU:O	2.24	0.69
1:CS:18:LEU:HG	1:DD:121:VAL:CG1	2.21	0.69
1:CX:42:LEU:O	1:CZ:94:ARG:NH1	2.24	0.69
1:DS:42:LEU:O	1:DU:94:ARG:NH1	2.24	0.69
1:DT:94:ARG:NH1	1:DU:42:LEU:O	2.24	0.69
1:EI:94:ARG:NH1	1:EJ:42:LEU:O	2.24	0.69
1:FS:72:VAL:HG22	1:FS:83:THR:HG22	1.73	0.69
1:AT:72:VAL:HG22	1:AT:83:THR:HG22	1.73	0.69
1:AT:94:ARG:NH1	1:AU:42:LEU:O	2.24	0.69
1:BC:94:ARG:NH1	1:BD:42:LEU:O	2.24	0.69
1:CA:94:ARG:NH1	1:CB:42:LEU:O	2.24	0.69
1:CJ:27:ASN:OD1	1:CJ:28:GLY:N	2.19	0.69
1:DB:94:ARG:NH1	1:DC:42:LEU:O	2.24	0.69
1:DZ:94:ARG:NH1	1:EA:42:LEU:O	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EC:94:ARG:NH1	1:ED:42:LEU:O	2.24	0.69
1:FJ:72:VAL:HG22	1:FJ:83:THR:HG22	1.73	0.69
1:FJ:94:ARG:NH1	1:FK:42:LEU:O	2.24	0.69
1:BK:137:LEU:HD13	1:DW:54:ILE:HG12	1.74	0.69
1:CD:94:ARG:NH1	1:CE:42:LEU:O	2.24	0.69
1:CS:73:VAL:CG1	1:DD:97:ALA:HB1	2.23	0.69
1:CV:94:ARG:NH1	1:CW:42:LEU:O	2.24	0.69
1:EX:94:ARG:NH1	1:EY:42:LEU:O	2.24	0.69
1:FA:72:VAL:HG22	1:FA:83:THR:HG22	1.73	0.69
1:AE:94:ARG:NH1	1:AF:42:LEU:O	2.24	0.69
1:BD:75:ASP:HA	1:EP:95:ASN:HD21	1.57	0.69
1:CB:118:SER:HB2	1:FN:8:VAL:HB	1.74	0.69
1:DJ:42:LEU:O	1:DL:94:ARG:NH1	2.24	0.69
1:DT:72:VAL:HG22	1:DT:83:THR:HG22	1.73	0.69
1:EU:72:VAL:HG22	1:EU:83:THR:HG22	1.73	0.69
1:FY:72:VAL:HG22	1:FY:83:THR:HG22	1.73	0.69
1:DB:54:ILE:HG12	1:GJ:137:LEU:HD13	1.74	0.69
1:DQ:94:ARG:NH1	1:DR:42:LEU:O	2.24	0.69
1:EB:42:LEU:O	1:ED:94:ARG:NH1	2.24	0.69
1:GB:94:ARG:NH1	1:GC:42:LEU:O	2.24	0.69
1:GH:72:VAL:HG22	1:GH:83:THR:HG22	1.73	0.69
1:AW:54:ILE:HG12	1:FC:137:LEU:HD13	1.72	0.69
1:CS:94:ARG:NH1	1:CT:42:LEU:O	2.24	0.69
1:CY:94:ARG:NH1	1:CZ:42:LEU:O	2.24	0.69
1:GT:94:ARG:NH1	1:GU:42:LEU:O	2.24	0.69
1:GN:94:ARG:NH1	1:GO:42:LEU:O	2.24	0.69
1:AE:27:ASN:OD1	1:AE:28:GLY:N	2.19	0.69
1:AZ:94:ARG:NH1	1:BA:42:LEU:O	2.24	0.69
1:BB:137:LEU:HD13	1:BR:54:ILE:HG12	1.73	0.69
1:BD:73:VAL:HG11	1:EP:97:ALA:O	1.93	0.69
1:CB:8:VAL:HB	1:FN:118:SER:HB2	1.74	0.69
1:CJ:94:ARG:NH1	1:CK:42:LEU:O	2.24	0.69
1:DB:27:ASN:OD1	1:DB:28:GLY:N	2.19	0.69
1:DG:42:LEU:O	1:DI:94:ARG:NH1	2.24	0.69
1:GH:27:ASN:OD1	1:GH:28:GLY:N	2.19	0.69
1:GQ:94:ARG:NH1	1:GR:42:LEU:O	2.24	0.69
1:AP:121:VAL:HG11	1:BU:18:LEU:HG	1.74	0.69
1:FA:52:PHE:CD1	1:FL:137:LEU:HD22	2.28	0.69
1:FS:112:ASP:HB2	1:FS:118:SER:HB3	1.75	0.69
1:GB:112:ASP:HB2	1:GB:118:SER:HB3	1.75	0.69
1:BR:112:ASP:HB2	1:BR:118:SER:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FM:94:ARG:NH1	1:FN:42:LEU:O	2.24	0.68
1:AE:112:ASP:HB2	1:AE:118:SER:HB3	1.75	0.68
1:AU:95:ASN:HD21	1:EG:75:ASP:HA	1.58	0.68
1:AW:94:ARG:NH1	1:AX:42:LEU:O	2.24	0.68
1:BU:27:ASN:OD1	1:BU:28:GLY:N	2.19	0.68
1:CJ:52:PHE:CD1	1:CO:137:LEU:HD22	2.27	0.68
1:DQ:27:ASN:OD1	1:DQ:28:GLY:N	2.19	0.68
1:FS:52:PHE:CD1	1:GP:137:LEU:HD22	2.29	0.68
1:GK:112:ASP:HB2	1:GK:118:SER:HB3	1.75	0.68
1:AV:63:ASP:HB3	1:EF:137:LEU:HD11	1.76	0.68
1:AZ:112:ASP:HB2	1:AZ:118:SER:HB3	1.75	0.68
1:EL:112:ASP:HB2	1:EL:118:SER:HB3	1.75	0.68
1:AP:54:ILE:HG12	1:BU:137:LEU:HD13	1.74	0.68
1:EB:73:VAL:HG11	1:GB:97:ALA:O	1.93	0.68
1:FJ:27:ASN:OD1	1:FJ:28:GLY:N	2.19	0.68
1:CJ:95:ASN:HD21	1:CO:75:ASP:HA	1.58	0.68
1:CS:75:ASP:OD1	1:DE:79:ASN:ND2	2.26	0.68
1:EI:112:ASP:HB2	1:EI:118:SER:HB3	1.75	0.68
1:EX:112:ASP:HB2	1:EX:118:SER:HB3	1.75	0.68
1:AE:95:ASN:HD21	1:GA:75:ASP:HA	1.59	0.68
1:DA:101:SER:HB2	1:DE:11:ASN:O	1.92	0.68
1:DE:112:ASP:HB2	1:DE:118:SER:HB3	1.75	0.68
1:DI:137:LEU:HD13	1:GU:54:ILE:HG12	1.76	0.68
1:EO:112:ASP:HB2	1:EO:118:SER:HB3	1.75	0.68
1:FV:112:ASP:HB2	1:FV:118:SER:HB3	1.75	0.68
1:FY:112:ASP:HB2	1:FY:118:SER:HB3	1.75	0.68
1:GT:112:ASP:HB2	1:GT:118:SER:HB3	1.75	0.68
1:CG:112:ASP:HB2	1:CG:118:SER:HB3	1.75	0.68
1:CY:112:ASP:HB2	1:CY:118:SER:HB3	1.75	0.68
1:FM:112:ASP:HB2	1:FM:118:SER:HB3	1.75	0.68
1:CU:137:LEU:HD11	1:DH:63:ASP:HB3	1.76	0.68
1:DZ:112:ASP:HB2	1:DZ:118:SER:HB3	1.75	0.68
1:GN:112:ASP:HB2	1:GN:118:SER:HB3	1.75	0.68
1:AH:112:ASP:HB2	1:AH:118:SER:HB3	1.75	0.68
1:AK:54:ILE:HG12	1:FO:137:LEU:HD13	1.76	0.68
1:DB:112:ASP:HB2	1:DB:118:SER:HB3	1.75	0.68
1:CW:118:SER:HB2	1:GI:8:VAL:HB	1.74	0.68
1:EF:112:ASP:HB2	1:EF:118:SER:HB3	1.75	0.68
1:EN:137:LEU:HD11	1:FJ:63:ASP:HB3	1.76	0.68
1:FP:112:ASP:HB2	1:FP:118:SER:HB3	1.75	0.68
1:AK:112:ASP:HB2	1:AK:118:SER:HB3	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:112:ASP:HB2	1:AT:118:SER:HB3	1.75	0.67
1:AZ:118:SER:HB2	1:EW:8:VAL:HB	1.76	0.67
1:GH:112:ASP:HB2	1:GH:118:SER:HB3	1.75	0.67
1:AB:112:ASP:HB2	1:AB:118:SER:HB3	1.75	0.67
1:CA:27:ASN:OD1	1:CA:28:GLY:N	2.19	0.67
1:FD:112:ASP:HB2	1:FD:118:SER:HB3	1.75	0.67
1:GE:112:ASP:HB2	1:GE:118:SER:HB3	1.75	0.67
1:AM:73:VAL:CG2	1:CA:102:MET:HE1	2.25	0.67
1:FG:112:ASP:HB2	1:FG:118:SER:HB3	1.75	0.67
1:FJ:112:ASP:HB2	1:FJ:118:SER:HB3	1.75	0.67
1:AP:18:LEU:HG	1:BU:121:VAL:HG11	1.75	0.67
1:AW:112:ASP:HB2	1:AW:118:SER:HB3	1.75	0.67
1:CA:112:ASP:HB2	1:CA:118:SER:HB3	1.75	0.67
1:DH:112:ASP:HB2	1:DH:118:SER:HB3	1.75	0.67
1:EU:112:ASP:HB2	1:EU:118:SER:HB3	1.75	0.67
1:BO:27:ASN:OD1	1:BO:28:GLY:N	2.19	0.67
1:CD:112:ASP:HB2	1:CD:118:SER:HB3	1.75	0.67
1:CM:112:ASP:HB2	1:CM:118:SER:HB3	1.75	0.67
1:CP:112:ASP:HB2	1:CP:118:SER:HB3	1.75	0.67
1:ER:112:ASP:HB2	1:ER:118:SER:HB3	1.75	0.67
1:FA:112:ASP:HB2	1:FA:118:SER:HB3	1.75	0.67
1:AN:112:ASP:HB2	1:AN:118:SER:HB3	1.75	0.67
1:AQ:112:ASP:HB2	1:AQ:118:SER:HB3	1.75	0.67
1:CE:95:ASN:HD21	1:FQ:75:ASP:HA	1.57	0.67
1:CJ:112:ASP:HB2	1:CJ:118:SER:HB3	1.75	0.67
1:CP:27:ASN:OD1	1:CP:28:GLY:N	2.19	0.67
1:BI:112:ASP:HB2	1:BI:118:SER:HB3	1.75	0.67
1:DL:73:VAL:HG11	1:GX:97:ALA:O	1.94	0.67
1:AH:137:LEU:HD13	1:GD:54:ILE:HG12	1.76	0.67
1:CV:112:ASP:HB2	1:CV:118:SER:HB3	1.75	0.67
1:DI:75:ASP:HA	1:GU:95:ASN:HD21	1.59	0.67
1:DN:112:ASP:HB2	1:DN:118:SER:HB3	1.75	0.67
1:DQ:112:ASP:HB2	1:DQ:118:SER:HB3	1.75	0.67
1:AI:75:ASP:HA	1:DU:95:ASN:HD21	1.60	0.67
1:BP:75:ASP:HA	1:FB:95:ASN:HD21	1.60	0.67
1:CN:95:ASN:HD21	1:FZ:75:ASP:HA	1.58	0.67
1:BG:95:ASN:HD21	1:ES:75:ASP:HA	1.60	0.67
1:BP:54:ILE:HG12	1:FB:137:LEU:HD13	1.75	0.67
1:BX:112:ASP:HB2	1:BX:118:SER:HB3	1.75	0.67
1:CS:27:ASN:OD1	1:CS:28:GLY:N	2.19	0.67
1:GQ:112:ASP:HB2	1:GQ:118:SER:HB3	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:112:ASP:HB2	1:BC:118:SER:HB3	1.75	0.66
1:BL:112:ASP:HB2	1:BL:118:SER:HB3	1.75	0.66
1:DA:18:LEU:HG	1:DE:121:VAL:HG11	1.75	0.66
1:DK:112:ASP:HB2	1:DK:118:SER:HB3	1.75	0.66
1:BU:112:ASP:HB2	1:BU:118:SER:HB3	1.75	0.66
1:CD:27:ASN:OD1	1:CD:28:GLY:N	2.19	0.66
1:CD:73:VAL:HG11	1:CR:97:ALA:O	1.94	0.66
1:AZ:54:ILE:HG12	1:EW:137:LEU:HD13	1.78	0.66
1:BF:112:ASP:HB2	1:BF:118:SER:HB3	1.75	0.66
1:BO:112:ASP:HB2	1:BO:118:SER:HB3	1.75	0.66
1:BS:75:ASP:HA	1:FE:95:ASN:HD21	1.61	0.66
1:DW:112:ASP:HB2	1:DW:118:SER:HB3	1.75	0.66
1:EN:118:SER:HB2	1:FJ:8:VAL:HB	1.75	0.66
1:AD:8:VAL:HB	1:BC:118:SER:HB2	1.78	0.66
1:CS:112:ASP:HB2	1:CS:118:SER:HB3	1.75	0.66
1:EC:112:ASP:HB2	1:EC:118:SER:HB3	1.75	0.66
1:GW:112:ASP:HB2	1:GW:118:SER:HB3	1.75	0.66
1:BS:95:ASN:HD21	1:FE:75:ASP:HA	1.61	0.66
1:CN:118:SER:HB2	1:FZ:8:VAL:HB	1.77	0.66
1:FA:54:ILE:HG12	1:FL:137:LEU:CD1	2.22	0.66
1:AO:118:SER:HB2	1:EA:8:VAL:HB	1.78	0.66
1:CZ:75:ASP:HA	1:GL:95:ASN:HD21	1.60	0.66
1:DT:112:ASP:HB2	1:DT:118:SER:HB3	1.75	0.66
1:AM:18:LEU:HG	1:CA:121:VAL:HG11	1.78	0.66
1:BZ:137:LEU:HD22	1:DT:52:PHE:CD1	2.31	0.66
1:CB:95:ASN:HD21	1:FN:75:ASP:HA	1.61	0.66
1:AK:8:VAL:HB	1:FO:118:SER:HB2	1.78	0.66
1:AQ:137:LEU:HA	1:FU:52:PHE:CE1	2.31	0.66
1:AQ:137:LEU:HA	1:FU:52:PHE:HE1	1.60	0.66
1:BP:19:VAL:HG21	1:FB:109:GLN:NE2	2.11	0.66
1:AR:102:MET:HE1	1:ED:73:VAL:CG2	2.26	0.65
1:AS:109:GLN:NE2	1:EL:19:VAL:HG21	2.11	0.65
1:CG:8:VAL:HB	1:CL:118:SER:HB2	1.78	0.65
1:CK:95:ASN:HD21	1:FW:75:ASP:HA	1.62	0.65
1:BT:118:SER:HB2	1:DN:8:VAL:HB	1.79	0.65
1:AR:8:VAL:HB	1:ED:118:SER:HB2	1.77	0.65
1:DA:8:VAL:HB	1:DE:118:SER:HB2	1.78	0.65
1:FP:118:SER:HB2	1:GV:8:VAL:HB	1.78	0.65
1:AU:54:ILE:HG12	1:EG:137:LEU:HD13	1.78	0.65
1:EQ:8:VAL:HB	1:FM:118:SER:HB2	1.79	0.65
1:ET:97:ALA:O	1:FG:73:VAL:HG11	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FD:137:LEU:HA	1:FF:52:PHE:HE1	1.61	0.65
1:BA:75:ASP:HA	1:EM:95:ASN:HD21	1.59	0.65
1:BP:118:SER:HB2	1:FB:8:VAL:HB	1.79	0.65
1:BP:137:LEU:HD11	1:FB:63:ASP:HB3	1.79	0.65
1:DB:137:LEU:HD13	1:GJ:54:ILE:HG12	1.77	0.65
1:CH:95:ASN:HD21	1:FT:75:ASP:HA	1.61	0.65
1:EB:109:GLN:NE2	1:GB:19:VAL:HG21	2.11	0.65
1:AX:97:ALA:O	1:EJ:73:VAL:HG11	1.97	0.65
1:CB:137:LEU:HD11	1:FN:63:ASP:HB3	1.79	0.65
1:CI:118:SER:HB2	1:GH:8:VAL:HB	1.79	0.65
1:CT:36:THR:HG22	1:DD:138:MET:HE3	1.79	0.65
1:CN:97:ALA:O	1:FZ:73:VAL:HG11	1.97	0.65
1:CQ:63:ASP:CB	1:GC:137:LEU:HD11	2.27	0.65
1:EB:8:VAL:HB	1:GB:118:SER:HB2	1.78	0.64
1:CT:118:SER:HB2	1:GF:8:VAL:HB	1.79	0.64
1:AN:52:PHE:CD1	1:FR:137:LEU:HD22	2.32	0.64
1:AX:73:VAL:HG11	1:EJ:97:ALA:O	1.97	0.64
1:CC:8:VAL:HB	1:GK:118:SER:HB2	1.79	0.64
1:CU:18:LEU:HG	1:DH:121:VAL:HG11	1.80	0.64
1:CZ:95:ASN:HD21	1:GL:75:ASP:HA	1.63	0.64
1:CS:118:SER:HB2	1:DD:8:VAL:HB	1.79	0.64
1:CV:24:ARG:HA	1:DH:138:MET:HE3	1.79	0.64
1:AI:137:LEU:HD13	1:DU:54:ILE:HG12	1.79	0.64
1:AR:98:TRP:CH2	1:ED:84:GLY:HA3	2.33	0.64
1:DF:121:VAL:HG11	1:GR:18:LEU:HG	1.80	0.64
1:CV:19:VAL:HG21	1:GM:109:GLN:NE2	2.12	0.64
1:EH:137:LEU:HD13	1:EO:54:ILE:HG12	1.79	0.64
1:FP:137:LEU:HD13	1:GV:54:ILE:HG12	1.78	0.64
1:AQ:54:ILE:HG12	1:FU:137:LEU:HD13	1.80	0.64
1:BY:95:ASN:HD21	1:FK:75:ASP:HA	1.62	0.64
1:CQ:75:ASP:HA	1:GC:95:ASN:HD21	1.61	0.64
1:AX:8:VAL:HB	1:EJ:118:SER:HB2	1.79	0.64
1:CT:54:ILE:HG12	1:GF:137:LEU:HD13	1.79	0.64
1:CU:121:VAL:HG11	1:DH:18:LEU:HG	1.79	0.64
1:EE:54:ILE:HG12	1:EU:137:LEU:HD13	1.79	0.64
1:FD:118:SER:HB2	1:FF:8:VAL:HB	1.79	0.64
1:AV:109:GLN:NE2	1:EF:19:VAL:HG21	2.12	0.63
1:BH:8:VAL:HB	1:BO:118:SER:HB2	1.80	0.63
1:AU:118:SER:HB2	1:EG:8:VAL:HB	1.79	0.63
1:CU:11:ASN:O	1:DH:101:SER:HB2	1.99	0.63
1:AQ:118:SER:HB2	1:FU:8:VAL:HB	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:137:LEU:HD22	1:EL:52:PHE:CD1	2.34	0.63
1:AX:89:GLN:HB3	1:EJ:87:THR:HG23	1.81	0.63
1:DA:29:ASN:HA	1:DE:139:PHE:HE2	1.64	0.63
1:AF:95:ASN:HD21	1:DR:75:ASP:HA	1.64	0.63
1:BJ:97:ALA:O	1:EV:73:VAL:HG11	1.97	0.63
1:CJ:101:SER:HB2	1:CO:11:ASN:O	1.98	0.63
1:FD:137:LEU:HA	1:FF:52:PHE:CE1	2.34	0.63
1:AE:10:ALA:HB1	1:AE:14:LEU:HA	1.81	0.63
1:AJ:118:SER:HB2	1:BX:8:VAL:HB	1.81	0.63
1:AH:10:ALA:HB1	1:AH:14:LEU:HA	1.81	0.63
1:BO:10:ALA:HB1	1:BO:14:LEU:HA	1.81	0.63
1:CY:52:PHE:CD1	1:GG:137:LEU:HD22	2.33	0.63
1:FV:137:LEU:HD13	1:GS:54:ILE:HG12	1.80	0.63
1:AS:54:ILE:HG12	1:EL:137:LEU:HD13	1.80	0.62
1:AV:8:VAL:HB	1:EF:118:SER:HB2	1.80	0.62
1:BV:87:THR:CG2	1:FH:89:GLN:HB3	2.29	0.62
1:CJ:10:ALA:HB1	1:CJ:14:LEU:HA	1.81	0.62
1:DL:118:SER:HB2	1:GX:8:VAL:HB	1.81	0.62
1:FD:8:VAL:HB	1:FF:118:SER:HB2	1.81	0.62
1:CG:10:ALA:HB1	1:CG:14:LEU:HA	1.81	0.62
1:CH:118:SER:HB2	1:FT:8:VAL:HB	1.80	0.62
1:CM:117:THR:HB	1:DG:117:THR:O	1.99	0.62
1:CW:137:LEU:HD11	1:GI:63:ASP:HB3	1.81	0.62
1:EN:125:THR:HG21	1:FJ:5:LEU:HA	1.80	0.62
1:BJ:118:SER:HB2	1:EV:8:VAL:HB	1.80	0.62
1:GW:10:ALA:HB1	1:GW:14:LEU:HA	1.81	0.62
1:BF:10:ALA:HB1	1:BF:14:LEU:HA	1.81	0.62
1:BV:95:ASN:ND2	1:FH:75:ASP:HA	2.13	0.62
1:BW:137:LEU:HD22	1:DQ:52:PHE:CD1	2.35	0.62
1:DL:137:LEU:HD12	1:GV:42:LEU:HD22	1.81	0.62
1:DZ:10:ALA:HB1	1:DZ:14:LEU:HA	1.81	0.62
1:EL:10:ALA:HB1	1:EL:14:LEU:HA	1.81	0.62
1:FA:101:SER:HB2	1:FL:11:ASN:O	1.98	0.62
1:FP:10:ALA:HB1	1:FP:14:LEU:HA	1.81	0.62
1:GK:10:ALA:HB1	1:GK:14:LEU:HA	1.81	0.62
1:BI:10:ALA:HB1	1:BI:14:LEU:HA	1.81	0.62
1:CI:73:VAL:CG2	1:GH:102:MET:HE1	2.29	0.62
1:DF:8:VAL:HB	1:GR:118:SER:HB2	1.81	0.62
1:EE:118:SER:HB2	1:EU:8:VAL:HB	1.82	0.62
1:AH:137:LEU:HA	1:GD:52:PHE:HE1	1.65	0.62
1:AO:75:ASP:HA	1:EA:95:ASN:HD21	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:10:ALA:HB1	1:AZ:14:LEU:HA	1.81	0.62
1:FD:10:ALA:HB1	1:FD:14:LEU:HA	1.81	0.62
1:FS:10:ALA:HB1	1:FS:14:LEU:HA	1.81	0.62
1:AQ:10:ALA:HB1	1:AQ:14:LEU:HA	1.81	0.62
1:BJ:89:GLN:HB3	1:EV:87:THR:CG2	2.30	0.62
1:BX:10:ALA:HB1	1:BX:14:LEU:HA	1.81	0.62
1:FV:10:ALA:HB1	1:FV:14:LEU:HA	1.81	0.62
1:GT:10:ALA:HB1	1:GT:14:LEU:HA	1.81	0.62
1:CC:54:ILE:HG12	1:GK:137:LEU:HD13	1.82	0.62
1:FM:10:ALA:HB1	1:FM:14:LEU:HA	1.81	0.62
1:AK:10:ALA:HB1	1:AK:14:LEU:HA	1.81	0.62
1:CY:10:ALA:HB1	1:CY:14:LEU:HA	1.81	0.62
1:DQ:10:ALA:HB1	1:DQ:14:LEU:HA	1.81	0.62
1:BR:10:ALA:HB1	1:BR:14:LEU:HA	1.81	0.62
1:CD:10:ALA:HB1	1:CD:14:LEU:HA	1.81	0.62
1:DW:10:ALA:HB1	1:DW:14:LEU:HA	1.81	0.62
1:EI:10:ALA:HB1	1:EI:14:LEU:HA	1.81	0.62
1:ER:10:ALA:HB1	1:ER:14:LEU:HA	1.81	0.62
1:FY:10:ALA:HB1	1:FY:14:LEU:HA	1.81	0.62
1:AN:10:ALA:HB1	1:AN:14:LEU:HA	1.81	0.61
1:AW:10:ALA:HB1	1:AW:14:LEU:HA	1.81	0.61
1:CB:6:ALA:HB3	1:FN:124:GLN:HA	1.82	0.61
1:CP:10:ALA:HB1	1:CP:14:LEU:HA	1.81	0.61
1:CS:10:ALA:HB1	1:CS:14:LEU:HA	1.81	0.61
1:DL:97:ALA:O	1:GX:73:VAL:HG11	2.00	0.61
1:AQ:19:VAL:HG21	1:FU:109:GLN:NE2	2.15	0.61
1:CW:8:VAL:HB	1:GI:118:SER:HB2	1.81	0.61
1:DB:137:LEU:HA	1:GJ:52:PHE:HE1	1.64	0.61
1:EE:18:LEU:HG	1:EU:121:VAL:CG1	2.30	0.61
1:EN:124:GLN:HA	1:FJ:6:ALA:HB3	1.81	0.61
1:BL:10:ALA:HB1	1:BL:14:LEU:HA	1.81	0.61
1:CV:118:SER:HB2	1:GM:8:VAL:HB	1.82	0.61
1:FG:10:ALA:HB1	1:FG:14:LEU:HA	1.81	0.61
1:GB:10:ALA:HB1	1:GB:14:LEU:HA	1.81	0.61
1:CM:10:ALA:HB1	1:CM:14:LEU:HA	1.81	0.61
1:CS:88:ILE:HD11	1:DD:110:ALA:HB1	1.83	0.61
1:CW:97:ALA:O	1:GI:73:VAL:HG11	2.01	0.61
1:DN:10:ALA:HB1	1:DN:14:LEU:HA	1.81	0.61
1:EF:10:ALA:HB1	1:EF:14:LEU:HA	1.81	0.61
1:EX:10:ALA:HB1	1:EX:14:LEU:HA	1.81	0.61
1:FJ:10:ALA:HB1	1:FJ:14:LEU:HA	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GE:10:ALA:HB1	1:GE:14:LEU:HA	1.81	0.61
1:AP:8:VAL:HB	1:BU:118:SER:HB2	1.82	0.61
1:DH:10:ALA:HB1	1:DH:14:LEU:HA	1.81	0.61
1:DK:10:ALA:HB1	1:DK:14:LEU:HA	1.81	0.61
1:CV:10:ALA:HB1	1:CV:14:LEU:HA	1.81	0.61
1:GH:10:ALA:HB1	1:GH:14:LEU:HA	1.81	0.61
1:EE:97:ALA:HB1	1:EU:73:VAL:HG12	1.82	0.61
1:AB:10:ALA:HB1	1:AB:14:LEU:HA	1.81	0.61
1:AJ:8:VAL:HB	1:BX:118:SER:HB2	1.82	0.61
1:AT:10:ALA:HB1	1:AT:14:LEU:HA	1.81	0.61
1:BU:10:ALA:HB1	1:BU:14:LEU:HA	1.81	0.61
1:CC:52:PHE:HE1	1:GK:137:LEU:HA	1.66	0.61
1:DT:10:ALA:HB1	1:DT:14:LEU:HA	1.81	0.61
1:EO:10:ALA:HB1	1:EO:14:LEU:HA	1.81	0.61
1:FA:10:ALA:HB1	1:FA:14:LEU:HA	1.81	0.61
1:FA:95:ASN:HD21	1:FL:75:ASP:HA	1.66	0.61
1:BD:118:SER:HB2	1:EP:8:VAL:HB	1.83	0.61
1:GN:10:ALA:HB1	1:GN:14:LEU:HA	1.81	0.61
1:AP:97:ALA:O	1:BU:73:VAL:HG11	2.01	0.61
1:BJ:8:VAL:HB	1:EV:118:SER:HB2	1.81	0.61
1:CU:52:PHE:HE1	1:DH:137:LEU:HA	1.66	0.61
1:DB:10:ALA:HB1	1:DB:14:LEU:HA	1.81	0.61
1:DC:117:THR:O	1:GO:117:THR:HB	2.01	0.61
1:DE:10:ALA:HB1	1:DE:14:LEU:HA	1.81	0.61
1:DY:8:VAL:HB	1:FY:118:SER:HB2	1.83	0.61
1:CA:10:ALA:HB1	1:CA:14:LEU:HA	1.81	0.60
1:CU:8:VAL:HB	1:DH:118:SER:HB2	1.83	0.60
1:BJ:90:VAL:HG22	1:EV:86:VAL:HG22	1.83	0.60
1:EU:10:ALA:HB1	1:EU:14:LEU:HA	1.81	0.60
1:AH:137:LEU:HA	1:GD:52:PHE:CE1	2.37	0.60
1:AX:118:SER:HB2	1:EJ:8:VAL:HB	1.83	0.60
1:BV:87:THR:HG23	1:FH:89:GLN:HB3	1.83	0.60
1:EB:137:LEU:HD22	1:GB:52:PHE:CD1	2.36	0.60
1:GQ:10:ALA:HB1	1:GQ:14:LEU:HA	1.81	0.60
1:CC:52:PHE:CE1	1:GK:137:LEU:HA	2.36	0.60
1:CD:118:SER:HB2	1:CR:8:VAL:HB	1.83	0.60
1:DP:137:LEU:HD13	1:GW:54:ILE:HG12	1.83	0.60
1:AR:73:VAL:HG11	1:ED:97:ALA:O	2.01	0.60
1:CP:8:VAL:HB	1:DJ:118:SER:HB2	1.83	0.60
1:DC:8:VAL:HB	1:GO:118:SER:HB2	1.82	0.60
1:DP:52:PHE:HE1	1:GW:137:LEU:HA	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EC:10:ALA:HB1	1:EC:14:LEU:HA	1.81	0.60
1:FS:54:ILE:HG12	1:GP:137:LEU:HD13	1.83	0.60
1:AE:105:SER:CB	1:GA:10:ALA:H	2.14	0.60
1:AL:75:ASP:HA	1:DX:95:ASN:HD21	1.67	0.60
1:BC:10:ALA:HB1	1:BC:14:LEU:HA	1.81	0.60
1:CD:97:ALA:O	1:CR:73:VAL:HG11	2.01	0.60
1:CS:137:LEU:HD13	1:DD:54:ILE:HG12	1.83	0.60
1:CT:86:VAL:HG22	1:GF:90:VAL:HG22	1.83	0.60
1:CT:87:THR:CG2	1:GF:89:GLN:HB3	2.32	0.60
1:AS:137:LEU:HD13	1:EL:54:ILE:HG12	1.83	0.60
1:FV:137:LEU:HA	1:GS:52:PHE:HE1	1.67	0.60
1:BJ:89:GLN:HB3	1:EV:87:THR:HG23	1.84	0.60
1:DA:137:LEU:HD11	1:DE:63:ASP:HB3	1.83	0.60
1:EE:110:ALA:HB1	1:EU:88:ILE:HD11	1.83	0.60
1:EN:29:ASN:HA	1:FJ:139:PHE:HE2	1.66	0.60
1:DF:19:VAL:HG21	1:GR:109:GLN:NE2	2.15	0.59
1:EN:52:PHE:CE1	1:FJ:137:LEU:HA	2.37	0.59
1:AE:109:GLN:NE2	1:GA:19:VAL:HG21	2.17	0.59
1:BP:95:ASN:ND2	1:FB:75:ASP:HA	2.14	0.59
1:EN:52:PHE:HE1	1:FJ:137:LEU:HA	1.67	0.59
1:AW:137:LEU:HA	1:FC:52:PHE:HE1	1.67	0.59
1:CJ:54:ILE:HG12	1:CO:137:LEU:CD1	2.27	0.59
1:AC:75:ASP:HA	1:DO:95:ASN:HD21	1.67	0.59
1:CG:137:LEU:HD13	1:CL:54:ILE:HG12	1.83	0.59
1:CT:8:VAL:HB	1:GF:118:SER:HB2	1.85	0.59
1:CK:117:THR:O	1:FW:117:THR:HB	2.02	0.59
1:DB:63:ASP:HB3	1:GJ:137:LEU:HD11	1.84	0.59
1:ET:73:VAL:HG11	1:FG:97:ALA:O	2.03	0.59
1:AZ:8:VAL:HB	1:EW:118:SER:HB2	1.85	0.59
1:CP:19:VAL:HG21	1:DJ:109:GLN:NE2	2.18	0.59
1:DS:117:THR:O	1:GQ:117:THR:HB	2.03	0.59
1:FS:19:VAL:HG21	1:GP:109:GLN:NE2	2.17	0.59
1:AW:112:ASP:OD1	1:AW:118:SER:OG	2.16	0.59
1:CU:52:PHE:CE1	1:DH:137:LEU:HA	2.37	0.59
1:DB:137:LEU:HA	1:GJ:52:PHE:CE1	2.37	0.59
1:AH:63:ASP:HB3	1:GD:137:LEU:HD11	1.84	0.59
1:AR:75:ASP:HA	1:ED:95:ASN:HD21	1.67	0.59
1:AX:87:THR:HG23	1:EJ:89:GLN:HB3	1.85	0.59
1:BH:52:PHE:HE1	1:BO:137:LEU:HA	1.68	0.59
1:BH:118:SER:HB2	1:BO:8:VAL:HB	1.85	0.59
1:CC:137:LEU:HD22	1:GK:52:PHE:CD1	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EH:109:GLN:NE2	1:EO:19:VAL:HG21	2.18	0.59
1:AP:42:LEU:HD22	1:ED:137:LEU:HD12	1.83	0.59
1:DS:8:VAL:HB	1:GQ:118:SER:HB2	1.85	0.59
1:ER:112:ASP:OD1	1:ER:118:SER:OG	2.16	0.59
1:CG:63:ASP:HB3	1:CL:137:LEU:HD11	1.85	0.59
1:EL:112:ASP:OD1	1:EL:118:SER:OG	2.16	0.59
1:BV:75:ASP:HA	1:FH:95:ASN:ND2	2.17	0.58
1:AG:137:LEU:HD13	1:BF:54:ILE:HG12	1.85	0.58
1:AW:137:LEU:HD13	1:FC:54:ILE:HG12	1.83	0.58
1:BB:137:LEU:HD22	1:BR:52:PHE:CD1	2.38	0.58
1:BM:8:VAL:HB	1:EY:118:SER:HB2	1.84	0.58
1:CQ:95:ASN:HD21	1:GC:75:ASP:HA	1.67	0.58
1:AD:118:SER:HB2	1:BC:8:VAL:HB	1.85	0.58
1:BZ:117:THR:O	1:DT:117:THR:HB	2.04	0.58
1:CW:121:VAL:HG11	1:GI:18:LEU:HG	1.86	0.58
1:FA:109:GLN:NE2	1:FL:19:VAL:HG21	2.19	0.58
1:AG:110:ALA:HB1	1:BF:88:ILE:HD11	1.85	0.58
1:BJ:87:THR:CG2	1:EV:89:GLN:HB3	2.33	0.58
1:BY:63:ASP:HB3	1:FK:137:LEU:HD11	1.84	0.58
1:CK:117:THR:OG1	1:FW:117:THR:OG1	2.21	0.58
1:BA:118:SER:HB2	1:EM:8:VAL:HB	1.85	0.58
1:BG:118:SER:HB2	1:ES:8:VAL:HB	1.85	0.58
1:BJ:19:VAL:HG21	1:EV:109:GLN:NE2	2.18	0.58
1:BJ:87:THR:HG23	1:EV:89:GLN:HB3	1.85	0.58
1:BJ:95:ASN:HD21	1:EV:75:ASP:CA	2.06	0.58
1:CG:18:LEU:HG	1:CL:121:VAL:HG11	1.86	0.58
1:EN:18:LEU:HG	1:FJ:121:VAL:CG1	2.30	0.58
1:BH:54:ILE:HG12	1:BO:137:LEU:HD13	1.84	0.58
1:CB:18:LEU:HG	1:FN:121:VAL:CG1	2.32	0.58
1:GT:112:ASP:OD1	1:GT:118:SER:OG	2.16	0.58
1:AB:54:ILE:HG12	1:FX:137:LEU:HD13	1.86	0.58
1:AM:118:SER:HB2	1:CA:8:VAL:HB	1.84	0.58
1:EE:122:SER:O	1:EU:18:LEU:HD11	2.03	0.58
1:BT:97:ALA:O	1:DN:73:VAL:HG11	2.03	0.58
1:DT:27:ASN:HB3	1:DT:30:ASN:OD1	2.04	0.58
1:AP:121:VAL:CG1	1:BU:18:LEU:HG	2.34	0.57
1:AV:18:LEU:HG	1:EF:121:VAL:HG11	1.85	0.57
1:BV:19:VAL:HG21	1:FH:109:GLN:NE2	2.19	0.57
1:EX:73:VAL:HG11	1:FI:97:ALA:O	2.04	0.57
1:AT:117:THR:HB	1:EZ:117:THR:O	2.04	0.57
1:CH:137:LEU:HD11	1:FT:63:ASP:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:27:ASN:HB3	1:CS:30:ASN:OD1	2.04	0.57
1:CV:97:ALA:O	1:GM:73:VAL:HG11	2.04	0.57
1:FG:27:ASN:HB3	1:FG:30:ASN:OD1	2.05	0.57
1:GQ:27:ASN:HB3	1:GQ:30:ASN:OD1	2.05	0.57
1:GT:27:ASN:HB3	1:GT:30:ASN:OD1	2.05	0.57
1:AE:42:LEU:HD22	1:BC:137:LEU:HD12	1.86	0.57
1:BG:8:VAL:HB	1:ES:118:SER:HB2	1.85	0.57
1:CB:63:ASP:CB	1:FN:137:LEU:HD11	2.35	0.57
1:CY:27:ASN:HB3	1:CY:30:ASN:OD1	2.04	0.57
1:DN:27:ASN:HB3	1:DN:30:ASN:OD1	2.05	0.57
1:DQ:27:ASN:HB3	1:DQ:30:ASN:OD1	2.04	0.57
1:EQ:88:ILE:HD11	1:FM:110:ALA:HB1	1.86	0.57
1:EX:27:ASN:HB3	1:EX:30:ASN:OD1	2.04	0.57
1:GK:27:ASN:HB3	1:GK:30:ASN:OD1	2.05	0.57
1:GN:27:ASN:HB3	1:GN:30:ASN:OD1	2.05	0.57
1:AT:27:ASN:HB3	1:AT:30:ASN:OD1	2.05	0.57
1:CJ:27:ASN:HB3	1:CJ:30:ASN:OD1	2.05	0.57
1:BP:10:ALA:H	1:FB:105:SER:CB	2.17	0.57
1:DW:27:ASN:HB3	1:DW:30:ASN:OD1	2.05	0.57
1:EF:27:ASN:HB3	1:EF:30:ASN:OD1	2.04	0.57
1:FA:27:ASN:HB3	1:FA:30:ASN:OD1	2.05	0.57
1:FM:27:ASN:HB3	1:FM:30:ASN:OD1	2.04	0.57
1:FP:27:ASN:HB3	1:FP:30:ASN:OD1	2.05	0.57
1:GH:27:ASN:HB3	1:GH:30:ASN:OD1	2.05	0.57
1:AN:27:ASN:HB3	1:AN:30:ASN:OD1	2.05	0.57
1:AW:137:LEU:HA	1:FC:52:PHE:CE1	2.39	0.57
1:BX:27:ASN:HB3	1:BX:30:ASN:OD1	2.04	0.57
1:CV:27:ASN:HB3	1:CV:30:ASN:OD1	2.04	0.57
1:DC:87:THR:HG23	1:GO:89:GLN:HB3	1.86	0.57
1:EC:27:ASN:HB3	1:EC:30:ASN:OD1	2.05	0.57
1:EE:102:MET:HE1	1:EU:73:VAL:HG22	1.85	0.57
1:FA:105:SER:CB	1:FL:10:ALA:H	2.17	0.57
1:FD:27:ASN:HB3	1:FD:30:ASN:OD1	2.04	0.57
1:GB:27:ASN:HB3	1:GB:30:ASN:OD1	2.04	0.57
1:AJ:117:THR:O	1:BX:117:THR:HB	2.04	0.57
1:AQ:27:ASN:HB3	1:AQ:30:ASN:OD1	2.04	0.57
1:AV:52:PHE:HD1	1:EF:137:LEU:HD22	1.70	0.57
1:AW:27:ASN:HB3	1:AW:30:ASN:OD1	2.04	0.57
1:CG:27:ASN:HB3	1:CG:30:ASN:OD1	2.05	0.57
1:CJ:89:GLN:HB3	1:CO:87:THR:OG1	2.04	0.57
1:DK:27:ASN:HB3	1:DK:30:ASN:OD1	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ER:27:ASN:HB3	1:ER:30:ASN:OD1	2.04	0.57
1:EU:27:ASN:HB3	1:EU:30:ASN:OD1	2.05	0.57
1:AD:52:PHE:HE2	1:BC:139:PHE:CE1	2.22	0.57
1:AE:27:ASN:HB3	1:AE:30:ASN:OD1	2.05	0.57
1:BD:18:LEU:HG	1:EP:121:VAL:HG11	1.86	0.57
1:BV:89:GLN:HB3	1:FH:87:THR:CG2	2.35	0.57
1:CQ:137:LEU:HD11	1:GC:63:ASP:CB	2.34	0.57
1:DP:54:ILE:HG12	1:GW:137:LEU:HD13	1.87	0.57
1:DZ:27:ASN:HB3	1:DZ:30:ASN:OD1	2.04	0.57
1:EK:137:LEU:HD22	1:ER:52:PHE:CD1	2.39	0.57
1:FS:27:ASN:HB3	1:FS:30:ASN:OD1	2.05	0.57
1:GW:27:ASN:HB3	1:GW:30:ASN:OD1	2.04	0.57
1:AH:27:ASN:HB3	1:AH:30:ASN:OD1	2.05	0.57
1:AO:8:VAL:HB	1:EA:118:SER:HB2	1.86	0.57
1:BC:55:LYS:HD2	1:BC:62:ASN:H	1.70	0.57
1:BY:101:SER:HB2	1:FK:11:ASN:O	2.04	0.57
1:CJ:105:SER:CB	1:CO:10:ALA:H	2.17	0.57
1:CP:27:ASN:HB3	1:CP:30:ASN:OD1	2.05	0.57
1:EF:112:ASP:OD1	1:EF:118:SER:OG	2.16	0.57
1:FG:55:LYS:HD2	1:FG:62:ASN:H	1.70	0.57
1:BF:27:ASN:HB3	1:BF:30:ASN:OD1	2.05	0.57
1:CC:118:SER:HB2	1:GK:8:VAL:HB	1.87	0.57
1:CV:52:PHE:CD1	1:GM:137:LEU:HD22	2.40	0.57
1:DF:102:MET:HE1	1:GR:73:VAL:CG2	2.35	0.57
1:DP:8:VAL:HB	1:GW:118:SER:HB2	1.85	0.57
1:GE:27:ASN:HB3	1:GE:30:ASN:OD1	2.04	0.57
1:GW:55:LYS:HD2	1:GW:62:ASN:H	1.70	0.57
1:AB:27:ASN:HB3	1:AB:30:ASN:OD1	2.05	0.56
1:AU:18:LEU:HG	1:EG:121:VAL:HG11	1.87	0.56
1:BC:27:ASN:HB3	1:BC:30:ASN:OD1	2.05	0.56
1:CD:27:ASN:HB3	1:CD:30:ASN:OD1	2.04	0.56
1:DZ:55:LYS:HD2	1:DZ:62:ASN:H	1.70	0.56
1:EO:55:LYS:HD2	1:EO:62:ASN:H	1.70	0.56
1:FJ:55:LYS:HD2	1:FJ:62:ASN:H	1.70	0.56
1:FY:27:ASN:HB3	1:FY:30:ASN:OD1	2.05	0.56
1:AM:88:ILE:HD11	1:CA:110:ALA:HB1	1.87	0.56
1:AZ:27:ASN:HB3	1:AZ:30:ASN:OD1	2.05	0.56
1:CM:27:ASN:HB3	1:CM:30:ASN:OD1	2.05	0.56
1:CM:117:THR:O	1:DG:117:THR:HB	2.05	0.56
1:CV:55:LYS:HD2	1:CV:62:ASN:H	1.70	0.56
1:EF:79:ASN:ND2	1:EU:75:ASP:OD1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EI:27:ASN:HB3	1:EI:30:ASN:OD1	2.04	0.56
1:AN:55:LYS:HD2	1:AN:62:ASN:H	1.70	0.56
1:AT:55:LYS:HD2	1:AT:62:ASN:H	1.70	0.56
1:BF:55:LYS:HD2	1:BF:62:ASN:H	1.70	0.56
1:BX:55:LYS:HD2	1:BX:62:ASN:H	1.70	0.56
1:CA:55:LYS:HD2	1:CA:62:ASN:H	1.70	0.56
1:CQ:18:LEU:HG	1:GC:121:VAL:CG1	2.31	0.56
1:DA:109:GLN:NE2	1:DE:19:VAL:HG21	2.20	0.56
1:DH:27:ASN:HB3	1:DH:30:ASN:OD1	2.04	0.56
1:EE:102:MET:HE1	1:EU:73:VAL:CG2	2.35	0.56
1:EN:122:SER:O	1:FJ:18:LEU:HD11	2.05	0.56
1:FA:55:LYS:HD2	1:FA:62:ASN:H	1.70	0.56
1:FJ:27:ASN:HB3	1:FJ:30:ASN:OD1	2.05	0.56
1:FV:137:LEU:HA	1:GS:52:PHE:CE1	2.40	0.56
1:GE:55:LYS:HD2	1:GE:62:ASN:H	1.70	0.56
1:AK:27:ASN:HB3	1:AK:30:ASN:OD1	2.04	0.56
1:BO:27:ASN:HB3	1:BO:30:ASN:OD1	2.04	0.56
1:CS:55:LYS:HD2	1:CS:62:ASN:H	1.70	0.56
1:DA:63:ASP:CB	1:DE:137:LEU:HD11	2.35	0.56
1:EF:24:ARG:HA	1:EU:138:MET:HE3	1.86	0.56
1:EH:54:ILE:HG12	1:EO:137:LEU:HD13	1.87	0.56
1:GQ:55:LYS:HD2	1:GQ:62:ASN:H	1.70	0.56
1:AE:55:LYS:HD2	1:AE:62:ASN:H	1.70	0.56
1:AK:112:ASP:OD1	1:AK:118:SER:OG	2.16	0.56
1:BY:105:SER:CB	1:FK:10:ALA:H	2.18	0.56
1:CF:137:LEU:HD13	1:GN:54:ILE:HG12	1.88	0.56
1:CQ:6:ALA:HB3	1:GC:124:GLN:HA	1.86	0.56
1:CZ:117:THR:HB	1:GL:117:THR:O	2.04	0.56
1:DB:27:ASN:HB3	1:DB:30:ASN:OD1	2.05	0.56
1:DL:95:ASN:HD21	1:GX:75:ASP:HA	1.70	0.56
1:DV:137:LEU:HD22	1:GE:52:PHE:CD1	2.41	0.56
1:AF:137:LEU:HD13	1:DR:54:ILE:HG12	1.88	0.56
1:AM:18:LEU:HG	1:CA:121:VAL:CG1	2.35	0.56
1:AM:84:GLY:HA3	1:CA:98:TRP:CH2	2.41	0.56
1:AR:121:VAL:HG11	1:ED:18:LEU:HG	1.86	0.56
1:AU:79:ASN:HD22	1:EZ:77:LYS:HZ3	1.53	0.56
1:BD:63:ASP:HB3	1:EP:137:LEU:HD11	1.87	0.56
1:CA:27:ASN:HB3	1:CA:30:ASN:OD1	2.04	0.56
1:CB:108:LYS:HB2	1:FN:9:GLY:HA2	1.88	0.56
1:CC:109:GLN:NE2	1:GK:19:VAL:HG21	2.20	0.56
1:CM:55:LYS:HD2	1:CM:62:ASN:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:54:ILE:HG12	1:EI:137:LEU:HD13	1.88	0.56
1:BA:8:VAL:HB	1:EM:118:SER:HB2	1.87	0.56
1:BD:54:ILE:HG12	1:EP:137:LEU:HD13	1.86	0.56
1:BI:27:ASN:HB3	1:BI:30:ASN:OD1	2.04	0.56
1:BQ:137:LEU:HD13	1:EC:54:ILE:HG12	1.86	0.56
1:CE:109:GLN:NE2	1:FQ:19:VAL:HG21	2.21	0.56
1:CJ:55:LYS:HD2	1:CJ:62:ASN:H	1.70	0.56
1:EC:55:LYS:HD2	1:EC:62:ASN:H	1.70	0.56
1:EL:27:ASN:HB3	1:EL:30:ASN:OD1	2.05	0.56
1:FD:52:PHE:CD1	1:FF:137:LEU:HD22	2.40	0.56
1:FD:63:ASP:HB3	1:FF:137:LEU:HD11	1.86	0.56
1:FV:27:ASN:HB3	1:FV:30:ASN:OD1	2.04	0.56
1:AH:55:LYS:HD2	1:AH:62:ASN:H	1.70	0.56
1:BL:55:LYS:HD2	1:BL:62:ASN:H	1.70	0.56
1:BU:27:ASN:HB3	1:BU:30:ASN:OD1	2.05	0.56
1:CC:52:PHE:CD1	1:GK:137:LEU:HD22	2.41	0.56
1:DY:118:SER:HB2	1:FY:8:VAL:HB	1.87	0.56
1:EI:55:LYS:HD2	1:EI:62:ASN:H	1.70	0.56
1:AW:55:LYS:HD2	1:AW:62:ASN:H	1.70	0.56
1:BH:137:LEU:HD11	1:BO:63:ASP:HB3	1.87	0.56
1:BI:55:LYS:HD2	1:BI:62:ASN:H	1.70	0.56
1:BR:27:ASN:HB3	1:BR:30:ASN:OD1	2.04	0.56
1:CC:52:PHE:HD1	1:GK:137:LEU:HD22	1.71	0.56
1:CD:8:VAL:HB	1:CR:118:SER:HB2	1.87	0.56
1:CD:55:LYS:HD2	1:CD:62:ASN:H	1.70	0.56
1:CH:54:ILE:HG12	1:FT:137:LEU:HD13	1.88	0.56
1:DL:84:GLY:HA3	1:GX:98:TRP:CH2	2.41	0.56
1:DL:97:ALA:HB1	1:GX:73:VAL:CG1	2.36	0.56
1:DT:55:LYS:HD2	1:DT:62:ASN:H	1.70	0.56
1:EO:27:ASN:HB3	1:EO:30:ASN:OD1	2.05	0.56
1:FD:137:LEU:HD22	1:FF:52:PHE:CD1	2.41	0.56
1:FP:137:LEU:HA	1:GV:52:PHE:CE1	2.41	0.56
1:GH:55:LYS:HD2	1:GH:62:ASN:H	1.70	0.56
1:AY:8:VAL:HB	1:EI:118:SER:HB2	1.88	0.56
1:BL:48:ILE:HG12	1:BL:69:LEU:HG	1.88	0.56
1:BU:55:LYS:HD2	1:BU:62:ASN:H	1.70	0.56
1:CP:48:ILE:HG12	1:CP:69:LEU:HG	1.88	0.56
1:DS:118:SER:HB2	1:GQ:8:VAL:HB	1.88	0.56
1:DW:55:LYS:HD2	1:DW:62:ASN:H	1.70	0.56
1:ET:8:VAL:HB	1:FG:118:SER:HB2	1.88	0.56
1:FD:55:LYS:HD2	1:FD:62:ASN:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FV:55:LYS:HD2	1:FV:62:ASN:H	1.70	0.56
1:GB:55:LYS:HD2	1:GB:62:ASN:H	1.70	0.56
1:AR:122:SER:O	1:ED:18:LEU:HD11	2.06	0.55
1:BR:48:ILE:HG12	1:BR:69:LEU:HG	1.88	0.55
1:BR:55:LYS:HD2	1:BR:62:ASN:H	1.70	0.55
1:CW:137:LEU:HD11	1:GI:63:ASP:CB	2.37	0.55
1:EX:55:LYS:HD2	1:EX:62:ASN:H	1.70	0.55
1:FY:48:ILE:HG12	1:FY:69:LEU:HG	1.89	0.55
1:GK:112:ASP:OD1	1:GK:118:SER:OG	2.16	0.55
1:AB:55:LYS:HD2	1:AB:62:ASN:H	1.70	0.55
1:AT:48:ILE:HG12	1:AT:69:LEU:HG	1.88	0.55
1:BL:27:ASN:HB3	1:BL:30:ASN:OD1	2.05	0.55
1:CB:9:GLY:HA2	1:FN:108:LYS:HB2	1.88	0.55
1:CB:101:SER:HB2	1:FN:11:ASN:O	2.05	0.55
1:CG:55:LYS:HD2	1:CG:62:ASN:H	1.70	0.55
1:DF:95:ASN:HD21	1:GR:75:ASP:CA	2.17	0.55
1:EL:55:LYS:HD2	1:EL:62:ASN:H	1.70	0.55
1:ER:55:LYS:HD2	1:ER:62:ASN:H	1.70	0.55
1:FM:55:LYS:HD2	1:FM:62:ASN:H	1.70	0.55
1:AI:95:ASN:ND2	1:DU:75:ASP:HA	2.20	0.55
1:BH:52:PHE:CE1	1:BO:137:LEU:HA	2.41	0.55
1:CB:124:GLN:HA	1:FN:6:ALA:HB3	1.88	0.55
1:DN:55:LYS:HD2	1:DN:62:ASN:H	1.70	0.55
1:FD:137:LEU:HD13	1:FF:54:ILE:HG12	1.88	0.55
1:GB:48:ILE:HG12	1:GB:69:LEU:HG	1.88	0.55
1:AP:11:ASN:O	1:BU:101:SER:HB2	2.06	0.55
1:BH:24:ARG:HG3	1:EV:137:LEU:O	2.06	0.55
1:BO:55:LYS:HD2	1:BO:62:ASN:H	1.70	0.55
1:CZ:117:THR:O	1:GL:117:THR:HB	2.06	0.55
1:DE:27:ASN:HB3	1:DE:30:ASN:OD1	2.04	0.55
1:DH:48:ILE:HG12	1:DH:69:LEU:HG	1.88	0.55
1:DK:48:ILE:HG12	1:DK:69:LEU:HG	1.89	0.55
1:DK:55:LYS:HD2	1:DK:62:ASN:H	1.70	0.55
1:DP:52:PHE:CE1	1:GW:137:LEU:HA	2.40	0.55
1:EF:55:LYS:HD2	1:EF:62:ASN:H	1.70	0.55
1:EL:48:ILE:HG12	1:EL:69:LEU:HG	1.89	0.55
1:FJ:48:ILE:HG12	1:FJ:69:LEU:HG	1.88	0.55
1:FS:55:LYS:HD2	1:FS:62:ASN:H	1.70	0.55
1:GK:55:LYS:HD2	1:GK:62:ASN:H	1.70	0.55
1:AK:55:LYS:HD2	1:AK:62:ASN:H	1.70	0.55
1:AQ:48:ILE:HG12	1:AQ:69:LEU:HG	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:89:GLN:HB3	1:EG:87:THR:HG23	1.89	0.55
1:BC:48:ILE:HG12	1:BC:69:LEU:HG	1.89	0.55
1:BO:48:ILE:HG12	1:BO:69:LEU:HG	1.88	0.55
1:BP:10:ALA:O	1:FB:105:SER:HB2	2.06	0.55
1:CA:48:ILE:HG12	1:CA:69:LEU:HG	1.88	0.55
1:CN:8:VAL:HB	1:FZ:118:SER:HB2	1.89	0.55
1:EU:55:LYS:HD2	1:EU:62:ASN:H	1.70	0.55
1:AN:95:ASN:HD21	1:FR:75:ASP:HA	1.71	0.55
1:BK:137:LEU:HD22	1:DW:52:PHE:CD1	2.41	0.55
1:BM:118:SER:HB2	1:EY:8:VAL:HB	1.88	0.55
1:BP:137:LEU:C	1:FB:52:PHE:CE2	2.84	0.55
1:CS:121:VAL:CG1	1:DD:18:LEU:HG	2.33	0.55
1:FM:48:ILE:HG12	1:FM:69:LEU:HG	1.89	0.55
1:FP:55:LYS:HD2	1:FP:62:ASN:H	1.70	0.55
1:GH:48:ILE:HG12	1:GH:69:LEU:HG	1.89	0.55
1:GN:55:LYS:HD2	1:GN:62:ASN:H	1.70	0.55
1:GT:55:LYS:HD2	1:GT:62:ASN:H	1.70	0.55
1:GW:48:ILE:HG12	1:GW:69:LEU:HG	1.88	0.55
1:AQ:55:LYS:HD2	1:AQ:62:ASN:H	1.70	0.55
1:BL:112:ASP:OD1	1:BL:118:SER:OG	2.16	0.55
1:CG:48:ILE:HG12	1:CG:69:LEU:HG	1.88	0.55
1:CP:55:LYS:HD2	1:CP:62:ASN:H	1.70	0.55
1:CU:118:SER:HB2	1:DH:8:VAL:HB	1.89	0.55
1:DE:55:LYS:HD2	1:DE:62:ASN:H	1.70	0.55
1:DN:48:ILE:HG12	1:DN:69:LEU:HG	1.88	0.55
1:DQ:55:LYS:HD2	1:DQ:62:ASN:H	1.70	0.55
1:GK:48:ILE:HG12	1:GK:69:LEU:HG	1.89	0.55
1:AH:48:ILE:HG12	1:AH:69:LEU:HG	1.88	0.55
1:AP:110:ALA:HB1	1:BU:88:ILE:HD11	1.89	0.55
1:AZ:55:LYS:HD2	1:AZ:62:ASN:H	1.70	0.55
1:BF:24:ARG:CZ	1:BF:34:VAL:HG21	2.37	0.55
1:BF:29:ASN:H	1:BG:25:SER:CB	2.20	0.55
1:BP:134:TRP:O	1:FB:65:ILE:HD11	2.06	0.55
1:CU:121:VAL:CG1	1:DH:18:LEU:HG	2.37	0.55
1:DE:24:ARG:CZ	1:DE:34:VAL:HG21	2.37	0.55
1:DE:48:ILE:HG12	1:DE:69:LEU:HG	1.89	0.55
1:EX:24:ARG:CZ	1:EX:34:VAL:HG21	2.37	0.55
1:AE:48:ILE:HG12	1:AE:69:LEU:HG	1.89	0.55
1:AE:137:LEU:HD22	1:GA:52:PHE:CD1	2.42	0.55
1:AH:29:ASN:H	1:AI:25:SER:CB	2.20	0.55
1:AQ:24:ARG:HA	1:BU:138:MET:HE3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:48:ILE:HG12	1:AZ:69:LEU:HG	1.88	0.55
1:BC:24:ARG:CZ	1:BC:34:VAL:HG21	2.37	0.55
1:BK:8:VAL:HB	1:DW:118:SER:HB2	1.89	0.55
1:BU:29:ASN:H	1:BV:25:SER:CB	2.20	0.55
1:BX:24:ARG:CZ	1:BX:34:VAL:HG21	2.37	0.55
1:CA:29:ASN:H	1:CB:25:SER:CB	2.20	0.55
1:CJ:109:GLN:NE2	1:CO:19:VAL:HG21	2.22	0.55
1:CY:48:ILE:HG12	1:CY:69:LEU:HG	1.88	0.55
1:DK:24:ARG:CZ	1:DK:34:VAL:HG21	2.37	0.55
1:DQ:24:ARG:CZ	1:DQ:34:VAL:HG21	2.37	0.55
1:DQ:29:ASN:H	1:DR:25:SER:CB	2.20	0.55
1:DT:29:ASN:H	1:DU:25:SER:CB	2.20	0.55
1:EC:24:ARG:CZ	1:EC:34:VAL:HG21	2.37	0.55
1:EC:48:ILE:HG12	1:EC:69:LEU:HG	1.88	0.55
1:EX:117:THR:HB	1:FI:117:THR:O	2.07	0.55
1:FA:8:VAL:HB	1:FL:118:SER:HB2	1.87	0.55
1:FG:48:ILE:HG12	1:FG:69:LEU:HG	1.89	0.55
1:FP:24:ARG:CZ	1:FP:34:VAL:HG21	2.37	0.55
1:FP:137:LEU:HA	1:GV:52:PHE:HE1	1.71	0.55
1:AZ:29:ASN:H	1:BA:25:SER:CB	2.20	0.55
1:BI:48:ILE:HG12	1:BI:69:LEU:HG	1.88	0.55
1:BL:24:ARG:CZ	1:BL:34:VAL:HG21	2.37	0.55
1:BY:109:GLN:NE2	1:FK:19:VAL:HG21	2.21	0.55
1:CD:29:ASN:H	1:CE:25:SER:CB	2.20	0.55
1:CV:48:ILE:HG12	1:CV:69:LEU:HG	1.89	0.55
1:CY:55:LYS:HD2	1:CY:62:ASN:H	1.70	0.55
1:DE:29:ASN:H	1:DF:25:SER:CB	2.20	0.55
1:DH:55:LYS:HD2	1:DH:62:ASN:H	1.70	0.55
1:DZ:29:ASN:H	1:EA:25:SER:CB	2.20	0.55
1:EE:97:ALA:HB1	1:EU:73:VAL:CG1	2.37	0.55
1:EI:24:ARG:CZ	1:EI:34:VAL:HG21	2.37	0.55
1:FG:24:ARG:CZ	1:FG:34:VAL:HG21	2.37	0.55
1:GQ:48:ILE:HG12	1:GQ:69:LEU:HG	1.88	0.55
1:GW:24:ARG:CZ	1:GW:34:VAL:HG21	2.37	0.55
1:AG:8:VAL:HB	1:BF:118:SER:HB2	1.89	0.54
1:AK:24:ARG:CZ	1:AK:34:VAL:HG21	2.37	0.54
1:AT:24:ARG:CZ	1:AT:34:VAL:HG21	2.37	0.54
1:AT:29:ASN:H	1:AU:25:SER:CB	2.20	0.54
1:AT:112:ASP:OD1	1:AT:118:SER:OG	2.17	0.54
1:BJ:86:VAL:HG22	1:EV:90:VAL:HG22	1.89	0.54
1:BR:24:ARG:CZ	1:BR:34:VAL:HG21	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:29:ASN:H	1:CK:25:SER:CB	2.20	0.54
1:CJ:89:GLN:HB3	1:CO:87:THR:HG1	1.72	0.54
1:CM:24:ARG:CZ	1:CM:34:VAL:HG21	2.37	0.54
1:CM:48:ILE:HG12	1:CM:69:LEU:HG	1.88	0.54
1:CS:48:ILE:HG12	1:CS:69:LEU:HG	1.88	0.54
1:DZ:48:ILE:HG12	1:DZ:69:LEU:HG	1.88	0.54
1:EU:48:ILE:HG12	1:EU:69:LEU:HG	1.88	0.54
1:EX:48:ILE:HG12	1:EX:69:LEU:HG	1.88	0.54
1:FC:24:ARG:CZ	1:FC:34:VAL:HG21	2.38	0.54
1:FY:55:LYS:HD2	1:FY:62:ASN:H	1.70	0.54
1:AB:48:ILE:HG12	1:AB:69:LEU:HG	1.88	0.54
1:AQ:24:ARG:CZ	1:AQ:34:VAL:HG21	2.37	0.54
1:AV:29:ASN:HA	1:EF:139:PHE:HE2	1.72	0.54
1:AZ:24:ARG:CZ	1:AZ:34:VAL:HG21	2.37	0.54
1:CD:24:ARG:CZ	1:CD:34:VAL:HG21	2.37	0.54
1:CS:24:ARG:CZ	1:CS:34:VAL:HG21	2.37	0.54
1:CV:24:ARG:CZ	1:CV:34:VAL:HG21	2.37	0.54
1:CV:29:ASN:H	1:CW:25:SER:CB	2.20	0.54
1:DF:87:THR:HG23	1:GR:89:GLN:HB3	1.89	0.54
1:DT:48:ILE:HG12	1:DT:69:LEU:HG	1.88	0.54
1:EX:29:ASN:H	1:EY:25:SER:CB	2.20	0.54
1:FA:24:ARG:CZ	1:FA:34:VAL:HG21	2.37	0.54
1:GH:29:ASN:H	1:GI:25:SER:CB	2.20	0.54
1:GQ:112:ASP:OD1	1:GQ:118:SER:OG	2.16	0.54
1:AW:29:ASN:H	1:AX:25:SER:CB	2.20	0.54
1:BE:137:LEU:HD13	1:BL:54:ILE:HG12	1.90	0.54
1:BW:24:ARG:CZ	1:BW:34:VAL:HG21	2.38	0.54
1:CF:24:ARG:CZ	1:CF:34:VAL:HG21	2.38	0.54
1:CK:117:THR:HB	1:FW:117:THR:O	2.07	0.54
1:CK:118:SER:HB2	1:FW:8:VAL:HB	1.90	0.54
1:CL:24:ARG:CZ	1:CL:34:VAL:HG21	2.38	0.54
1:CT:87:THR:HG23	1:GF:89:GLN:HB3	1.88	0.54
1:DB:55:LYS:HD2	1:DB:62:ASN:H	1.70	0.54
1:DT:24:ARG:CZ	1:DT:34:VAL:HG21	2.37	0.54
1:EI:29:ASN:H	1:EJ:25:SER:CB	2.20	0.54
1:ER:48:ILE:HG12	1:ER:69:LEU:HG	1.88	0.54
1:FA:48:ILE:HG12	1:FA:69:LEU:HG	1.88	0.54
1:FF:24:ARG:CZ	1:FF:34:VAL:HG21	2.38	0.54
1:FS:24:ARG:CZ	1:FS:34:VAL:HG21	2.37	0.54
1:FV:24:ARG:CZ	1:FV:34:VAL:HG21	2.37	0.54
1:GE:29:ASN:H	1:GF:25:SER:CB	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GT:24:ARG:CZ	1:GT:34:VAL:HG21	2.37	0.54
1:GW:29:ASN:H	1:GX:25:SER:CB	2.20	0.54
1:AO:97:ALA:O	1:EA:73:VAL:HG11	2.07	0.54
1:CJ:24:ARG:CZ	1:CJ:34:VAL:HG21	2.37	0.54
1:DS:24:ARG:CZ	1:DS:34:VAL:HG21	2.38	0.54
1:EC:29:ASN:H	1:ED:25:SER:CB	2.20	0.54
1:EF:24:ARG:CZ	1:EF:34:VAL:HG21	2.37	0.54
1:EL:29:ASN:H	1:EM:25:SER:CB	2.20	0.54
1:EO:24:ARG:CZ	1:EO:34:VAL:HG21	2.37	0.54
1:FS:48:ILE:HG12	1:FS:69:LEU:HG	1.89	0.54
1:FV:29:ASN:H	1:FW:25:SER:CB	2.20	0.54
1:GB:24:ARG:CZ	1:GB:34:VAL:HG21	2.37	0.54
1:GK:29:ASN:H	1:GL:25:SER:CB	2.20	0.54
1:GM:24:ARG:CZ	1:GM:34:VAL:HG21	2.38	0.54
1:GN:24:ARG:CZ	1:GN:34:VAL:HG21	2.37	0.54
1:AA:24:ARG:CZ	1:AA:34:VAL:HG21	2.38	0.54
1:AH:24:ARG:CZ	1:AH:34:VAL:HG21	2.37	0.54
1:AI:137:LEU:HD11	1:DU:63:ASP:HB3	1.89	0.54
1:AQ:29:ASN:H	1:AR:25:SER:CB	2.20	0.54
1:AW:24:ARG:CZ	1:AW:34:VAL:HG21	2.37	0.54
1:BD:18:LEU:HD11	1:EP:122:SER:O	2.07	0.54
1:BL:29:ASN:H	1:BM:25:SER:CB	2.20	0.54
1:BU:48:ILE:HG12	1:BU:69:LEU:HG	1.89	0.54
1:BX:48:ILE:HG12	1:BX:69:LEU:HG	1.88	0.54
1:CE:8:VAL:HB	1:FQ:118:SER:HB2	1.89	0.54
1:DB:24:ARG:CZ	1:DB:34:VAL:HG21	2.37	0.54
1:DB:29:ASN:H	1:DC:25:SER:CB	2.20	0.54
1:DH:24:ARG:CZ	1:DH:34:VAL:HG21	2.37	0.54
1:DQ:48:ILE:HG12	1:DQ:69:LEU:HG	1.88	0.54
1:DW:48:ILE:HG12	1:DW:69:LEU:HG	1.88	0.54
1:DW:112:ASP:OD1	1:DW:118:SER:OG	2.16	0.54
1:EB:137:LEU:HD13	1:GB:54:ILE:HG12	1.90	0.54
1:EE:137:LEU:HD11	1:EU:63:ASP:CG	2.32	0.54
1:FA:29:ASN:H	1:FB:25:SER:CB	2.20	0.54
1:FD:29:ASN:H	1:FE:25:SER:CB	2.20	0.54
1:FO:24:ARG:CZ	1:FO:34:VAL:HG21	2.38	0.54
1:FP:29:ASN:H	1:FQ:25:SER:CB	2.20	0.54
1:FP:48:ILE:HG12	1:FP:69:LEU:HG	1.88	0.54
1:FY:29:ASN:H	1:FZ:25:SER:CB	2.20	0.54
1:GT:48:ILE:HG12	1:GT:69:LEU:HG	1.88	0.54
1:AG:118:SER:HB2	1:BF:8:VAL:HB	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:79:ASN:HD22	1:EZ:77:LYS:NZ	2.05	0.54
1:AW:48:ILE:HG12	1:AW:69:LEU:HG	1.88	0.54
1:BB:24:ARG:CZ	1:BB:34:VAL:HG21	2.38	0.54
1:BC:29:ASN:H	1:BD:25:SER:CB	2.20	0.54
1:BO:112:ASP:OD1	1:BO:118:SER:OG	2.16	0.54
1:BU:24:ARG:CZ	1:BU:34:VAL:HG21	2.37	0.54
1:BZ:24:ARG:CZ	1:BZ:34:VAL:HG21	2.38	0.54
1:CP:29:ASN:H	1:CQ:25:SER:CB	2.20	0.54
1:CS:6:ALA:HB3	1:DD:124:GLN:HA	1.90	0.54
1:CS:29:ASN:H	1:CT:25:SER:CB	2.20	0.54
1:CX:24:ARG:CZ	1:CX:34:VAL:HG21	2.38	0.54
1:DG:24:ARG:CZ	1:DG:34:VAL:HG21	2.38	0.54
1:DW:24:ARG:CZ	1:DW:34:VAL:HG21	2.37	0.54
1:ER:24:ARG:CZ	1:ER:34:VAL:HG21	2.37	0.54
1:ER:29:ASN:H	1:ES:25:SER:CB	2.20	0.54
1:EZ:24:ARG:CZ	1:EZ:34:VAL:HG21	2.38	0.54
1:FD:24:ARG:CZ	1:FD:34:VAL:HG21	2.37	0.54
1:FX:24:ARG:CZ	1:FX:34:VAL:HG21	2.38	0.54
1:FY:24:ARG:CZ	1:FY:34:VAL:HG21	2.37	0.54
1:GA:24:ARG:CZ	1:GA:34:VAL:HG21	2.38	0.54
1:GB:29:ASN:H	1:GC:25:SER:CB	2.20	0.54
1:GE:48:ILE:HG12	1:GE:69:LEU:HG	1.88	0.54
1:GN:29:ASN:H	1:GO:25:SER:CB	2.20	0.54
1:GS:24:ARG:CZ	1:GS:34:VAL:HG21	2.38	0.54
1:AN:24:ARG:CZ	1:AN:34:VAL:HG21	2.37	0.54
1:AS:52:PHE:HE1	1:EL:137:LEU:HA	1.72	0.54
1:AV:24:ARG:CZ	1:AV:34:VAL:HG21	2.38	0.54
1:BO:24:ARG:CZ	1:BO:34:VAL:HG21	2.37	0.54
1:CA:24:ARG:CZ	1:CA:34:VAL:HG21	2.37	0.54
1:CI:24:ARG:CZ	1:CI:34:VAL:HG21	2.38	0.54
1:DM:117:THR:O	1:GT:117:THR:HB	2.06	0.54
1:DP:109:GLN:NE2	1:GW:19:VAL:HG21	2.22	0.54
1:DZ:24:ARG:CZ	1:DZ:34:VAL:HG21	2.37	0.54
1:EF:48:ILE:HG12	1:EF:69:LEU:HG	1.88	0.54
1:FD:48:ILE:HG12	1:FD:69:LEU:HG	1.88	0.54
1:FL:24:ARG:CZ	1:FL:34:VAL:HG21	2.38	0.54
1:AE:29:ASN:H	1:AF:25:SER:CB	2.20	0.54
1:AJ:24:ARG:CZ	1:AJ:34:VAL:HG21	2.38	0.54
1:AK:48:ILE:HG12	1:AK:69:LEU:HG	1.88	0.54
1:AW:63:ASP:HB3	1:FC:137:LEU:HD11	1.88	0.54
1:BH:24:ARG:CZ	1:BH:34:VAL:HG21	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:24:ARG:CZ	1:BI:34:VAL:HG21	2.37	0.54
1:BV:86:VAL:HG22	1:FH:90:VAL:HG22	1.90	0.54
1:CD:48:ILE:HG12	1:CD:69:LEU:HG	1.88	0.54
1:CG:24:ARG:CZ	1:CG:34:VAL:HG21	2.37	0.54
1:CH:8:VAL:HB	1:FT:118:SER:HB2	1.90	0.54
1:CO:24:ARG:CZ	1:CO:34:VAL:HG21	2.38	0.54
1:CP:121:VAL:HG11	1:DJ:18:LEU:HG	1.89	0.54
1:DZ:112:ASP:OD1	1:DZ:118:SER:OG	2.16	0.54
1:EB:54:ILE:HG12	1:GB:137:LEU:HD13	1.89	0.54
1:ET:24:ARG:CZ	1:ET:34:VAL:HG21	2.38	0.54
1:EU:24:ARG:CZ	1:EU:34:VAL:HG21	2.37	0.54
1:EU:29:ASN:H	1:EV:25:SER:CB	2.20	0.54
1:FI:24:ARG:CZ	1:FI:34:VAL:HG21	2.38	0.54
1:FM:24:ARG:CZ	1:FM:34:VAL:HG21	2.37	0.54
1:FM:29:ASN:H	1:FN:25:SER:CB	2.20	0.54
1:FV:48:ILE:HG12	1:FV:69:LEU:HG	1.89	0.54
1:GE:24:ARG:CZ	1:GE:34:VAL:HG21	2.37	0.54
1:GJ:24:ARG:CZ	1:GJ:34:VAL:HG21	2.38	0.54
1:GP:24:ARG:CZ	1:GP:34:VAL:HG21	2.38	0.54
1:GQ:29:ASN:H	1:GR:25:SER:CB	2.20	0.54
1:AT:137:LEU:HD12	1:FA:42:LEU:HD22	1.90	0.54
1:BX:29:ASN:H	1:BY:25:SER:CB	2.20	0.54
1:CG:18:LEU:HG	1:CL:121:VAL:CG1	2.37	0.54
1:CQ:5:LEU:HA	1:GC:125:THR:HG21	1.90	0.54
1:CU:24:ARG:CZ	1:CU:34:VAL:HG21	2.38	0.54
1:DA:24:ARG:CZ	1:DA:34:VAL:HG21	2.38	0.54
1:DT:42:LEU:HD22	1:GQ:137:LEU:HD12	1.88	0.54
1:DW:29:ASN:H	1:DX:25:SER:CB	2.20	0.54
1:EE:137:LEU:HD11	1:EU:63:ASP:HB3	1.89	0.54
1:EK:24:ARG:CZ	1:EK:34:VAL:HG21	2.38	0.54
1:EL:24:ARG:CZ	1:EL:34:VAL:HG21	2.37	0.54
1:EN:97:ALA:O	1:FJ:73:VAL:HG11	2.08	0.54
1:EQ:24:ARG:CZ	1:EQ:34:VAL:HG21	2.38	0.54
1:FP:8:VAL:HB	1:GV:118:SER:HB2	1.89	0.54
1:FV:52:PHE:CD1	1:GS:137:LEU:HD22	2.43	0.54
1:GT:29:ASN:H	1:GU:25:SER:CB	2.20	0.54
1:AB:24:ARG:CZ	1:AB:34:VAL:HG21	2.37	0.54
1:AB:52:PHE:CD1	1:FX:137:LEU:HD22	2.43	0.54
1:AE:24:ARG:CZ	1:AE:34:VAL:HG21	2.37	0.54
1:AX:89:GLN:HB3	1:EJ:87:THR:CG2	2.38	0.54
1:BI:29:ASN:H	1:BJ:25:SER:CB	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:29:ASN:H	1:BP:25:SER:CB	2.20	0.54
1:BZ:75:ASP:HA	1:DT:95:ASN:HD21	1.72	0.54
1:CD:88:ILE:HD11	1:CR:110:ALA:HB1	1.91	0.54
1:CG:137:LEU:HA	1:CL:52:PHE:HE1	1.72	0.54
1:CJ:48:ILE:HG12	1:CJ:69:LEU:HG	1.88	0.54
1:CN:75:ASP:HA	1:FZ:95:ASN:HD21	1.72	0.54
1:CP:24:ARG:CZ	1:CP:34:VAL:HG21	2.37	0.54
1:DN:29:ASN:H	1:DO:25:SER:CB	2.20	0.54
1:DY:24:ARG:CZ	1:DY:34:VAL:HG21	2.38	0.54
1:EF:29:ASN:H	1:EG:25:SER:CB	2.20	0.54
1:ET:110:ALA:HB1	1:FG:88:ILE:HD11	1.90	0.54
1:EX:117:THR:O	1:FI:117:THR:HB	2.08	0.54
1:FJ:24:ARG:CZ	1:FJ:34:VAL:HG21	2.37	0.54
1:FU:24:ARG:CZ	1:FU:34:VAL:HG21	2.38	0.54
1:GQ:24:ARG:CZ	1:GQ:34:VAL:HG21	2.37	0.54
1:GV:24:ARG:CZ	1:GV:34:VAL:HG21	2.38	0.54
1:AD:24:ARG:CZ	1:AD:34:VAL:HG21	2.38	0.53
1:AH:118:SER:HB2	1:GD:8:VAL:HB	1.90	0.53
1:AJ:73:VAL:HG11	1:BX:97:ALA:O	2.08	0.53
1:AJ:137:LEU:HD13	1:BX:54:ILE:HG12	1.89	0.53
1:AK:29:ASN:H	1:AL:25:SER:CB	2.20	0.53
1:AN:29:ASN:H	1:AO:25:SER:CB	2.20	0.53
1:BI:112:ASP:OD1	1:BI:118:SER:OG	2.17	0.53
1:BQ:137:LEU:HD22	1:EC:52:PHE:CD1	2.44	0.53
1:CC:24:ARG:CZ	1:CC:34:VAL:HG21	2.38	0.53
1:CP:52:PHE:CD1	1:DJ:137:LEU:HD22	2.43	0.53
1:CY:24:ARG:CZ	1:CY:34:VAL:HG21	2.37	0.53
1:DN:24:ARG:CZ	1:DN:34:VAL:HG21	2.37	0.53
1:DV:8:VAL:HB	1:GE:118:SER:HB2	1.89	0.53
1:EH:24:ARG:CZ	1:EH:34:VAL:HG21	2.38	0.53
1:EI:48:ILE:HG12	1:EI:69:LEU:HG	1.88	0.53
1:EN:63:ASP:HB3	1:FJ:137:LEU:HD11	1.90	0.53
1:FR:24:ARG:CZ	1:FR:34:VAL:HG21	2.38	0.53
1:AD:73:VAL:CG2	1:BC:102:MET:HE1	2.38	0.53
1:AP:24:ARG:CZ	1:AP:34:VAL:HG21	2.38	0.53
1:AY:24:ARG:CZ	1:AY:34:VAL:HG21	2.38	0.53
1:BQ:24:ARG:CZ	1:BQ:34:VAL:HG21	2.38	0.53
1:BR:29:ASN:H	1:BS:25:SER:CB	2.20	0.53
1:CG:121:VAL:CG1	1:CL:18:LEU:HG	2.39	0.53
1:CG:138:MET:HE3	1:CM:24:ARG:HA	1.90	0.53
1:CR:24:ARG:CZ	1:CR:34:VAL:HG21	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:97:ALA:O	1:DD:73:VAL:HG11	2.09	0.53
1:DC:95:ASN:HD21	1:GO:75:ASP:CA	2.15	0.53
1:DT:112:ASP:OD1	1:DT:118:SER:OG	2.16	0.53
1:EO:29:ASN:H	1:EP:25:SER:CB	2.20	0.53
1:FG:29:ASN:H	1:FH:25:SER:CB	2.20	0.53
1:FS:29:ASN:H	1:FT:25:SER:CB	2.20	0.53
1:AB:29:ASN:H	1:AC:25:SER:CB	2.20	0.53
1:AB:117:THR:HB	1:FX:117:THR:O	2.08	0.53
1:BE:24:ARG:CZ	1:BE:34:VAL:HG21	2.38	0.53
1:BN:117:THR:O	1:DZ:117:THR:HB	2.09	0.53
1:CG:29:ASN:H	1:CH:25:SER:CB	2.20	0.53
1:CT:109:GLN:NE2	1:GF:19:VAL:HG21	2.22	0.53
1:CY:19:VAL:HG21	1:GG:109:GLN:NE2	2.24	0.53
1:DD:24:ARG:CZ	1:DD:34:VAL:HG21	2.38	0.53
1:DJ:24:ARG:CZ	1:DJ:34:VAL:HG21	2.38	0.53
1:DK:29:ASN:H	1:DL:25:SER:CB	2.20	0.53
1:DL:73:VAL:CG2	1:GX:102:MET:HE1	2.38	0.53
1:EO:48:ILE:HG12	1:EO:69:LEU:HG	1.89	0.53
1:AM:24:ARG:CZ	1:AM:34:VAL:HG21	2.38	0.53
1:AN:19:VAL:HG21	1:FR:109:GLN:NE2	2.24	0.53
1:AR:73:VAL:CG1	1:ED:97:ALA:HB1	2.38	0.53
1:AT:117:THR:O	1:EZ:117:THR:HB	2.08	0.53
1:BF:48:ILE:HG12	1:BF:69:LEU:HG	1.89	0.53
1:BM:117:THR:HB	1:EY:117:THR:O	2.09	0.53
1:BO:29:ASN:H	1:BP:25:SER:HB2	1.74	0.53
1:BP:86:VAL:HG22	1:FB:90:VAL:HG22	1.90	0.53
1:DS:77:LYS:NZ	1:GR:79:ASN:HD22	2.06	0.53
1:DV:24:ARG:CZ	1:DV:34:VAL:HG21	2.38	0.53
1:FD:112:ASP:OD1	1:FD:118:SER:OG	2.16	0.53
1:FD:137:LEU:HD22	1:FF:52:PHE:HD1	1.73	0.53
1:FL:120:THR:HA	1:FL:124:GLN:HE22	1.74	0.53
1:FP:29:ASN:H	1:FQ:25:SER:HB2	1.74	0.53
1:GD:24:ARG:CZ	1:GD:34:VAL:HG21	2.38	0.53
1:GH:24:ARG:CZ	1:GH:34:VAL:HG21	2.37	0.53
1:AE:90:VAL:HG22	1:GA:86:VAL:HG22	1.90	0.53
1:AK:137:LEU:HA	1:FO:52:PHE:HE1	1.73	0.53
1:AN:137:LEU:HA	1:FR:52:PHE:HE1	1.73	0.53
1:AT:29:ASN:H	1:AU:25:SER:HB2	1.74	0.53
1:CA:29:ASN:H	1:CB:25:SER:HB2	1.74	0.53
1:CP:29:ASN:H	1:CQ:25:SER:HB2	1.74	0.53
1:CY:29:ASN:H	1:CZ:25:SER:CB	2.20	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EB:24:ARG:CZ	1:EB:34:VAL:HG21	2.38	0.53
1:EE:24:ARG:CZ	1:EE:34:VAL:HG21	2.38	0.53
1:EE:138:MET:HE3	1:EV:36:THR:HG22	1.91	0.53
1:EW:24:ARG:CZ	1:EW:34:VAL:HG21	2.38	0.53
1:GG:24:ARG:CZ	1:GG:34:VAL:HG21	2.38	0.53
1:AQ:137:LEU:HD22	1:FU:52:PHE:HD1	1.71	0.53
1:BR:29:ASN:H	1:BS:25:SER:HB2	1.74	0.53
1:BT:24:ARG:CZ	1:BT:34:VAL:HG21	2.38	0.53
1:BU:29:ASN:H	1:BV:25:SER:HB2	1.74	0.53
1:CC:120:THR:HA	1:CC:124:GLN:HE22	1.74	0.53
1:CF:120:THR:HA	1:CF:124:GLN:HE22	1.74	0.53
1:CI:18:LEU:HG	1:GH:121:VAL:HG11	1.90	0.53
1:CM:29:ASN:H	1:CN:25:SER:CB	2.20	0.53
1:DH:29:ASN:H	1:DI:25:SER:HB2	1.74	0.53
1:FJ:29:ASN:H	1:FK:25:SER:CB	2.20	0.53
1:FS:29:ASN:H	1:FT:25:SER:HB2	1.74	0.53
1:GK:24:ARG:CZ	1:GK:34:VAL:HG21	2.37	0.53
1:AH:29:ASN:H	1:AI:25:SER:HB2	1.74	0.53
1:AM:18:LEU:HD11	1:CA:123:GLY:H	1.74	0.53
1:AN:48:ILE:HG12	1:AN:69:LEU:HG	1.89	0.53
1:AP:120:THR:HA	1:AP:124:GLN:HE22	1.74	0.53
1:AS:24:ARG:CZ	1:AS:34:VAL:HG21	2.38	0.53
1:CL:120:THR:HA	1:CL:124:GLN:HE22	1.74	0.53
1:CY:29:ASN:H	1:CZ:25:SER:HB2	1.74	0.53
1:CZ:117:THR:OG1	1:GL:117:THR:OG1	2.25	0.53
1:DB:48:ILE:HG12	1:DB:69:LEU:HG	1.89	0.53
1:DH:29:ASN:H	1:DI:25:SER:CB	2.20	0.53
1:DM:24:ARG:CZ	1:DM:34:VAL:HG21	2.38	0.53
1:EQ:73:VAL:CG2	1:FM:102:MET:HE1	2.39	0.53
1:GP:120:THR:HA	1:GP:124:GLN:HE22	1.74	0.53
1:GS:120:THR:HA	1:GS:124:GLN:HE22	1.74	0.53
1:AB:29:ASN:H	1:AC:25:SER:HB2	1.74	0.53
1:AE:30:ASN:HA	1:AE:50:ALA:O	2.09	0.53
1:AG:24:ARG:CZ	1:AG:34:VAL:HG21	2.38	0.53
1:AJ:48:ILE:HG12	1:AJ:69:LEU:HG	1.91	0.53
1:AT:27:ASN:CG	1:AT:28:GLY:H	2.16	0.53
1:AY:120:THR:HA	1:AY:124:GLN:HE22	1.74	0.53
1:BK:24:ARG:CZ	1:BK:34:VAL:HG21	2.38	0.53
1:BK:48:ILE:HG12	1:BK:69:LEU:HG	1.91	0.53
1:BK:120:THR:HA	1:BK:124:GLN:HE22	1.74	0.53
1:BL:29:ASN:H	1:BM:25:SER:HB2	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:24:ARG:CZ	1:BN:34:VAL:HG21	2.38	0.53
1:BV:54:ILE:HG12	1:FH:137:LEU:HD13	1.91	0.53
1:BZ:19:VAL:HG21	1:DT:109:GLN:NE2	2.23	0.53
1:CJ:137:LEU:HD22	1:CO:52:PHE:CD1	2.43	0.53
1:CR:48:ILE:HG12	1:CR:69:LEU:HG	1.91	0.53
1:CS:29:ASN:H	1:CT:25:SER:HB2	1.74	0.53
1:DS:120:THR:HA	1:DS:124:GLN:HE22	1.74	0.53
1:DV:48:ILE:HG12	1:DV:69:LEU:HG	1.91	0.53
1:EH:48:ILE:HG12	1:EH:69:LEU:HG	1.91	0.53
1:GH:29:ASN:H	1:GI:25:SER:HB2	1.74	0.53
1:AD:120:THR:HA	1:AD:124:GLN:HE22	1.74	0.53
1:AH:112:ASP:OD1	1:AH:118:SER:OG	2.17	0.53
1:AV:120:THR:HA	1:AV:124:GLN:HE22	1.74	0.53
1:BK:118:SER:HB2	1:DW:8:VAL:HB	1.91	0.53
1:BZ:120:THR:HA	1:BZ:124:GLN:HE22	1.74	0.53
1:CI:120:THR:HA	1:CI:124:GLN:HE22	1.74	0.53
1:CJ:19:VAL:HG21	1:CO:109:GLN:NE2	2.24	0.53
1:DG:48:ILE:HG12	1:DG:69:LEU:HG	1.91	0.53
1:DK:30:ASN:HA	1:DK:50:ALA:O	2.09	0.53
1:DV:118:SER:HB2	1:GE:8:VAL:HB	1.91	0.53
1:DY:120:THR:HA	1:DY:124:GLN:HE22	1.74	0.53
1:EE:48:ILE:HG12	1:EE:69:LEU:HG	1.91	0.53
1:FD:29:ASN:H	1:FE:25:SER:HB2	1.74	0.53
1:FO:48:ILE:HG12	1:FO:69:LEU:HG	1.91	0.53
1:FP:27:ASN:CG	1:FP:28:GLY:H	2.16	0.53
1:FR:48:ILE:HG12	1:FR:69:LEU:HG	1.91	0.53
1:FV:30:ASN:HA	1:FV:50:ALA:O	2.09	0.53
1:GJ:120:THR:HA	1:GJ:124:GLN:HE22	1.74	0.53
1:GS:48:ILE:HG12	1:GS:69:LEU:HG	1.91	0.53
1:AB:19:VAL:HG21	1:FX:109:GLN:NE2	2.24	0.53
1:AU:73:VAL:CG2	1:EG:102:MET:HE1	2.39	0.53
1:BN:73:VAL:HG11	1:DZ:97:ALA:O	2.09	0.53
1:BQ:48:ILE:HG12	1:BQ:69:LEU:HG	1.91	0.53
1:BT:48:ILE:HG12	1:BT:69:LEU:HG	1.91	0.53
1:BW:120:THR:HA	1:BW:124:GLN:HE22	1.74	0.53
1:CL:48:ILE:HG12	1:CL:69:LEU:HG	1.91	0.53
1:CO:120:THR:HA	1:CO:124:GLN:HE22	1.74	0.53
1:CP:137:LEU:HD13	1:DJ:54:ILE:HG12	1.90	0.53
1:CT:89:GLN:HB3	1:GF:87:THR:CG2	2.38	0.53
1:CV:30:ASN:HA	1:CV:50:ALA:O	2.09	0.53
1:DB:27:ASN:CG	1:DB:28:GLY:H	2.16	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DS:117:THR:HB	1:GQ:117:THR:O	2.09	0.53
1:EI:29:ASN:H	1:EJ:25:SER:HB2	1.74	0.53
1:EL:29:ASN:H	1:EM:25:SER:HB2	1.74	0.53
1:EN:24:ARG:CZ	1:EN:34:VAL:HG21	2.38	0.53
1:EZ:120:THR:HA	1:EZ:124:GLN:HE22	1.74	0.53
1:FF:48:ILE:HG12	1:FF:69:LEU:HG	1.91	0.53
1:FX:48:ILE:HG12	1:FX:69:LEU:HG	1.91	0.53
1:FY:30:ASN:HA	1:FY:50:ALA:O	2.09	0.53
1:GM:48:ILE:HG12	1:GM:69:LEU:HG	1.91	0.53
1:GW:30:ASN:HA	1:GW:50:ALA:O	2.09	0.53
1:AK:29:ASN:H	1:AL:25:SER:HB2	1.74	0.52
1:AK:73:VAL:HG11	1:FO:97:ALA:O	2.08	0.52
1:AS:8:VAL:HB	1:EL:118:SER:HB2	1.90	0.52
1:AT:30:ASN:HA	1:AT:50:ALA:O	2.09	0.52
1:AW:30:ASN:HA	1:AW:50:ALA:O	2.09	0.52
1:BN:48:ILE:HG12	1:BN:69:LEU:HG	1.91	0.52
1:BU:30:ASN:HA	1:BU:50:ALA:O	2.09	0.52
1:BW:11:ASN:O	1:DQ:101:SER:HB2	2.09	0.52
1:CC:48:ILE:HG12	1:CC:69:LEU:HG	1.91	0.52
1:CD:30:ASN:HA	1:CD:50:ALA:O	2.09	0.52
1:DA:120:THR:HA	1:DA:124:GLN:HE22	1.74	0.52
1:DD:48:ILE:HG12	1:DD:69:LEU:HG	1.91	0.52
1:DP:24:ARG:CZ	1:DP:34:VAL:HG21	2.38	0.52
1:EN:110:ALA:HB1	1:FJ:88:ILE:HD11	1.91	0.52
1:EQ:120:THR:HA	1:EQ:124:GLN:HE22	1.74	0.52
1:ET:120:THR:HA	1:ET:124:GLN:HE22	1.74	0.52
1:EW:48:ILE:HG12	1:EW:69:LEU:HG	1.91	0.52
1:EX:30:ASN:HA	1:EX:50:ALA:O	2.09	0.52
1:FA:30:ASN:HA	1:FA:50:ALA:O	2.09	0.52
1:FI:120:THR:HA	1:FI:124:GLN:HE22	1.74	0.52
1:FS:30:ASN:HA	1:FS:50:ALA:O	2.09	0.52
1:FY:29:ASN:H	1:FZ:25:SER:HB2	1.74	0.52
1:GH:30:ASN:HA	1:GH:50:ALA:O	2.09	0.52
1:GN:48:ILE:HG12	1:GN:69:LEU:HG	1.88	0.52
1:AH:30:ASN:HA	1:AH:50:ALA:O	2.09	0.52
1:AN:137:LEU:HD13	1:FR:54:ILE:HG12	1.91	0.52
1:AV:137:LEU:HD11	1:EF:63:ASP:HB3	1.92	0.52
1:BD:73:VAL:CG2	1:EP:102:MET:HE1	2.39	0.52
1:BE:120:THR:HA	1:BE:124:GLN:HE22	1.74	0.52
1:BQ:117:THR:O	1:EC:117:THR:HB	2.09	0.52
1:BT:120:THR:HA	1:BT:124:GLN:HE22	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:30:ASN:HA	1:BX:50:ALA:O	2.09	0.52
1:CJ:30:ASN:HA	1:CJ:50:ALA:O	2.09	0.52
1:CU:63:ASP:HB3	1:DH:137:LEU:HD11	1.90	0.52
1:DA:48:ILE:HG12	1:DA:69:LEU:HG	1.91	0.52
1:EF:30:ASN:HA	1:EF:50:ALA:O	2.10	0.52
1:EO:29:ASN:H	1:EP:25:SER:HB2	1.74	0.52
1:FA:29:ASN:H	1:FB:25:SER:HB2	1.74	0.52
1:FA:88:ILE:HD11	1:FL:110:ALA:HB1	1.92	0.52
1:FD:30:ASN:HA	1:FD:50:ALA:O	2.09	0.52
1:FF:120:THR:HA	1:FF:124:GLN:HE22	1.74	0.52
1:FL:48:ILE:HG12	1:FL:69:LEU:HG	1.91	0.52
1:GG:48:ILE:HG12	1:GG:69:LEU:HG	1.91	0.52
1:GN:29:ASN:H	1:GO:25:SER:HB2	1.74	0.52
1:GN:30:ASN:HA	1:GN:50:ALA:O	2.10	0.52
1:GT:30:ASN:HA	1:GT:50:ALA:O	2.09	0.52
1:GV:120:THR:HA	1:GV:124:GLN:HE22	1.74	0.52
1:AK:30:ASN:HA	1:AK:50:ALA:O	2.09	0.52
1:AM:48:ILE:HG12	1:AM:69:LEU:HG	1.91	0.52
1:AS:52:PHE:CE1	1:EL:137:LEU:HA	2.44	0.52
1:AW:29:ASN:H	1:AX:25:SER:HB2	1.74	0.52
1:AZ:30:ASN:HA	1:AZ:50:ALA:O	2.09	0.52
1:BC:27:ASN:CG	1:BC:28:GLY:H	2.16	0.52
1:BF:30:ASN:HA	1:BF:50:ALA:O	2.09	0.52
1:BH:120:THR:HA	1:BH:124:GLN:HE22	1.74	0.52
1:BK:109:GLN:NE2	1:DW:19:VAL:HG21	2.25	0.52
1:CB:11:ASN:O	1:FN:101:SER:HB2	2.09	0.52
1:CX:117:THR:O	1:DK:117:THR:HB	2.09	0.52
1:CY:30:ASN:HA	1:CY:50:ALA:O	2.10	0.52
1:DE:29:ASN:H	1:DF:25:SER:HB2	1.74	0.52
1:DM:48:ILE:HG12	1:DM:69:LEU:HG	1.91	0.52
1:DW:30:ASN:HA	1:DW:50:ALA:O	2.09	0.52
1:EF:27:ASN:CG	1:EF:28:GLY:H	2.16	0.52
1:EH:120:THR:HA	1:EH:124:GLN:HE22	1.74	0.52
1:EH:137:LEU:HD22	1:EO:52:PHE:CD1	2.44	0.52
1:EK:48:ILE:HG12	1:EK:69:LEU:HG	1.91	0.52
1:FM:29:ASN:H	1:FN:25:SER:HB2	1.74	0.52
1:FO:120:THR:HA	1:FO:124:GLN:HE22	1.74	0.52
1:GB:29:ASN:H	1:GC:25:SER:HB2	1.74	0.52
1:GG:120:THR:HA	1:GG:124:GLN:HE22	1.74	0.52
1:AA:48:ILE:HG12	1:AA:69:LEU:HG	1.91	0.52
1:AA:110:ALA:HB1	1:BI:88:ILE:HD11	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:53:ASP:HB3	1:AD:64:ARG:HB2	1.92	0.52
1:AQ:29:ASN:H	1:AR:25:SER:HB2	1.74	0.52
1:AS:120:THR:HA	1:AS:124:GLN:HE22	1.74	0.52
1:AV:48:ILE:HG12	1:AV:69:LEU:HG	1.91	0.52
1:BI:30:ASN:HA	1:BI:50:ALA:O	2.09	0.52
1:CE:75:ASP:HA	1:FQ:95:ASN:ND2	2.17	0.52
1:CH:63:ASP:HB3	1:FT:137:LEU:HD11	1.90	0.52
1:CJ:29:ASN:H	1:CK:25:SER:HB2	1.74	0.52
1:CU:48:ILE:HG12	1:CU:69:LEU:HG	1.91	0.52
1:DC:89:GLN:HB3	1:GO:87:THR:HG23	1.91	0.52
1:DG:120:THR:HA	1:DG:124:GLN:HE22	1.74	0.52
1:DH:30:ASN:HA	1:DH:50:ALA:O	2.09	0.52
1:EI:30:ASN:HA	1:EI:50:ALA:O	2.09	0.52
1:ET:48:ILE:HG12	1:ET:69:LEU:HG	1.91	0.52
1:FI:48:ILE:HG12	1:FI:69:LEU:HG	1.91	0.52
1:FJ:29:ASN:H	1:FK:25:SER:HB2	1.74	0.52
1:FU:120:THR:HA	1:FU:124:GLN:HE22	1.74	0.52
1:GM:53:ASP:HB3	1:GM:64:ARG:HB2	1.92	0.52
1:AE:29:ASN:H	1:AF:25:SER:HB2	1.74	0.52
1:AN:30:ASN:HA	1:AN:50:ALA:O	2.09	0.52
1:AR:137:LEU:HD13	1:ED:54:ILE:HG12	1.90	0.52
1:AZ:137:LEU:HA	1:EW:52:PHE:HE1	1.74	0.52
1:BB:120:THR:HA	1:BB:124:GLN:HE22	1.74	0.52
1:BV:89:GLN:HB3	1:FH:87:THR:HG23	1.91	0.52
1:CI:53:ASP:HB3	1:CI:64:ARG:HB2	1.92	0.52
1:CS:30:ASN:HA	1:CS:50:ALA:O	2.09	0.52
1:CX:48:ILE:HG12	1:CX:69:LEU:HG	1.91	0.52
1:DD:53:ASP:HB3	1:DD:64:ARG:HB2	1.92	0.52
1:DE:30:ASN:HA	1:DE:50:ALA:O	2.09	0.52
1:DK:29:ASN:H	1:DL:25:SER:HB2	1.74	0.52
1:DS:53:ASP:HB3	1:DS:64:ARG:HB2	1.92	0.52
1:EK:53:ASP:HB3	1:EK:64:ARG:HB2	1.92	0.52
1:EL:27:ASN:CG	1:EL:28:GLY:H	2.16	0.52
1:FC:48:ILE:HG12	1:FC:69:LEU:HG	1.91	0.52
1:FC:53:ASP:HB3	1:FC:64:ARG:HB2	1.92	0.52
1:FX:120:THR:HA	1:FX:124:GLN:HE22	1.74	0.52
1:GE:112:ASP:OD1	1:GE:118:SER:OG	2.16	0.52
1:GK:29:ASN:H	1:GL:25:SER:HB2	1.74	0.52
1:GQ:30:ASN:HA	1:GQ:50:ALA:O	2.10	0.52
1:GS:53:ASP:HB3	1:GS:64:ARG:HB2	1.92	0.52
1:AB:30:ASN:HA	1:AB:50:ALA:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:89:GLN:HB3	1:GA:87:THR:OG1	2.10	0.52
1:AZ:29:ASN:H	1:BA:25:SER:HB2	1.74	0.52
1:BB:53:ASP:HB3	1:BB:64:ARG:HB2	1.92	0.52
1:BH:53:ASP:HB3	1:BH:64:ARG:HB2	1.92	0.52
1:BL:30:ASN:HA	1:BL:50:ALA:O	2.09	0.52
1:BP:75:ASP:HA	1:FB:95:ASN:ND2	2.23	0.52
1:BQ:73:VAL:HG11	1:EC:97:ALA:O	2.10	0.52
1:BZ:48:ILE:HG12	1:BZ:69:LEU:HG	1.91	0.52
1:CF:48:ILE:HG12	1:CF:69:LEU:HG	1.91	0.52
1:CM:30:ASN:HA	1:CM:50:ALA:O	2.09	0.52
1:CR:120:THR:HA	1:CR:124:GLN:HE22	1.74	0.52
1:CU:53:ASP:HB3	1:CU:64:ARG:HB2	1.92	0.52
1:CV:29:ASN:H	1:CW:25:SER:HB2	1.74	0.52
1:DB:29:ASN:H	1:DC:25:SER:HB2	1.74	0.52
1:DJ:120:THR:HA	1:DJ:124:GLN:HE22	1.74	0.52
1:DL:97:ALA:HB1	1:GX:73:VAL:HG11	1.92	0.52
1:DY:53:ASP:HB3	1:DY:64:ARG:HB2	1.92	0.52
1:DZ:29:ASN:H	1:EA:25:SER:HB2	1.74	0.52
1:EE:120:THR:HA	1:EE:124:GLN:HE22	1.74	0.52
1:EO:30:ASN:HA	1:EO:50:ALA:O	2.09	0.52
1:EU:30:ASN:HA	1:EU:50:ALA:O	2.09	0.52
1:EZ:53:ASP:HB3	1:EZ:64:ARG:HB2	1.92	0.52
1:FO:53:ASP:HB3	1:FO:64:ARG:HB2	1.92	0.52
1:FV:29:ASN:H	1:FW:25:SER:HB2	1.74	0.52
1:GD:120:THR:HA	1:GD:124:GLN:HE22	1.74	0.52
1:GE:30:ASN:HA	1:GE:50:ALA:O	2.09	0.52
1:AF:118:SER:HB2	1:DR:8:VAL:HB	1.91	0.52
1:AP:137:LEU:HD11	1:BU:63:ASP:HB3	1.92	0.52
1:AQ:11:ASN:O	1:FU:101:SER:HB2	2.10	0.52
1:BA:137:LEU:HD13	1:EM:54:ILE:HG12	1.92	0.52
1:BQ:53:ASP:HB3	1:BQ:64:ARG:HB2	1.92	0.52
1:CI:48:ILE:HG12	1:CI:69:LEU:HG	1.91	0.52
1:CU:110:ALA:HB1	1:DH:88:ILE:HD11	1.90	0.52
1:DF:121:VAL:CG1	1:GR:18:LEU:HG	2.40	0.52
1:DN:30:ASN:HA	1:DN:50:ALA:O	2.09	0.52
1:DT:30:ASN:HA	1:DT:50:ALA:O	2.09	0.52
1:DW:29:ASN:H	1:DX:25:SER:HB2	1.74	0.52
1:EB:120:THR:HA	1:EB:124:GLN:HE22	1.74	0.52
1:EC:30:ASN:HA	1:EC:50:ALA:O	2.09	0.52
1:EU:27:ASN:CG	1:EU:28:GLY:H	2.16	0.52
1:FJ:30:ASN:HA	1:FJ:50:ALA:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FP:19:VAL:HG21	1:GV:109:GLN:NE2	2.25	0.52
1:FU:53:ASP:HB3	1:FU:64:ARG:HB2	1.92	0.52
1:GA:53:ASP:HB3	1:GA:64:ARG:HB2	1.92	0.52
1:GA:120:THR:HA	1:GA:124:GLN:HE22	1.74	0.52
1:GG:53:ASP:HB3	1:GG:64:ARG:HB2	1.92	0.52
1:GP:48:ILE:HG12	1:GP:69:LEU:HG	1.91	0.52
1:GQ:29:ASN:H	1:GR:25:SER:HB2	1.74	0.52
1:GV:53:ASP:HB3	1:GV:64:ARG:HB2	1.92	0.52
1:AN:29:ASN:H	1:AO:25:SER:HB2	1.74	0.52
1:AQ:30:ASN:HA	1:AQ:50:ALA:O	2.09	0.52
1:AV:105:SER:CB	1:EF:10:ALA:H	2.22	0.52
1:AV:137:LEU:HD22	1:EF:52:PHE:CD1	2.45	0.52
1:BC:30:ASN:HA	1:BC:50:ALA:O	2.09	0.52
1:BT:53:ASP:HB3	1:BT:64:ARG:HB2	1.92	0.52
1:CG:30:ASN:HA	1:CG:50:ALA:O	2.09	0.52
1:CT:19:VAL:HG21	1:GF:109:GLN:NE2	2.25	0.52
1:CV:54:ILE:HG12	1:GM:137:LEU:HD13	1.91	0.52
1:DA:53:ASP:HB3	1:DA:64:ARG:HB2	1.92	0.52
1:DM:8:VAL:HB	1:GT:118:SER:HB2	1.90	0.52
1:DY:137:LEU:HD13	1:FY:54:ILE:HG12	1.91	0.52
1:EF:29:ASN:H	1:EG:25:SER:HB2	1.74	0.52
1:ER:30:ASN:HA	1:ER:50:ALA:O	2.09	0.52
1:FM:30:ASN:HA	1:FM:50:ALA:O	2.09	0.52
1:FS:95:ASN:HD21	1:GP:75:ASP:HA	1.74	0.52
1:GD:53:ASP:HB3	1:GD:64:ARG:HB2	1.92	0.52
1:GT:27:ASN:CG	1:GT:28:GLY:H	2.16	0.52
1:AG:48:ILE:HG12	1:AG:69:LEU:HG	1.91	0.52
1:AM:73:VAL:HG22	1:CA:102:MET:HE1	1.92	0.52
1:AT:118:SER:HB2	1:EZ:8:VAL:HB	1.91	0.52
1:AV:53:ASP:HB3	1:AV:64:ARG:HB2	1.92	0.52
1:AY:27:ASN:HB3	1:AY:30:ASN:HB3	1.92	0.52
1:BK:27:ASN:HB3	1:BK:30:ASN:HB3	1.92	0.52
1:BL:27:ASN:CG	1:BL:28:GLY:H	2.16	0.52
1:BW:53:ASP:HB3	1:BW:64:ARG:HB2	1.92	0.52
1:CG:137:LEU:HA	1:CL:52:PHE:CE1	2.45	0.52
1:CQ:121:VAL:CG1	1:GC:18:LEU:HG	2.37	0.52
1:CQ:124:GLN:HA	1:GC:6:ALA:HB3	1.92	0.52
1:CX:120:THR:HA	1:CX:124:GLN:HE22	1.74	0.52
1:DB:30:ASN:HA	1:DB:50:ALA:O	2.09	0.52
1:DY:117:THR:O	1:FY:117:THR:HB	2.10	0.52
1:EH:53:ASP:HB3	1:EH:64:ARG:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EN:9:GLY:HA2	1:FJ:108:LYS:HB2	1.92	0.52
1:FC:120:THR:HA	1:FC:124:GLN:HE22	1.74	0.52
1:FL:53:ASP:HB3	1:FL:64:ARG:HB2	1.92	0.52
1:FR:53:ASP:HB3	1:FR:64:ARG:HB2	1.92	0.52
1:GJ:48:ILE:HG12	1:GJ:69:LEU:HG	1.91	0.52
1:AG:27:ASN:HB3	1:AG:30:ASN:HB3	1.92	0.52
1:AI:19:VAL:HG21	1:DU:109:GLN:NE2	2.24	0.52
1:AP:53:ASP:HB3	1:AP:64:ARG:HB2	1.92	0.52
1:BC:29:ASN:H	1:BD:25:SER:HB2	1.74	0.52
1:BV:10:ALA:H	1:FH:105:SER:CB	2.22	0.52
1:BW:27:ASN:HB3	1:BW:30:ASN:HB3	1.92	0.52
1:BX:29:ASN:H	1:BY:25:SER:HB2	1.74	0.52
1:BX:112:ASP:OD1	1:BX:118:SER:OG	2.16	0.52
1:CA:27:ASN:CG	1:CA:28:GLY:H	2.15	0.52
1:CG:29:ASN:H	1:CH:25:SER:HB2	1.74	0.52
1:CH:11:ASN:O	1:FT:101:SER:HB2	2.10	0.52
1:CL:27:ASN:HB3	1:CL:30:ASN:HB3	1.92	0.52
1:DM:118:SER:HB2	1:GT:8:VAL:HB	1.92	0.52
1:DN:29:ASN:H	1:DO:25:SER:HB2	1.74	0.52
1:DP:27:ASN:HB3	1:DP:30:ASN:HB3	1.92	0.52
1:EC:29:ASN:H	1:ED:25:SER:HB2	1.74	0.52
1:EE:121:VAL:CG1	1:EU:18:LEU:CG	2.83	0.52
1:EN:11:ASN:O	1:FJ:101:SER:HB2	2.10	0.52
1:EW:27:ASN:HB3	1:EW:30:ASN:HB3	1.92	0.52
1:EW:120:THR:HA	1:EW:124:GLN:HE22	1.74	0.52
1:FF:27:ASN:HB3	1:FF:30:ASN:HB3	1.92	0.52
1:FO:27:ASN:HB3	1:FO:30:ASN:HB3	1.92	0.52
1:FX:27:ASN:HB3	1:FX:30:ASN:HB3	1.92	0.52
1:GJ:27:ASN:HB3	1:GJ:30:ASN:HB3	1.92	0.52
1:GJ:53:ASP:HB3	1:GJ:64:ARG:HB2	1.92	0.52
1:GM:120:THR:HA	1:GM:124:GLN:HE22	1.74	0.52
1:GT:29:ASN:H	1:GU:25:SER:HB2	1.74	0.52
1:AD:48:ILE:HG12	1:AD:69:LEU:HG	1.91	0.51
1:AF:117:THR:HG1	1:DR:117:THR:HG1	1.58	0.51
1:BB:48:ILE:HG12	1:BB:69:LEU:HG	1.91	0.51
1:BE:27:ASN:HB3	1:BE:30:ASN:HB3	1.92	0.51
1:BN:27:ASN:HB3	1:BN:30:ASN:HB3	1.92	0.51
1:BN:53:ASP:HB3	1:BN:64:ARG:HB2	1.92	0.51
1:BW:48:ILE:HG12	1:BW:69:LEU:HG	1.91	0.51
1:CF:53:ASP:HB3	1:CF:64:ARG:HB2	1.92	0.51
1:CX:27:ASN:HB3	1:CX:30:ASN:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DC:6:ALA:HB3	1:GO:125:THR:HG23	1.93	0.51
1:DF:122:SER:O	1:GR:18:LEU:HD11	2.09	0.51
1:DJ:53:ASP:HB3	1:DJ:64:ARG:HB2	1.92	0.51
1:DM:27:ASN:HB3	1:DM:30:ASN:HB3	1.92	0.51
1:DQ:30:ASN:HA	1:DQ:50:ALA:O	2.09	0.51
1:DV:120:THR:HA	1:DV:124:GLN:HE22	1.74	0.51
1:DZ:30:ASN:HA	1:DZ:50:ALA:O	2.09	0.51
1:EB:53:ASP:HB3	1:EB:64:ARG:HB2	1.92	0.51
1:EK:120:THR:HA	1:EK:124:GLN:HE22	1.74	0.51
1:EN:48:ILE:HG12	1:EN:69:LEU:HG	1.91	0.51
1:ER:29:ASN:H	1:ES:25:SER:HB2	1.74	0.51
1:EX:27:ASN:CG	1:EX:28:GLY:H	2.16	0.51
1:FP:30:ASN:HA	1:FP:50:ALA:O	2.09	0.51
1:GK:30:ASN:HA	1:GK:50:ALA:O	2.09	0.51
1:GV:48:ILE:HG12	1:GV:69:LEU:HG	1.91	0.51
1:AA:120:THR:HA	1:AA:124:GLN:HE22	1.74	0.51
1:AP:27:ASN:HB3	1:AP:30:ASN:HB3	1.92	0.51
1:AY:48:ILE:HG12	1:AY:69:LEU:HG	1.91	0.51
1:BB:27:ASN:HB3	1:BB:30:ASN:HB3	1.92	0.51
1:BO:30:ASN:HA	1:BO:50:ALA:O	2.09	0.51
1:BT:27:ASN:HB3	1:BT:30:ASN:HB3	1.92	0.51
1:CA:30:ASN:HA	1:CA:50:ALA:O	2.09	0.51
1:CO:27:ASN:HB3	1:CO:30:ASN:HB3	1.92	0.51
1:CX:53:ASP:HB3	1:CX:64:ARG:HB2	1.92	0.51
1:DY:48:ILE:HG12	1:DY:69:LEU:HG	1.91	0.51
1:EU:29:ASN:H	1:EV:25:SER:HB2	1.74	0.51
1:FG:29:ASN:H	1:FH:25:SER:HB2	1.74	0.51
1:FU:27:ASN:HB3	1:FU:30:ASN:HB3	1.92	0.51
1:GA:48:ILE:HG12	1:GA:69:LEU:HG	1.91	0.51
1:AA:27:ASN:HB3	1:AA:30:ASN:HB3	1.92	0.51
1:AJ:120:THR:HA	1:AJ:124:GLN:HE22	1.74	0.51
1:AV:63:ASP:CB	1:EF:137:LEU:HD11	2.40	0.51
1:BA:137:LEU:HD11	1:EM:63:ASP:HB3	1.92	0.51
1:BE:8:VAL:HB	1:BL:118:SER:HB2	1.91	0.51
1:BF:27:ASN:CG	1:BF:28:GLY:H	2.16	0.51
1:BS:117:THR:HB	1:FE:117:THR:O	2.10	0.51
1:BZ:53:ASP:HB3	1:BZ:64:ARG:HB2	1.92	0.51
1:CD:29:ASN:H	1:CE:25:SER:HB2	1.74	0.51
1:CF:27:ASN:HB3	1:CF:30:ASN:HB3	1.92	0.51
1:CM:19:VAL:HG21	1:DG:109:GLN:NE2	2.25	0.51
1:CP:54:ILE:HG12	1:DJ:137:LEU:HD13	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:53:ASP:HB3	1:DP:64:ARG:HB2	1.92	0.51
1:DT:29:ASN:H	1:DU:25:SER:HB2	1.74	0.51
1:DY:73:VAL:HG11	1:FY:97:ALA:O	2.10	0.51
1:EN:53:ASP:HB3	1:EN:64:ARG:HB2	1.92	0.51
1:EN:120:THR:HA	1:EN:124:GLN:HE22	1.74	0.51
1:EQ:53:ASP:HB3	1:EQ:64:ARG:HB2	1.92	0.51
1:FD:109:GLN:NE2	1:FF:19:VAL:HG21	2.25	0.51
1:FG:30:ASN:HA	1:FG:50:ALA:O	2.09	0.51
1:FR:120:THR:HA	1:FR:124:GLN:HE22	1.74	0.51
1:FV:19:VAL:HG21	1:GS:109:GLN:NE2	2.25	0.51
1:GB:30:ASN:HA	1:GB:50:ALA:O	2.09	0.51
1:GH:27:ASN:CG	1:GH:28:GLY:H	2.16	0.51
1:AG:120:THR:HA	1:AG:124:GLN:HE22	1.74	0.51
1:AJ:27:ASN:HB3	1:AJ:30:ASN:HB3	1.92	0.51
1:AK:137:LEU:HA	1:FO:52:PHE:CE1	2.45	0.51
1:AT:139:PHE:CE1	1:EZ:52:PHE:HE2	2.28	0.51
1:AU:109:GLN:NE2	1:EG:19:VAL:HG21	2.25	0.51
1:BB:109:GLN:NE2	1:BR:19:VAL:HG21	2.25	0.51
1:BF:29:ASN:H	1:BG:25:SER:HB2	1.74	0.51
1:BH:48:ILE:HG12	1:BH:69:LEU:HG	1.91	0.51
1:BI:29:ASN:H	1:BJ:25:SER:HB2	1.74	0.51
1:BQ:120:THR:HA	1:BQ:124:GLN:HE22	1.74	0.51
1:CC:27:ASN:HB3	1:CC:30:ASN:HB3	1.93	0.51
1:CO:48:ILE:HG12	1:CO:69:LEU:HG	1.91	0.51
1:CP:30:ASN:HA	1:CP:50:ALA:O	2.10	0.51
1:CS:84:GLY:HA2	1:DD:93:PRO:HD3	1.91	0.51
1:CV:27:ASN:CG	1:CV:28:GLY:H	2.15	0.51
1:DF:86:VAL:HG22	1:GR:90:VAL:HG22	1.92	0.51
1:DM:120:THR:HA	1:DM:124:GLN:HE22	1.74	0.51
1:DS:27:ASN:HB3	1:DS:30:ASN:HB3	1.92	0.51
1:EE:53:ASP:HB3	1:EE:64:ARG:HB2	1.92	0.51
1:EQ:48:ILE:HG12	1:EQ:69:LEU:HG	1.91	0.51
1:ET:118:SER:HB2	1:FG:8:VAL:HB	1.92	0.51
1:EX:29:ASN:H	1:EY:25:SER:HB2	1.74	0.51
1:FV:63:ASP:HB3	1:GS:137:LEU:HD11	1.92	0.51
1:GM:27:ASN:HB3	1:GM:30:ASN:HB3	1.92	0.51
1:AP:118:SER:HB2	1:BU:8:VAL:HB	1.91	0.51
1:AR:87:THR:HG23	1:ED:89:GLN:HB3	1.93	0.51
1:AS:27:ASN:HB3	1:AS:30:ASN:HB3	1.92	0.51
1:AZ:137:LEU:HD13	1:EW:54:ILE:HG12	1.92	0.51
1:BA:54:ILE:HG12	1:EM:137:LEU:HD13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:95:ASN:HD21	1:EP:75:ASP:HA	1.74	0.51
1:BE:48:ILE:HG12	1:BE:69:LEU:HG	1.91	0.51
1:BH:27:ASN:HB3	1:BH:30:ASN:HB3	1.93	0.51
1:BN:120:THR:HA	1:BN:124:GLN:HE22	1.74	0.51
1:BS:117:THR:O	1:FE:117:THR:HB	2.10	0.51
1:BZ:118:SER:HB2	1:DT:8:VAL:HB	1.93	0.51
1:CG:5:LEU:HA	1:CL:125:THR:HG21	1.93	0.51
1:CU:120:THR:HA	1:CU:124:GLN:HE22	1.74	0.51
1:CW:137:LEU:HD13	1:GI:54:ILE:HG12	1.91	0.51
1:DJ:48:ILE:HG12	1:DJ:69:LEU:HG	1.91	0.51
1:EE:27:ASN:HB3	1:EE:30:ASN:HB3	1.92	0.51
1:EK:27:ASN:HB3	1:EK:30:ASN:HB3	1.92	0.51
1:FS:112:ASP:OD1	1:FS:118:SER:OG	2.16	0.51
1:GW:29:ASN:H	1:GX:25:SER:HB2	1.74	0.51
1:AD:27:ASN:HB3	1:AD:30:ASN:HB3	1.92	0.51
1:AN:54:ILE:HG12	1:FR:137:LEU:CD1	2.37	0.51
1:AY:53:ASP:HB3	1:AY:64:ARG:HB2	1.92	0.51
1:CA:112:ASP:OD1	1:CA:118:SER:OG	2.16	0.51
1:CQ:125:THR:HG21	1:GC:5:LEU:HA	1.93	0.51
1:DQ:29:ASN:H	1:DR:25:SER:HB2	1.74	0.51
1:EL:30:ASN:HA	1:EL:50:ALA:O	2.09	0.51
1:EN:27:ASN:HB3	1:EN:30:ASN:HB3	1.93	0.51
1:EQ:27:ASN:HB3	1:EQ:30:ASN:HB3	1.92	0.51
1:EZ:48:ILE:HG12	1:EZ:69:LEU:HG	1.91	0.51
1:GD:48:ILE:HG12	1:GD:69:LEU:HG	1.91	0.51
1:GG:27:ASN:HB3	1:GG:30:ASN:HB3	1.92	0.51
1:AG:53:ASP:HB3	1:AG:64:ARG:HB2	1.92	0.51
1:AM:53:ASP:HB3	1:AM:64:ARG:HB2	1.92	0.51
1:AM:120:THR:HA	1:AM:124:GLN:HE22	1.74	0.51
1:AQ:27:ASN:CG	1:AQ:28:GLY:H	2.15	0.51
1:BE:53:ASP:HB3	1:BE:64:ARG:HB2	1.92	0.51
1:BI:27:ASN:CG	1:BI:28:GLY:H	2.16	0.51
1:CI:84:GLY:HA3	1:GH:98:TRP:CH2	2.45	0.51
1:CM:27:ASN:CG	1:CM:28:GLY:H	2.16	0.51
1:DA:27:ASN:HB3	1:DA:30:ASN:HB3	1.92	0.51
1:DJ:28:GLY:HA3	1:DK:27:ASN:HB2	1.93	0.51
1:FC:27:ASN:HB3	1:FC:30:ASN:HB3	1.92	0.51
1:FR:27:ASN:HB3	1:FR:30:ASN:HB3	1.92	0.51
1:GS:27:ASN:HB3	1:GS:30:ASN:HB3	1.92	0.51
1:AD:77:LYS:HG3	1:AD:78:THR:HG23	1.93	0.51
1:AS:48:ILE:HG12	1:AS:69:LEU:HG	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:112:ASP:OD1	1:BF:118:SER:OG	2.16	0.51
1:BZ:27:ASN:HB3	1:BZ:30:ASN:HB3	1.92	0.51
1:CM:29:ASN:H	1:CN:25:SER:HB2	1.74	0.51
1:CM:117:THR:OG1	1:DG:117:THR:OG1	2.25	0.51
1:CO:53:ASP:HB3	1:CO:64:ARG:HB2	1.92	0.51
1:DP:120:THR:HA	1:DP:124:GLN:HE22	1.74	0.51
1:DV:27:ASN:HB3	1:DV:30:ASN:HB3	1.92	0.51
1:DY:27:ASN:HB3	1:DY:30:ASN:HB3	1.92	0.51
1:EB:27:ASN:HB3	1:EB:30:ASN:HB3	1.92	0.51
1:EH:77:LYS:HG3	1:EH:78:THR:HG23	1.93	0.51
1:FI:27:ASN:HB3	1:FI:30:ASN:HB3	1.92	0.51
1:FL:27:ASN:HB3	1:FL:30:ASN:HB3	1.92	0.51
1:FU:48:ILE:HG12	1:FU:69:LEU:HG	1.91	0.51
1:AK:137:LEU:HD13	1:FO:54:ILE:HG12	1.93	0.51
1:AP:48:ILE:HG12	1:AP:69:LEU:HG	1.91	0.51
1:AQ:137:LEU:HD22	1:FU:52:PHE:CD1	2.46	0.51
1:AR:95:ASN:HD21	1:ED:75:ASP:HA	1.76	0.51
1:BB:77:LYS:HG3	1:BB:78:THR:HG23	1.93	0.51
1:BK:53:ASP:HB3	1:BK:64:ARG:HB2	1.92	0.51
1:BR:30:ASN:HA	1:BR:50:ALA:O	2.09	0.51
1:CB:121:VAL:CG1	1:FN:18:LEU:HG	2.38	0.51
1:CI:27:ASN:HB3	1:CI:30:ASN:HB3	1.93	0.51
1:CI:77:LYS:HG3	1:CI:78:THR:HG23	1.93	0.51
1:CL:53:ASP:HB3	1:CL:64:ARG:HB2	1.92	0.51
1:CR:28:GLY:HA3	1:CS:27:ASN:HB2	1.93	0.51
1:DH:112:ASP:OD1	1:DH:118:SER:OG	2.16	0.51
1:DS:28:GLY:HA3	1:DT:27:ASN:HB2	1.93	0.51
1:DS:48:ILE:HG12	1:DS:69:LEU:HG	1.91	0.51
1:DS:52:PHE:HE2	1:GQ:139:PHE:CE1	2.28	0.51
1:EB:77:LYS:HG3	1:EB:78:THR:HG23	1.93	0.51
1:EK:117:THR:O	1:ER:117:THR:HB	2.10	0.51
1:GA:77:LYS:HG3	1:GA:78:THR:HG23	1.93	0.51
1:GV:27:ASN:HB3	1:GV:30:ASN:HB3	1.92	0.51
1:AA:53:ASP:HB3	1:AA:64:ARG:HB2	1.92	0.51
1:AD:28:GLY:HA3	1:AE:27:ASN:HB2	1.93	0.51
1:BP:10:ALA:HB1	1:BP:14:LEU:HA	1.93	0.51
1:CC:53:ASP:HB3	1:CC:64:ARG:HB2	1.92	0.51
1:CD:54:ILE:HG12	1:CR:137:LEU:HD13	1.92	0.51
1:CR:53:ASP:HB3	1:CR:64:ARG:HB2	1.92	0.51
1:CV:137:LEU:HD22	1:GM:52:PHE:CD1	2.46	0.51
1:CZ:10:ALA:HB1	1:CZ:14:LEU:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DD:120:THR:HA	1:DD:124:GLN:HE22	1.74	0.51
1:DG:28:GLY:HA3	1:DH:27:ASN:HB2	1.93	0.51
1:DP:77:LYS:HG3	1:DP:78:THR:HG23	1.93	0.51
1:DX:10:ALA:HB1	1:DX:14:LEU:HA	1.93	0.51
1:EE:29:ASN:HA	1:EU:139:PHE:HE2	1.76	0.51
1:EM:10:ALA:HB1	1:EM:14:LEU:HA	1.93	0.51
1:ET:28:GLY:HA3	1:EU:27:ASN:HB2	1.93	0.51
1:EU:42:LEU:HD22	1:FG:137:LEU:HD12	1.93	0.51
1:EW:53:ASP:HB3	1:EW:64:ARG:HB2	1.92	0.51
1:FC:77:LYS:HG3	1:FC:78:THR:HG23	1.93	0.51
1:GD:27:ASN:HB3	1:GD:30:ASN:HB3	1.92	0.51
1:GM:77:LYS:HG3	1:GM:78:THR:HG23	1.93	0.51
1:GQ:27:ASN:CG	1:GQ:28:GLY:H	2.16	0.51
1:GS:28:GLY:HA3	1:GT:27:ASN:HB2	1.93	0.51
1:GU:10:ALA:HB1	1:GU:14:LEU:HA	1.93	0.51
1:AE:8:VAL:HB	1:GA:118:SER:HB2	1.92	0.50
1:AE:105:SER:HB2	1:GA:10:ALA:O	2.11	0.50
1:BN:77:LYS:HG3	1:BN:78:THR:HG23	1.93	0.50
1:BQ:27:ASN:HB3	1:BQ:30:ASN:HB3	1.93	0.50
1:CJ:90:VAL:HG22	1:CO:86:VAL:HG22	1.92	0.50
1:CT:89:GLN:HB3	1:GF:87:THR:HG23	1.93	0.50
1:CY:112:ASP:OD1	1:CY:118:SER:OG	2.16	0.50
1:DH:27:ASN:CG	1:DH:28:GLY:H	2.16	0.50
1:DP:48:ILE:HG12	1:DP:69:LEU:HG	1.91	0.50
1:EK:110:ALA:HB1	1:ER:88:ILE:HD11	1.92	0.50
1:EQ:77:LYS:HG3	1:EQ:78:THR:HG23	1.93	0.50
1:EZ:28:GLY:HA3	1:FA:27:ASN:HB2	1.93	0.50
1:FD:19:VAL:HG21	1:FF:109:GLN:NE2	2.26	0.50
1:FJ:27:ASN:CG	1:FJ:28:GLY:H	2.16	0.50
1:FR:28:GLY:HA3	1:FS:27:ASN:HB2	1.93	0.50
1:FU:77:LYS:HG3	1:FU:78:THR:HG23	1.93	0.50
1:FX:28:GLY:HA3	1:FY:27:ASN:HB2	1.93	0.50
1:FX:53:ASP:HB3	1:FX:64:ARG:HB2	1.92	0.50
1:GA:28:GLY:HA3	1:GB:27:ASN:HB2	1.93	0.50
1:GE:29:ASN:H	1:GF:25:SER:HB2	1.74	0.50
1:GG:77:LYS:HG3	1:GG:78:THR:HG23	1.93	0.50
1:GH:112:ASP:OD1	1:GH:118:SER:OG	2.16	0.50
1:AG:77:LYS:HG3	1:AG:78:THR:HG23	1.93	0.50
1:AI:10:ALA:HB1	1:AI:14:LEU:HA	1.93	0.50
1:AJ:53:ASP:HB3	1:AJ:64:ARG:HB2	1.92	0.50
1:AS:53:ASP:HB3	1:AS:64:ARG:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:73:VAL:HG11	1:EL:97:ALA:O	2.11	0.50
1:CC:77:LYS:HG3	1:CC:78:THR:HG23	1.93	0.50
1:CI:88:ILE:HD11	1:GH:110:ALA:HB1	1.91	0.50
1:CT:95:ASN:ND2	1:GF:75:ASP:HA	2.24	0.50
1:DM:77:LYS:HG3	1:DM:78:THR:HG23	1.93	0.50
1:EB:28:GLY:HA3	1:EC:27:ASN:HB2	1.93	0.50
1:ED:10:ALA:HB1	1:ED:14:LEU:HA	1.93	0.50
1:EH:27:ASN:HB3	1:EH:30:ASN:HB3	1.92	0.50
1:ES:10:ALA:HB1	1:ES:14:LEU:HA	1.93	0.50
1:FI:28:GLY:HA3	1:FJ:27:ASN:HB2	1.93	0.50
1:GP:27:ASN:HB3	1:GP:30:ASN:HB3	1.93	0.50
1:GW:27:ASN:CG	1:GW:28:GLY:H	2.16	0.50
1:AD:117:THR:HB	1:BC:117:THR:O	2.12	0.50
1:AH:52:PHE:CD1	1:GD:137:LEU:HD22	2.47	0.50
1:AV:27:ASN:HB3	1:AV:30:ASN:HB3	1.92	0.50
1:AX:10:ALA:HB1	1:AX:14:LEU:HA	1.93	0.50
1:BH:137:LEU:HD22	1:BO:52:PHE:CD1	2.46	0.50
1:BY:10:ALA:HB1	1:BY:14:LEU:HA	1.93	0.50
1:CF:28:GLY:HA3	1:CG:27:ASN:HB2	1.93	0.50
1:CM:125:THR:HG23	1:DG:6:ALA:HB3	1.93	0.50
1:CT:137:LEU:O	1:GD:24:ARG:HG3	2.11	0.50
1:CX:28:GLY:HA3	1:CY:27:ASN:HB2	1.93	0.50
1:DM:53:ASP:HB3	1:DM:64:ARG:HB2	1.92	0.50
1:DN:112:ASP:OD1	1:DN:118:SER:OG	2.16	0.50
1:DV:53:ASP:HB3	1:DV:64:ARG:HB2	1.92	0.50
1:EB:48:ILE:HG12	1:EB:69:LEU:HG	1.91	0.50
1:EN:77:LYS:HG3	1:EN:78:THR:HG23	1.93	0.50
1:FF:77:LYS:HG3	1:FF:78:THR:HG23	1.93	0.50
1:FI:77:LYS:HG3	1:FI:78:THR:HG23	1.93	0.50
1:FT:10:ALA:HB1	1:FT:14:LEU:HA	1.93	0.50
1:GP:53:ASP:HB3	1:GP:64:ARG:HB2	1.92	0.50
1:GV:77:LYS:HG3	1:GV:78:THR:HG23	1.93	0.50
1:AD:88:ILE:HD11	1:BC:110:ALA:HB1	1.92	0.50
1:AJ:97:ALA:O	1:BX:73:VAL:HG11	2.12	0.50
1:BK:52:PHE:CD1	1:DW:137:LEU:HD22	2.46	0.50
1:BV:11:ASN:O	1:FH:101:SER:HB2	2.11	0.50
1:CF:77:LYS:HG3	1:CF:78:THR:HG23	1.93	0.50
1:DD:27:ASN:HB3	1:DD:30:ASN:HB3	1.92	0.50
1:DY:77:LYS:HG3	1:DY:78:THR:HG23	1.93	0.50
1:EK:77:LYS:HG3	1:EK:78:THR:HG23	1.93	0.50
1:FF:28:GLY:HA3	1:FG:27:ASN:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FL:28:GLY:HA3	1:FM:27:ASN:HB2	1.93	0.50
1:FQ:10:ALA:HB1	1:FQ:14:LEU:HA	1.93	0.50
1:GD:28:GLY:HA3	1:GE:27:ASN:HB2	1.93	0.50
1:GP:28:GLY:HA3	1:GQ:27:ASN:HB2	1.93	0.50
1:AC:10:ALA:HB1	1:AC:14:LEU:HA	1.93	0.50
1:AJ:42:LEU:HD22	1:DX:137:LEU:HD12	1.94	0.50
1:BK:28:GLY:HA3	1:BL:27:ASN:HB2	1.93	0.50
1:BS:10:ALA:HB1	1:BS:14:LEU:HA	1.93	0.50
1:BW:10:ALA:HB1	1:BW:14:LEU:HA	1.94	0.50
1:CF:10:ALA:HB1	1:CF:14:LEU:HA	1.94	0.50
1:CI:28:GLY:HA3	1:CJ:27:ASN:HB2	1.93	0.50
1:CY:27:ASN:CG	1:CY:28:GLY:H	2.16	0.50
1:DD:28:GLY:HA3	1:DE:27:ASN:HB2	1.93	0.50
1:EH:52:PHE:HD1	1:EO:137:LEU:HD22	1.76	0.50
1:ET:77:LYS:HG3	1:ET:78:THR:HG23	1.93	0.50
1:EZ:27:ASN:HB3	1:EZ:30:ASN:HB3	1.92	0.50
1:GA:27:ASN:HB3	1:GA:30:ASN:HB3	1.92	0.50
1:GD:10:ALA:HB1	1:GD:14:LEU:HA	1.94	0.50
1:GG:28:GLY:HA3	1:GH:27:ASN:HB2	1.93	0.50
1:GJ:10:ALA:HB1	1:GJ:14:LEU:HA	1.94	0.50
1:AA:117:THR:O	1:BI:117:THR:HB	2.12	0.50
1:AJ:10:ALA:HB1	1:AJ:14:LEU:HA	1.94	0.50
1:AM:77:LYS:HG3	1:AM:78:THR:HG23	1.93	0.50
1:AM:97:ALA:O	1:CA:73:VAL:HG11	2.11	0.50
1:AY:10:ALA:HB1	1:AY:14:LEU:HA	1.94	0.50
1:AY:28:GLY:HA3	1:AZ:27:ASN:HB2	1.93	0.50
1:BG:10:ALA:HB1	1:BG:14:LEU:HA	1.93	0.50
1:BJ:10:ALA:HB1	1:BJ:14:LEU:HA	1.93	0.50
1:BW:54:ILE:HG12	1:DQ:137:LEU:HD13	1.94	0.50
1:CC:10:ALA:HB1	1:CC:14:LEU:HA	1.94	0.50
1:CU:27:ASN:HB3	1:CU:30:ASN:HB3	1.92	0.50
1:CU:101:SER:HB2	1:DH:11:ASN:O	2.11	0.50
1:DA:28:GLY:HA3	1:DB:27:ASN:HB2	1.93	0.50
1:DF:9:GLY:HA2	1:GR:108:LYS:HB2	1.93	0.50
1:EB:10:ALA:HB1	1:EB:14:LEU:HA	1.94	0.50
1:EE:125:THR:HG21	1:EU:5:LEU:HA	1.93	0.50
1:EV:10:ALA:HB1	1:EV:14:LEU:HA	1.93	0.50
1:EY:10:ALA:HB1	1:EY:14:LEU:HA	1.93	0.50
1:EZ:10:ALA:HB1	1:EZ:14:LEU:HA	1.94	0.50
1:FH:10:ALA:HB1	1:FH:14:LEU:HA	1.94	0.50
1:FL:77:LYS:HG3	1:FL:78:THR:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FU:10:ALA:HB1	1:FU:14:LEU:HA	1.94	0.50
1:GI:10:ALA:HB1	1:GI:14:LEU:HA	1.93	0.50
1:GJ:77:LYS:HG3	1:GJ:78:THR:HG23	1.93	0.50
1:GM:28:GLY:HA3	1:GN:27:ASN:HB2	1.93	0.50
1:GR:10:ALA:HB1	1:GR:14:LEU:HA	1.93	0.50
1:GS:77:LYS:HG3	1:GS:78:THR:HG23	1.93	0.50
1:AM:10:ALA:HB1	1:AM:14:LEU:HA	1.94	0.50
1:AP:77:LYS:HG3	1:AP:78:THR:HG23	1.93	0.50
1:AR:10:ALA:HB1	1:AR:14:LEU:HA	1.93	0.50
1:AY:77:LYS:HG3	1:AY:78:THR:HG23	1.93	0.50
1:BQ:77:LYS:HG3	1:BQ:78:THR:HG23	1.93	0.50
1:BY:65:ILE:HD11	1:FK:134:TRP:O	2.12	0.50
1:CS:27:ASN:CG	1:CS:28:GLY:H	2.15	0.50
1:DJ:77:LYS:HG3	1:DJ:78:THR:HG23	1.93	0.50
1:DL:10:ALA:HB1	1:DL:14:LEU:HA	1.93	0.50
1:DV:10:ALA:HB1	1:DV:14:LEU:HA	1.94	0.50
1:DY:10:ALA:HB1	1:DY:14:LEU:HA	1.94	0.50
1:EG:10:ALA:HB1	1:EG:14:LEU:HA	1.93	0.50
1:EN:10:ALA:HB1	1:EN:14:LEU:HA	1.94	0.50
1:ET:53:ASP:HB3	1:ET:64:ARG:HB2	1.92	0.50
1:FA:117:THR:HB	1:FL:117:THR:O	2.10	0.50
1:FI:53:ASP:HB3	1:FI:64:ARG:HB2	1.92	0.50
1:FU:28:GLY:HA3	1:FV:27:ASN:HB2	1.93	0.50
1:GC:10:ALA:HB1	1:GC:14:LEU:HA	1.93	0.50
1:GP:77:LYS:HG3	1:GP:78:THR:HG23	1.93	0.50
1:AE:19:VAL:HG21	1:GA:109:GLN:NE2	2.27	0.50
1:AH:101:SER:HB2	1:GD:11:ASN:O	2.12	0.50
1:AM:109:GLN:NE2	1:CA:19:VAL:HG21	2.26	0.50
1:AN:137:LEU:HD22	1:FR:52:PHE:CD1	2.47	0.50
1:AO:10:ALA:HB1	1:AO:14:LEU:HA	1.93	0.50
1:AV:77:LYS:HG3	1:AV:78:THR:HG23	1.93	0.50
1:AX:87:THR:CG2	1:EJ:89:GLN:HB3	2.42	0.50
1:BE:28:GLY:HA3	1:BF:27:ASN:HB2	1.93	0.50
1:BM:117:THR:OG1	1:EY:117:THR:OG1	2.29	0.50
1:BN:28:GLY:HA3	1:BO:27:ASN:HB2	1.93	0.50
1:BN:137:LEU:HD13	1:DZ:54:ILE:HG12	1.93	0.50
1:BW:28:GLY:HA3	1:BX:27:ASN:HB2	1.93	0.50
1:BZ:10:ALA:HB1	1:BZ:14:LEU:HA	1.94	0.50
1:CX:10:ALA:HB1	1:CX:14:LEU:HA	1.94	0.50
1:DD:10:ALA:HB1	1:DD:14:LEU:HA	1.94	0.50
1:DG:10:ALA:HB1	1:DG:14:LEU:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DG:53:ASP:HB3	1:DG:64:ARG:HB2	1.92	0.50
1:DO:10:ALA:HB1	1:DO:14:LEU:HA	1.93	0.50
1:DV:28:GLY:HA3	1:DW:27:ASN:HB2	1.93	0.50
1:EK:28:GLY:HA3	1:EL:27:ASN:HB2	1.93	0.50
1:EN:137:LEU:HD11	1:FJ:63:ASP:CB	2.41	0.50
1:EQ:28:GLY:HA3	1:ER:27:ASN:HB2	1.93	0.50
1:EW:77:LYS:HG3	1:EW:78:THR:HG23	1.93	0.50
1:FC:10:ALA:HB1	1:FC:14:LEU:HA	1.94	0.50
1:FF:53:ASP:HB3	1:FF:64:ARG:HB2	1.92	0.50
1:FW:10:ALA:HB1	1:FW:14:LEU:HA	1.93	0.50
1:AA:10:ALA:HB1	1:AA:14:LEU:HA	1.94	0.50
1:AJ:28:GLY:HA3	1:AK:27:ASN:HB2	1.93	0.50
1:AN:112:ASP:OD1	1:AN:118:SER:OG	2.16	0.50
1:BB:28:GLY:HA3	1:BC:27:ASN:HB2	1.93	0.50
1:BT:77:LYS:HG3	1:BT:78:THR:HG23	1.93	0.50
1:CR:10:ALA:HB1	1:CR:14:LEU:HA	1.94	0.50
1:CU:10:ALA:HB1	1:CU:14:LEU:HA	1.94	0.50
1:DS:10:ALA:HB1	1:DS:14:LEU:HA	1.94	0.50
1:DU:10:ALA:HB1	1:DU:14:LEU:HA	1.93	0.50
1:DY:28:GLY:HA3	1:DZ:27:ASN:HB2	1.93	0.50
1:EJ:10:ALA:HB1	1:EJ:14:LEU:HA	1.93	0.50
1:ET:27:ASN:HB3	1:ET:30:ASN:HB3	1.92	0.50
1:EZ:77:LYS:HG3	1:EZ:78:THR:HG23	1.93	0.50
1:FI:10:ALA:HB1	1:FI:14:LEU:HA	1.94	0.50
1:FP:52:PHE:CD1	1:GV:137:LEU:HD22	2.46	0.50
1:GS:10:ALA:HB1	1:GS:14:LEU:HA	1.94	0.50
1:AN:101:SER:HB2	1:FR:11:ASN:O	2.12	0.49
1:AR:121:VAL:CG1	1:ED:18:LEU:HG	2.42	0.49
1:AS:77:LYS:HG3	1:AS:78:THR:HG23	1.93	0.49
1:BH:28:GLY:HA3	1:BI:27:ASN:HB2	1.93	0.49
1:BQ:28:GLY:HA3	1:BR:27:ASN:HB2	1.93	0.49
1:BV:10:ALA:HB1	1:BV:14:LEU:HA	1.93	0.49
1:CK:8:VAL:HB	1:FW:118:SER:HB2	1.92	0.49
1:CO:77:LYS:HG3	1:CO:78:THR:HG23	1.93	0.49
1:CS:137:LEU:O	1:DE:24:ARG:NE	2.44	0.49
1:CU:125:THR:HG21	1:DH:5:LEU:HA	1.93	0.49
1:DJ:10:ALA:HB1	1:DJ:14:LEU:HA	1.94	0.49
1:DJ:27:ASN:HB3	1:DJ:30:ASN:HB3	1.92	0.49
1:DM:110:ALA:HB1	1:GT:88:ILE:HD11	1.94	0.49
1:EE:77:LYS:HG3	1:EE:78:THR:HG23	1.93	0.49
1:EH:52:PHE:CD1	1:EO:137:LEU:HD22	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ET:10:ALA:HB1	1:ET:14:LEU:HA	1.94	0.49
1:FA:105:SER:HB2	1:FL:10:ALA:O	2.12	0.49
1:FK:10:ALA:HB1	1:FK:14:LEU:HA	1.93	0.49
1:AG:28:GLY:HA3	1:AH:27:ASN:HB2	1.93	0.49
1:AG:97:ALA:O	1:BF:73:VAL:HG11	2.12	0.49
1:AI:118:SER:HB2	1:DU:8:VAL:HB	1.94	0.49
1:AJ:77:LYS:HG3	1:AJ:78:THR:HG23	1.93	0.49
1:AM:27:ASN:HB3	1:AM:30:ASN:HB3	1.92	0.49
1:AS:28:GLY:HA3	1:AT:27:ASN:HB2	1.93	0.49
1:BC:112:ASP:OD1	1:BC:118:SER:OG	2.16	0.49
1:BH:10:ALA:HB1	1:BH:14:LEU:HA	1.94	0.49
1:BK:52:PHE:HE1	1:DW:137:LEU:HA	1.76	0.49
1:BK:77:LYS:HG3	1:BK:78:THR:HG23	1.93	0.49
1:BY:95:ASN:ND2	1:FK:75:ASP:HA	2.26	0.49
1:CE:105:SER:CB	1:FQ:10:ALA:H	2.25	0.49
1:CL:10:ALA:HB1	1:CL:14:LEU:HA	1.94	0.49
1:DA:77:LYS:HG3	1:DA:78:THR:HG23	1.93	0.49
1:DD:77:LYS:HG3	1:DD:78:THR:HG23	1.93	0.49
1:DM:10:ALA:HB1	1:DM:14:LEU:HA	1.94	0.49
1:DM:28:GLY:HA3	1:DN:27:ASN:HB2	1.93	0.49
1:DP:28:GLY:HA3	1:DQ:27:ASN:HB2	1.93	0.49
1:AI:117:THR:O	1:DU:117:THR:HB	2.12	0.49
1:BE:77:LYS:HG3	1:BE:78:THR:HG23	1.93	0.49
1:CK:10:ALA:HB1	1:CK:14:LEU:HA	1.93	0.49
1:CN:10:ALA:HB1	1:CN:14:LEU:HA	1.93	0.49
1:CS:112:ASP:OD1	1:CS:118:SER:OG	2.16	0.49
1:CV:137:LEU:HD13	1:GM:54:ILE:HG12	1.93	0.49
1:DG:27:ASN:HB3	1:DG:30:ASN:HB3	1.92	0.49
1:DV:52:PHE:HE1	1:GE:137:LEU:HA	1.77	0.49
1:EE:28:GLY:HA3	1:EF:27:ASN:HB2	1.93	0.49
1:GM:10:ALA:HB1	1:GM:14:LEU:HA	1.94	0.49
1:AF:10:ALA:HB1	1:AF:14:LEU:HA	1.93	0.49
1:AM:28:GLY:HA3	1:AN:27:ASN:HB2	1.93	0.49
1:AN:137:LEU:HA	1:FR:52:PHE:CE1	2.47	0.49
1:AV:10:ALA:HB1	1:AV:14:LEU:HA	1.94	0.49
1:AW:137:LEU:HD22	1:FC:52:PHE:HD1	1.78	0.49
1:BJ:102:MET:HE2	1:EV:71:LYS:HG2	1.94	0.49
1:BZ:28:GLY:HA3	1:CA:27:ASN:HB2	1.93	0.49
1:CC:28:GLY:HA3	1:CD:27:ASN:HB2	1.93	0.49
1:CR:77:LYS:HG3	1:CR:78:THR:HG23	1.93	0.49
1:CU:77:LYS:HG3	1:CU:78:THR:HG23	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:117:THR:HB	1:DK:117:THR:O	2.12	0.49
1:CX:137:LEU:HD13	1:DK:54:ILE:HG12	1.94	0.49
1:DB:137:LEU:HD22	1:GJ:52:PHE:HD1	1.77	0.49
1:EE:10:ALA:HB1	1:EE:14:LEU:HA	1.94	0.49
1:EP:10:ALA:HB1	1:EP:14:LEU:HA	1.94	0.49
1:EQ:10:ALA:HB1	1:EQ:14:LEU:HA	1.94	0.49
1:EX:118:SER:HB2	1:FI:8:VAL:HB	1.94	0.49
1:FO:77:LYS:HG3	1:FO:78:THR:HG23	1.93	0.49
1:GD:77:LYS:HG3	1:GD:78:THR:HG23	1.93	0.49
1:AA:28:GLY:HA3	1:AB:27:ASN:HB2	1.93	0.49
1:AB:117:THR:O	1:FX:117:THR:HB	2.11	0.49
1:AD:52:PHE:CD2	1:BC:139:PHE:CZ	3.00	0.49
1:AP:28:GLY:HA3	1:AQ:27:ASN:HB2	1.93	0.49
1:AP:52:PHE:CE1	1:BU:137:LEU:HA	2.47	0.49
1:AU:10:ALA:HB1	1:AU:14:LEU:HA	1.93	0.49
1:BE:88:ILE:HD11	1:BL:110:ALA:HB1	1.93	0.49
1:BJ:98:TRP:CH2	1:EV:71:LYS:HB3	2.47	0.49
1:BW:118:SER:HB2	1:DQ:8:VAL:HB	1.93	0.49
1:CG:88:ILE:HD11	1:CL:110:ALA:HB1	1.94	0.49
1:CG:137:LEU:HD11	1:CL:63:ASP:HB3	1.95	0.49
1:CO:28:GLY:HA3	1:CP:27:ASN:HB2	1.93	0.49
1:CV:137:LEU:HD22	1:GM:52:PHE:HD1	1.78	0.49
1:CW:10:ALA:HB1	1:CW:14:LEU:HA	1.93	0.49
1:DA:10:ALA:HB1	1:DA:14:LEU:HA	1.94	0.49
1:DC:87:THR:CG2	1:GO:89:GLN:HB3	2.42	0.49
1:DG:77:LYS:HG3	1:DG:78:THR:HG23	1.93	0.49
1:DP:10:ALA:HB1	1:DP:14:LEU:HA	1.94	0.49
1:DR:10:ALA:HB1	1:DR:14:LEU:HA	1.93	0.49
1:DV:77:LYS:HG3	1:DV:78:THR:HG23	1.93	0.49
1:EN:28:GLY:HA3	1:EO:27:ASN:HB2	1.93	0.49
1:GV:28:GLY:HA3	1:GW:27:ASN:HB2	1.93	0.49
1:AN:27:ASN:CG	1:AN:28:GLY:H	2.16	0.49
1:AQ:52:PHE:CD1	1:FU:137:LEU:HD22	2.47	0.49
1:AX:97:ALA:HB1	1:EJ:73:VAL:CG1	2.42	0.49
1:BD:84:GLY:HA3	1:EP:98:TRP:CH2	2.48	0.49
1:BT:137:LEU:HD13	1:DN:54:ILE:HG12	1.94	0.49
1:CQ:10:ALA:HB1	1:CQ:14:LEU:HA	1.93	0.49
1:CR:27:ASN:HB3	1:CR:30:ASN:HB3	1.92	0.49
1:DF:10:ALA:HB1	1:DF:14:LEU:HA	1.93	0.49
1:DK:27:ASN:CG	1:DK:28:GLY:H	2.16	0.49
1:DS:77:LYS:HG3	1:DS:78:THR:HG23	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FF:10:ALA:HB1	1:FF:14:LEU:HA	1.94	0.49
1:FO:28:GLY:HA3	1:FP:27:ASN:HB2	1.93	0.49
1:GL:10:ALA:HB1	1:GL:14:LEU:HA	1.93	0.49
1:GO:10:ALA:HB1	1:GO:14:LEU:HA	1.94	0.49
1:AG:99:ASN:OD1	1:AG:102:MET:HG3	2.13	0.49
1:AR:73:VAL:HG11	1:ED:97:ALA:HB1	1.94	0.49
1:AY:109:GLN:NE2	1:EI:19:VAL:HG21	2.28	0.49
1:BE:10:ALA:HB1	1:BE:14:LEU:HA	1.94	0.49
1:BP:8:VAL:HB	1:FB:118:SER:HB2	1.94	0.49
1:BW:99:ASN:OD1	1:BW:102:MET:HG3	2.13	0.49
1:CE:10:ALA:HB1	1:CE:14:LEU:HA	1.93	0.49
1:CE:89:GLN:HB3	1:FQ:87:THR:HG23	1.95	0.49
1:CL:77:LYS:HG3	1:CL:78:THR:HG23	1.93	0.49
1:DP:99:ASN:OD1	1:DP:102:MET:HG3	2.13	0.49
1:DV:99:ASN:OD1	1:DV:102:MET:HG3	2.13	0.49
1:EB:77:LYS:NZ	1:GC:79:ASN:HD22	2.10	0.49
1:EO:112:ASP:OD1	1:EO:118:SER:OG	2.16	0.49
1:FC:99:ASN:OD1	1:FC:102:MET:HG3	2.13	0.49
1:AU:73:VAL:CG1	1:EG:97:ALA:HB1	2.43	0.49
1:BK:10:ALA:HB1	1:BK:14:LEU:HA	1.94	0.49
1:BN:10:ALA:HB1	1:BN:14:LEU:HA	1.94	0.49
1:CU:137:LEU:HD11	1:DH:63:ASP:CB	2.42	0.49
1:CX:77:LYS:HG3	1:CX:78:THR:HG23	1.93	0.49
1:DA:88:ILE:HD11	1:DE:110:ALA:HB1	1.94	0.49
1:DI:10:ALA:HB1	1:DI:14:LEU:HA	1.93	0.49
1:DP:137:LEU:HD22	1:GW:52:PHE:CD1	2.48	0.49
1:EW:28:GLY:HA3	1:EX:27:ASN:HB2	1.93	0.49
1:EW:99:ASN:OD1	1:EW:102:MET:HG3	2.13	0.49
1:EZ:99:ASN:OD1	1:EZ:102:MET:HG3	2.13	0.49
1:FN:10:ALA:HB1	1:FN:14:LEU:HA	1.93	0.49
1:FR:10:ALA:HB1	1:FR:14:LEU:HA	1.94	0.49
1:GF:10:ALA:HB1	1:GF:14:LEU:HA	1.94	0.49
1:GG:10:ALA:HB1	1:GG:14:LEU:HA	1.94	0.49
1:GX:10:ALA:HB1	1:GX:14:LEU:HA	1.93	0.49
1:AL:10:ALA:HB1	1:AL:14:LEU:HA	1.93	0.49
1:BB:117:THR:O	1:BR:117:THR:HB	2.11	0.49
1:BK:117:THR:O	1:DW:117:THR:HB	2.12	0.49
1:BM:10:ALA:HB1	1:BM:14:LEU:HA	1.93	0.49
1:BQ:10:ALA:HB1	1:BQ:14:LEU:HA	1.94	0.49
1:CB:10:ALA:HB1	1:CB:14:LEU:HA	1.94	0.49
1:CG:139:PHE:HE2	1:CL:29:ASN:HA	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:108:LYS:HB2	1:GC:9:GLY:HA2	1.94	0.49
1:CS:139:PHE:HE2	1:DD:29:ASN:HA	1.78	0.49
1:DF:87:THR:CG2	1:GR:89:GLN:HB3	2.43	0.49
1:EH:28:GLY:HA3	1:EI:27:ASN:HB2	1.93	0.49
1:EW:10:ALA:HB1	1:EW:14:LEU:HA	1.94	0.49
1:FF:99:ASN:OD1	1:FF:102:MET:HG3	2.13	0.49
1:FL:10:ALA:HB1	1:FL:14:LEU:HA	1.94	0.49
1:FP:137:LEU:HD22	1:GV:52:PHE:HD1	1.77	0.49
1:FR:77:LYS:HG3	1:FR:78:THR:HG23	1.93	0.49
1:GJ:28:GLY:HA3	1:GK:27:ASN:HB2	1.93	0.49
1:GS:99:ASN:OD1	1:GS:102:MET:HG3	2.13	0.49
1:AA:77:LYS:HG3	1:AA:78:THR:HG23	1.93	0.49
1:AD:117:THR:O	1:BC:117:THR:HB	2.13	0.49
1:AP:10:ALA:HB1	1:AP:14:LEU:HA	1.94	0.49
1:AP:99:ASN:OD1	1:AP:102:MET:HG3	2.13	0.49
1:AY:99:ASN:OD1	1:AY:102:MET:HG3	2.13	0.49
1:BD:10:ALA:HB1	1:BD:14:LEU:HA	1.93	0.49
1:BW:19:VAL:HG21	1:DQ:109:GLN:NE2	2.27	0.49
1:CT:36:THR:HG22	1:DD:138:MET:CE	2.42	0.49
1:CU:28:GLY:HA3	1:CV:27:ASN:HB2	1.93	0.49
1:DC:10:ALA:HB1	1:DC:14:LEU:HA	1.93	0.49
1:EA:10:ALA:HB1	1:EA:14:LEU:HA	1.93	0.49
1:EE:9:GLY:HA2	1:EU:108:LYS:HB2	1.94	0.49
1:EQ:99:ASN:OD1	1:EQ:102:MET:HG3	2.13	0.49
1:FC:28:GLY:HA3	1:FD:27:ASN:HB2	1.93	0.49
1:AG:117:THR:O	1:BF:117:THR:HB	2.13	0.48
1:AJ:99:ASN:OD1	1:AJ:102:MET:HG3	2.13	0.48
1:AN:109:GLN:NE2	1:FR:19:VAL:HG21	2.28	0.48
1:BD:63:ASP:CB	1:EP:137:LEU:HD11	2.43	0.48
1:BT:99:ASN:OD1	1:BT:102:MET:HG3	2.13	0.48
1:BW:75:ASP:HA	1:DQ:95:ASN:HD21	1.78	0.48
1:CH:10:ALA:HB1	1:CH:14:LEU:HA	1.94	0.48
1:CI:52:PHE:HE2	1:GH:139:PHE:CE1	2.32	0.48
1:CI:99:ASN:OD1	1:CI:102:MET:HG3	2.13	0.48
1:CL:28:GLY:HA3	1:CM:27:ASN:HB2	1.93	0.48
1:CT:10:ALA:HB1	1:CT:14:LEU:HA	1.93	0.48
1:CT:90:VAL:HG22	1:GF:86:VAL:HG22	1.95	0.48
1:CU:29:ASN:HA	1:DH:139:PHE:HE2	1.78	0.48
1:DY:99:ASN:OD1	1:DY:102:MET:HG3	2.13	0.48
1:DZ:27:ASN:CG	1:DZ:28:GLY:H	2.15	0.48
1:EB:118:SER:HB2	1:GB:8:VAL:HB	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EC:27:ASN:CG	1:EC:28:GLY:H	2.16	0.48
1:EH:10:ALA:HB1	1:EH:14:LEU:HA	1.94	0.48
1:FX:99:ASN:OD1	1:FX:102:MET:HG3	2.13	0.48
1:GB:27:ASN:CG	1:GB:28:GLY:H	2.16	0.48
1:AI:54:ILE:HG12	1:DU:137:LEU:HD13	1.94	0.48
1:AS:99:ASN:OD1	1:AS:102:MET:HG3	2.13	0.48
1:AU:75:ASP:CA	1:EG:95:ASN:HD21	2.20	0.48
1:AW:19:VAL:HG21	1:FC:109:GLN:NE2	2.29	0.48
1:AW:137:LEU:HD22	1:FC:52:PHE:CD1	2.49	0.48
1:AZ:121:VAL:HG11	1:EW:18:LEU:HG	1.95	0.48
1:BE:99:ASN:OD1	1:BE:102:MET:HG3	2.13	0.48
1:BT:10:ALA:HB1	1:BT:14:LEU:HA	1.94	0.48
1:BW:52:PHE:HE1	1:DQ:137:LEU:HA	1.79	0.48
1:BW:77:LYS:HG3	1:BW:78:THR:HG23	1.93	0.48
1:BW:137:LEU:CD1	1:DQ:54:ILE:HG12	2.33	0.48
1:CD:137:LEU:HD12	1:CS:42:LEU:HD22	1.95	0.48
1:CI:18:LEU:HD11	1:GH:123:GLY:H	1.77	0.48
1:EH:99:ASN:OD1	1:EH:102:MET:HG3	2.13	0.48
1:EN:99:ASN:OD1	1:EN:102:MET:HG3	2.13	0.48
1:EQ:97:ALA:O	1:FM:73:VAL:HG11	2.13	0.48
1:FO:10:ALA:HB1	1:FO:14:LEU:HA	1.94	0.48
1:FX:10:ALA:HB1	1:FX:14:LEU:HA	1.94	0.48
1:AA:99:ASN:OD1	1:AA:102:MET:HG3	2.13	0.48
1:AD:10:ALA:HB1	1:AD:14:LEU:HA	1.94	0.48
1:AH:137:LEU:HD22	1:GD:52:PHE:HD1	1.78	0.48
1:AV:28:GLY:HA3	1:AW:27:ASN:HB2	1.93	0.48
1:BB:10:ALA:HB1	1:BB:14:LEU:HA	1.94	0.48
1:BZ:24:ARG:NE	1:FN:137:LEU:O	2.47	0.48
1:BZ:77:LYS:HG3	1:BZ:78:THR:HG23	1.93	0.48
1:CO:10:ALA:HB1	1:CO:14:LEU:HA	1.94	0.48
1:CS:63:ASP:CG	1:DD:137:LEU:HD11	2.38	0.48
1:DF:11:ASN:O	1:GR:101:SER:HB2	2.14	0.48
1:DJ:99:ASN:OD1	1:DJ:102:MET:HG3	2.13	0.48
1:EB:99:ASN:OD1	1:EB:102:MET:HG3	2.13	0.48
1:EQ:84:GLY:HA3	1:FM:98:TRP:CH2	2.48	0.48
1:ET:99:ASN:OD1	1:ET:102:MET:HG3	2.13	0.48
1:FA:89:GLN:HB3	1:FL:87:THR:OG1	2.13	0.48
1:FM:27:ASN:CG	1:FM:28:GLY:H	2.16	0.48
1:FS:117:THR:HB	1:GP:117:THR:O	2.12	0.48
1:AT:8:VAL:HB	1:EZ:118:SER:HB2	1.96	0.48
1:CI:10:ALA:HB1	1:CI:14:LEU:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:65:ILE:HD11	1:GC:134:TRP:O	2.13	0.48
1:DM:99:ASN:OD1	1:DM:102:MET:HG3	2.13	0.48
1:EK:11:ASN:O	1:ER:101:SER:HB2	2.14	0.48
1:FS:117:THR:O	1:GP:117:THR:HB	2.13	0.48
1:FU:99:ASN:OD1	1:FU:102:MET:HG3	2.13	0.48
1:FX:77:LYS:HG3	1:FX:78:THR:HG23	1.93	0.48
1:BH:77:LYS:HG3	1:BH:78:THR:HG23	1.93	0.48
1:BO:27:ASN:CG	1:BO:28:GLY:H	2.16	0.48
1:CD:73:VAL:CG2	1:CR:102:MET:HE1	2.44	0.48
1:CE:89:GLN:HB3	1:FQ:87:THR:CG2	2.43	0.48
1:CF:99:ASN:OD1	1:CF:102:MET:HG3	2.13	0.48
1:CU:137:LEU:CD1	1:DH:54:ILE:HG12	2.27	0.48
1:DL:75:ASP:HA	1:GX:95:ASN:HD21	1.78	0.48
1:FR:99:ASN:OD1	1:FR:102:MET:HG3	2.13	0.48
1:FY:27:ASN:CG	1:FY:28:GLY:H	2.15	0.48
1:GD:99:ASN:OD1	1:GD:102:MET:HG3	2.13	0.48
1:GP:10:ALA:HB1	1:GP:14:LEU:HA	1.94	0.48
1:GV:10:ALA:HB1	1:GV:14:LEU:HA	1.94	0.48
1:AS:10:ALA:HB1	1:AS:14:LEU:HA	1.94	0.48
1:BT:28:GLY:HA3	1:BU:27:ASN:HB2	1.93	0.48
1:BX:27:ASN:CG	1:BX:28:GLY:H	2.16	0.48
1:BY:8:VAL:HB	1:FK:118:SER:HB2	1.94	0.48
1:DA:52:PHE:HD1	1:DE:137:LEU:HD22	1.77	0.48
1:DG:99:ASN:OD1	1:DG:102:MET:HG3	2.13	0.48
1:DJ:42:LEU:HD22	1:GX:137:LEU:HD12	1.95	0.48
1:DS:99:ASN:OD1	1:DS:102:MET:HG3	2.13	0.48
1:DV:117:THR:O	1:GE:117:THR:HB	2.13	0.48
1:EQ:109:GLN:NE2	1:FM:19:VAL:HG21	2.28	0.48
1:FB:10:ALA:HB1	1:FB:14:LEU:HA	1.94	0.48
1:FZ:10:ALA:HB1	1:FZ:14:LEU:HA	1.93	0.48
1:AD:97:ALA:O	1:BC:73:VAL:HG11	2.14	0.48
1:BA:10:ALA:HB1	1:BA:14:LEU:HA	1.93	0.48
1:BE:110:ALA:HB1	1:BL:88:ILE:HD11	1.96	0.48
1:BN:8:VAL:HB	1:DZ:118:SER:HB2	1.95	0.48
1:BQ:109:GLN:NE2	1:EC:19:VAL:HG21	2.29	0.48
1:BZ:99:ASN:OD1	1:BZ:102:MET:HG3	2.13	0.48
1:CJ:137:LEU:HD22	1:CO:52:PHE:HD1	1.78	0.48
1:CS:73:VAL:HG11	1:DD:97:ALA:C	2.35	0.48
1:DB:11:ASN:O	1:GJ:101:SER:HB2	2.14	0.48
1:EX:19:VAL:HG21	1:FI:109:GLN:NE2	2.28	0.48
1:EX:125:THR:HG23	1:FI:6:ALA:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FE:10:ALA:HB1	1:FE:14:LEU:HA	1.93	0.48
1:GA:99:ASN:OD1	1:GA:102:MET:HG3	2.13	0.48
1:GP:99:ASN:OD1	1:GP:102:MET:HG3	2.13	0.48
1:AH:137:LEU:HD11	1:GD:63:ASP:HB3	1.96	0.48
1:AW:118:SER:HB2	1:FC:8:VAL:HB	1.94	0.48
1:AX:137:LEU:HD12	1:EH:42:LEU:HD22	1.95	0.48
1:BN:99:ASN:OD1	1:BN:102:MET:HG3	2.13	0.48
1:CJ:112:ASP:OD1	1:CJ:118:SER:OG	2.16	0.48
1:CO:99:ASN:OD1	1:CO:102:MET:HG3	2.13	0.48
1:CU:99:ASN:OD1	1:CU:102:MET:HG3	2.13	0.48
1:DA:99:ASN:OD1	1:DA:102:MET:HG3	2.13	0.48
1:DB:19:VAL:HG21	1:GJ:109:GLN:NE2	2.28	0.48
1:FL:99:ASN:OD1	1:FL:102:MET:HG3	2.13	0.48
1:AG:10:ALA:HB1	1:AG:14:LEU:HA	1.94	0.48
1:AR:97:ALA:HB1	1:ED:73:VAL:CG1	2.44	0.48
1:AZ:63:ASP:HB3	1:EW:137:LEU:HD11	1.96	0.48
1:BH:99:ASN:OD1	1:BH:102:MET:HG3	2.13	0.48
1:BQ:99:ASN:OD1	1:BQ:102:MET:HG3	2.13	0.48
1:BW:109:GLN:NE2	1:DQ:19:VAL:HG21	2.29	0.48
1:BY:105:SER:HB2	1:FK:10:ALA:O	2.13	0.48
1:CV:8:VAL:HB	1:GM:118:SER:HB2	1.96	0.48
1:CX:99:ASN:OD1	1:CX:102:MET:HG3	2.13	0.48
1:DD:40:SER:HB2	1:DD:45:PRO:HA	1.96	0.48
1:DP:118:SER:HB2	1:GW:8:VAL:HB	1.96	0.48
1:EE:40:SER:HB2	1:EE:45:PRO:HA	1.96	0.48
1:EK:10:ALA:HB1	1:EK:14:LEU:HA	1.94	0.48
1:FA:27:ASN:CG	1:FA:28:GLY:H	2.16	0.48
1:GV:99:ASN:OD1	1:GV:102:MET:HG3	2.13	0.48
1:AB:27:ASN:CG	1:AB:28:GLY:H	2.16	0.48
1:AE:137:LEU:HD22	1:GA:52:PHE:HD1	1.77	0.48
1:AF:117:THR:O	1:DR:117:THR:HB	2.13	0.48
1:AM:99:ASN:OD1	1:AM:102:MET:HG3	2.13	0.48
1:AY:52:PHE:HE1	1:EI:137:LEU:HA	1.79	0.48
1:BW:8:VAL:HB	1:DQ:118:SER:HB2	1.96	0.48
1:CF:40:SER:HB2	1:CF:45:PRO:HA	1.96	0.48
1:CQ:101:SER:HB2	1:GC:11:ASN:O	2.14	0.48
1:CS:8:VAL:HB	1:DD:118:SER:HB2	1.95	0.48
1:CY:95:ASN:HD21	1:GG:75:ASP:HA	1.79	0.48
1:DD:99:ASN:OD1	1:DD:102:MET:HG3	2.13	0.48
1:EI:27:ASN:CG	1:EI:28:GLY:H	2.16	0.48
1:AD:99:ASN:OD1	1:AD:102:MET:HG3	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:40:SER:HB2	1:AY:45:PRO:HA	1.96	0.47
1:CC:99:ASN:OD1	1:CC:102:MET:HG3	2.13	0.47
1:CI:117:THR:HB	1:GH:117:THR:O	2.14	0.47
1:FI:99:ASN:OD1	1:FI:102:MET:HG3	2.13	0.47
1:FR:40:SER:HB2	1:FR:45:PRO:HA	1.96	0.47
1:AN:137:LEU:HD22	1:FR:52:PHE:HD1	1.79	0.47
1:AO:137:LEU:HD13	1:EA:54:ILE:HG12	1.94	0.47
1:AT:117:THR:OG1	1:EZ:117:THR:OG1	2.31	0.47
1:BV:118:SER:HB2	1:FH:8:VAL:HB	1.96	0.47
1:CF:110:ALA:HB1	1:GN:88:ILE:HD11	1.96	0.47
1:CQ:9:GLY:HA2	1:GC:108:LYS:HB2	1.95	0.47
1:CR:99:ASN:OD1	1:CR:102:MET:HG3	2.13	0.47
1:CW:122:SER:O	1:GI:18:LEU:HD11	2.14	0.47
1:DB:137:LEU:HD22	1:GJ:52:PHE:CD1	2.49	0.47
1:DV:109:GLN:NE2	1:GE:19:VAL:HG21	2.29	0.47
1:DY:40:SER:HB2	1:DY:45:PRO:HA	1.96	0.47
1:EH:8:VAL:HB	1:EO:118:SER:HB2	1.96	0.47
1:FL:40:SER:HB2	1:FL:45:PRO:HA	1.96	0.47
1:FO:99:ASN:OD1	1:FO:102:MET:HG3	2.13	0.47
1:GP:40:SER:HB2	1:GP:45:PRO:HA	1.96	0.47
1:AM:130:PHE:CD1	1:AM:140:PRO:HB3	2.50	0.47
1:AT:97:ALA:HB1	1:EZ:73:VAL:CG1	2.44	0.47
1:AZ:27:ASN:CG	1:AZ:28:GLY:H	2.16	0.47
1:BQ:40:SER:HB2	1:BQ:45:PRO:HA	1.96	0.47
1:CI:105:SER:O	1:CI:109:GLN:HG3	2.15	0.47
1:CL:99:ASN:OD1	1:CL:102:MET:HG3	2.13	0.47
1:CP:137:LEU:HA	1:DJ:52:PHE:HE1	1.78	0.47
1:DC:89:GLN:HB3	1:GO:87:THR:CG2	2.44	0.47
1:DK:112:ASP:OD1	1:DK:118:SER:OG	2.16	0.47
1:EK:40:SER:HB2	1:EK:45:PRO:HA	1.96	0.47
1:FS:95:ASN:HD21	1:GP:75:ASP:CA	2.27	0.47
1:FV:27:ASN:CG	1:FV:28:GLY:H	2.15	0.47
1:GA:10:ALA:HB1	1:GA:14:LEU:HA	1.94	0.47
1:GA:40:SER:HB2	1:GA:45:PRO:HA	1.96	0.47
1:GG:99:ASN:OD1	1:GG:102:MET:HG3	2.13	0.47
1:GJ:40:SER:HB2	1:GJ:45:PRO:HA	1.96	0.47
1:AD:40:SER:HB2	1:AD:45:PRO:HA	1.96	0.47
1:AJ:137:LEU:HD22	1:BX:52:PHE:CD1	2.49	0.47
1:AN:105:SER:CB	1:FR:10:ALA:H	2.28	0.47
1:AS:40:SER:HB2	1:AS:45:PRO:HA	1.96	0.47
1:AV:99:ASN:OD1	1:AV:102:MET:HG3	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:105:SER:O	1:AY:109:GLN:HG3	2.15	0.47
1:BB:99:ASN:OD1	1:BB:102:MET:HG3	2.13	0.47
1:BB:105:SER:O	1:BB:109:GLN:HG3	2.15	0.47
1:BD:27:ASN:O	1:BD:30:ASN:HB3	2.15	0.47
1:BK:99:ASN:OD1	1:BK:102:MET:HG3	2.13	0.47
1:BT:102:MET:HE1	1:DN:73:VAL:CG2	2.44	0.47
1:BT:105:SER:O	1:BT:109:GLN:HG3	2.15	0.47
1:BW:130:PHE:CD1	1:BW:140:PRO:HB3	2.50	0.47
1:CR:130:PHE:CD1	1:CR:140:PRO:HB3	2.50	0.47
1:DG:130:PHE:CD1	1:DG:140:PRO:HB3	2.50	0.47
1:DL:89:GLN:HB3	1:GX:87:THR:HG23	1.97	0.47
1:DP:130:PHE:CD1	1:DP:140:PRO:HB3	2.50	0.47
1:EE:99:ASN:OD1	1:EE:102:MET:HG3	2.13	0.47
1:EH:105:SER:O	1:EH:109:GLN:HG3	2.15	0.47
1:EK:99:ASN:OD1	1:EK:102:MET:HG3	2.13	0.47
1:EN:130:PHE:CD1	1:EN:140:PRO:HB3	2.50	0.47
1:ES:27:ASN:O	1:ES:30:ASN:HB3	2.15	0.47
1:EZ:40:SER:HB2	1:EZ:45:PRO:HA	1.96	0.47
1:FU:105:SER:O	1:FU:109:GLN:HG3	2.15	0.47
1:GD:105:SER:O	1:GD:109:GLN:HG3	2.15	0.47
1:GM:99:ASN:OD1	1:GM:102:MET:HG3	2.13	0.47
1:GM:105:SER:O	1:GM:109:GLN:HG3	2.15	0.47
1:GR:27:ASN:O	1:GR:30:ASN:HB3	2.15	0.47
1:GV:105:SER:O	1:GV:109:GLN:HG3	2.15	0.47
1:AF:27:ASN:O	1:AF:30:ASN:HB3	2.15	0.47
1:AN:117:THR:HB	1:FR:117:THR:O	2.15	0.47
1:AV:105:SER:O	1:AV:109:GLN:HG3	2.15	0.47
1:AY:52:PHE:CE1	1:EI:137:LEU:HA	2.49	0.47
1:BA:27:ASN:O	1:BA:30:ASN:HB3	2.15	0.47
1:BJ:24:ARG:NH2	1:BJ:34:VAL:HG21	2.30	0.47
1:BK:52:PHE:CE1	1:DW:137:LEU:HA	2.49	0.47
1:BS:27:ASN:O	1:BS:30:ASN:HB3	2.15	0.47
1:CC:19:VAL:HG21	1:GK:109:GLN:NE2	2.29	0.47
1:CF:130:PHE:CD1	1:CF:140:PRO:HB3	2.50	0.47
1:CI:52:PHE:CD2	1:GH:139:PHE:CZ	3.02	0.47
1:CR:105:SER:O	1:CR:109:GLN:HG3	2.15	0.47
1:DA:105:SER:O	1:DA:109:GLN:HG3	2.15	0.47
1:DO:27:ASN:O	1:DO:30:ASN:HB3	2.15	0.47
1:DP:105:SER:O	1:DP:109:GLN:HG3	2.15	0.47
1:DS:73:VAL:CG1	1:GQ:97:ALA:HB1	2.45	0.47
1:EE:130:PHE:CD1	1:EE:140:PRO:HB3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EN:105:SER:O	1:EN:109:GLN:HG3	2.15	0.47
1:FG:27:ASN:CG	1:FG:28:GLY:H	2.16	0.47
1:GU:27:ASN:O	1:GU:30:ASN:HB3	2.15	0.47
1:GX:24:ARG:NH2	1:GX:34:VAL:HG21	2.30	0.47
1:AA:137:LEU:HD22	1:BI:52:PHE:CD1	2.48	0.47
1:AC:24:ARG:NH2	1:AC:34:VAL:HG21	2.30	0.47
1:AD:102:MET:HE1	1:BC:73:VAL:CG2	2.44	0.47
1:AD:105:SER:O	1:AD:109:GLN:HG3	2.15	0.47
1:AH:11:ASN:O	1:GD:101:SER:HB2	2.15	0.47
1:AU:27:ASN:O	1:AU:30:ASN:HB3	2.15	0.47
1:AV:40:SER:HB2	1:AV:45:PRO:HA	1.96	0.47
1:AX:27:ASN:O	1:AX:30:ASN:HB3	2.15	0.47
1:AZ:112:ASP:OD1	1:AZ:118:SER:OG	2.16	0.47
1:BJ:27:ASN:O	1:BJ:30:ASN:HB3	2.15	0.47
1:CE:27:ASN:O	1:CE:30:ASN:HB3	2.15	0.47
1:CG:139:PHE:CZ	1:CL:52:PHE:HD2	2.33	0.47
1:CL:130:PHE:CD1	1:CL:140:PRO:HB3	2.50	0.47
1:CM:73:VAL:HG11	1:DG:97:ALA:O	2.15	0.47
1:CM:112:ASP:OD1	1:CM:118:SER:OG	2.16	0.47
1:CN:24:ARG:NH2	1:CN:34:VAL:HG21	2.30	0.47
1:CS:138:MET:HE3	1:DE:24:ARG:HA	1.97	0.47
1:CT:24:ARG:NH2	1:CT:34:VAL:HG21	2.30	0.47
1:CZ:27:ASN:O	1:CZ:30:ASN:HB3	2.15	0.47
1:DC:27:ASN:O	1:DC:30:ASN:HB3	2.15	0.47
1:DD:130:PHE:CD1	1:DD:140:PRO:HB3	2.50	0.47
1:DF:24:ARG:NH2	1:DF:34:VAL:HG21	2.30	0.47
1:DL:73:VAL:CG1	1:GX:97:ALA:HB1	2.44	0.47
1:DR:24:ARG:NH2	1:DR:34:VAL:HG21	2.30	0.47
1:EB:105:SER:O	1:EB:109:GLN:HG3	2.15	0.47
1:ED:27:ASN:O	1:ED:30:ASN:HB3	2.15	0.47
1:EE:105:SER:O	1:EE:109:GLN:HG3	2.15	0.47
1:EH:52:PHE:CE1	1:EO:137:LEU:HA	2.50	0.47
1:EP:27:ASN:O	1:EP:30:ASN:HB3	2.15	0.47
1:EQ:130:PHE:CD1	1:EQ:140:PRO:HB3	2.50	0.47
1:EW:130:PHE:CD1	1:EW:140:PRO:HB3	2.50	0.47
1:EY:27:ASN:O	1:EY:30:ASN:HB3	2.15	0.47
1:FC:40:SER:HB2	1:FC:45:PRO:HA	1.96	0.47
1:FF:130:PHE:CD1	1:FF:140:PRO:HB3	2.50	0.47
1:FP:137:LEU:HD22	1:GV:52:PHE:CD1	2.50	0.47
1:FS:27:ASN:CG	1:FS:28:GLY:H	2.16	0.47
1:FU:130:PHE:CD1	1:FU:140:PRO:HB3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FX:130:PHE:CD1	1:FX:140:PRO:HB3	2.50	0.47
1:GJ:105:SER:O	1:GJ:109:GLN:HG3	2.15	0.47
1:GL:27:ASN:O	1:GL:30:ASN:HB3	2.15	0.47
1:GO:24:ARG:NH2	1:GO:34:VAL:HG21	2.30	0.47
1:GV:40:SER:HB2	1:GV:45:PRO:HA	1.96	0.47
1:AA:130:PHE:CD1	1:AA:140:PRO:HB3	2.50	0.47
1:AD:130:PHE:CD1	1:AD:140:PRO:HB3	2.50	0.47
1:AG:52:PHE:HE2	1:BF:139:PHE:CE1	2.33	0.47
1:AG:130:PHE:CD1	1:AG:140:PRO:HB3	2.50	0.47
1:AH:8:VAL:HB	1:GD:118:SER:HB2	1.96	0.47
1:AI:24:ARG:NH2	1:AI:34:VAL:HG21	2.30	0.47
1:AP:101:SER:HB2	1:BU:11:ASN:O	2.14	0.47
1:AR:24:ARG:NH2	1:AR:34:VAL:HG21	2.30	0.47
1:AS:52:PHE:HD1	1:EL:137:LEU:HD22	1.80	0.47
1:AS:130:PHE:CD1	1:AS:140:PRO:HB3	2.50	0.47
1:AY:130:PHE:CD1	1:AY:140:PRO:HB3	2.50	0.47
1:AZ:137:LEU:HA	1:EW:52:PHE:CE1	2.49	0.47
1:BA:24:ARG:NH2	1:BA:34:VAL:HG21	2.30	0.47
1:BE:130:PHE:CD1	1:BE:140:PRO:HB3	2.50	0.47
1:BG:117:THR:HB	1:ES:117:THR:O	2.15	0.47
1:BH:130:PHE:CD1	1:BH:140:PRO:HB3	2.50	0.47
1:BJ:91:SER:O	1:EV:84:GLY:HA2	2.15	0.47
1:BM:117:THR:O	1:EY:117:THR:HB	2.15	0.47
1:BQ:8:VAL:HB	1:EC:118:SER:HB2	1.96	0.47
1:BT:130:PHE:CD1	1:BT:140:PRO:HB3	2.50	0.47
1:BZ:130:PHE:CD1	1:BZ:140:PRO:HB3	2.50	0.47
1:CE:24:ARG:NH2	1:CE:34:VAL:HG21	2.30	0.47
1:CH:27:ASN:O	1:CH:30:ASN:HB3	2.15	0.47
1:CL:105:SER:O	1:CL:109:GLN:HG3	2.15	0.47
1:CO:130:PHE:CD1	1:CO:140:PRO:HB3	2.50	0.47
1:CQ:27:ASN:O	1:CQ:30:ASN:HB3	2.15	0.47
1:CU:130:PHE:CD1	1:CU:140:PRO:HB3	2.50	0.47
1:CW:24:ARG:NH2	1:CW:34:VAL:HG21	2.30	0.47
1:CX:40:SER:HB2	1:CX:45:PRO:HA	1.96	0.47
1:DI:24:ARG:NH2	1:DI:34:VAL:HG21	2.30	0.47
1:DM:40:SER:HB2	1:DM:45:PRO:HA	1.96	0.47
1:DM:105:SER:O	1:DM:109:GLN:HG3	2.15	0.47
1:DM:130:PHE:CD1	1:DM:140:PRO:HB3	2.50	0.47
1:DS:40:SER:HB2	1:DS:45:PRO:HA	1.96	0.47
1:DS:130:PHE:CD1	1:DS:140:PRO:HB3	2.50	0.47
1:DU:27:ASN:O	1:DU:30:ASN:HB3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DY:105:SER:O	1:DY:109:GLN:HG3	2.15	0.47
1:DY:117:THR:HB	1:FY:117:THR:O	2.14	0.47
1:EA:24:ARG:NH2	1:EA:34:VAL:HG21	2.30	0.47
1:EA:27:ASN:O	1:EA:30:ASN:HB3	2.15	0.47
1:EG:24:ARG:NH2	1:EG:34:VAL:HG21	2.30	0.47
1:EH:130:PHE:CD1	1:EH:140:PRO:HB3	2.50	0.47
1:EJ:27:ASN:O	1:EJ:30:ASN:HB3	2.15	0.47
1:EK:75:ASP:HA	1:ER:95:ASN:HD21	1.79	0.47
1:EK:130:PHE:CD1	1:EK:140:PRO:HB3	2.50	0.47
1:EN:40:SER:HB2	1:EN:45:PRO:HA	1.96	0.47
1:EP:24:ARG:NH2	1:EP:34:VAL:HG21	2.30	0.47
1:ET:40:SER:HB2	1:ET:45:PRO:HA	1.96	0.47
1:ET:130:PHE:CD1	1:ET:140:PRO:HB3	2.50	0.47
1:EW:40:SER:HB2	1:EW:45:PRO:HA	1.96	0.47
1:EZ:105:SER:O	1:EZ:109:GLN:HG3	2.15	0.47
1:EZ:130:PHE:CD1	1:EZ:140:PRO:HB3	2.50	0.47
1:FA:90:VAL:HG22	1:FL:86:VAL:HG22	1.96	0.47
1:FI:40:SER:HB2	1:FI:45:PRO:HA	1.96	0.47
1:FI:130:PHE:CD1	1:FI:140:PRO:HB3	2.50	0.47
1:FR:105:SER:O	1:FR:109:GLN:HG3	2.15	0.47
1:FS:97:ALA:O	1:GP:73:VAL:HG11	2.15	0.47
1:FS:117:THR:HG1	1:GP:117:THR:HG1	1.57	0.47
1:FT:24:ARG:NH2	1:FT:34:VAL:HG21	2.30	0.47
1:FT:27:ASN:O	1:FT:30:ASN:HB3	2.15	0.47
1:GA:130:PHE:CD1	1:GA:140:PRO:HB3	2.50	0.47
1:GD:130:PHE:CD1	1:GD:140:PRO:HB3	2.50	0.47
1:GJ:99:ASN:OD1	1:GJ:102:MET:HG3	2.13	0.47
1:GM:130:PHE:CD1	1:GM:140:PRO:HB3	2.50	0.47
1:GP:130:PHE:CD1	1:GP:140:PRO:HB3	2.50	0.47
1:GS:40:SER:HB2	1:GS:45:PRO:HA	1.96	0.47
1:GS:130:PHE:CD1	1:GS:140:PRO:HB3	2.50	0.47
1:GU:24:ARG:NH2	1:GU:34:VAL:HG21	2.30	0.47
1:AH:19:VAL:HG21	1:GD:109:GLN:NE2	2.30	0.47
1:AL:24:ARG:NH2	1:AL:34:VAL:HG21	2.30	0.47
1:AM:105:SER:O	1:AM:109:GLN:HG3	2.15	0.47
1:AO:27:ASN:O	1:AO:30:ASN:HB3	2.15	0.47
1:AU:24:ARG:NH2	1:AU:34:VAL:HG21	2.30	0.47
1:AV:130:PHE:CD1	1:AV:140:PRO:HB3	2.50	0.47
1:BK:105:SER:O	1:BK:109:GLN:HG3	2.15	0.47
1:BQ:105:SER:O	1:BQ:109:GLN:HG3	2.15	0.47
1:BY:24:ARG:NH2	1:BY:34:VAL:HG21	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:105:SER:O	1:CO:109:GLN:HG3	2.15	0.47
1:CU:40:SER:HB2	1:CU:45:PRO:HA	1.96	0.47
1:CW:75:ASP:HA	1:GI:95:ASN:HD21	1.79	0.47
1:DA:130:PHE:CD1	1:DA:140:PRO:HB3	2.50	0.47
1:EC:112:ASP:OD1	1:EC:118:SER:OG	2.16	0.47
1:EE:137:LEU:HD11	1:EU:63:ASP:CB	2.45	0.47
1:EQ:40:SER:HB2	1:EQ:45:PRO:HA	1.96	0.47
1:ET:52:PHE:HE2	1:FG:139:PHE:CE1	2.33	0.47
1:FB:24:ARG:NH2	1:FB:34:VAL:HG21	2.30	0.47
1:FE:27:ASN:O	1:FE:30:ASN:HB3	2.15	0.47
1:GD:40:SER:HB2	1:GD:45:PRO:HA	1.96	0.47
1:GG:105:SER:O	1:GG:109:GLN:HG3	2.15	0.47
1:GJ:130:PHE:CD1	1:GJ:140:PRO:HB3	2.50	0.47
1:GM:40:SER:HB2	1:GM:45:PRO:HA	1.96	0.47
1:GV:130:PHE:CD1	1:GV:140:PRO:HB3	2.50	0.47
1:GX:27:ASN:O	1:GX:30:ASN:HB3	2.15	0.47
1:AP:52:PHE:HE1	1:BU:137:LEU:HA	1.80	0.47
1:AS:105:SER:O	1:AS:109:GLN:HG3	2.15	0.47
1:BG:24:ARG:NH2	1:BG:34:VAL:HG21	2.30	0.47
1:BM:24:ARG:NH2	1:BM:34:VAL:HG21	2.30	0.47
1:BN:40:SER:HB2	1:BN:45:PRO:HA	1.96	0.47
1:BT:52:PHE:HE1	1:DN:137:LEU:HA	1.79	0.47
1:BY:137:LEU:HD13	1:FK:54:ILE:HG12	1.96	0.47
1:CC:105:SER:O	1:CC:109:GLN:HG3	2.15	0.47
1:CI:40:SER:HB2	1:CI:45:PRO:HA	1.96	0.47
1:CW:27:ASN:O	1:CW:30:ASN:HB3	2.15	0.47
1:DL:18:LEU:HG	1:GX:121:VAL:HG11	1.96	0.47
1:DM:137:LEU:HD13	1:GT:54:ILE:HG12	1.95	0.47
1:DX:27:ASN:O	1:DX:30:ASN:HB3	2.15	0.47
1:EK:10:ALA:H	1:ER:105:SER:CB	2.28	0.47
1:EM:24:ARG:NH2	1:EM:34:VAL:HG21	2.30	0.47
1:FC:105:SER:O	1:FC:109:GLN:HG3	2.15	0.47
1:FN:24:ARG:NH2	1:FN:34:VAL:HG21	2.30	0.47
1:FO:130:PHE:CD1	1:FO:140:PRO:HB3	2.50	0.47
1:AA:40:SER:HB2	1:AA:45:PRO:HA	1.96	0.47
1:AD:84:GLY:HA3	1:BC:98:TRP:CH2	2.50	0.47
1:AJ:40:SER:HB2	1:AJ:45:PRO:HA	1.96	0.47
1:AK:27:ASN:CG	1:AK:28:GLY:H	2.15	0.47
1:AP:130:PHE:CD1	1:AP:140:PRO:HB3	2.50	0.47
1:AX:24:ARG:NH2	1:AX:34:VAL:HG21	2.30	0.47
1:AY:118:SER:HB2	1:EI:8:VAL:HB	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:130:PHE:CD1	1:BB:140:PRO:HB3	2.50	0.47
1:BE:40:SER:HB2	1:BE:45:PRO:HA	1.96	0.47
1:BG:27:ASN:O	1:BG:30:ASN:HB3	2.15	0.47
1:BS:24:ARG:NH2	1:BS:34:VAL:HG21	2.30	0.47
1:BZ:105:SER:O	1:BZ:109:GLN:HG3	2.15	0.47
1:CK:27:ASN:O	1:CK:30:ASN:HB3	2.15	0.47
1:CN:27:ASN:O	1:CN:30:ASN:HB3	2.15	0.47
1:CP:137:LEU:HA	1:DJ:52:PHE:CE1	2.50	0.47
1:CU:105:SER:O	1:CU:109:GLN:HG3	2.15	0.47
1:CY:8:VAL:HB	1:GG:118:SER:HB2	1.97	0.47
1:DA:40:SER:HB2	1:DA:45:PRO:HA	1.96	0.47
1:DJ:130:PHE:CD1	1:DJ:140:PRO:HB3	2.50	0.47
1:DL:27:ASN:O	1:DL:30:ASN:HB3	2.15	0.47
1:DV:105:SER:O	1:DV:109:GLN:HG3	2.15	0.47
1:EQ:52:PHE:HE2	1:FM:139:PHE:CE1	2.33	0.47
1:FH:24:ARG:NH2	1:FH:34:VAL:HG21	2.30	0.47
1:FI:105:SER:O	1:FI:109:GLN:HG3	2.15	0.47
1:FL:130:PHE:CD1	1:FL:140:PRO:HB3	2.50	0.47
1:FR:130:PHE:CD1	1:FR:140:PRO:HB3	2.50	0.47
1:FV:137:LEU:HD11	1:GS:63:ASP:HB3	1.97	0.47
1:GN:27:ASN:CG	1:GN:28:GLY:H	2.15	0.47
1:GR:24:ARG:NH2	1:GR:34:VAL:HG21	2.30	0.47
1:GW:112:ASP:OD1	1:GW:118:SER:OG	2.16	0.47
1:AJ:102:MET:HE1	1:BX:73:VAL:CG2	2.45	0.46
1:AJ:130:PHE:CD1	1:AJ:140:PRO:HB3	2.50	0.46
1:AL:27:ASN:O	1:AL:30:ASN:HB3	2.15	0.46
1:AO:24:ARG:NH2	1:AO:34:VAL:HG21	2.30	0.46
1:AR:27:ASN:O	1:AR:30:ASN:HB3	2.15	0.46
1:BE:105:SER:O	1:BE:109:GLN:HG3	2.15	0.46
1:BH:105:SER:O	1:BH:109:GLN:HG3	2.15	0.46
1:BZ:137:LEU:CD1	1:DT:54:ILE:HG12	2.39	0.46
1:CC:130:PHE:CD1	1:CC:140:PRO:HB3	2.50	0.46
1:CI:97:ALA:O	1:GH:73:VAL:HG11	2.15	0.46
1:CX:105:SER:O	1:CX:109:GLN:HG3	2.15	0.46
1:DS:105:SER:O	1:DS:109:GLN:HG3	2.15	0.46
1:DV:130:PHE:CD1	1:DV:140:PRO:HB3	2.50	0.46
1:DY:130:PHE:CD1	1:DY:140:PRO:HB3	2.50	0.46
1:EB:52:PHE:HE1	1:GB:137:LEU:HA	1.80	0.46
1:EH:52:PHE:HE1	1:EO:137:LEU:HA	1.80	0.46
1:EK:105:SER:O	1:EK:109:GLN:HG3	2.15	0.46
1:ES:24:ARG:NH2	1:ES:34:VAL:HG21	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EW:105:SER:O	1:EW:109:GLN:HG3	2.15	0.46
1:FK:27:ASN:O	1:FK:30:ASN:HB3	2.15	0.46
1:FN:27:ASN:O	1:FN:30:ASN:HB3	2.15	0.46
1:FP:121:VAL:HG11	1:GV:18:LEU:HG	1.97	0.46
1:FQ:24:ARG:NH2	1:FQ:34:VAL:HG21	2.30	0.46
1:FU:40:SER:HB2	1:FU:45:PRO:HA	1.96	0.46
1:GG:40:SER:HB2	1:GG:45:PRO:HA	1.96	0.46
1:GO:27:ASN:O	1:GO:30:ASN:HB3	2.15	0.46
1:AQ:137:LEU:HD11	1:FU:63:ASP:HB3	1.98	0.46
1:BH:40:SER:HB2	1:BH:45:PRO:HA	1.96	0.46
1:BK:130:PHE:CD1	1:BK:140:PRO:HB3	2.50	0.46
1:BN:130:PHE:CD1	1:BN:140:PRO:HB3	2.50	0.46
1:BP:24:ARG:NH2	1:BP:34:VAL:HG21	2.30	0.46
1:CI:130:PHE:CD1	1:CI:140:PRO:HB3	2.50	0.46
1:CR:40:SER:HB2	1:CR:45:PRO:HA	1.96	0.46
1:CX:109:GLN:NE2	1:DK:19:VAL:HG21	2.30	0.46
1:DP:40:SER:HB2	1:DP:45:PRO:HA	1.96	0.46
1:DQ:27:ASN:CG	1:DQ:28:GLY:H	2.16	0.46
1:EB:77:LYS:HZ3	1:GC:79:ASN:HD22	1.64	0.46
1:EE:52:PHE:CE1	1:EU:137:LEU:HA	2.50	0.46
1:EQ:105:SER:O	1:EQ:109:GLN:HG3	2.15	0.46
1:ET:105:SER:O	1:ET:109:GLN:HG3	2.15	0.46
1:FD:27:ASN:CG	1:FD:28:GLY:H	2.16	0.46
1:FO:40:SER:HB2	1:FO:45:PRO:HA	1.96	0.46
1:FQ:27:ASN:O	1:FQ:30:ASN:HB3	2.15	0.46
1:GG:130:PHE:CD1	1:GG:140:PRO:HB3	2.50	0.46
1:GI:27:ASN:O	1:GI:30:ASN:HB3	2.15	0.46
1:GP:105:SER:O	1:GP:109:GLN:HG3	2.15	0.46
1:AC:105:SER:O	1:AC:109:GLN:HG3	2.16	0.46
1:AG:102:MET:HE1	1:BF:73:VAL:CG2	2.46	0.46
1:AG:105:SER:O	1:AG:109:GLN:HG3	2.15	0.46
1:AI:105:SER:O	1:AI:109:GLN:HG3	2.16	0.46
1:BB:40:SER:HB2	1:BB:45:PRO:HA	1.96	0.46
1:BK:19:VAL:HG21	1:DW:109:GLN:NE2	2.30	0.46
1:BP:27:ASN:O	1:BP:30:ASN:HB3	2.15	0.46
1:BQ:130:PHE:CD1	1:BQ:140:PRO:HB3	2.50	0.46
1:BR:27:ASN:CG	1:BR:28:GLY:H	2.16	0.46
1:BW:52:PHE:CD1	1:DQ:137:LEU:HD22	2.51	0.46
1:BW:105:SER:O	1:BW:109:GLN:HG3	2.15	0.46
1:BZ:40:SER:HB2	1:BZ:45:PRO:HA	1.96	0.46
1:CF:105:SER:O	1:CF:109:GLN:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:19:VAL:HG21	1:FT:109:GLN:NE2	2.31	0.46
1:CK:105:SER:O	1:CK:109:GLN:HG3	2.16	0.46
1:CN:137:LEU:HD13	1:FZ:54:ILE:HG12	1.96	0.46
1:CO:40:SER:HB2	1:CO:45:PRO:HA	1.96	0.46
1:DA:105:SER:CB	1:DE:10:ALA:H	2.29	0.46
1:DG:40:SER:HB2	1:DG:45:PRO:HA	1.96	0.46
1:DM:117:THR:HB	1:GT:117:THR:O	2.16	0.46
1:DN:27:ASN:CG	1:DN:28:GLY:H	2.15	0.46
1:DO:24:ARG:NH2	1:DO:34:VAL:HG21	2.30	0.46
1:DX:24:ARG:NH2	1:DX:34:VAL:HG21	2.30	0.46
1:DX:105:SER:O	1:DX:109:GLN:HG3	2.16	0.46
1:ED:24:ARG:NH2	1:ED:34:VAL:HG21	2.30	0.46
1:ED:105:SER:O	1:ED:109:GLN:HG3	2.16	0.46
1:EQ:18:LEU:HG	1:FM:121:VAL:HG11	1.98	0.46
1:EV:24:ARG:NH2	1:EV:34:VAL:HG21	2.30	0.46
1:FC:130:PHE:CD1	1:FC:140:PRO:HB3	2.50	0.46
1:FN:105:SER:O	1:FN:109:GLN:HG3	2.16	0.46
1:FV:137:LEU:HD22	1:GS:52:PHE:HD1	1.80	0.46
1:FW:24:ARG:NH2	1:FW:34:VAL:HG21	2.30	0.46
1:FZ:24:ARG:NH2	1:FZ:34:VAL:HG21	2.30	0.46
1:GC:24:ARG:NH2	1:GC:34:VAL:HG21	2.30	0.46
1:GC:105:SER:O	1:GC:109:GLN:HG3	2.16	0.46
1:GF:24:ARG:NH2	1:GF:34:VAL:HG21	2.30	0.46
1:GS:105:SER:O	1:GS:109:GLN:HG3	2.15	0.46
1:AD:52:PHE:CE2	1:BC:139:PHE:CE1	3.02	0.46
1:AL:105:SER:O	1:AL:109:GLN:HG3	2.16	0.46
1:AM:40:SER:HB2	1:AM:45:PRO:HA	1.96	0.46
1:AT:16:SER:HB3	1:EZ:121:VAL:HG21	1.98	0.46
1:BT:40:SER:HB2	1:BT:45:PRO:HA	1.96	0.46
1:BZ:110:ALA:HB1	1:DT:88:ILE:HD11	1.98	0.46
1:CB:137:LEU:HD11	1:FN:63:ASP:CB	2.44	0.46
1:CC:40:SER:HB2	1:CC:45:PRO:HA	1.96	0.46
1:CH:24:ARG:NH2	1:CH:34:VAL:HG21	2.30	0.46
1:CQ:105:SER:O	1:CQ:109:GLN:HG3	2.16	0.46
1:CZ:24:ARG:NH2	1:CZ:34:VAL:HG21	2.30	0.46
1:DC:19:VAL:HG21	1:GO:109:GLN:NE2	2.31	0.46
1:DG:105:SER:O	1:DG:109:GLN:HG3	2.15	0.46
1:DL:24:ARG:NH2	1:DL:34:VAL:HG21	2.30	0.46
1:DL:105:SER:O	1:DL:109:GLN:HG3	2.16	0.46
1:EB:52:PHE:CE1	1:GB:137:LEU:HA	2.51	0.46
1:ES:105:SER:O	1:ES:109:GLN:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EY:24:ARG:NH2	1:EY:34:VAL:HG21	2.30	0.46
1:FE:24:ARG:NH2	1:FE:34:VAL:HG21	2.30	0.46
1:FK:24:ARG:NH2	1:FK:34:VAL:HG21	2.30	0.46
1:FX:40:SER:HB2	1:FX:45:PRO:HA	1.96	0.46
1:GA:105:SER:O	1:GA:109:GLN:HG3	2.15	0.46
1:GI:105:SER:O	1:GI:109:GLN:HG3	2.16	0.46
1:GL:24:ARG:NH2	1:GL:34:VAL:HG21	2.30	0.46
1:AA:105:SER:O	1:AA:109:GLN:HG3	2.15	0.46
1:AE:27:ASN:CG	1:AE:28:GLY:H	2.16	0.46
1:AE:137:LEU:HD13	1:GA:54:ILE:HG12	1.97	0.46
1:AF:105:SER:O	1:AF:109:GLN:HG3	2.16	0.46
1:AG:40:SER:HB2	1:AG:45:PRO:HA	1.96	0.46
1:AI:40:SER:HB2	1:AI:46:GLY:H	1.81	0.46
1:AP:105:SER:O	1:AP:109:GLN:HG3	2.15	0.46
1:AW:27:ASN:CG	1:AW:28:GLY:H	2.15	0.46
1:BJ:40:SER:HB2	1:BJ:46:GLY:H	1.81	0.46
1:BM:27:ASN:O	1:BM:30:ASN:HB3	2.15	0.46
1:BN:118:SER:HB2	1:DZ:8:VAL:HB	1.97	0.46
1:BP:105:SER:O	1:BP:109:GLN:HG3	2.16	0.46
1:BV:24:ARG:NH2	1:BV:34:VAL:HG21	2.30	0.46
1:CL:40:SER:HB2	1:CL:45:PRO:HA	1.96	0.46
1:CM:137:LEU:HD22	1:DG:52:PHE:CD1	2.49	0.46
1:CX:130:PHE:CD1	1:CX:140:PRO:HB3	2.50	0.46
1:CY:117:THR:HB	1:GG:117:THR:O	2.15	0.46
1:DM:97:ALA:O	1:GT:73:VAL:HG11	2.16	0.46
1:DR:40:SER:HB2	1:DR:46:GLY:H	1.81	0.46
1:DR:105:SER:O	1:DR:109:GLN:HG3	2.16	0.46
1:EB:130:PHE:CD1	1:EB:140:PRO:HB3	2.50	0.46
1:EG:27:ASN:O	1:EG:30:ASN:HB3	2.15	0.46
1:EN:121:VAL:HG12	1:FJ:18:LEU:HG	1.97	0.46
1:EV:27:ASN:O	1:EV:30:ASN:HB3	2.15	0.46
1:EY:105:SER:O	1:EY:109:GLN:HG3	2.16	0.46
1:FH:27:ASN:O	1:FH:30:ASN:HB3	2.15	0.46
1:AC:40:SER:HB2	1:AC:46:GLY:H	1.81	0.46
1:AM:52:PHE:CD2	1:CA:139:PHE:CZ	3.03	0.46
1:AP:29:ASN:HA	1:BU:139:PHE:HE2	1.81	0.46
1:AP:40:SER:HB2	1:AP:45:PRO:HA	1.96	0.46
1:AU:89:GLN:HB3	1:EG:87:THR:CG2	2.46	0.46
1:BG:73:VAL:HG11	1:ES:97:ALA:O	2.16	0.46
1:BG:105:SER:O	1:BG:109:GLN:HG3	2.16	0.46
1:BJ:105:SER:O	1:BJ:109:GLN:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:63:ASP:HB3	1:FB:137:LEU:HD11	1.97	0.46
1:BV:40:SER:HB2	1:BV:46:GLY:H	1.81	0.46
1:BW:40:SER:HB2	1:BW:45:PRO:HA	1.96	0.46
1:BZ:109:GLN:NE2	1:DT:19:VAL:HG21	2.31	0.46
1:CB:5:LEU:HA	1:FN:125:THR:HG21	1.98	0.46
1:CB:105:SER:O	1:CB:109:GLN:HG3	2.16	0.46
1:CI:18:LEU:HG	1:GH:121:VAL:CG1	2.45	0.46
1:CK:125:THR:HG23	1:FW:6:ALA:HB3	1.98	0.46
1:DC:24:ARG:NH2	1:DC:34:VAL:HG21	2.30	0.46
1:DC:40:SER:HB2	1:DC:46:GLY:H	1.81	0.46
1:DC:117:THR:HB	1:GO:117:THR:O	2.15	0.46
1:DE:27:ASN:CG	1:DE:28:GLY:H	2.15	0.46
1:DI:27:ASN:O	1:DI:30:ASN:HB3	2.15	0.46
1:DU:24:ARG:NH2	1:DU:34:VAL:HG21	2.30	0.46
1:DV:40:SER:HB2	1:DV:45:PRO:HA	1.96	0.46
1:ED:40:SER:HB2	1:ED:46:GLY:H	1.81	0.46
1:FB:27:ASN:O	1:FB:30:ASN:HB3	2.15	0.46
1:FH:105:SER:O	1:FH:109:GLN:HG3	2.16	0.46
1:FQ:40:SER:HB2	1:FQ:46:GLY:H	1.81	0.46
1:FX:105:SER:O	1:FX:109:GLN:HG3	2.15	0.46
1:GI:40:SER:HB2	1:GI:46:GLY:H	1.81	0.46
1:GR:105:SER:O	1:GR:109:GLN:HG3	2.16	0.46
1:GX:105:SER:O	1:GX:109:GLN:HG3	2.16	0.46
1:AF:24:ARG:NH2	1:AF:34:VAL:HG21	2.30	0.46
1:AQ:112:ASP:OD1	1:AQ:118:SER:OG	2.16	0.46
1:AU:18:LEU:HD11	1:EG:122:SER:O	2.16	0.46
1:BB:75:ASP:HA	1:BR:95:ASN:HD21	1.80	0.46
1:BD:18:LEU:HG	1:EP:121:VAL:CG1	2.46	0.46
1:BK:40:SER:HB2	1:BK:45:PRO:HA	1.96	0.46
1:BM:40:SER:HB2	1:BM:46:GLY:H	1.81	0.46
1:BN:105:SER:O	1:BN:109:GLN:HG3	2.15	0.46
1:BN:110:ALA:HB1	1:DZ:88:ILE:HD11	1.97	0.46
1:CG:99:ASN:HB2	1:CG:102:MET:HG3	1.98	0.46
1:CK:24:ARG:NH2	1:CK:34:VAL:HG21	2.30	0.46
1:CS:18:LEU:HD11	1:DD:122:SER:O	2.15	0.46
1:CS:108:LYS:HZ2	1:DD:117:THR:HG22	1.81	0.46
1:CW:105:SER:O	1:CW:109:GLN:HG3	2.16	0.46
1:CZ:105:SER:O	1:CZ:109:GLN:HG3	2.16	0.46
1:DJ:105:SER:O	1:DJ:109:GLN:HG3	2.15	0.46
1:DO:105:SER:O	1:DO:109:GLN:HG3	2.16	0.46
1:DU:105:SER:O	1:DU:109:GLN:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DX:40:SER:HB2	1:DX:46:GLY:H	1.81	0.46
1:EF:23:LEU:O	1:EU:138:MET:HE3	2.14	0.46
1:EH:40:SER:HB2	1:EH:45:PRO:HA	1.96	0.46
1:EM:27:ASN:O	1:EM:30:ASN:HB3	2.15	0.46
1:FF:105:SER:O	1:FF:109:GLN:HG3	2.15	0.46
1:FP:99:ASN:HB2	1:FP:102:MET:HG3	1.98	0.46
1:FT:40:SER:HB2	1:FT:46:GLY:H	1.81	0.46
1:FW:27:ASN:O	1:FW:30:ASN:HB3	2.15	0.46
1:FZ:40:SER:HB2	1:FZ:46:GLY:H	1.81	0.46
1:GF:27:ASN:O	1:GF:30:ASN:HB3	2.15	0.46
1:AA:52:PHE:HE2	1:BI:139:PHE:CE1	2.34	0.46
1:AA:66:HIS:CD2	1:AA:89:GLN:HG3	2.51	0.46
1:AE:88:ILE:HD11	1:GA:110:ALA:HB1	1.98	0.46
1:AH:137:LEU:HD22	1:GD:52:PHE:CD1	2.51	0.46
1:AJ:66:HIS:CD2	1:AJ:89:GLN:HG3	2.51	0.46
1:AR:40:SER:HB2	1:AR:46:GLY:H	1.81	0.46
1:AZ:52:PHE:CD1	1:EW:137:LEU:HD22	2.51	0.46
1:BD:40:SER:HB2	1:BD:46:GLY:H	1.81	0.46
1:BF:99:ASN:HB2	1:BF:102:MET:HG3	1.98	0.46
1:BQ:118:SER:HB2	1:EC:8:VAL:HB	1.98	0.46
1:BT:110:ALA:HB1	1:DN:88:ILE:HD11	1.96	0.46
1:BY:27:ASN:O	1:BY:30:ASN:HB3	2.15	0.46
1:CB:24:ARG:NH2	1:CB:34:VAL:HG21	2.30	0.46
1:CE:101:SER:HB2	1:FQ:11:ASN:O	2.16	0.46
1:CG:73:VAL:HG11	1:CL:97:ALA:O	2.16	0.46
1:CI:73:VAL:HG22	1:GH:102:MET:HE1	1.97	0.46
1:CJ:99:ASN:HB2	1:CJ:102:MET:HG3	1.98	0.46
1:CQ:24:ARG:NH2	1:CQ:34:VAL:HG21	2.30	0.46
1:CT:9:GLY:HA2	1:GF:108:LYS:HB2	1.98	0.46
1:CY:118:SER:HB2	1:GG:8:VAL:HB	1.96	0.46
1:DD:105:SER:O	1:DD:109:GLN:HG3	2.15	0.46
1:DF:105:SER:O	1:DF:109:GLN:HG3	2.16	0.46
1:DF:125:THR:HG21	1:GR:5:LEU:HA	1.98	0.46
1:DH:99:ASN:HB2	1:DH:102:MET:HG3	1.98	0.46
1:DI:19:VAL:HG21	1:GU:109:GLN:NE2	2.31	0.46
1:DI:105:SER:O	1:DI:109:GLN:HG3	2.16	0.46
1:DL:18:LEU:HD11	1:GX:122:SER:O	2.15	0.46
1:EA:40:SER:HB2	1:EA:46:GLY:H	1.81	0.46
1:EA:105:SER:O	1:EA:109:GLN:HG3	2.16	0.46
1:EB:40:SER:HB2	1:EB:45:PRO:HA	1.96	0.46
1:EV:105:SER:O	1:EV:109:GLN:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GC:40:SER:HB2	1:GC:46:GLY:H	1.81	0.46
1:GR:40:SER:HB2	1:GR:46:GLY:H	1.81	0.46
1:AC:118:SER:HB2	1:DO:8:VAL:HB	1.97	0.46
1:BD:24:ARG:NH2	1:BD:34:VAL:HG21	2.30	0.46
1:BY:40:SER:HB2	1:BY:46:GLY:H	1.81	0.46
1:CB:27:ASN:O	1:CB:30:ASN:HB3	2.15	0.46
1:CC:66:HIS:CD2	1:CC:89:GLN:HG3	2.51	0.46
1:CD:75:ASP:OD1	1:CS:79:ASN:ND2	2.47	0.46
1:CJ:27:ASN:CG	1:CJ:28:GLY:H	2.15	0.46
1:CM:99:ASN:HB2	1:CM:102:MET:HG3	1.98	0.46
1:CX:66:HIS:CD2	1:CX:89:GLN:HG3	2.51	0.46
1:CZ:40:SER:HB2	1:CZ:46:GLY:H	1.81	0.46
1:DB:99:ASN:HB2	1:DB:102:MET:HG3	1.98	0.46
1:DF:40:SER:HB2	1:DF:46:GLY:H	1.81	0.46
1:DG:66:HIS:CD2	1:DG:89:GLN:HG3	2.51	0.46
1:DP:52:PHE:HD1	1:GW:137:LEU:HD22	1.81	0.46
1:DR:27:ASN:O	1:DR:30:ASN:HB3	2.15	0.46
1:DV:66:HIS:CD2	1:DV:89:GLN:HG3	2.51	0.46
1:EH:66:HIS:CD2	1:EH:89:GLN:HG3	2.51	0.46
1:EJ:24:ARG:NH2	1:EJ:34:VAL:HG21	2.30	0.46
1:EP:40:SER:HB2	1:EP:46:GLY:H	1.81	0.46
1:ET:137:LEU:HD13	1:FG:54:ILE:HG12	1.97	0.46
1:EX:137:LEU:HD22	1:FI:52:PHE:CD1	2.51	0.46
1:FB:105:SER:O	1:FB:109:GLN:HG3	2.16	0.46
1:FF:66:HIS:CD2	1:FF:89:GLN:HG3	2.51	0.46
1:FN:40:SER:HB2	1:FN:46:GLY:H	1.81	0.46
1:FO:105:SER:O	1:FO:109:GLN:HG3	2.15	0.46
1:FT:105:SER:O	1:FT:109:GLN:HG3	2.16	0.46
1:FU:66:HIS:CD2	1:FU:89:GLN:HG3	2.51	0.46
1:GS:66:HIS:CD2	1:GS:89:GLN:HG3	2.51	0.46
1:AC:27:ASN:O	1:AC:30:ASN:HB3	2.15	0.46
1:AI:27:ASN:O	1:AI:30:ASN:HB3	2.15	0.46
1:AJ:105:SER:O	1:AJ:109:GLN:HG3	2.15	0.46
1:BH:66:HIS:CD2	1:BH:89:GLN:HG3	2.51	0.46
1:BJ:108:LYS:HB2	1:EV:9:GLY:HA2	1.96	0.46
1:BN:66:HIS:CD2	1:BN:89:GLN:HG3	2.51	0.46
1:BT:66:HIS:CD2	1:BT:89:GLN:HG3	2.51	0.46
1:BV:105:SER:O	1:BV:109:GLN:HG3	2.16	0.46
1:BY:105:SER:O	1:BY:109:GLN:HG3	2.16	0.46
1:BY:117:THR:HB	1:FK:117:THR:O	2.16	0.46
1:CD:99:ASN:HB2	1:CD:102:MET:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:66:HIS:CD2	1:CI:89:GLN:HG3	2.51	0.46
1:CN:98:TRP:CH2	1:FZ:84:GLY:HA3	2.52	0.46
1:CS:99:ASN:HB2	1:CS:102:MET:HG3	1.98	0.46
1:CW:40:SER:HB2	1:CW:46:GLY:H	1.81	0.46
1:DJ:66:HIS:CD2	1:DJ:89:GLN:HG3	2.51	0.46
1:DM:66:HIS:CD2	1:DM:89:GLN:HG3	2.51	0.46
1:DT:99:ASN:HB2	1:DT:102:MET:HG3	1.98	0.46
1:DZ:99:ASN:HB2	1:DZ:102:MET:HG3	1.98	0.46
1:EB:66:HIS:CD2	1:EB:89:GLN:HG3	2.51	0.46
1:EJ:40:SER:HB2	1:EJ:46:GLY:H	1.81	0.46
1:EK:66:HIS:CD2	1:EK:89:GLN:HG3	2.51	0.46
1:EM:40:SER:HB2	1:EM:46:GLY:H	1.81	0.46
1:EW:66:HIS:CD2	1:EW:89:GLN:HG3	2.51	0.46
1:FF:40:SER:HB2	1:FF:45:PRO:HA	1.96	0.46
1:FJ:99:ASN:HB2	1:FJ:102:MET:HG3	1.98	0.46
1:FK:40:SER:HB2	1:FK:46:GLY:H	1.81	0.46
1:FK:105:SER:O	1:FK:109:GLN:HG3	2.16	0.46
1:FV:99:ASN:HB2	1:FV:102:MET:HG3	1.98	0.46
1:FW:105:SER:O	1:FW:109:GLN:HG3	2.16	0.46
1:GC:27:ASN:O	1:GC:30:ASN:HB3	2.15	0.46
1:GF:40:SER:HB2	1:GF:46:GLY:H	1.81	0.46
1:GK:27:ASN:CG	1:GK:28:GLY:H	2.16	0.46
1:AD:66:HIS:CD2	1:AD:89:GLN:HG3	2.51	0.45
1:AH:99:ASN:HB2	1:AH:102:MET:HG3	1.98	0.45
1:AO:40:SER:HB2	1:AO:46:GLY:H	1.81	0.45
1:AO:105:SER:O	1:AO:109:GLN:HG3	2.16	0.45
1:AR:98:TRP:CZ2	1:ED:84:GLY:HA3	2.51	0.45
1:AR:105:SER:O	1:AR:109:GLN:HG3	2.16	0.45
1:AV:66:HIS:CD2	1:AV:89:GLN:HG3	2.51	0.45
1:AX:40:SER:HB2	1:AX:46:GLY:H	1.81	0.45
1:BQ:66:HIS:CD2	1:BQ:89:GLN:HG3	2.51	0.45
1:BS:117:THR:HG1	1:FE:117:THR:HG1	1.59	0.45
1:BU:99:ASN:HB2	1:BU:102:MET:HG3	1.98	0.45
1:BW:52:PHE:CE1	1:DQ:137:LEU:HA	2.51	0.45
1:CE:40:SER:HB2	1:CE:46:GLY:H	1.81	0.45
1:CI:73:VAL:HG21	1:GH:102:MET:HE1	1.98	0.45
1:CN:40:SER:HB2	1:CN:46:GLY:H	1.81	0.45
1:CS:97:ALA:HB1	1:DD:73:VAL:CG1	2.45	0.45
1:CT:27:ASN:O	1:CT:30:ASN:HB3	2.15	0.45
1:CY:109:GLN:NE2	1:GG:19:VAL:HG21	2.31	0.45
1:DO:40:SER:HB2	1:DO:46:GLY:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DS:66:HIS:CD2	1:DS:89:GLN:HG3	2.51	0.45
1:EI:99:ASN:HB2	1:EI:102:MET:HG3	1.98	0.45
1:EJ:105:SER:O	1:EJ:109:GLN:HG3	2.16	0.45
1:EM:105:SER:O	1:EM:109:GLN:HG3	2.16	0.45
1:ES:40:SER:HB2	1:ES:46:GLY:H	1.81	0.45
1:EV:40:SER:HB2	1:EV:46:GLY:H	1.81	0.45
1:FW:40:SER:HB2	1:FW:46:GLY:H	1.81	0.45
1:GD:66:HIS:CD2	1:GD:89:GLN:HG3	2.51	0.45
1:GI:24:ARG:NH2	1:GI:34:VAL:HG21	2.30	0.45
1:GU:105:SER:O	1:GU:109:GLN:HG3	2.16	0.45
1:GW:99:ASN:HB2	1:GW:102:MET:HG3	1.98	0.45
1:AL:104:VAL:HG13	1:DX:131:PRO:HB2	1.99	0.45
1:AM:52:PHE:HE2	1:CA:139:PHE:CE1	2.34	0.45
1:AM:66:HIS:CD2	1:AM:89:GLN:HG3	2.51	0.45
1:AQ:99:ASN:HB2	1:AQ:102:MET:HG3	1.98	0.45
1:AS:66:HIS:CD2	1:AS:89:GLN:HG3	2.51	0.45
1:AZ:99:ASN:HB2	1:AZ:102:MET:HG3	1.98	0.45
1:BG:40:SER:HB2	1:BG:46:GLY:H	1.81	0.45
1:CB:86:VAL:HG22	1:FN:90:VAL:HG22	1.97	0.45
1:CD:27:ASN:CG	1:CD:28:GLY:H	2.16	0.45
1:CH:40:SER:HB2	1:CH:46:GLY:H	1.81	0.45
1:CN:102:MET:HE1	1:FZ:73:VAL:CG2	2.46	0.45
1:CT:11:ASN:O	1:GF:101:SER:HB2	2.16	0.45
1:CV:137:LEU:HA	1:GM:52:PHE:CE1	2.51	0.45
1:DC:102:MET:HE1	1:GO:73:VAL:CG2	2.47	0.45
1:DF:27:ASN:O	1:DF:30:ASN:HB3	2.15	0.45
1:EQ:66:HIS:CD2	1:EQ:89:GLN:HG3	2.51	0.45
1:ET:66:HIS:CD2	1:ET:89:GLN:HG3	2.51	0.45
1:GH:99:ASN:HB2	1:GH:102:MET:HG3	1.98	0.45
1:AL:40:SER:HB2	1:AL:46:GLY:H	1.81	0.45
1:AY:52:PHE:HD1	1:EI:137:LEU:HD22	1.81	0.45
1:BK:52:PHE:HD1	1:DW:137:LEU:HD22	1.80	0.45
1:BP:40:SER:HB2	1:BP:46:GLY:H	1.81	0.45
1:BP:109:GLN:NE2	1:FB:19:VAL:HG21	2.31	0.45
1:CF:66:HIS:CD2	1:CF:89:GLN:HG3	2.51	0.45
1:CQ:40:SER:HB2	1:CQ:46:GLY:H	1.81	0.45
1:CQ:63:ASP:CG	1:GC:137:LEU:HD11	2.41	0.45
1:CS:73:VAL:HG22	1:DD:102:MET:HE1	1.97	0.45
1:DJ:40:SER:HB2	1:DJ:45:PRO:HA	1.96	0.45
1:DQ:99:ASN:HB2	1:DQ:102:MET:HG3	1.98	0.45
1:DS:121:VAL:HG21	1:GQ:16:SER:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EO:27:ASN:CG	1:EO:28:GLY:H	2.15	0.45
1:EZ:66:HIS:CD2	1:EZ:89:GLN:HG3	2.51	0.45
1:FE:105:SER:O	1:FE:109:GLN:HG3	2.16	0.45
1:FL:66:HIS:CD2	1:FL:89:GLN:HG3	2.51	0.45
1:GD:55:LYS:O	1:GD:94:ARG:NH2	2.50	0.45
1:GN:99:ASN:HB2	1:GN:102:MET:HG3	1.98	0.45
1:AG:137:LEU:HD11	1:BF:63:ASP:HB3	1.98	0.45
1:AP:42:LEU:CD2	1:ED:137:LEU:HD12	2.47	0.45
1:AU:40:SER:HB2	1:AU:46:GLY:H	1.81	0.45
1:AU:105:SER:O	1:AU:109:GLN:HG3	2.16	0.45
1:AY:137:LEU:HD22	1:EI:52:PHE:CD1	2.51	0.45
1:AZ:97:ALA:O	1:EW:73:VAL:HG11	2.16	0.45
1:BE:54:ILE:HG12	1:BL:137:LEU:HD13	1.97	0.45
1:BH:55:LYS:O	1:BH:94:ARG:NH2	2.50	0.45
1:BJ:97:ALA:HB1	1:EV:73:VAL:CG1	2.47	0.45
1:BN:55:LYS:O	1:BN:94:ARG:NH2	2.50	0.45
1:BS:105:SER:O	1:BS:109:GLN:HG3	2.16	0.45
1:BT:55:LYS:O	1:BT:94:ARG:NH2	2.50	0.45
1:BT:117:THR:O	1:DN:117:THR:HB	2.17	0.45
1:BV:27:ASN:O	1:BV:30:ASN:HB3	2.15	0.45
1:BV:130:PHE:CD1	1:BV:140:PRO:HB3	2.52	0.45
1:BW:66:HIS:CD2	1:BW:89:GLN:HG3	2.51	0.45
1:BY:130:PHE:CD1	1:BY:140:PRO:HB3	2.52	0.45
1:BZ:66:HIS:CD2	1:BZ:89:GLN:HG3	2.51	0.45
1:CI:109:GLN:NE2	1:GH:19:VAL:HG21	2.31	0.45
1:CK:130:PHE:CD1	1:CK:140:PRO:HB3	2.52	0.45
1:CL:55:LYS:O	1:CL:94:ARG:NH2	2.50	0.45
1:CL:66:HIS:CD2	1:CL:89:GLN:HG3	2.51	0.45
1:CT:105:SER:O	1:CT:109:GLN:HG3	2.16	0.45
1:CT:130:PHE:CD1	1:CT:140:PRO:HB3	2.52	0.45
1:CU:52:PHE:HD1	1:DH:137:LEU:HD22	1.81	0.45
1:CV:99:ASN:HB2	1:CV:102:MET:HG3	1.98	0.45
1:CZ:130:PHE:CD1	1:CZ:140:PRO:HB3	2.52	0.45
1:DC:73:VAL:HG11	1:GO:97:ALA:O	2.15	0.45
1:DY:137:LEU:HD22	1:FY:52:PHE:CD1	2.51	0.45
1:EQ:55:LYS:O	1:EQ:94:ARG:NH2	2.50	0.45
1:EQ:118:SER:HB2	1:FM:8:VAL:HB	1.97	0.45
1:EU:99:ASN:HB2	1:EU:102:MET:HG3	1.98	0.45
1:EW:55:LYS:O	1:EW:94:ARG:NH2	2.50	0.45
1:FI:66:HIS:CD2	1:FI:89:GLN:HG3	2.51	0.45
1:FZ:27:ASN:O	1:FZ:30:ASN:HB3	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GE:99:ASN:HB2	1:GE:102:MET:HG3	1.98	0.45
1:GJ:66:HIS:CD2	1:GJ:89:GLN:HG3	2.51	0.45
1:GS:55:LYS:O	1:GS:94:ARG:NH2	2.50	0.45
1:AC:117:THR:O	1:DO:117:THR:HB	2.16	0.45
1:AE:99:ASN:HB2	1:AE:102:MET:HG3	1.98	0.45
1:AG:55:LYS:O	1:AG:94:ARG:NH2	2.50	0.45
1:AL:95:ASN:HD21	1:DX:75:ASP:HA	1.81	0.45
1:AP:52:PHE:HD1	1:BU:137:LEU:HD22	1.82	0.45
1:AT:99:ASN:HB2	1:AT:102:MET:HG3	1.98	0.45
1:AW:99:ASN:HB2	1:AW:102:MET:HG3	1.98	0.45
1:AX:105:SER:O	1:AX:109:GLN:HG3	2.16	0.45
1:BH:109:GLN:NE2	1:BO:19:VAL:HG21	2.31	0.45
1:BK:55:LYS:O	1:BK:94:ARG:NH2	2.50	0.45
1:BK:66:HIS:CD2	1:BK:89:GLN:HG3	2.51	0.45
1:BM:105:SER:O	1:BM:109:GLN:HG3	2.16	0.45
1:BS:40:SER:HB2	1:BS:46:GLY:H	1.81	0.45
1:BV:48:ILE:HG12	1:BV:69:LEU:HG	1.99	0.45
1:BX:99:ASN:HB2	1:BX:102:MET:HG3	1.98	0.45
1:CB:40:SER:HB2	1:CB:46:GLY:H	1.81	0.45
1:CG:97:ALA:O	1:CL:73:VAL:HG11	2.17	0.45
1:CK:48:ILE:HG12	1:CK:69:LEU:HG	1.99	0.45
1:CN:48:ILE:HG12	1:CN:69:LEU:HG	1.99	0.45
1:CR:66:HIS:CD2	1:CR:89:GLN:HG3	2.51	0.45
1:CV:137:LEU:HA	1:GM:52:PHE:HE1	1.81	0.45
1:DC:130:PHE:CD1	1:DC:140:PRO:HB3	2.52	0.45
1:DL:48:ILE:HG12	1:DL:69:LEU:HG	1.99	0.45
1:DP:55:LYS:O	1:DP:94:ARG:NH2	2.50	0.45
1:EM:130:PHE:CD1	1:EM:140:PRO:HB3	2.52	0.45
1:EX:99:ASN:HB2	1:EX:102:MET:HG3	1.98	0.45
1:EY:40:SER:HB2	1:EY:46:GLY:H	1.81	0.45
1:FA:99:ASN:HB2	1:FA:102:MET:HG3	1.98	0.45
1:FD:77:LYS:HG2	1:FG:79:ASN:ND2	2.31	0.45
1:FG:99:ASN:HB2	1:FG:102:MET:HG3	1.98	0.45
1:FK:130:PHE:CD1	1:FK:140:PRO:HB3	2.52	0.45
1:FL:55:LYS:O	1:FL:94:ARG:NH2	2.50	0.45
1:FQ:105:SER:O	1:FQ:109:GLN:HG3	2.16	0.45
1:FQ:130:PHE:CD1	1:FQ:140:PRO:HB3	2.52	0.45
1:FW:48:ILE:HG12	1:FW:69:LEU:HG	1.99	0.45
1:FZ:48:ILE:HG12	1:FZ:69:LEU:HG	1.99	0.45
1:GL:40:SER:HB2	1:GL:46:GLY:H	1.81	0.45
1:GO:40:SER:HB2	1:GO:46:GLY:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GU:40:SER:HB2	1:GU:46:GLY:H	1.81	0.45
1:GU:130:PHE:CD1	1:GU:140:PRO:HB3	2.52	0.45
1:GX:40:SER:HB2	1:GX:46:GLY:H	1.81	0.45
1:AF:48:ILE:HG12	1:AF:69:LEU:HG	1.99	0.45
1:AV:52:PHE:CD1	1:EF:137:LEU:HD22	2.50	0.45
1:AV:55:LYS:O	1:AV:94:ARG:NH2	2.50	0.45
1:BA:63:ASP:HB3	1:EM:137:LEU:HD11	1.97	0.45
1:BE:55:LYS:O	1:BE:94:ARG:NH2	2.50	0.45
1:BE:66:HIS:CD2	1:BE:89:GLN:HG3	2.51	0.45
1:BG:130:PHE:CD1	1:BG:140:PRO:HB3	2.52	0.45
1:BN:52:PHE:HE2	1:DZ:139:PHE:CE1	2.35	0.45
1:CE:48:ILE:HG12	1:CE:69:LEU:HG	1.99	0.45
1:CE:105:SER:O	1:CE:109:GLN:HG3	2.16	0.45
1:CG:27:ASN:CG	1:CG:28:GLY:H	2.16	0.45
1:CH:130:PHE:CD1	1:CH:140:PRO:HB3	2.52	0.45
1:CS:73:VAL:CG2	1:DD:102:MET:HE1	2.46	0.45
1:CT:40:SER:HB2	1:CT:46:GLY:H	1.81	0.45
1:DD:66:HIS:CD2	1:DD:89:GLN:HG3	2.51	0.45
1:DE:99:ASN:HB2	1:DE:102:MET:HG3	1.98	0.45
1:DG:55:LYS:O	1:DG:94:ARG:NH2	2.50	0.45
1:DI:40:SER:HB2	1:DI:46:GLY:H	1.81	0.45
1:DL:40:SER:HB2	1:DL:46:GLY:H	1.81	0.45
1:DL:130:PHE:CD1	1:DL:140:PRO:HB3	2.52	0.45
1:DN:99:ASN:HB2	1:DN:102:MET:HG3	1.98	0.45
1:DR:48:ILE:HG12	1:DR:69:LEU:HG	1.99	0.45
1:DS:55:LYS:O	1:DS:94:ARG:NH2	2.50	0.45
1:DU:130:PHE:CD1	1:DU:140:PRO:HB3	2.52	0.45
1:DW:27:ASN:CG	1:DW:28:GLY:H	2.16	0.45
1:EN:102:MET:HE1	1:FJ:73:VAL:CG2	2.47	0.45
1:EQ:117:THR:HB	1:FM:117:THR:O	2.17	0.45
1:FE:130:PHE:CD1	1:FE:140:PRO:HB3	2.52	0.45
1:FI:55:LYS:O	1:FI:94:ARG:NH2	2.50	0.45
1:FM:99:ASN:HB2	1:FM:102:MET:HG3	1.98	0.45
1:FQ:48:ILE:HG12	1:FQ:69:LEU:HG	1.99	0.45
1:FR:66:HIS:CD2	1:FR:89:GLN:HG3	2.51	0.45
1:FS:99:ASN:HB2	1:FS:102:MET:HG3	1.98	0.45
1:GK:99:ASN:HB2	1:GK:102:MET:HG3	1.98	0.45
1:GP:55:LYS:O	1:GP:94:ARG:NH2	2.50	0.45
1:AF:40:SER:HB2	1:AF:46:GLY:H	1.81	0.45
1:AH:88:ILE:HD11	1:GD:110:ALA:HB1	1.97	0.45
1:AI:48:ILE:HG12	1:AI:69:LEU:HG	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:19:VAL:HG21	1:FO:109:GLN:NE2	2.32	0.45
1:AL:48:ILE:HG12	1:AL:69:LEU:HG	1.99	0.45
1:AM:55:LYS:O	1:AM:94:ARG:NH2	2.50	0.45
1:AP:66:HIS:CD2	1:AP:89:GLN:HG3	2.51	0.45
1:BB:55:LYS:O	1:BB:94:ARG:NH2	2.50	0.45
1:BP:48:ILE:HG12	1:BP:69:LEU:HG	1.99	0.45
1:BW:55:LYS:O	1:BW:94:ARG:NH2	2.50	0.45
1:CA:99:ASN:HB2	1:CA:102:MET:HG3	1.98	0.45
1:CD:139:PHE:CE1	1:CR:52:PHE:HE2	2.34	0.45
1:CE:95:ASN:ND2	1:FQ:75:ASP:HA	2.28	0.45
1:CI:55:LYS:O	1:CI:94:ARG:NH2	2.50	0.45
1:CN:130:PHE:CD1	1:CN:140:PRO:HB3	2.52	0.45
1:CU:122:SER:O	1:DH:18:LEU:HD11	2.17	0.45
1:DI:10:ALA:H	1:GU:105:SER:CB	2.29	0.45
1:DM:55:LYS:O	1:DM:94:ARG:NH2	2.50	0.45
1:DM:117:THR:OG1	1:GT:117:THR:OG1	2.34	0.45
1:DP:66:HIS:CD2	1:DP:89:GLN:HG3	2.51	0.45
1:DU:48:ILE:HG12	1:DU:69:LEU:HG	1.99	0.45
1:ED:130:PHE:CD1	1:ED:140:PRO:HB3	2.52	0.45
1:EE:136:GLY:C	1:EV:42:LEU:HD21	2.42	0.45
1:EG:40:SER:HB2	1:EG:46:GLY:H	1.81	0.45
1:EH:55:LYS:O	1:EH:94:ARG:NH2	2.50	0.45
1:EP:105:SER:O	1:EP:109:GLN:HG3	2.16	0.45
1:EY:130:PHE:CD1	1:EY:140:PRO:HB3	2.52	0.45
1:FB:40:SER:HB2	1:FB:46:GLY:H	1.81	0.45
1:FC:66:HIS:CD2	1:FC:89:GLN:HG3	2.51	0.45
1:FH:48:ILE:HG12	1:FH:69:LEU:HG	1.99	0.45
1:FH:130:PHE:CD1	1:FH:140:PRO:HB3	2.52	0.45
1:FL:105:SER:O	1:FL:109:GLN:HG3	2.15	0.45
1:FN:130:PHE:CD1	1:FN:140:PRO:HB3	2.52	0.45
1:FT:79:ASN:HD22	1:GP:77:LYS:NZ	2.14	0.45
1:FZ:105:SER:O	1:FZ:109:GLN:HG3	2.16	0.45
1:GF:105:SER:O	1:GF:109:GLN:HG3	2.16	0.45
1:AE:112:ASP:OD1	1:AE:118:SER:OG	2.16	0.45
1:AI:130:PHE:CD1	1:AI:140:PRO:HB3	2.52	0.45
1:AU:130:PHE:CD1	1:AU:140:PRO:HB3	2.52	0.45
1:AV:88:ILE:HD11	1:EF:110:ALA:HB1	1.98	0.45
1:AX:48:ILE:HG12	1:AX:69:LEU:HG	1.99	0.45
1:AY:52:PHE:CD1	1:EI:137:LEU:HD22	2.51	0.45
1:BB:66:HIS:CD2	1:BB:89:GLN:HG3	2.51	0.45
1:BH:110:ALA:HB1	1:BO:88:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:48:ILE:HG12	1:BM:69:LEU:HG	1.99	0.45
1:BY:48:ILE:HG12	1:BY:69:LEU:HG	1.99	0.45
1:CE:130:PHE:CD1	1:CE:140:PRO:HB3	2.52	0.45
1:CK:40:SER:HB2	1:CK:46:GLY:H	1.81	0.45
1:CM:118:SER:HB2	1:DG:8:VAL:HB	1.98	0.45
1:CP:102:MET:HE1	1:DJ:73:VAL:CG2	2.46	0.45
1:CU:66:HIS:CD2	1:CU:89:GLN:HG3	2.51	0.45
1:CX:55:LYS:O	1:CX:94:ARG:NH2	2.50	0.45
1:DA:18:LEU:HG	1:DE:121:VAL:CG1	2.43	0.45
1:DB:88:ILE:HD11	1:GJ:110:ALA:HB1	1.99	0.45
1:DI:48:ILE:HG12	1:DI:69:LEU:HG	1.99	0.45
1:DJ:55:LYS:O	1:DJ:94:ARG:NH2	2.50	0.45
1:DL:54:ILE:HG12	1:GX:137:LEU:HD13	1.97	0.45
1:DU:40:SER:HB2	1:DU:46:GLY:H	1.81	0.45
1:DV:55:LYS:O	1:DV:94:ARG:NH2	2.50	0.45
1:DX:48:ILE:HG12	1:DX:69:LEU:HG	1.99	0.45
1:EA:130:PHE:CD1	1:EA:140:PRO:HB3	2.52	0.45
1:EN:55:LYS:O	1:EN:94:ARG:NH2	2.50	0.45
1:EN:66:HIS:CD2	1:EN:89:GLN:HG3	2.51	0.45
1:EY:48:ILE:HG12	1:EY:69:LEU:HG	1.99	0.45
1:FB:48:ILE:HG12	1:FB:69:LEU:HG	1.99	0.45
1:FU:55:LYS:O	1:FU:94:ARG:NH2	2.50	0.45
1:FW:130:PHE:CD1	1:FW:140:PRO:HB3	2.52	0.45
1:FX:55:LYS:O	1:FX:94:ARG:NH2	2.50	0.45
1:GF:48:ILE:HG12	1:GF:69:LEU:HG	1.99	0.45
1:GM:55:LYS:O	1:GM:94:ARG:NH2	2.50	0.45
1:GX:48:ILE:HG12	1:GX:69:LEU:HG	1.99	0.45
1:AG:66:HIS:CD2	1:AG:89:GLN:HG3	2.51	0.45
1:AO:48:ILE:HG12	1:AO:69:LEU:HG	1.99	0.45
1:AX:117:THR:HB	1:EJ:117:THR:O	2.17	0.45
1:BD:130:PHE:CD1	1:BD:140:PRO:HB3	2.52	0.45
1:CC:55:LYS:O	1:CC:94:ARG:NH2	2.50	0.45
1:CJ:42:LEU:HD22	1:GH:137:LEU:HD12	1.98	0.45
1:CQ:130:PHE:CD1	1:CQ:140:PRO:HB3	2.52	0.45
1:CR:55:LYS:O	1:CR:94:ARG:NH2	2.50	0.45
1:CS:110:ALA:HB1	1:DD:88:ILE:HD11	1.99	0.45
1:CT:73:VAL:HG11	1:GF:97:ALA:O	2.17	0.45
1:DI:137:LEU:HD11	1:GU:63:ASP:HB3	1.99	0.45
1:DS:117:THR:HG1	1:GQ:117:THR:HG1	1.60	0.45
1:DY:55:LYS:O	1:DY:94:ARG:NH2	2.50	0.45
1:EE:11:ASN:O	1:EU:101:SER:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ET:55:LYS:O	1:ET:94:ARG:NH2	2.50	0.45
1:ET:102:MET:HE1	1:FG:73:VAL:CG2	2.46	0.45
1:EV:130:PHE:CD1	1:EV:140:PRO:HB3	2.52	0.45
1:GA:55:LYS:O	1:GA:94:ARG:NH2	2.50	0.45
1:GE:27:ASN:CG	1:GE:28:GLY:H	2.16	0.45
1:GQ:99:ASN:HB2	1:GQ:102:MET:HG3	1.98	0.45
1:GU:48:ILE:HG12	1:GU:69:LEU:HG	1.99	0.45
1:GV:66:HIS:CD2	1:GV:89:GLN:HG3	2.51	0.45
1:AD:110:ALA:HB1	1:BC:88:ILE:HD11	1.98	0.45
1:AF:130:PHE:CD1	1:AF:140:PRO:HB3	2.52	0.45
1:AN:99:ASN:HB2	1:AN:102:MET:HG3	1.98	0.45
1:AR:130:PHE:CD1	1:AR:140:PRO:HB3	2.52	0.45
1:AS:55:LYS:O	1:AS:94:ARG:NH2	2.50	0.45
1:AW:88:ILE:HD11	1:FC:110:ALA:HB1	1.99	0.45
1:AX:93:PRO:HD3	1:EJ:84:GLY:HA2	1.97	0.45
1:AZ:19:VAL:HG21	1:EW:109:GLN:NE2	2.32	0.45
1:AZ:137:LEU:HD11	1:EW:63:ASP:HB3	1.99	0.45
1:BD:105:SER:O	1:BD:109:GLN:HG3	2.16	0.45
1:BJ:48:ILE:HG12	1:BJ:69:LEU:HG	1.99	0.45
1:BJ:130:PHE:CD1	1:BJ:140:PRO:HB3	2.52	0.45
1:BL:99:ASN:HB2	1:BL:102:MET:HG3	1.98	0.45
1:BO:99:ASN:HB2	1:BO:102:MET:HG3	1.98	0.45
1:BW:110:ALA:HB1	1:DQ:88:ILE:HD11	1.98	0.45
1:BY:52:PHE:CE2	1:FK:137:LEU:C	2.95	0.45
1:BY:101:SER:HA	1:FK:14:LEU:HD21	1.99	0.45
1:BZ:55:LYS:O	1:BZ:94:ARG:NH2	2.50	0.45
1:BZ:87:THR:OG1	1:DT:89:GLN:HB3	2.16	0.45
1:CH:105:SER:O	1:CH:109:GLN:HG3	2.16	0.45
1:CI:52:PHE:HD2	1:GH:139:PHE:CZ	2.35	0.45
1:CN:105:SER:O	1:CN:109:GLN:HG3	2.16	0.45
1:CN:117:THR:O	1:FZ:117:THR:HB	2.16	0.45
1:CO:55:LYS:O	1:CO:94:ARG:NH2	2.50	0.45
1:CO:66:HIS:CD2	1:CO:89:GLN:HG3	2.51	0.45
1:CT:48:ILE:HG12	1:CT:69:LEU:HG	1.99	0.45
1:DR:130:PHE:CD1	1:DR:140:PRO:HB3	2.52	0.45
1:DS:97:ALA:O	1:GQ:73:VAL:HG11	2.17	0.45
1:DY:66:HIS:CD2	1:DY:89:GLN:HG3	2.51	0.45
1:EG:105:SER:O	1:EG:109:GLN:HG3	2.16	0.45
1:EJ:48:ILE:HG12	1:EJ:69:LEU:HG	1.99	0.45
1:EJ:130:PHE:CD1	1:EJ:140:PRO:HB3	2.52	0.45
1:ER:27:ASN:CG	1:ER:28:GLY:H	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ER:99:ASN:HB2	1:ER:102:MET:HG3	1.98	0.45
1:ES:48:ILE:HG12	1:ES:69:LEU:HG	1.99	0.45
1:FH:40:SER:HB2	1:FH:46:GLY:H	1.81	0.45
1:FN:48:ILE:HG12	1:FN:69:LEU:HG	1.99	0.45
1:GC:130:PHE:CD1	1:GC:140:PRO:HB3	2.52	0.45
1:GL:105:SER:O	1:GL:109:GLN:HG3	2.16	0.45
1:GO:130:PHE:CD1	1:GO:140:PRO:HB3	2.52	0.45
1:GR:130:PHE:CD1	1:GR:140:PRO:HB3	2.52	0.45
1:AC:48:ILE:HG12	1:AC:69:LEU:HG	1.99	0.44
1:AJ:110:ALA:HB1	1:BX:88:ILE:HD11	2.00	0.44
1:AK:137:LEU:HD22	1:FO:52:PHE:CD1	2.52	0.44
1:AY:66:HIS:CD2	1:AY:89:GLN:HG3	2.51	0.44
1:BG:48:ILE:HG12	1:BG:69:LEU:HG	1.99	0.44
1:BK:54:ILE:HG12	1:DW:137:LEU:HD13	1.99	0.44
1:CG:18:LEU:HD11	1:CL:122:SER:O	2.17	0.44
1:CV:117:THR:O	1:GM:117:THR:HB	2.17	0.44
1:CW:48:ILE:HG12	1:CW:69:LEU:HG	1.99	0.44
1:DA:55:LYS:O	1:DA:94:ARG:NH2	2.50	0.44
1:DB:24:ARG:HG3	1:DE:138:MET:HG2	1.98	0.44
1:DC:105:SER:O	1:DC:109:GLN:HG3	2.16	0.44
1:DF:102:MET:HE1	1:GR:73:VAL:HG22	1.99	0.44
1:DK:99:ASN:HB2	1:DK:102:MET:HG3	1.98	0.44
1:DO:48:ILE:HG12	1:DO:69:LEU:HG	1.99	0.44
1:DT:27:ASN:CG	1:DT:28:GLY:H	2.16	0.44
1:DX:130:PHE:CD1	1:DX:140:PRO:HB3	2.52	0.44
1:DY:52:PHE:HE2	1:FY:139:PHE:CE1	2.35	0.44
1:EA:48:ILE:HG12	1:EA:69:LEU:HG	1.99	0.44
1:EB:55:LYS:O	1:EB:94:ARG:NH2	2.50	0.44
1:ED:48:ILE:HG12	1:ED:69:LEU:HG	1.99	0.44
1:EE:66:HIS:CD2	1:EE:89:GLN:HG3	2.51	0.44
1:EK:19:VAL:HG21	1:ER:109:GLN:NE2	2.32	0.44
1:ES:130:PHE:CD1	1:ES:140:PRO:HB3	2.52	0.44
1:EV:48:ILE:HG12	1:EV:69:LEU:HG	1.99	0.44
1:FD:99:ASN:HB2	1:FD:102:MET:HG3	1.98	0.44
1:FE:40:SER:HB2	1:FE:46:GLY:H	1.81	0.44
1:FK:48:ILE:HG12	1:FK:69:LEU:HG	1.99	0.44
1:FO:66:HIS:CD2	1:FO:89:GLN:HG3	2.51	0.44
1:FT:130:PHE:CD1	1:FT:140:PRO:HB3	2.52	0.44
1:GA:66:HIS:CD2	1:GA:89:GLN:HG3	2.51	0.44
1:GF:130:PHE:CD1	1:GF:140:PRO:HB3	2.52	0.44
1:GG:55:LYS:O	1:GG:94:ARG:NH2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GJ:55:LYS:O	1:GJ:94:ARG:NH2	2.50	0.44
1:GP:66:HIS:CD2	1:GP:89:GLN:HG3	2.51	0.44
1:GX:130:PHE:CD1	1:GX:140:PRO:HB3	2.52	0.44
1:AA:55:LYS:O	1:AA:94:ARG:NH2	2.50	0.44
1:AD:55:LYS:O	1:AD:94:ARG:NH2	2.50	0.44
1:AE:95:ASN:HD21	1:GA:75:ASP:CA	2.28	0.44
1:AK:137:LEU:HD22	1:FO:52:PHE:HD1	1.83	0.44
1:AR:84:GLY:HA2	1:ED:93:PRO:HD3	1.99	0.44
1:AY:97:ALA:O	1:EI:73:VAL:HG11	2.17	0.44
1:BA:105:SER:O	1:BA:109:GLN:HG3	2.16	0.44
1:BC:99:ASN:HB2	1:BC:102:MET:HG3	1.98	0.44
1:BI:99:ASN:HB2	1:BI:102:MET:HG3	1.98	0.44
1:BN:97:ALA:O	1:DZ:73:VAL:HG11	2.18	0.44
1:BP:130:PHE:CD1	1:BP:140:PRO:HB3	2.52	0.44
1:BZ:10:ALA:H	1:DT:105:SER:CB	2.30	0.44
1:CB:90:VAL:HG22	1:FN:86:VAL:HG22	1.98	0.44
1:CG:139:PHE:CZ	1:CL:52:PHE:CD2	3.05	0.44
1:CP:99:ASN:HB2	1:CP:102:MET:HG3	1.98	0.44
1:CS:97:ALA:HB1	1:DD:73:VAL:HG11	1.99	0.44
1:CU:137:LEU:HD22	1:DH:52:PHE:CD1	2.52	0.44
1:CV:86:VAL:HG22	1:GM:90:VAL:HG22	1.99	0.44
1:CW:130:PHE:CD1	1:CW:140:PRO:HB3	2.52	0.44
1:DI:130:PHE:CD1	1:DI:140:PRO:HB3	2.52	0.44
1:DO:130:PHE:CD1	1:DO:140:PRO:HB3	2.52	0.44
1:DS:102:MET:HE1	1:GQ:73:VAL:CG2	2.47	0.44
1:EE:138:MET:CE	1:EV:36:THR:HG22	2.47	0.44
1:EG:130:PHE:CD1	1:EG:140:PRO:HB3	2.52	0.44
1:EK:137:LEU:CD1	1:ER:54:ILE:HG12	2.40	0.44
1:EL:99:ASN:HB2	1:EL:102:MET:HG3	1.98	0.44
1:FV:137:LEU:HD22	1:GS:52:PHE:CD1	2.53	0.44
1:GO:105:SER:O	1:GO:109:GLN:HG3	2.16	0.44
1:GV:55:LYS:O	1:GV:94:ARG:NH2	2.50	0.44
1:AF:8:VAL:HB	1:DR:118:SER:HB2	1.99	0.44
1:AK:63:ASP:HB3	1:FO:137:LEU:HD11	1.97	0.44
1:AM:18:LEU:HD11	1:CA:123:GLY:N	2.32	0.44
1:AY:55:LYS:O	1:AY:94:ARG:NH2	2.50	0.44
1:BE:52:PHE:HE2	1:BL:139:PHE:CE1	2.35	0.44
1:BN:117:THR:HB	1:DZ:117:THR:O	2.18	0.44
1:BZ:11:ASN:O	1:DT:101:SER:HB2	2.16	0.44
1:CJ:95:ASN:HD21	1:CO:75:ASP:CA	2.26	0.44
1:DD:55:LYS:O	1:DD:94:ARG:NH2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:130:PHE:CD1	1:FB:140:PRO:HB3	2.52	0.44
1:FO:55:LYS:O	1:FO:94:ARG:NH2	2.50	0.44
1:GL:130:PHE:CD1	1:GL:140:PRO:HB3	2.52	0.44
1:AJ:55:LYS:O	1:AJ:94:ARG:NH2	2.50	0.44
1:AK:99:ASN:HB2	1:AK:102:MET:HG3	1.98	0.44
1:AM:73:VAL:HG21	1:CA:102:MET:HE1	1.97	0.44
1:AM:75:ASP:HB2	1:CA:95:ASN:HD21	1.83	0.44
1:AO:130:PHE:CD1	1:AO:140:PRO:HB3	2.52	0.44
1:AP:55:LYS:O	1:AP:94:ARG:NH2	2.50	0.44
1:AX:130:PHE:CD1	1:AX:140:PRO:HB3	2.52	0.44
1:BA:48:ILE:HG12	1:BA:69:LEU:HG	1.99	0.44
1:BG:117:THR:O	1:ES:117:THR:HB	2.17	0.44
1:BP:9:GLY:HA2	1:FB:108:LYS:HB2	1.99	0.44
1:BR:99:ASN:HB2	1:BR:102:MET:HG3	1.98	0.44
1:BS:130:PHE:CD1	1:BS:140:PRO:HB3	2.52	0.44
1:BW:52:PHE:HD1	1:DQ:137:LEU:HD22	1.83	0.44
1:CB:65:ILE:HD11	1:FN:134:TRP:O	2.17	0.44
1:CB:125:THR:HG21	1:FN:5:LEU:HA	2.00	0.44
1:CB:130:PHE:CD1	1:CB:140:PRO:HB3	2.52	0.44
1:CB:137:LEU:O	1:FL:24:ARG:NE	2.50	0.44
1:CE:117:THR:HB	1:FQ:117:THR:O	2.18	0.44
1:CF:55:LYS:O	1:CF:94:ARG:NH2	2.50	0.44
1:DA:66:HIS:CD2	1:DA:89:GLN:HG3	2.51	0.44
1:DF:89:GLN:O	1:GR:87:THR:HG22	2.17	0.44
1:DW:99:ASN:HB2	1:DW:102:MET:HG3	1.98	0.44
1:EE:98:TRP:CH2	1:EU:84:GLY:HA3	2.52	0.44
1:EF:99:ASN:HB2	1:EF:102:MET:HG3	1.98	0.44
1:FR:55:LYS:O	1:FR:94:ARG:NH2	2.50	0.44
1:GI:130:PHE:CD1	1:GI:140:PRO:HB3	2.52	0.44
1:GT:99:ASN:HB2	1:GT:102:MET:HG3	1.98	0.44
1:AL:130:PHE:CD1	1:AL:140:PRO:HB3	2.52	0.44
1:AO:137:LEU:HD11	1:EA:63:ASP:HB3	1.99	0.44
1:AP:9:GLY:HA2	1:BU:108:LYS:HB2	1.99	0.44
1:AP:124:GLN:HA	1:BU:6:ALA:HB3	1.99	0.44
1:BJ:97:ALA:C	1:EV:73:VAL:HG11	2.43	0.44
1:BJ:121:VAL:HG11	1:EV:18:LEU:HG	1.99	0.44
1:BS:48:ILE:HG12	1:BS:69:LEU:HG	1.99	0.44
1:BY:137:LEU:HD11	1:FK:63:ASP:HB3	1.98	0.44
1:CE:137:LEU:HD13	1:FQ:54:ILE:HG12	1.99	0.44
1:CW:54:ILE:HG12	1:GI:137:LEU:HD13	1.99	0.44
1:CY:89:GLN:HB3	1:GG:87:THR:OG1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:99:ASN:HB2	1:CY:102:MET:HG3	1.98	0.44
1:CY:137:LEU:HD22	1:GG:52:PHE:CD1	2.53	0.44
1:DI:54:ILE:HG12	1:GU:137:LEU:HD13	1.99	0.44
1:DI:117:THR:O	1:GU:117:THR:HB	2.17	0.44
1:DL:93:PRO:HD3	1:GX:84:GLY:HA2	2.00	0.44
1:DP:52:PHE:CD1	1:GW:137:LEU:HD22	2.52	0.44
1:DV:54:ILE:HG12	1:GE:137:LEU:HD13	2.00	0.44
1:EE:55:LYS:O	1:EE:94:ARG:NH2	2.50	0.44
1:EE:121:VAL:HG11	1:EU:18:LEU:CG	2.30	0.44
1:EK:55:LYS:O	1:EK:94:ARG:NH2	2.50	0.44
1:EM:48:ILE:HG12	1:EM:69:LEU:HG	1.99	0.44
1:FF:55:LYS:O	1:FF:94:ARG:NH2	2.50	0.44
1:FP:112:ASP:OD1	1:FP:118:SER:OG	2.16	0.44
1:FY:99:ASN:HB2	1:FY:102:MET:HG3	1.98	0.44
1:FZ:130:PHE:CD1	1:FZ:140:PRO:HB3	2.52	0.44
1:GB:99:ASN:HB2	1:GB:102:MET:HG3	1.98	0.44
1:GG:66:HIS:CD2	1:GG:89:GLN:HG3	2.51	0.44
1:GM:66:HIS:CD2	1:GM:89:GLN:HG3	2.51	0.44
1:GO:48:ILE:HG12	1:GO:69:LEU:HG	1.99	0.44
1:AM:52:PHE:HD2	1:CA:139:PHE:CZ	2.35	0.44
1:AR:48:ILE:HG12	1:AR:69:LEU:HG	1.99	0.44
1:BE:73:VAL:HG11	1:BL:97:ALA:O	2.18	0.44
1:BJ:9:GLY:HA2	1:EV:108:LYS:HB2	2.00	0.44
1:BM:130:PHE:CD1	1:BM:140:PRO:HB3	2.52	0.44
1:BT:52:PHE:CE1	1:DN:137:LEU:HA	2.53	0.44
1:CP:27:ASN:CG	1:CP:28:GLY:H	2.15	0.44
1:CQ:48:ILE:HG12	1:CQ:69:LEU:HG	1.99	0.44
1:CQ:134:TRP:O	1:GC:65:ILE:HD11	2.17	0.44
1:CT:42:LEU:HD21	1:DD:136:GLY:C	2.43	0.44
1:EE:73:VAL:HG11	1:EU:97:ALA:O	2.17	0.44
1:EN:101:SER:HB2	1:FJ:11:ASN:O	2.18	0.44
1:FJ:112:ASP:OD1	1:FJ:118:SER:OG	2.16	0.44
1:FT:48:ILE:HG12	1:FT:69:LEU:HG	1.99	0.44
1:FX:66:HIS:CD2	1:FX:89:GLN:HG3	2.51	0.44
1:AB:99:ASN:HB2	1:AB:102:MET:HG3	1.98	0.44
1:AB:137:LEU:HA	1:FX:52:PHE:HE1	1.81	0.44
1:AQ:8:VAL:HB	1:FU:118:SER:HB2	1.99	0.44
1:AR:125:THR:HG21	1:ED:5:LEU:HA	2.00	0.44
1:BV:90:VAL:HG22	1:FH:86:VAL:HG22	1.99	0.44
1:CB:137:LEU:C	1:FN:52:PHE:CE2	2.96	0.44
1:CE:90:VAL:HG22	1:FQ:86:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:48:ILE:HG12	1:CH:69:LEU:HG	1.99	0.44
1:CI:18:LEU:HD11	1:GH:123:GLY:N	2.32	0.44
1:CJ:137:LEU:HD13	1:CO:54:ILE:HG12	2.00	0.44
1:CU:55:LYS:O	1:CU:94:ARG:NH2	2.50	0.44
1:DF:130:PHE:CD1	1:DF:140:PRO:HB3	2.52	0.44
1:DV:52:PHE:CE1	1:GE:137:LEU:HA	2.52	0.44
1:EG:48:ILE:HG12	1:EG:69:LEU:HG	1.99	0.44
1:EP:130:PHE:CD1	1:EP:140:PRO:HB3	2.52	0.44
1:EX:117:THR:OG1	1:FI:117:THR:OG1	2.32	0.44
1:FC:55:LYS:O	1:FC:94:ARG:NH2	2.50	0.44
1:FE:48:ILE:HG12	1:FE:69:LEU:HG	1.99	0.44
1:GC:48:ILE:HG12	1:GC:69:LEU:HG	1.99	0.44
1:AK:52:PHE:CD1	1:FO:137:LEU:HD22	2.53	0.44
1:AR:106:LEU:HD13	1:ED:85:SER:HA	2.00	0.44
1:AV:52:PHE:CE1	1:EF:137:LEU:CA	2.98	0.44
1:AX:73:VAL:CG1	1:EJ:97:ALA:HB1	2.48	0.44
1:BA:40:SER:HB2	1:BA:46:GLY:H	1.81	0.44
1:BD:48:ILE:HG12	1:BD:69:LEU:HG	1.99	0.44
1:CJ:105:SER:HB2	1:CO:10:ALA:O	2.18	0.44
1:DA:29:ASN:HA	1:DE:139:PHE:CE2	2.50	0.44
1:DC:48:ILE:HG12	1:DC:69:LEU:HG	1.99	0.44
1:DC:97:ALA:HB1	1:GO:73:VAL:CG1	2.48	0.44
1:EO:99:ASN:HB2	1:EO:102:MET:HG3	1.98	0.44
1:FS:137:LEU:HD13	1:GP:54:ILE:HG12	1.99	0.44
1:FV:118:SER:HB2	1:GS:8:VAL:HB	2.00	0.44
1:AC:8:VAL:HB	1:DO:118:SER:HB2	1.99	0.44
1:AC:130:PHE:CD1	1:AC:140:PRO:HB3	2.52	0.44
1:AM:54:ILE:HG12	1:CA:137:LEU:HD13	1.99	0.44
1:AR:137:LEU:HD12	1:EB:42:LEU:HD22	1.99	0.44
1:BA:130:PHE:CD1	1:BA:140:PRO:HB3	2.52	0.44
1:BH:63:ASP:HB3	1:BO:137:LEU:HD11	2.00	0.44
1:BK:127:THR:HG22	1:BK:130:PHE:CE2	2.53	0.44
1:BT:137:LEU:HD11	1:DN:63:ASP:HB3	2.00	0.44
1:CC:127:THR:HG22	1:CC:130:PHE:CE2	2.53	0.44
1:CI:127:THR:HG22	1:CI:130:PHE:CE2	2.53	0.44
1:CQ:11:ASN:O	1:GC:101:SER:HB2	2.18	0.44
1:CT:139:PHE:CG	1:GF:31:VAL:HG21	2.53	0.44
1:CV:89:GLN:HB3	1:GM:87:THR:OG1	2.17	0.44
1:CX:137:LEU:HD22	1:DK:52:PHE:CD1	2.53	0.44
1:DD:127:THR:HG22	1:DD:130:PHE:CE2	2.53	0.44
1:DF:98:TRP:CH2	1:GR:84:GLY:HA3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:137:LEU:HD11	1:GW:63:ASP:HB3	2.00	0.44
1:EE:52:PHE:HD1	1:EU:137:LEU:HD22	1.82	0.44
1:EN:52:PHE:HD2	1:FJ:139:PHE:CZ	2.36	0.44
1:GA:127:THR:HG22	1:GA:130:PHE:CE2	2.53	0.44
1:GI:48:ILE:HG12	1:GI:69:LEU:HG	1.99	0.44
1:AH:27:ASN:CG	1:AH:28:GLY:H	2.16	0.43
1:AR:102:MET:HE1	1:ED:73:VAL:HG21	1.98	0.43
1:AU:48:ILE:HG12	1:AU:69:LEU:HG	1.99	0.43
1:BH:52:PHE:HD1	1:BO:137:LEU:HD22	1.83	0.43
1:BH:127:THR:HG22	1:BH:130:PHE:CE2	2.53	0.43
1:BQ:55:LYS:O	1:BQ:94:ARG:NH2	2.50	0.43
1:BQ:127:THR:HG22	1:BQ:130:PHE:CE2	2.53	0.43
1:CB:48:ILE:HG12	1:CB:69:LEU:HG	1.99	0.43
1:CR:127:THR:HG22	1:CR:130:PHE:CE2	2.53	0.43
1:DG:127:THR:HG22	1:DG:130:PHE:CE2	2.53	0.43
1:DP:127:THR:HG22	1:DP:130:PHE:CE2	2.53	0.43
1:DY:52:PHE:CD2	1:FY:139:PHE:CZ	3.06	0.43
1:EK:127:THR:HG22	1:EK:130:PHE:CE2	2.53	0.43
1:FF:127:THR:HG22	1:FF:130:PHE:CE2	2.53	0.43
1:FS:137:LEU:HA	1:GP:52:PHE:HE1	1.83	0.43
1:GS:127:THR:HG22	1:GS:130:PHE:CE2	2.53	0.43
1:AI:75:ASP:HA	1:DU:95:ASN:ND2	2.29	0.43
1:AS:105:SER:CB	1:EL:10:ALA:H	2.31	0.43
1:AT:19:VAL:HG21	1:EZ:109:GLN:NE2	2.33	0.43
1:AT:52:PHE:CD1	1:EZ:137:LEU:HD22	2.53	0.43
1:BD:5:LEU:HA	1:EP:125:THR:HG21	1.99	0.43
1:BJ:31:VAL:HG21	1:EV:139:PHE:CG	2.53	0.43
1:CI:102:MET:HE1	1:GH:73:VAL:CG2	2.48	0.43
1:CJ:86:VAL:HG22	1:CO:90:VAL:HG22	2.00	0.43
1:CJ:88:ILE:HD11	1:CO:110:ALA:HB1	2.00	0.43
1:CY:27:ASN:CG	1:CY:28:GLY:N	2.76	0.43
1:DF:10:ALA:O	1:GR:105:SER:HB2	2.19	0.43
1:DS:127:THR:HG22	1:DS:130:PHE:CE2	2.53	0.43
1:EB:75:ASP:CB	1:GB:95:ASN:HD21	2.31	0.43
1:EE:127:THR:HG22	1:EE:130:PHE:CE2	2.53	0.43
1:FL:127:THR:HG22	1:FL:130:PHE:CE2	2.53	0.43
1:FO:127:THR:HG22	1:FO:130:PHE:CE2	2.53	0.43
1:GG:127:THR:HG22	1:GG:130:PHE:CE2	2.53	0.43
1:GP:127:THR:HG22	1:GP:130:PHE:CE2	2.53	0.43
1:AK:118:SER:CB	1:FO:8:VAL:HB	2.46	0.43
1:AU:18:LEU:HG	1:EG:121:VAL:CG1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:127:THR:HG22	1:AZ:130:PHE:CE2	2.54	0.43
1:BA:127:THR:HG22	1:BA:130:PHE:CE2	2.54	0.43
1:BT:127:THR:HG22	1:BT:130:PHE:CE2	2.53	0.43
1:BU:27:ASN:CG	1:BU:28:GLY:H	2.16	0.43
1:BZ:127:THR:HG22	1:BZ:130:PHE:CE2	2.53	0.43
1:CD:127:THR:HG22	1:CD:130:PHE:CE2	2.54	0.43
1:CH:127:THR:HG22	1:CH:130:PHE:CE2	2.54	0.43
1:CM:127:THR:HG22	1:CM:130:PHE:CE2	2.54	0.43
1:CS:138:MET:HE3	1:DE:23:LEU:O	2.18	0.43
1:CU:97:ALA:O	1:DH:73:VAL:HG11	2.18	0.43
1:CU:127:THR:HG22	1:CU:130:PHE:CE2	2.53	0.43
1:CX:127:THR:HG22	1:CX:130:PHE:CE2	2.53	0.43
1:DM:127:THR:HG22	1:DM:130:PHE:CE2	2.53	0.43
1:EB:52:PHE:HD1	1:GB:137:LEU:HD22	1.83	0.43
1:EZ:55:LYS:O	1:EZ:94:ARG:NH2	2.50	0.43
1:EZ:127:THR:HG22	1:EZ:130:PHE:CE2	2.53	0.43
1:FR:127:THR:HG22	1:FR:130:PHE:CE2	2.53	0.43
1:FU:127:THR:HG22	1:FU:130:PHE:CE2	2.53	0.43
1:GR:127:THR:HG22	1:GR:130:PHE:CE2	2.54	0.43
1:GX:127:THR:HG22	1:GX:130:PHE:CE2	2.54	0.43
1:AP:127:THR:HG22	1:AP:130:PHE:CE2	2.54	0.43
1:BB:19:VAL:HG21	1:BR:109:GLN:NE2	2.33	0.43
1:BV:127:THR:HG22	1:BV:130:PHE:CE2	2.54	0.43
1:CD:97:ALA:HB1	1:CR:73:VAL:CG1	2.49	0.43
1:CM:52:PHE:CD1	1:DG:137:LEU:HD22	2.54	0.43
1:CO:127:THR:HG22	1:CO:130:PHE:CE2	2.53	0.43
1:CU:9:GLY:HA2	1:DH:108:LYS:HB2	1.99	0.43
1:CV:127:THR:HG22	1:CV:130:PHE:CE2	2.54	0.43
1:DA:127:THR:HG22	1:DA:130:PHE:CE2	2.53	0.43
1:DE:112:ASP:OD1	1:DE:118:SER:OG	2.16	0.43
1:DL:127:THR:HG22	1:DL:130:PHE:CE2	2.54	0.43
1:DQ:112:ASP:OD1	1:DQ:118:SER:OG	2.16	0.43
1:DS:77:LYS:HZ3	1:GR:79:ASN:HD22	1.66	0.43
1:DX:127:THR:HG22	1:DX:130:PHE:CE2	2.54	0.43
1:EC:99:ASN:HB2	1:EC:102:MET:HG3	1.98	0.43
1:EN:63:ASP:CB	1:FJ:137:LEU:HD11	2.48	0.43
1:FP:11:ASN:O	1:GV:101:SER:HB2	2.18	0.43
1:FT:127:THR:HG22	1:FT:130:PHE:CE2	2.54	0.43
1:GC:127:THR:HG22	1:GC:130:PHE:CE2	2.54	0.43
1:GK:127:THR:HG22	1:GK:130:PHE:CE2	2.54	0.43
1:GM:127:THR:HG22	1:GM:130:PHE:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:127:THR:HG22	1:AA:130:PHE:CE2	2.53	0.43
1:AG:127:THR:HG22	1:AG:130:PHE:CE2	2.53	0.43
1:AS:117:THR:HB	1:EL:117:THR:O	2.19	0.43
1:AS:127:THR:HG22	1:AS:130:PHE:CE2	2.53	0.43
1:AU:108:LYS:HB2	1:EG:9:GLY:HA2	2.01	0.43
1:AY:110:ALA:HB1	1:EI:88:ILE:HD11	2.00	0.43
1:BE:118:SER:HB2	1:BL:8:VAL:HB	2.01	0.43
1:BJ:75:ASP:HA	1:EV:95:ASN:ND2	2.29	0.43
1:BN:127:THR:HG22	1:BN:130:PHE:CE2	2.53	0.43
1:BP:127:THR:HG22	1:BP:130:PHE:CE2	2.54	0.43
1:BU:127:THR:HG22	1:BU:130:PHE:CE2	2.54	0.43
1:BZ:52:PHE:CD1	1:DT:137:LEU:HD22	2.53	0.43
1:DE:127:THR:HG22	1:DE:130:PHE:CE2	2.54	0.43
1:DJ:127:THR:HG22	1:DJ:130:PHE:CE2	2.53	0.43
1:DM:52:PHE:HE2	1:GT:139:PHE:CE1	2.37	0.43
1:DU:127:THR:HG22	1:DU:130:PHE:CE2	2.54	0.43
1:EC:27:ASN:CG	1:EC:28:GLY:N	2.76	0.43
1:ED:127:THR:HG22	1:ED:130:PHE:CE2	2.54	0.43
1:EL:127:THR:HG22	1:EL:130:PHE:CE2	2.54	0.43
1:EO:127:THR:HG22	1:EO:130:PHE:CE2	2.54	0.43
1:EP:48:ILE:HG12	1:EP:69:LEU:HG	1.99	0.43
1:EU:127:THR:HG22	1:EU:130:PHE:CE2	2.54	0.43
1:EY:127:THR:HG22	1:EY:130:PHE:CE2	2.54	0.43
1:GH:127:THR:HG22	1:GH:130:PHE:CE2	2.54	0.43
1:GT:127:THR:HG22	1:GT:130:PHE:CE2	2.54	0.43
1:AD:127:THR:HG22	1:AD:130:PHE:CE2	2.53	0.43
1:AF:127:THR:HG22	1:AF:130:PHE:CE2	2.54	0.43
1:AL:127:THR:HG22	1:AL:130:PHE:CE2	2.54	0.43
1:AS:52:PHE:CD1	1:EL:137:LEU:HD22	2.53	0.43
1:BE:52:PHE:CD2	1:BL:139:PHE:CZ	3.07	0.43
1:BE:127:THR:HG22	1:BE:130:PHE:CE2	2.53	0.43
1:BG:127:THR:HG22	1:BG:130:PHE:CE2	2.54	0.43
1:BG:137:LEU:HD13	1:ES:54:ILE:HG12	2.00	0.43
1:BQ:87:THR:OG1	1:EC:89:GLN:HB3	2.19	0.43
1:BV:10:ALA:O	1:FH:105:SER:HB2	2.19	0.43
1:CK:127:THR:HG22	1:CK:130:PHE:CE2	2.54	0.43
1:CL:127:THR:HG22	1:CL:130:PHE:CE2	2.53	0.43
1:CQ:18:LEU:HD11	1:GC:122:SER:O	2.19	0.43
1:CQ:127:THR:HG22	1:CQ:130:PHE:CE2	2.54	0.43
1:CS:127:THR:HG22	1:CS:130:PHE:CE2	2.54	0.43
1:DR:127:THR:HG22	1:DR:130:PHE:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DS:75:ASP:HB2	1:GQ:95:ASN:HD21	1.84	0.43
1:EG:127:THR:HG22	1:EG:130:PHE:CE2	2.54	0.43
1:EN:127:THR:HG22	1:EN:130:PHE:CE2	2.53	0.43
1:ET:127:THR:HG22	1:ET:130:PHE:CE2	2.53	0.43
1:EU:79:ASN:ND2	1:FG:75:ASP:OD1	2.46	0.43
1:FK:127:THR:HG22	1:FK:130:PHE:CE2	2.54	0.43
1:GB:27:ASN:CG	1:GB:28:GLY:N	2.76	0.43
1:AB:117:THR:OG1	1:FX:117:THR:OG1	2.33	0.43
1:AB:137:LEU:HD13	1:FX:54:ILE:HG12	2.01	0.43
1:AD:73:VAL:CG1	1:BC:97:ALA:HB1	2.49	0.43
1:AK:127:THR:HG22	1:AK:130:PHE:CE2	2.54	0.43
1:AL:117:THR:O	1:DX:117:THR:HB	2.18	0.43
1:AO:117:THR:O	1:EA:117:THR:HB	2.17	0.43
1:AW:52:PHE:CD1	1:FC:137:LEU:HD22	2.54	0.43
1:AY:127:THR:HG22	1:AY:130:PHE:CE2	2.53	0.43
1:BR:27:ASN:CG	1:BR:28:GLY:N	2.76	0.43
1:CD:24:ARG:NE	1:CD:34:VAL:HG21	2.34	0.43
1:CD:79:ASN:ND2	1:GK:77:LYS:HG2	2.33	0.43
1:CE:127:THR:HG22	1:CE:130:PHE:CE2	2.54	0.43
1:CP:110:ALA:HB1	1:DJ:88:ILE:HD11	2.01	0.43
1:CY:127:THR:HG22	1:CY:130:PHE:CE2	2.54	0.43
1:CZ:127:THR:HG22	1:CZ:130:PHE:CE2	2.54	0.43
1:DH:127:THR:HG22	1:DH:130:PHE:CE2	2.54	0.43
1:DT:24:ARG:NE	1:DT:34:VAL:HG21	2.34	0.43
1:EN:137:LEU:HD11	1:FJ:63:ASP:CG	2.43	0.43
1:EO:24:ARG:NE	1:EO:34:VAL:HG21	2.34	0.43
1:ET:88:ILE:HD11	1:FG:110:ALA:HB1	2.00	0.43
1:FI:127:THR:HG22	1:FI:130:PHE:CE2	2.53	0.43
1:FZ:127:THR:HG22	1:FZ:130:PHE:CE2	2.54	0.43
1:GH:27:ASN:CG	1:GH:28:GLY:N	2.76	0.43
1:AB:24:ARG:NE	1:AB:34:VAL:HG21	2.34	0.43
1:AC:127:THR:HG22	1:AC:130:PHE:CE2	2.54	0.43
1:AJ:127:THR:HG22	1:AJ:130:PHE:CE2	2.53	0.43
1:AT:24:ARG:NE	1:AT:34:VAL:HG21	2.34	0.43
1:AU:127:THR:HG22	1:AU:130:PHE:CE2	2.54	0.43
1:AW:127:THR:HG22	1:AW:130:PHE:CE2	2.54	0.43
1:BF:24:ARG:NE	1:BF:34:VAL:HG21	2.34	0.43
1:BI:24:ARG:NE	1:BI:34:VAL:HG21	2.34	0.43
1:BI:127:THR:HG22	1:BI:130:PHE:CE2	2.54	0.43
1:BO:42:LEU:HD22	1:DZ:137:LEU:HD12	2.01	0.43
1:BS:127:THR:HG22	1:BS:130:PHE:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:127:THR:HG22	1:BY:130:PHE:CE2	2.54	0.43
1:CD:27:ASN:CG	1:CD:28:GLY:N	2.76	0.43
1:CF:8:VAL:HB	1:GN:118:SER:HB2	2.00	0.43
1:CF:109:GLN:NE2	1:GN:19:VAL:HG21	2.34	0.43
1:CF:117:THR:O	1:GN:117:THR:HB	2.18	0.43
1:CF:127:THR:HG22	1:CF:130:PHE:CE2	2.53	0.43
1:CJ:127:THR:HG22	1:CJ:130:PHE:CE2	2.54	0.43
1:CM:24:ARG:NE	1:CM:34:VAL:HG21	2.34	0.43
1:CV:24:ARG:NE	1:CV:34:VAL:HG21	2.34	0.43
1:CY:24:ARG:NE	1:CY:34:VAL:HG21	2.34	0.43
1:CZ:48:ILE:HG12	1:CZ:69:LEU:HG	1.99	0.43
1:DC:127:THR:HG22	1:DC:130:PHE:CE2	2.54	0.43
1:DF:48:ILE:HG12	1:DF:69:LEU:HG	1.99	0.43
1:DO:127:THR:HG22	1:DO:130:PHE:CE2	2.54	0.43
1:EA:127:THR:HG22	1:EA:130:PHE:CE2	2.54	0.43
1:EJ:127:THR:HG22	1:EJ:130:PHE:CE2	2.54	0.43
1:EO:27:ASN:CG	1:EO:28:GLY:N	2.76	0.43
1:EP:127:THR:HG22	1:EP:130:PHE:CE2	2.54	0.43
1:ES:127:THR:HG22	1:ES:130:PHE:CE2	2.54	0.43
1:ET:117:THR:O	1:FG:117:THR:HB	2.19	0.43
1:EV:127:THR:HG22	1:EV:130:PHE:CE2	2.54	0.43
1:FB:127:THR:HG22	1:FB:130:PHE:CE2	2.54	0.43
1:FE:127:THR:HG22	1:FE:130:PHE:CE2	2.54	0.43
1:FG:24:ARG:NE	1:FG:34:VAL:HG21	2.34	0.43
1:FG:127:THR:HG22	1:FG:130:PHE:CE2	2.54	0.43
1:FJ:127:THR:HG22	1:FJ:130:PHE:CE2	2.54	0.43
1:FP:127:THR:HG22	1:FP:130:PHE:CE2	2.54	0.43
1:FS:127:THR:HG22	1:FS:130:PHE:CE2	2.54	0.43
1:GE:127:THR:HG22	1:GE:130:PHE:CE2	2.54	0.43
1:AB:127:THR:HG22	1:AB:130:PHE:CE2	2.54	0.43
1:AC:117:THR:HG1	1:DO:117:THR:HG1	1.66	0.43
1:AD:52:PHE:CE2	1:BC:139:PHE:CZ	3.06	0.43
1:AG:52:PHE:CD2	1:BF:139:PHE:CZ	3.07	0.43
1:AK:88:ILE:HD11	1:FO:110:ALA:HB1	2.00	0.43
1:AL:117:THR:HB	1:DX:117:THR:O	2.19	0.43
1:AM:127:THR:HG22	1:AM:130:PHE:CE2	2.53	0.43
1:AO:19:VAL:HG21	1:EA:109:GLN:NE2	2.34	0.43
1:AO:127:THR:HG22	1:AO:130:PHE:CE2	2.54	0.43
1:AU:84:GLY:HA3	1:EG:98:TRP:CH2	2.53	0.43
1:AU:90:VAL:HG22	1:EG:86:VAL:HG22	1.99	0.43
1:AZ:139:PHE:CZ	1:EW:52:PHE:CD2	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:109:GLN:NE2	1:EP:19:VAL:HG21	2.33	0.43
1:BR:127:THR:HG22	1:BR:130:PHE:CE2	2.54	0.43
1:BT:8:VAL:HB	1:DN:118:SER:CB	2.44	0.43
1:CB:127:THR:HG22	1:CB:130:PHE:CE2	2.54	0.43
1:DB:137:LEU:HD11	1:GJ:63:ASP:HB3	1.99	0.43
1:DH:24:ARG:NE	1:DH:34:VAL:HG21	2.34	0.43
1:DY:127:THR:HG22	1:DY:130:PHE:CE2	2.53	0.43
1:DZ:24:ARG:NE	1:DZ:34:VAL:HG21	2.34	0.43
1:EB:52:PHE:CD1	1:GB:137:LEU:HD22	2.54	0.43
1:EE:24:ARG:HB2	1:EE:34:VAL:HG23	2.01	0.43
1:EE:119:ALA:O	1:EU:8:VAL:HG21	2.18	0.43
1:EH:87:THR:OG1	1:EO:89:GLN:HB3	2.19	0.43
1:EM:127:THR:HG22	1:EM:130:PHE:CE2	2.54	0.43
1:EQ:127:THR:HG22	1:EQ:130:PHE:CE2	2.53	0.43
1:ET:73:VAL:CG1	1:FG:97:ALA:HB1	2.49	0.43
1:EU:24:ARG:NE	1:EU:34:VAL:HG21	2.34	0.43
1:EW:127:THR:HG22	1:EW:130:PHE:CE2	2.53	0.43
1:FC:24:ARG:HB2	1:FC:34:VAL:HG23	2.01	0.43
1:FD:117:THR:HB	1:FF:117:THR:O	2.19	0.43
1:FS:118:SER:HB2	1:GP:8:VAL:HB	2.01	0.43
1:GD:127:THR:HG22	1:GD:130:PHE:CE2	2.53	0.43
1:GO:127:THR:HG22	1:GO:130:PHE:CE2	2.54	0.43
1:GQ:127:THR:HG22	1:GQ:130:PHE:CE2	2.54	0.43
1:AJ:109:GLN:NE2	1:BX:19:VAL:HG21	2.34	0.43
1:AN:24:ARG:NE	1:AN:34:VAL:HG21	2.34	0.43
1:AN:42:LEU:HD22	1:CA:137:LEU:HD12	2.00	0.43
1:AN:127:THR:HG22	1:AN:130:PHE:CE2	2.54	0.43
1:AQ:24:ARG:NE	1:AQ:34:VAL:HG21	2.34	0.43
1:AS:24:ARG:HB2	1:AS:34:VAL:HG23	2.01	0.43
1:AV:24:ARG:HB2	1:AV:34:VAL:HG23	2.01	0.43
1:BO:27:ASN:CG	1:BO:28:GLY:N	2.76	0.43
1:BQ:24:ARG:HB2	1:BQ:34:VAL:HG23	2.01	0.43
1:BQ:117:THR:HB	1:EC:117:THR:O	2.19	0.43
1:BU:24:ARG:NE	1:BU:34:VAL:HG21	2.34	0.43
1:BV:109:GLN:NE2	1:FH:19:VAL:HG21	2.33	0.43
1:BW:127:THR:HG22	1:BW:130:PHE:CE2	2.53	0.43
1:CA:127:THR:HG22	1:CA:130:PHE:CE2	2.54	0.43
1:CG:24:ARG:NE	1:CG:34:VAL:HG21	2.34	0.43
1:CT:73:VAL:HG21	1:GF:98:TRP:HE3	1.84	0.43
1:CU:124:GLN:HA	1:DH:6:ALA:HB3	2.01	0.43
1:DA:24:ARG:HB2	1:DA:34:VAL:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DT:127:THR:HG22	1:DT:130:PHE:CE2	2.54	0.43
1:EE:97:ALA:C	1:EU:73:VAL:HG11	2.40	0.43
1:EH:24:ARG:HB2	1:EH:34:VAL:HG23	2.01	0.43
1:EU:112:ASP:OD1	1:EU:118:SER:OG	2.16	0.43
1:FC:127:THR:HG22	1:FC:130:PHE:CE2	2.53	0.43
1:FD:127:THR:HG22	1:FD:130:PHE:CE2	2.54	0.43
1:FV:11:ASN:O	1:GS:101:SER:HB2	2.18	0.43
1:FV:24:ARG:NE	1:FV:34:VAL:HG21	2.34	0.43
1:GB:24:ARG:NE	1:GB:34:VAL:HG21	2.34	0.43
1:GH:24:ARG:NE	1:GH:34:VAL:HG21	2.34	0.43
1:GI:127:THR:HG22	1:GI:130:PHE:CE2	2.54	0.43
1:GL:48:ILE:HG12	1:GL:69:LEU:HG	1.99	0.43
1:GM:24:ARG:HB2	1:GM:34:VAL:HG23	2.01	0.43
1:AR:127:THR:HG22	1:AR:130:PHE:CE2	2.54	0.42
1:AT:89:GLN:HB3	1:EZ:87:THR:OG1	2.19	0.42
1:AT:127:THR:HG22	1:AT:130:PHE:CE2	2.54	0.42
1:AV:127:THR:HG22	1:AV:130:PHE:CE2	2.53	0.42
1:AZ:110:ALA:HB1	1:EW:88:ILE:HD11	2.01	0.42
1:AZ:139:PHE:CZ	1:EW:52:PHE:HD2	2.37	0.42
1:BB:24:ARG:HB2	1:BB:34:VAL:HG23	2.01	0.42
1:BB:52:PHE:CD1	1:BR:137:LEU:HD22	2.54	0.42
1:BC:24:ARG:NE	1:BC:34:VAL:HG21	2.34	0.42
1:BC:127:THR:HG22	1:BC:130:PHE:CE2	2.54	0.42
1:BO:24:ARG:NE	1:BO:34:VAL:HG21	2.34	0.42
1:BT:24:ARG:HB2	1:BT:34:VAL:HG23	2.01	0.42
1:BW:10:ALA:H	1:DQ:105:SER:CB	2.31	0.42
1:CA:24:ARG:NE	1:CA:34:VAL:HG21	2.34	0.42
1:CJ:24:ARG:NE	1:CJ:34:VAL:HG21	2.34	0.42
1:CU:137:LEU:HD11	1:DH:63:ASP:CG	2.44	0.42
1:DS:137:LEU:HD22	1:GQ:52:PHE:CD1	2.54	0.42
1:DZ:127:THR:HG22	1:DZ:130:PHE:CE2	2.54	0.42
1:EH:90:VAL:HG22	1:EO:86:VAL:HG22	2.01	0.42
1:EK:24:ARG:HB2	1:EK:34:VAL:HG23	2.01	0.42
1:EN:24:ARG:HB2	1:EN:34:VAL:HG23	2.01	0.42
1:FA:24:ARG:NE	1:FA:34:VAL:HG21	2.34	0.42
1:FH:127:THR:HG22	1:FH:130:PHE:CE2	2.54	0.42
1:FJ:24:ARG:NE	1:FJ:34:VAL:HG21	2.34	0.42
1:GB:127:THR:HG22	1:GB:130:PHE:CE2	2.54	0.42
1:GJ:127:THR:HG22	1:GJ:130:PHE:CE2	2.53	0.42
1:GK:24:ARG:NE	1:GK:34:VAL:HG21	2.34	0.42
1:GL:127:THR:HG22	1:GL:130:PHE:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GQ:27:ASN:CG	1:GQ:28:GLY:N	2.76	0.42
1:AD:98:TRP:CH2	1:BC:84:GLY:HA3	2.55	0.42
1:AE:24:ARG:NE	1:AE:34:VAL:HG21	2.34	0.42
1:AH:127:THR:HG22	1:AH:130:PHE:CE2	2.54	0.42
1:AM:73:VAL:CG1	1:CA:97:ALA:HB1	2.49	0.42
1:AM:73:VAL:HG12	1:CA:97:ALA:HB1	2.00	0.42
1:AY:24:ARG:HB2	1:AY:34:VAL:HG23	2.01	0.42
1:BB:127:THR:HG22	1:BB:130:PHE:CE2	2.53	0.42
1:BL:24:ARG:NE	1:BL:34:VAL:HG21	2.34	0.42
1:BL:127:THR:HG22	1:BL:130:PHE:CE2	2.54	0.42
1:BR:24:ARG:NE	1:BR:34:VAL:HG21	2.34	0.42
1:BX:24:ARG:NE	1:BX:34:VAL:HG21	2.34	0.42
1:CE:63:ASP:HB3	1:FQ:137:LEU:HD11	2.01	0.42
1:CE:87:THR:CG2	1:FQ:89:GLN:HB3	2.50	0.42
1:CG:127:THR:HG22	1:CG:130:PHE:CE2	2.54	0.42
1:CZ:68:ASN:ND2	1:CZ:70:ARG:HH11	2.18	0.42
1:DE:24:ARG:NE	1:DE:34:VAL:HG21	2.34	0.42
1:DF:127:THR:HG22	1:DF:130:PHE:CE2	2.54	0.42
1:DF:137:LEU:O	1:GP:24:ARG:NE	2.52	0.42
1:DK:127:THR:HG22	1:DK:130:PHE:CE2	2.54	0.42
1:DN:127:THR:HG22	1:DN:130:PHE:CE2	2.54	0.42
1:EB:127:THR:HG22	1:EB:130:PHE:CE2	2.53	0.42
1:EF:24:ARG:NE	1:EF:34:VAL:HG21	2.34	0.42
1:EX:117:THR:HG1	1:FI:117:THR:HG1	1.62	0.42
1:EX:127:THR:HG22	1:EX:130:PHE:CE2	2.54	0.42
1:GE:24:ARG:NE	1:GE:34:VAL:HG21	2.34	0.42
1:GG:24:ARG:HB2	1:GG:34:VAL:HG23	2.01	0.42
1:GR:48:ILE:HG12	1:GR:69:LEU:HG	1.99	0.42
1:AC:97:ALA:O	1:DO:73:VAL:HG11	2.20	0.42
1:AE:118:SER:HB2	1:GA:8:VAL:HB	2.02	0.42
1:AH:24:ARG:NE	1:AH:34:VAL:HG21	2.34	0.42
1:AJ:117:THR:HB	1:BX:117:THR:O	2.18	0.42
1:AP:122:SER:O	1:BU:18:LEU:HD11	2.19	0.42
1:BE:24:ARG:HB2	1:BE:34:VAL:HG23	2.01	0.42
1:CS:52:PHE:CD2	1:DD:139:PHE:CZ	3.07	0.42
1:CT:127:THR:HG22	1:CT:130:PHE:CE2	2.54	0.42
1:CW:127:THR:HG22	1:CW:130:PHE:CE2	2.54	0.42
1:CX:52:PHE:HE2	1:DK:139:PHE:CE1	2.37	0.42
1:DA:29:ASN:C	1:DE:139:PHE:HZ	2.28	0.42
1:DU:68:ASN:ND2	1:DU:70:ARG:HH11	2.18	0.42
1:DV:127:THR:HG22	1:DV:130:PHE:CE2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DW:24:ARG:NE	1:DW:34:VAL:HG21	2.34	0.42
1:EC:24:ARG:NE	1:EC:34:VAL:HG21	2.34	0.42
1:EF:127:THR:HG22	1:EF:130:PHE:CE2	2.54	0.42
1:EH:127:THR:HG22	1:EH:130:PHE:CE2	2.53	0.42
1:EN:124:GLN:HA	1:FJ:6:ALA:CB	2.49	0.42
1:EQ:24:ARG:HB2	1:EQ:34:VAL:HG23	2.01	0.42
1:ER:127:THR:HG22	1:ER:130:PHE:CE2	2.54	0.42
1:GP:24:ARG:HB2	1:GP:34:VAL:HG23	2.01	0.42
1:AT:110:ALA:HB1	1:EZ:88:ILE:HD11	2.01	0.42
1:AU:87:THR:HG22	1:EG:89:GLN:O	2.18	0.42
1:BB:68:ASN:ND2	1:BB:70:ARG:HH11	2.18	0.42
1:BD:88:ILE:HD11	1:EP:110:ALA:HB1	2.01	0.42
1:CF:24:ARG:HB2	1:CF:34:VAL:HG23	2.01	0.42
1:CK:68:ASN:ND2	1:CK:70:ARG:HH11	2.18	0.42
1:CL:24:ARG:HB2	1:CL:34:VAL:HG23	2.01	0.42
1:CP:95:ASN:HD21	1:DJ:75:ASP:HB2	1.85	0.42
1:CU:24:ARG:HB2	1:CU:34:VAL:HG23	2.01	0.42
1:CW:68:ASN:ND2	1:CW:70:ARG:HH11	2.18	0.42
1:CW:121:VAL:CG1	1:GI:18:LEU:HG	2.50	0.42
1:CX:117:THR:HG1	1:DK:117:THR:HG1	1.63	0.42
1:DC:68:ASN:ND2	1:DC:70:ARG:HH11	2.18	0.42
1:DO:68:ASN:ND2	1:DO:70:ARG:HH11	2.18	0.42
1:DP:24:ARG:HB2	1:DP:34:VAL:HG23	2.01	0.42
1:DQ:24:ARG:NE	1:DQ:34:VAL:HG21	2.34	0.42
1:DX:68:ASN:ND2	1:DX:70:ARG:HH11	2.18	0.42
1:EA:68:ASN:ND2	1:EA:70:ARG:HH11	2.18	0.42
1:ER:42:LEU:HD22	1:FM:137:LEU:HD12	2.00	0.42
1:ET:97:ALA:HB1	1:FG:73:VAL:HG12	2.01	0.42
1:FD:24:ARG:NE	1:FD:34:VAL:HG21	2.34	0.42
1:FM:24:ARG:NE	1:FM:34:VAL:HG21	2.34	0.42
1:FM:127:THR:HG22	1:FM:130:PHE:CE2	2.54	0.42
1:FN:127:THR:HG22	1:FN:130:PHE:CE2	2.54	0.42
1:FV:127:THR:HG22	1:FV:130:PHE:CE2	2.54	0.42
1:FY:127:THR:HG22	1:FY:130:PHE:CE2	2.54	0.42
1:AE:86:VAL:HG22	1:GA:90:VAL:HG22	2.01	0.42
1:AI:10:ALA:H	1:DU:105:SER:CB	2.32	0.42
1:AO:68:ASN:ND2	1:AO:70:ARG:HH11	2.18	0.42
1:AP:24:ARG:HB2	1:AP:34:VAL:HG23	2.01	0.42
1:AZ:24:ARG:NE	1:AZ:34:VAL:HG21	2.34	0.42
1:BD:127:THR:HG22	1:BD:130:PHE:CE2	2.54	0.42
1:CL:68:ASN:ND2	1:CL:70:ARG:HH11	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CN:137:LEU:HD11	1:FZ:63:ASP:HB3	2.01	0.42
1:CO:24:ARG:HB2	1:CO:34:VAL:HG23	2.01	0.42
1:CP:127:THR:HG22	1:CP:130:PHE:CE2	2.54	0.42
1:CS:24:ARG:NE	1:CS:34:VAL:HG21	2.34	0.42
1:CX:24:ARG:HB2	1:CX:34:VAL:HG23	2.02	0.42
1:DK:24:ARG:NE	1:DK:34:VAL:HG21	2.34	0.42
1:DQ:127:THR:HG22	1:DQ:130:PHE:CE2	2.54	0.42
1:DR:68:ASN:ND2	1:DR:70:ARG:HH11	2.18	0.42
1:DW:127:THR:HG22	1:DW:130:PHE:CE2	2.54	0.42
1:EG:68:ASN:ND2	1:EG:70:ARG:HH11	2.18	0.42
1:ET:68:ASN:ND2	1:ET:70:ARG:HH11	2.18	0.42
1:FA:137:LEU:HD22	1:FL:52:PHE:CD1	2.53	0.42
1:FF:68:ASN:ND2	1:FF:70:ARG:HH11	2.18	0.42
1:FH:68:ASN:ND2	1:FH:70:ARG:HH11	2.18	0.42
1:FO:24:ARG:HB2	1:FO:34:VAL:HG23	2.01	0.42
1:FR:24:ARG:HB2	1:FR:34:VAL:HG23	2.01	0.42
1:FR:68:ASN:ND2	1:FR:70:ARG:HH11	2.18	0.42
1:GJ:24:ARG:HB2	1:GJ:34:VAL:HG23	2.01	0.42
1:GJ:68:ASN:ND2	1:GJ:70:ARG:HH11	2.18	0.42
1:GP:68:ASN:ND2	1:GP:70:ARG:HH11	2.18	0.42
1:GQ:24:ARG:NE	1:GQ:34:VAL:HG21	2.34	0.42
1:GV:24:ARG:HB2	1:GV:34:VAL:HG23	2.01	0.42
1:GV:127:THR:HG22	1:GV:130:PHE:CE2	2.53	0.42
1:GW:127:THR:HG22	1:GW:130:PHE:CE2	2.54	0.42
1:AG:24:ARG:HB2	1:AG:34:VAL:HG23	2.01	0.42
1:AH:138:MET:HE3	1:GE:24:ARG:HA	2.01	0.42
1:AL:117:THR:HG1	1:DX:117:THR:HG1	1.68	0.42
1:AS:68:ASN:ND2	1:AS:70:ARG:HH11	2.18	0.42
1:AX:68:ASN:ND2	1:AX:70:ARG:HH11	2.18	0.42
1:BF:127:THR:HG22	1:BF:130:PHE:CE2	2.54	0.42
1:BJ:93:PRO:HD3	1:EV:84:GLY:HA2	2.02	0.42
1:BJ:127:THR:HG22	1:BJ:130:PHE:CE2	2.54	0.42
1:BX:127:THR:HG22	1:BX:130:PHE:CE2	2.54	0.42
1:BZ:24:ARG:HB2	1:BZ:34:VAL:HG23	2.01	0.42
1:CF:68:ASN:ND2	1:CF:70:ARG:HH11	2.18	0.42
1:CP:24:ARG:NE	1:CP:34:VAL:HG21	2.34	0.42
1:CT:68:ASN:ND2	1:CT:70:ARG:HH11	2.18	0.42
1:DB:118:SER:HB2	1:GJ:8:VAL:HB	2.00	0.42
1:DD:24:ARG:HB2	1:DD:34:VAL:HG23	2.01	0.42
1:EB:24:ARG:HB2	1:EB:34:VAL:HG23	2.01	0.42
1:EM:68:ASN:ND2	1:EM:70:ARG:HH11	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ES:68:ASN:ND2	1:ES:70:ARG:HH11	2.18	0.42
1:EW:68:ASN:ND2	1:EW:70:ARG:HH11	2.18	0.42
1:FA:127:THR:HG22	1:FA:130:PHE:CE2	2.54	0.42
1:FW:68:ASN:ND2	1:FW:70:ARG:HH11	2.18	0.42
1:FW:127:THR:HG22	1:FW:130:PHE:CE2	2.54	0.42
1:FX:68:ASN:ND2	1:FX:70:ARG:HH11	2.18	0.42
1:FY:24:ARG:NE	1:FY:34:VAL:HG21	2.34	0.42
1:GF:127:THR:HG22	1:GF:130:PHE:CE2	2.54	0.42
1:GM:68:ASN:ND2	1:GM:70:ARG:HH11	2.18	0.42
1:GN:127:THR:HG22	1:GN:130:PHE:CE2	2.54	0.42
1:GT:24:ARG:NE	1:GT:34:VAL:HG21	2.34	0.42
1:GX:68:ASN:ND2	1:GX:70:ARG:HH11	2.18	0.42
1:AC:68:ASN:ND2	1:AC:70:ARG:HH11	2.18	0.42
1:AG:98:TRP:CH2	1:BF:84:GLY:HA3	2.55	0.42
1:AI:127:THR:HG22	1:AI:130:PHE:CE2	2.54	0.42
1:AP:138:MET:HE3	1:BV:36:THR:HG22	2.01	0.42
1:AW:8:VAL:HB	1:FC:118:SER:HB2	2.01	0.42
1:AX:127:THR:HG22	1:AX:130:PHE:CE2	2.54	0.42
1:BE:68:ASN:ND2	1:BE:70:ARG:HH11	2.18	0.42
1:BJ:11:ASN:O	1:EV:101:SER:HB2	2.20	0.42
1:BK:68:ASN:ND2	1:BK:70:ARG:HH11	2.18	0.42
1:BW:137:LEU:HD11	1:DQ:63:ASP:HB3	2.02	0.42
1:CC:137:LEU:HD11	1:GK:63:ASP:HB3	2.02	0.42
1:CE:68:ASN:ND2	1:CE:70:ARG:HH11	2.18	0.42
1:CN:127:THR:HG22	1:CN:130:PHE:CE2	2.54	0.42
1:DA:118:SER:HB2	1:DE:8:VAL:HB	2.01	0.42
1:DF:110:ALA:HB1	1:GR:88:ILE:HD11	2.01	0.42
1:DI:127:THR:HG22	1:DI:130:PHE:CE2	2.54	0.42
1:DJ:24:ARG:HB2	1:DJ:34:VAL:HG23	2.01	0.42
1:DM:73:VAL:HG11	1:GT:97:ALA:O	2.19	0.42
1:DV:110:ALA:HB1	1:GE:88:ILE:HD11	2.02	0.42
1:DY:68:ASN:ND2	1:DY:70:ARG:HH11	2.18	0.42
1:DY:110:ALA:HB1	1:FY:88:ILE:HD11	2.01	0.42
1:EB:117:THR:HB	1:GB:117:THR:O	2.19	0.42
1:EK:109:GLN:NE2	1:ER:19:VAL:HG21	2.35	0.42
1:EU:27:ASN:CG	1:EU:28:GLY:N	2.76	0.42
1:EY:68:ASN:ND2	1:EY:70:ARG:HH11	2.18	0.42
1:FF:24:ARG:HB2	1:FF:34:VAL:HG23	2.01	0.42
1:FT:68:ASN:ND2	1:FT:70:ARG:HH11	2.18	0.42
1:FX:127:THR:HG22	1:FX:130:PHE:CE2	2.53	0.42
1:GR:68:ASN:ND2	1:GR:70:ARG:HH11	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GU:127:THR:HG22	1:GU:130:PHE:CE2	2.54	0.42
1:AC:54:ILE:HG12	1:DO:137:LEU:HD13	2.01	0.42
1:AE:127:THR:HG22	1:AE:130:PHE:CE2	2.54	0.42
1:AE:137:LEU:HA	1:GA:52:PHE:CE1	2.55	0.42
1:AN:63:ASP:HB3	1:FR:137:LEU:HD11	2.02	0.42
1:BN:24:ARG:HB2	1:BN:34:VAL:HG23	2.01	0.42
1:BT:68:ASN:ND2	1:BT:70:ARG:HH11	2.18	0.42
1:BY:68:ASN:ND2	1:BY:70:ARG:HH11	2.18	0.42
1:CC:90:VAL:HG22	1:GK:86:VAL:HG22	2.02	0.42
1:CD:73:VAL:HG12	1:CR:97:ALA:HB1	2.02	0.42
1:CE:105:SER:HB2	1:FQ:10:ALA:O	2.19	0.42
1:CT:71:LYS:HB3	1:GF:98:TRP:CH2	2.55	0.42
1:DF:68:ASN:ND2	1:DF:70:ARG:HH11	2.18	0.42
1:DN:24:ARG:NE	1:DN:34:VAL:HG21	2.34	0.42
1:DV:137:LEU:HD11	1:GE:63:ASP:HB3	2.02	0.42
1:EH:68:ASN:ND2	1:EH:70:ARG:HH11	2.18	0.42
1:EI:24:ARG:NE	1:EI:34:VAL:HG21	2.34	0.42
1:EW:24:ARG:HB2	1:EW:34:VAL:HG23	2.01	0.42
1:EZ:68:ASN:ND2	1:EZ:70:ARG:HH11	2.18	0.42
1:FA:73:VAL:HG11	1:FL:97:ALA:O	2.19	0.42
1:FQ:127:THR:HG22	1:FQ:130:PHE:CE2	2.54	0.42
1:FS:24:ARG:NE	1:FS:34:VAL:HG21	2.34	0.42
1:FU:68:ASN:ND2	1:FU:70:ARG:HH11	2.18	0.42
1:FV:101:SER:HB2	1:GS:11:ASN:O	2.19	0.42
1:FX:24:ARG:HB2	1:FX:34:VAL:HG23	2.01	0.42
1:GO:68:ASN:ND2	1:GO:70:ARG:HH11	2.18	0.42
1:AH:27:ASN:CG	1:AH:28:GLY:N	2.76	0.42
1:AQ:127:THR:HG22	1:AQ:130:PHE:CE2	2.54	0.42
1:AW:27:ASN:CG	1:AW:28:GLY:N	2.76	0.42
1:AZ:27:ASN:CG	1:AZ:28:GLY:N	2.76	0.42
1:BA:68:ASN:ND2	1:BA:70:ARG:HH11	2.18	0.42
1:BH:18:LEU:HG	1:BO:121:VAL:HG11	2.02	0.42
1:BH:24:ARG:HB2	1:BH:34:VAL:HG23	2.01	0.42
1:BV:68:ASN:ND2	1:BV:70:ARG:HH11	2.18	0.42
1:BW:24:ARG:HB2	1:BW:34:VAL:HG23	2.01	0.42
1:CJ:117:THR:HB	1:CO:117:THR:O	2.20	0.42
1:CM:77:LYS:HG2	1:DH:79:ASN:ND2	2.35	0.42
1:CS:88:ILE:CD1	1:DD:110:ALA:HB1	2.49	0.42
1:DF:137:LEU:HD11	1:GR:63:ASP:HB3	2.00	0.42
1:DH:13:THR:O	1:DH:14:LEU:HB2	2.20	0.42
1:DL:68:ASN:ND2	1:DL:70:ARG:HH11	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:117:THR:O	1:GW:117:THR:HB	2.19	0.42
1:DP:117:THR:HB	1:GW:117:THR:O	2.19	0.42
1:DS:68:ASN:ND2	1:DS:70:ARG:HH11	2.18	0.42
1:DS:109:GLN:NE2	1:GQ:19:VAL:HG21	2.35	0.42
1:DY:24:ARG:HB2	1:DY:34:VAL:HG23	2.01	0.42
1:EE:68:ASN:ND2	1:EE:70:ARG:HH11	2.18	0.42
1:EI:13:THR:O	1:EI:14:LEU:HB2	2.20	0.42
1:EI:127:THR:HG22	1:EI:130:PHE:CE2	2.54	0.42
1:EL:24:ARG:NE	1:EL:34:VAL:HG21	2.34	0.42
1:EN:18:LEU:HD21	1:FJ:121:VAL:HB	2.02	0.42
1:EN:68:ASN:ND2	1:EN:70:ARG:HH11	2.18	0.42
1:EN:102:MET:HE1	1:FJ:73:VAL:HG22	2.02	0.42
1:EX:24:ARG:NE	1:EX:34:VAL:HG21	2.34	0.42
1:FP:73:VAL:HG11	1:GV:97:ALA:O	2.19	0.42
1:FV:27:ASN:CG	1:FV:28:GLY:N	2.76	0.42
1:GI:68:ASN:ND2	1:GI:70:ARG:HH11	2.18	0.42
1:GN:24:ARG:NE	1:GN:34:VAL:HG21	2.34	0.42
1:AA:68:ASN:ND2	1:AA:70:ARG:HH11	2.18	0.42
1:AG:68:ASN:ND2	1:AG:70:ARG:HH11	2.18	0.42
1:AL:68:ASN:ND2	1:AL:70:ARG:HH11	2.18	0.42
1:BH:52:PHE:CD1	1:BO:137:LEU:HD22	2.55	0.42
1:BM:54:ILE:HG12	1:EY:137:LEU:HD13	2.01	0.42
1:BM:127:THR:HG22	1:BM:130:PHE:CE2	2.54	0.42
1:BO:127:THR:HG22	1:BO:130:PHE:CE2	2.54	0.42
1:CB:68:ASN:ND2	1:CB:70:ARG:HH11	2.18	0.42
1:CF:88:ILE:HD11	1:GN:110:ALA:HB1	2.01	0.42
1:CH:134:TRP:O	1:FT:65:ILE:HD11	2.20	0.42
1:CQ:68:ASN:ND2	1:CQ:70:ARG:HH11	2.18	0.42
1:CS:13:THR:O	1:CS:14:LEU:HB2	2.20	0.42
1:DB:24:ARG:NE	1:DB:34:VAL:HG21	2.34	0.42
1:DP:68:ASN:ND2	1:DP:70:ARG:HH11	2.18	0.42
1:EQ:73:VAL:CG1	1:FM:97:ALA:HB1	2.50	0.42
1:FE:68:ASN:ND2	1:FE:70:ARG:HH11	2.18	0.42
1:FO:68:ASN:ND2	1:FO:70:ARG:HH11	2.18	0.42
1:FP:24:ARG:NE	1:FP:34:VAL:HG21	2.34	0.42
1:FP:63:ASP:HB3	1:GV:137:LEU:HD11	2.02	0.42
1:GV:68:ASN:ND2	1:GV:70:ARG:HH11	2.18	0.42
1:AD:24:ARG:HB2	1:AD:34:VAL:HG23	2.01	0.41
1:AD:68:ASN:ND2	1:AD:70:ARG:HH11	2.18	0.41
1:AK:24:ARG:NE	1:AK:34:VAL:HG21	2.34	0.41
1:AW:24:ARG:NE	1:AW:34:VAL:HG21	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:68:ASN:ND2	1:AY:70:ARG:HH11	2.18	0.41
1:BJ:68:ASN:ND2	1:BJ:70:ARG:HH11	2.18	0.41
1:BQ:68:ASN:ND2	1:BQ:70:ARG:HH11	2.18	0.41
1:BU:27:ASN:CG	1:BU:28:GLY:N	2.76	0.41
1:CI:68:ASN:ND2	1:CI:70:ARG:HH11	2.18	0.41
1:CU:63:ASP:CB	1:DH:137:LEU:HD11	2.50	0.41
1:CX:68:ASN:ND2	1:CX:70:ARG:HH11	2.18	0.41
1:DG:68:ASN:ND2	1:DG:70:ARG:HH11	2.18	0.41
1:DI:68:ASN:ND2	1:DI:70:ARG:HH11	2.18	0.41
1:DI:118:SER:HB2	1:GU:8:VAL:HB	2.01	0.41
1:DN:13:THR:O	1:DN:14:LEU:HB2	2.20	0.41
1:DT:13:THR:O	1:DT:14:LEU:HB2	2.20	0.41
1:DY:109:GLN:NE2	1:FY:19:VAL:HG21	2.35	0.41
1:ED:68:ASN:ND2	1:ED:70:ARG:HH11	2.18	0.41
1:EJ:68:ASN:ND2	1:EJ:70:ARG:HH11	2.18	0.41
1:EL:27:ASN:CG	1:EL:28:GLY:N	2.76	0.41
1:ER:27:ASN:CG	1:ER:28:GLY:N	2.76	0.41
1:FB:68:ASN:ND2	1:FB:70:ARG:HH11	2.18	0.41
1:FP:13:THR:O	1:FP:14:LEU:HB2	2.20	0.41
1:GU:68:ASN:ND2	1:GU:70:ARG:HH11	2.18	0.41
1:GW:24:ARG:NE	1:GW:34:VAL:HG21	2.34	0.41
1:AF:68:ASN:ND2	1:AF:70:ARG:HH11	2.18	0.41
1:AK:27:ASN:CG	1:AK:28:GLY:N	2.76	0.41
1:AR:68:ASN:ND2	1:AR:70:ARG:HH11	2.18	0.41
1:AV:68:ASN:ND2	1:AV:70:ARG:HH11	2.18	0.41
1:BF:13:THR:O	1:BF:14:LEU:HB2	2.20	0.41
1:BZ:86:VAL:HG22	1:DT:90:VAL:HG22	2.02	0.41
1:CC:24:ARG:HB2	1:CC:34:VAL:HG23	2.01	0.41
1:CI:52:PHE:CE2	1:GH:139:PHE:CE1	3.08	0.41
1:CI:75:ASP:HB2	1:GH:95:ASN:HD21	1.85	0.41
1:CJ:13:THR:O	1:CJ:14:LEU:HB2	2.20	0.41
1:CP:27:ASN:CG	1:CP:28:GLY:N	2.76	0.41
1:CX:110:ALA:HB1	1:DK:88:ILE:HD11	2.01	0.41
1:DL:73:VAL:HG11	1:GX:97:ALA:HB1	2.02	0.41
1:DS:125:THR:HG23	1:GQ:6:ALA:HB3	2.02	0.41
1:EC:127:THR:HG22	1:EC:130:PHE:CE2	2.54	0.41
1:EF:24:ARG:NE	1:EU:137:LEU:O	2.53	0.41
1:EN:137:LEU:HD22	1:FJ:52:PHE:CD1	2.55	0.41
1:FC:68:ASN:ND2	1:FC:70:ARG:HH11	2.18	0.41
1:FM:13:THR:O	1:FM:14:LEU:HB2	2.20	0.41
1:FQ:68:ASN:ND2	1:FQ:70:ARG:HH11	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GD:24:ARG:HB2	1:GD:34:VAL:HG23	2.01	0.41
1:GF:68:ASN:ND2	1:GF:70:ARG:HH11	2.18	0.41
1:GG:68:ASN:ND2	1:GG:70:ARG:HH11	2.18	0.41
1:GH:13:THR:O	1:GH:14:LEU:HB2	2.20	0.41
1:AA:24:ARG:HB2	1:AA:34:VAL:HG23	2.01	0.41
1:AJ:68:ASN:ND2	1:AJ:70:ARG:HH11	2.18	0.41
1:AK:13:THR:O	1:AK:14:LEU:HB2	2.20	0.41
1:AQ:138:MET:HE3	1:FV:24:ARG:HA	2.01	0.41
1:AS:75:ASP:HA	1:EL:95:ASN:HD21	1.85	0.41
1:AU:87:THR:HG23	1:EG:89:GLN:HB3	2.01	0.41
1:AZ:88:ILE:HD11	1:EW:110:ALA:HB1	2.01	0.41
1:BG:68:ASN:ND2	1:BG:70:ARG:HH11	2.18	0.41
1:BK:24:ARG:HB2	1:BK:34:VAL:HG23	2.01	0.41
1:BW:68:ASN:ND2	1:BW:70:ARG:HH11	2.18	0.41
1:CB:63:ASP:CG	1:FN:137:LEU:HD11	2.44	0.41
1:CD:84:GLY:HA3	1:CR:98:TRP:CH2	2.55	0.41
1:CM:54:ILE:HG12	1:DG:137:LEU:HD13	2.01	0.41
1:CO:68:ASN:ND2	1:CO:70:ARG:HH11	2.18	0.41
1:CR:68:ASN:ND2	1:CR:70:ARG:HH11	2.18	0.41
1:DA:137:LEU:HD22	1:DE:52:PHE:CD1	2.55	0.41
1:DS:87:THR:OG1	1:GQ:89:GLN:HB3	2.21	0.41
1:DS:88:ILE:HD11	1:GQ:110:ALA:HB1	2.03	0.41
1:DS:110:ALA:HB1	1:GQ:88:ILE:HD11	2.01	0.41
1:EE:18:LEU:HD21	1:EU:121:VAL:HB	2.03	0.41
1:EL:13:THR:O	1:EL:14:LEU:HB2	2.20	0.41
1:EQ:68:ASN:ND2	1:EQ:70:ARG:HH11	2.18	0.41
1:AE:108:LYS:HB2	1:GA:9:GLY:HA2	2.02	0.41
1:AP:68:ASN:ND2	1:AP:70:ARG:HH11	2.18	0.41
1:AV:42:LEU:HD22	1:EJ:137:LEU:HD12	2.02	0.41
1:BB:87:THR:OG1	1:BR:89:GLN:HB3	2.21	0.41
1:BM:68:ASN:ND2	1:BM:70:ARG:HH11	2.18	0.41
1:BO:105:SER:O	1:BO:109:GLN:HG3	2.21	0.41
1:BP:90:VAL:HG22	1:FB:86:VAL:HG22	2.01	0.41
1:BS:68:ASN:ND2	1:BS:70:ARG:HH11	2.18	0.41
1:BY:90:VAL:HG22	1:FK:86:VAL:HG22	2.03	0.41
1:CC:68:ASN:ND2	1:CC:70:ARG:HH11	2.18	0.41
1:CI:24:ARG:HB2	1:CI:34:VAL:HG23	2.01	0.41
1:CN:68:ASN:ND2	1:CN:70:ARG:HH11	2.18	0.41
1:CV:13:THR:O	1:CV:14:LEU:HB2	2.20	0.41
1:CY:13:THR:O	1:CY:14:LEU:HB2	2.20	0.41
1:DC:137:LEU:HD12	1:GM:42:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DM:24:ARG:HB2	1:DM:34:VAL:HG23	2.01	0.41
1:EB:68:ASN:ND2	1:EB:70:ARG:HH11	2.18	0.41
1:EQ:18:LEU:HD11	1:FM:123:GLY:H	1.83	0.41
1:EU:105:SER:O	1:EU:109:GLN:HG3	2.21	0.41
1:EX:8:VAL:HB	1:FI:118:SER:HB2	2.02	0.41
1:FI:68:ASN:ND2	1:FI:70:ARG:HH11	2.18	0.41
1:FM:27:ASN:CG	1:FM:28:GLY:N	2.76	0.41
1:FU:24:ARG:HB2	1:FU:34:VAL:HG23	2.01	0.41
1:GC:68:ASN:ND2	1:GC:70:ARG:HH11	2.18	0.41
1:GN:105:SER:O	1:GN:109:GLN:HG3	2.21	0.41
1:GT:105:SER:O	1:GT:109:GLN:HG3	2.21	0.41
1:AC:117:THR:HB	1:DO:117:THR:O	2.21	0.41
1:AJ:24:ARG:HB2	1:AJ:34:VAL:HG23	2.01	0.41
1:AQ:13:THR:O	1:AQ:14:LEU:HB2	2.20	0.41
1:AU:68:ASN:ND2	1:AU:70:ARG:HH11	2.18	0.41
1:BE:109:GLN:NE2	1:BL:19:VAL:HG21	2.36	0.41
1:BL:105:SER:O	1:BL:109:GLN:HG3	2.21	0.41
1:CG:105:SER:O	1:CG:109:GLN:HG3	2.21	0.41
1:CG:110:ALA:HB1	1:CL:88:ILE:HD11	2.02	0.41
1:CG:137:LEU:HD11	1:CL:63:ASP:CB	2.51	0.41
1:CP:13:THR:O	1:CP:14:LEU:HB2	2.20	0.41
1:DA:68:ASN:ND2	1:DA:70:ARG:HH11	2.18	0.41
1:DB:127:THR:HG22	1:DB:130:PHE:CE2	2.54	0.41
1:DF:10:ALA:H	1:GR:105:SER:CB	2.33	0.41
1:DL:137:LEU:HD12	1:GV:42:LEU:CD2	2.48	0.41
1:EX:105:SER:O	1:EX:109:GLN:HG3	2.21	0.41
1:FD:13:THR:O	1:FD:14:LEU:HB2	2.20	0.41
1:FJ:105:SER:O	1:FJ:109:GLN:HG3	2.21	0.41
1:FL:24:ARG:HB2	1:FL:34:VAL:HG23	2.01	0.41
1:FN:68:ASN:ND2	1:FN:70:ARG:HH11	2.18	0.41
1:FP:105:SER:O	1:FP:109:GLN:HG3	2.21	0.41
1:FY:13:THR:O	1:FY:14:LEU:HB2	2.20	0.41
1:AE:105:SER:O	1:AE:109:GLN:HG3	2.21	0.41
1:AM:24:ARG:HB2	1:AM:34:VAL:HG23	2.01	0.41
1:AN:27:ASN:CG	1:AN:28:GLY:N	2.76	0.41
1:AP:125:THR:HG21	1:BU:5:LEU:HA	2.02	0.41
1:AR:102:MET:HE1	1:ED:73:VAL:HG22	2.01	0.41
1:AT:27:ASN:CG	1:AT:28:GLY:N	2.76	0.41
1:AT:105:SER:O	1:AT:109:GLN:HG3	2.21	0.41
1:AZ:105:SER:O	1:AZ:109:GLN:HG3	2.21	0.41
1:BO:13:THR:O	1:BO:14:LEU:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:13:THR:O	1:BR:14:LEU:HB2	2.20	0.41
1:BR:105:SER:O	1:BR:109:GLN:HG3	2.21	0.41
1:BZ:8:VAL:HB	1:DT:118:SER:HB2	2.02	0.41
1:CM:8:VAL:HB	1:DG:118:SER:HB2	2.02	0.41
1:CT:75:ASP:CA	1:GF:95:ASN:HD21	2.15	0.41
1:CU:68:ASN:ND2	1:CU:70:ARG:HH11	2.18	0.41
1:DA:29:ASN:C	1:DE:139:PHE:CZ	2.99	0.41
1:DB:13:THR:O	1:DB:14:LEU:HB2	2.20	0.41
1:DF:8:VAL:CB	1:GR:118:SER:HB2	2.50	0.41
1:DI:95:ASN:ND2	1:GU:75:ASP:HA	2.31	0.41
1:DV:68:ASN:ND2	1:DV:70:ARG:HH11	2.18	0.41
1:EL:105:SER:O	1:EL:109:GLN:HG3	2.21	0.41
1:EN:108:LYS:HB2	1:FJ:9:GLY:HA2	2.02	0.41
1:EP:68:ASN:ND2	1:EP:70:ARG:HH11	2.18	0.41
1:EQ:52:PHE:CD2	1:FM:139:PHE:CZ	3.07	0.41
1:ER:24:ARG:NE	1:ER:34:VAL:HG21	2.34	0.41
1:EX:13:THR:O	1:EX:14:LEU:HB2	2.20	0.41
1:FA:118:SER:HB2	1:FL:8:VAL:HB	2.03	0.41
1:FB:65:ILE:HB	1:FB:90:VAL:HB	2.03	0.41
1:FL:68:ASN:ND2	1:FL:70:ARG:HH11	2.18	0.41
1:FT:65:ILE:HB	1:FT:90:VAL:HB	2.03	0.41
1:FV:88:ILE:HD11	1:GS:110:ALA:HB1	2.01	0.41
1:GA:24:ARG:HB2	1:GA:34:VAL:HG23	2.02	0.41
1:GE:105:SER:O	1:GE:109:GLN:HG3	2.21	0.41
1:AM:68:ASN:ND2	1:AM:70:ARG:HH11	2.18	0.41
1:AN:13:THR:O	1:AN:14:LEU:HB2	2.20	0.41
1:AZ:13:THR:O	1:AZ:14:LEU:HB2	2.20	0.41
1:BD:68:ASN:ND2	1:BD:70:ARG:HH11	2.18	0.41
1:BI:105:SER:O	1:BI:109:GLN:HG3	2.21	0.41
1:BJ:98:TRP:HE3	1:EV:73:VAL:HG21	1.85	0.41
1:BP:68:ASN:ND2	1:BP:70:ARG:HH11	2.18	0.41
1:BT:102:MET:HE1	1:DN:73:VAL:HG22	2.02	0.41
1:CC:97:ALA:O	1:GK:73:VAL:HG11	2.21	0.41
1:CD:105:SER:O	1:CD:109:GLN:HG3	2.21	0.41
1:CD:110:ALA:HB1	1:CR:88:ILE:HD11	2.02	0.41
1:CM:105:SER:O	1:CM:109:GLN:HG3	2.21	0.41
1:CP:121:VAL:CG1	1:DJ:18:LEU:HG	2.50	0.41
1:CS:69:LEU:HB3	1:DD:106:LEU:HD22	2.03	0.41
1:CY:137:LEU:HD13	1:GG:54:ILE:HG12	2.03	0.41
1:DD:68:ASN:ND2	1:DD:70:ARG:HH11	2.18	0.41
1:DL:65:ILE:HB	1:DL:90:VAL:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DS:24:ARG:HB2	1:DS:34:VAL:HG23	2.01	0.41
1:DV:24:ARG:HB2	1:DV:34:VAL:HG23	2.01	0.41
1:EC:13:THR:O	1:EC:14:LEU:HB2	2.20	0.41
1:EE:52:PHE:CD1	1:EU:137:LEU:HD22	2.56	0.41
1:FA:13:THR:O	1:FA:14:LEU:HB2	2.20	0.41
1:FD:73:VAL:HG11	1:FF:97:ALA:O	2.20	0.41
1:FD:114:LEU:HD22	1:FF:88:ILE:CD1	2.50	0.41
1:FG:105:SER:O	1:FG:109:GLN:HG3	2.21	0.41
1:FK:68:ASN:ND2	1:FK:70:ARG:HH11	2.18	0.41
1:FS:105:SER:O	1:FS:109:GLN:HG3	2.21	0.41
1:FW:65:ILE:HB	1:FW:90:VAL:HB	2.03	0.41
1:GB:13:THR:O	1:GB:14:LEU:HB2	2.20	0.41
1:GS:68:ASN:ND2	1:GS:70:ARG:HH11	2.18	0.41
1:AB:105:SER:O	1:AB:109:GLN:HG3	2.21	0.41
1:AE:77:LYS:HG2	1:GB:79:ASN:ND2	2.36	0.41
1:AO:65:ILE:HB	1:AO:90:VAL:HB	2.03	0.41
1:AP:97:ALA:HB1	1:BU:73:VAL:CG1	2.51	0.41
1:AT:13:THR:O	1:AT:14:LEU:HB2	2.20	0.41
1:AV:90:VAL:HG22	1:EF:86:VAL:HG22	2.03	0.41
1:BA:65:ILE:HB	1:BA:90:VAL:HB	2.03	0.41
1:BL:79:ASN:ND2	1:DW:77:LYS:HG2	2.35	0.41
1:BN:68:ASN:ND2	1:BN:70:ARG:HH11	2.18	0.41
1:BZ:10:ALA:O	1:DT:105:SER:HB2	2.20	0.41
1:BZ:68:ASN:ND2	1:BZ:70:ARG:HH11	2.18	0.41
1:CD:13:THR:O	1:CD:14:LEU:HB2	2.20	0.41
1:CG:13:THR:O	1:CG:14:LEU:HB2	2.20	0.41
1:CH:139:PHE:HA	1:CH:140:PRO:HD3	1.96	0.41
1:CV:105:SER:O	1:CV:109:GLN:HG3	2.21	0.41
1:CX:73:VAL:HG11	1:DK:97:ALA:O	2.21	0.41
1:CZ:65:ILE:HB	1:CZ:90:VAL:HB	2.03	0.41
1:DB:63:ASP:CB	1:GJ:137:LEU:HD11	2.51	0.41
1:DG:24:ARG:HB2	1:DG:34:VAL:HG23	2.01	0.41
1:DH:105:SER:O	1:DH:109:GLN:HG3	2.21	0.41
1:DN:105:SER:O	1:DN:109:GLN:HG3	2.21	0.41
1:DQ:13:THR:O	1:DQ:14:LEU:HB2	2.20	0.41
1:DR:65:ILE:HB	1:DR:90:VAL:HB	2.03	0.41
1:DT:13:THR:O	1:DT:13:THR:HG22	2.21	0.41
1:EB:75:ASP:HB2	1:GB:95:ASN:HD21	1.86	0.41
1:EE:124:GLN:HA	1:EU:6:ALA:CB	2.47	0.41
1:EH:101:SER:HB2	1:EO:11:ASN:O	2.21	0.41
1:EN:52:PHE:HD1	1:FJ:137:LEU:HD22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ES:65:ILE:HB	1:ES:90:VAL:HB	2.03	0.41
1:ET:24:ARG:HB2	1:ET:34:VAL:HG23	2.01	0.41
1:EX:75:ASP:OD1	1:FJ:79:ASN:ND2	2.45	0.41
1:FY:105:SER:O	1:FY:109:GLN:HG3	2.21	0.41
1:GQ:105:SER:O	1:GQ:109:GLN:HG3	2.21	0.41
1:AM:117:THR:HB	1:CA:117:THR:O	2.21	0.41
1:AS:63:ASP:HB3	1:EL:137:LEU:HD11	2.03	0.41
1:AS:101:SER:HB2	1:EL:11:ASN:O	2.21	0.41
1:AU:99:ASN:HB2	1:AU:102:MET:HG3	2.03	0.41
1:AW:105:SER:O	1:AW:109:GLN:HG3	2.21	0.41
1:AX:95:ASN:HD21	1:EJ:75:ASP:CA	2.26	0.41
1:BC:105:SER:O	1:BC:109:GLN:HG3	2.21	0.41
1:BG:65:ILE:HB	1:BG:90:VAL:HB	2.03	0.41
1:BH:19:VAL:HG21	1:BO:109:GLN:NE2	2.36	0.41
1:BH:68:ASN:ND2	1:BH:70:ARG:HH11	2.18	0.41
1:BI:13:THR:HG22	1:BI:13:THR:O	2.21	0.41
1:BJ:97:ALA:CB	1:EV:73:VAL:CG1	2.99	0.41
1:BJ:98:TRP:CZ3	1:EV:71:LYS:HB3	2.56	0.41
1:BU:105:SER:O	1:BU:109:GLN:HG3	2.21	0.41
1:BV:65:ILE:HB	1:BV:90:VAL:HB	2.03	0.41
1:BW:117:THR:O	1:DQ:117:THR:HB	2.21	0.41
1:BY:139:PHE:HA	1:BY:140:PRO:HD3	1.96	0.41
1:CF:52:PHE:HE2	1:GN:139:PHE:CE1	2.39	0.41
1:CF:97:ALA:O	1:GN:73:VAL:HG11	2.20	0.41
1:CH:68:ASN:ND2	1:CH:70:ARG:HH11	2.18	0.41
1:CH:86:VAL:HG22	1:FT:90:VAL:HG22	2.03	0.41
1:CM:13:THR:HG22	1:CM:13:THR:O	2.21	0.41
1:CS:105:SER:O	1:CS:109:GLN:HG3	2.21	0.41
1:CS:139:PHE:CE2	1:DD:29:ASN:HA	2.55	0.41
1:CT:84:GLY:HA2	1:GF:91:SER:O	2.20	0.41
1:CW:99:ASN:HB2	1:CW:102:MET:HG3	2.03	0.41
1:CW:102:MET:HE1	1:GI:73:VAL:CG2	2.51	0.41
1:CX:88:ILE:HD11	1:DK:110:ALA:HB1	2.02	0.41
1:CY:13:THR:O	1:CY:13:THR:HG22	2.21	0.41
1:CY:97:ALA:O	1:GG:73:VAL:HG11	2.20	0.41
1:DE:13:THR:O	1:DE:14:LEU:HB2	2.20	0.41
1:DI:11:ASN:O	1:GU:101:SER:HB2	2.20	0.41
1:DK:13:THR:HG22	1:DK:13:THR:O	2.21	0.41
1:DK:13:THR:O	1:DK:14:LEU:HB2	2.20	0.41
1:DM:88:ILE:HD11	1:GT:110:ALA:HB1	2.03	0.41
1:DN:13:THR:O	1:DN:13:THR:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:88:ILE:CD1	1:GW:114:LEU:HD22	2.51	0.41
1:DS:73:VAL:HG12	1:GQ:97:ALA:HB1	2.03	0.41
1:DU:65:ILE:HB	1:DU:90:VAL:HB	2.03	0.41
1:DU:112:ASP:HB2	1:DU:118:SER:HB3	2.03	0.41
1:DY:88:ILE:HD11	1:FY:110:ALA:HB1	2.02	0.41
1:EA:65:ILE:HB	1:EA:90:VAL:HB	2.03	0.41
1:EB:90:VAL:HG22	1:GB:86:VAL:HG22	2.02	0.41
1:EI:13:THR:O	1:EI:13:THR:HG22	2.21	0.41
1:EI:27:ASN:CG	1:EI:28:GLY:N	2.76	0.41
1:EK:68:ASN:ND2	1:EK:70:ARG:HH11	2.18	0.41
1:EL:13:THR:O	1:EL:13:THR:HG22	2.21	0.41
1:EO:13:THR:O	1:EO:14:LEU:HB2	2.21	0.41
1:EO:105:SER:O	1:EO:109:GLN:HG3	2.21	0.41
1:ER:13:THR:HG22	1:ER:13:THR:O	2.21	0.41
1:EU:13:THR:HG22	1:EU:13:THR:O	2.21	0.41
1:FA:95:ASN:HD21	1:FL:75:ASP:CA	2.32	0.41
1:FD:105:SER:O	1:FD:109:GLN:HG3	2.21	0.41
1:FG:13:THR:O	1:FG:14:LEU:HB2	2.20	0.41
1:FI:24:ARG:HB2	1:FI:34:VAL:HG23	2.01	0.41
1:FM:13:THR:O	1:FM:13:THR:HG22	2.21	0.41
1:FP:13:THR:O	1:FP:13:THR:HG22	2.21	0.41
1:FQ:65:ILE:HB	1:FQ:90:VAL:HB	2.03	0.41
1:FS:13:THR:O	1:FS:14:LEU:HB2	2.20	0.41
1:FY:27:ASN:CG	1:FY:28:GLY:N	2.76	0.41
1:FZ:68:ASN:ND2	1:FZ:70:ARG:HH11	2.18	0.41
1:GF:65:ILE:HB	1:GF:90:VAL:HB	2.03	0.41
1:GH:105:SER:O	1:GH:109:GLN:HG3	2.21	0.41
1:GS:24:ARG:HB2	1:GS:34:VAL:HG23	2.01	0.41
1:GW:105:SER:O	1:GW:109:GLN:HG3	2.21	0.41
1:AB:27:ASN:CG	1:AB:28:GLY:N	2.76	0.41
1:AI:109:GLN:NE2	1:DU:19:VAL:HG21	2.36	0.41
1:AK:105:SER:O	1:AK:109:GLN:HG3	2.21	0.41
1:AT:95:ASN:HD21	1:EZ:75:ASP:HB2	1.86	0.41
1:AW:13:THR:O	1:AW:14:LEU:HB2	2.20	0.41
1:BD:73:VAL:CG1	1:EP:97:ALA:HB1	2.51	0.41
1:BF:105:SER:O	1:BF:109:GLN:HG3	2.21	0.41
1:BJ:107:LEU:HD23	1:EV:86:VAL:HG21	2.03	0.41
1:BJ:109:GLN:NE2	1:EV:19:VAL:HG21	2.35	0.41
1:BQ:77:LYS:NZ	1:ED:79:ASN:HD22	2.18	0.41
1:BR:13:THR:O	1:BR:13:THR:HG22	2.21	0.41
1:BX:105:SER:O	1:BX:109:GLN:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:65:ILE:HB	1:CB:90:VAL:HB	2.03	0.41
1:CG:64:ARG:HD2	1:CG:89:GLN:NE2	2.36	0.41
1:CM:13:THR:O	1:CM:14:LEU:HB2	2.20	0.41
1:DE:13:THR:O	1:DE:13:THR:HG22	2.21	0.41
1:DH:13:THR:O	1:DH:13:THR:HG22	2.21	0.41
1:DM:68:ASN:ND2	1:DM:70:ARG:HH11	2.18	0.41
1:DQ:27:ASN:CG	1:DQ:28:GLY:N	2.76	0.41
1:DT:105:SER:O	1:DT:109:GLN:HG3	2.21	0.41
1:DZ:13:THR:O	1:DZ:14:LEU:HB2	2.20	0.41
1:ED:65:ILE:HB	1:ED:90:VAL:HB	2.03	0.41
1:ED:112:ASP:HB2	1:ED:118:SER:HB3	2.03	0.41
1:EF:13:THR:O	1:EF:14:LEU:HB2	2.20	0.41
1:EH:130:PHE:N	1:EH:131:PRO:HD2	2.36	0.41
1:EM:112:ASP:HB2	1:EM:118:SER:HB3	2.03	0.41
1:EN:137:LEU:CD1	1:FJ:54:ILE:HG12	2.33	0.41
1:FC:130:PHE:N	1:FC:131:PRO:HD2	2.36	0.41
1:FD:88:ILE:HD11	1:FF:110:ALA:HB1	2.03	0.41
1:FE:139:PHE:HA	1:FE:140:PRO:HD3	1.96	0.41
1:FO:130:PHE:N	1:FO:131:PRO:HD2	2.36	0.41
1:GB:13:THR:O	1:GB:13:THR:HG22	2.21	0.41
1:GL:68:ASN:ND2	1:GL:70:ARG:HH11	2.18	0.41
1:GP:130:PHE:N	1:GP:131:PRO:HD2	2.36	0.41
1:AE:18:LEU:HD23	1:AE:18:LEU:HA	1.96	0.40
1:AF:112:ASP:HB2	1:AF:118:SER:HB3	2.04	0.40
1:AI:65:ILE:HB	1:AI:90:VAL:HB	2.03	0.40
1:AL:107:LEU:HD13	1:DX:114:LEU:O	2.22	0.40
1:AQ:86:VAL:HG22	1:FU:90:VAL:HG22	2.04	0.40
1:AQ:110:ALA:HB1	1:FU:88:ILE:HD11	2.03	0.40
1:AW:11:ASN:O	1:FC:101:SER:HB2	2.21	0.40
1:BL:13:THR:O	1:BL:14:LEU:HB2	2.20	0.40
1:BN:137:LEU:HD22	1:DZ:52:PHE:CD1	2.56	0.40
1:BO:13:THR:O	1:BO:13:THR:HG22	2.21	0.40
1:BU:13:THR:O	1:BU:14:LEU:HB2	2.20	0.40
1:CA:13:THR:O	1:CA:13:THR:HG22	2.21	0.40
1:CE:65:ILE:HB	1:CE:90:VAL:HB	2.03	0.40
1:CI:8:VAL:HB	1:GH:118:SER:CB	2.43	0.40
1:CO:130:PHE:N	1:CO:131:PRO:HD2	2.36	0.40
1:CQ:137:LEU:C	1:GC:52:PHE:CE2	3.00	0.40
1:CW:137:LEU:HD11	1:GI:63:ASP:CG	2.45	0.40
1:DA:52:PHE:CE1	1:DE:137:LEU:CA	3.00	0.40
1:DL:112:ASP:HB2	1:DL:118:SER:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DW:105:SER:O	1:DW:109:GLN:HG3	2.21	0.40
1:ES:112:ASP:HB2	1:ES:118:SER:HB3	2.04	0.40
1:EV:65:ILE:HB	1:EV:90:VAL:HB	2.03	0.40
1:EY:112:ASP:HB2	1:EY:118:SER:HB3	2.04	0.40
1:EZ:24:ARG:HB2	1:EZ:34:VAL:HG23	2.01	0.40
1:FA:13:THR:O	1:FA:13:THR:HG22	2.21	0.40
1:FG:13:THR:O	1:FG:13:THR:HG22	2.21	0.40
1:FQ:112:ASP:HB2	1:FQ:118:SER:HB3	2.03	0.40
1:FR:130:PHE:N	1:FR:131:PRO:HD2	2.37	0.40
1:FV:13:THR:O	1:FV:14:LEU:HB2	2.20	0.40
1:GC:99:ASN:HB2	1:GC:102:MET:HG3	2.03	0.40
1:GE:13:THR:HG22	1:GE:13:THR:O	2.21	0.40
1:GH:64:ARG:HD2	1:GH:89:GLN:NE2	2.37	0.40
1:GO:112:ASP:HB2	1:GO:118:SER:HB3	2.03	0.40
1:GW:18:LEU:HD23	1:GW:18:LEU:HA	1.96	0.40
1:AE:13:THR:O	1:AE:14:LEU:HB2	2.20	0.40
1:AF:65:ILE:HB	1:AF:90:VAL:HB	2.03	0.40
1:AG:88:ILE:HD11	1:BF:110:ALA:HB1	2.02	0.40
1:AH:13:THR:O	1:AH:14:LEU:HB2	2.21	0.40
1:AS:88:ILE:HD11	1:EL:110:ALA:HB1	2.03	0.40
1:AS:130:PHE:N	1:AS:131:PRO:HD2	2.37	0.40
1:AV:130:PHE:N	1:AV:131:PRO:HD2	2.36	0.40
1:AY:130:PHE:N	1:AY:131:PRO:HD2	2.37	0.40
1:BA:99:ASN:HB2	1:BA:102:MET:HG3	2.03	0.40
1:BM:109:GLN:NE2	1:EY:19:VAL:HG21	2.35	0.40
1:BN:109:GLN:NE2	1:DZ:19:VAL:HG21	2.35	0.40
1:BQ:130:PHE:N	1:BQ:131:PRO:HD2	2.37	0.40
1:BR:64:ARG:HD2	1:BR:89:GLN:NE2	2.36	0.40
1:BS:8:VAL:HB	1:FE:118:SER:HB2	2.03	0.40
1:BZ:75:ASP:CA	1:DT:95:ASN:HD21	2.34	0.40
1:CA:13:THR:O	1:CA:14:LEU:HB2	2.20	0.40
1:CA:27:ASN:CG	1:CA:28:GLY:N	2.76	0.40
1:CC:101:SER:HB2	1:GK:11:ASN:O	2.21	0.40
1:CF:130:PHE:N	1:CF:131:PRO:HD2	2.36	0.40
1:CH:65:ILE:HB	1:CH:90:VAL:HB	2.03	0.40
1:CH:99:ASN:HB2	1:CH:102:MET:HG3	2.04	0.40
1:CN:97:ALA:HB1	1:FZ:73:VAL:CG1	2.51	0.40
1:CP:13:THR:O	1:CP:13:THR:HG22	2.21	0.40
1:CR:24:ARG:HB2	1:CR:34:VAL:HG23	2.01	0.40
1:DB:13:THR:O	1:DB:13:THR:HG22	2.21	0.40
1:DF:97:ALA:HB1	1:GR:73:VAL:CG1	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DF:99:ASN:HB2	1:DF:102:MET:HG3	2.04	0.40
1:DH:27:ASN:CG	1:DH:28:GLY:N	2.76	0.40
1:DJ:68:ASN:ND2	1:DJ:70:ARG:HH11	2.18	0.40
1:DJ:130:PHE:N	1:DJ:131:PRO:HD2	2.37	0.40
1:DK:105:SER:O	1:DK:109:GLN:HG3	2.21	0.40
1:DP:63:ASP:HB3	1:GW:137:LEU:HD11	2.03	0.40
1:EB:130:PHE:N	1:EB:131:PRO:HD2	2.36	0.40
1:EC:105:SER:O	1:EC:109:GLN:HG3	2.21	0.40
1:EI:105:SER:O	1:EI:109:GLN:HG3	2.21	0.40
1:EK:130:PHE:N	1:EK:131:PRO:HD2	2.37	0.40
1:EL:64:ARG:HD2	1:EL:89:GLN:NE2	2.37	0.40
1:EO:13:THR:O	1:EO:13:THR:HG22	2.21	0.40
1:ET:98:TRP:CH2	1:FG:84:GLY:HA3	2.56	0.40
1:EU:13:THR:O	1:EU:14:LEU:HB2	2.20	0.40
1:FE:99:ASN:HB2	1:FE:102:MET:HG3	2.03	0.40
1:FF:130:PHE:N	1:FF:131:PRO:HD2	2.37	0.40
1:FH:99:ASN:HB2	1:FH:102:MET:HG3	2.04	0.40
1:FJ:13:THR:O	1:FJ:14:LEU:HB2	2.20	0.40
1:FM:64:ARG:HD2	1:FM:89:GLN:NE2	2.37	0.40
1:FM:105:SER:O	1:FM:109:GLN:HG3	2.21	0.40
1:FT:99:ASN:HB2	1:FT:102:MET:HG3	2.04	0.40
1:FT:112:ASP:HB2	1:FT:118:SER:HB3	2.04	0.40
1:FV:64:ARG:HD2	1:FV:89:GLN:NE2	2.37	0.40
1:GE:64:ARG:HD2	1:GE:89:GLN:NE2	2.37	0.40
1:GG:130:PHE:N	1:GG:131:PRO:HD2	2.37	0.40
1:GK:105:SER:O	1:GK:109:GLN:HG3	2.21	0.40
1:GL:99:ASN:HB2	1:GL:102:MET:HG3	2.03	0.40
1:GT:64:ARG:HD2	1:GT:89:GLN:NE2	2.37	0.40
1:GU:99:ASN:HB2	1:GU:102:MET:HG3	2.03	0.40
1:AB:13:THR:O	1:AB:13:THR:HG22	2.21	0.40
1:AB:13:THR:O	1:AB:14:LEU:HB2	2.20	0.40
1:AH:105:SER:O	1:AH:109:GLN:HG3	2.21	0.40
1:AI:68:ASN:ND2	1:AI:70:ARG:HH11	2.18	0.40
1:AK:13:THR:O	1:AK:13:THR:HG22	2.21	0.40
1:AL:65:ILE:HB	1:AL:90:VAL:HB	2.03	0.40
1:AN:105:SER:O	1:AN:109:GLN:HG3	2.21	0.40
1:AQ:10:ALA:H	1:FU:105:SER:CB	2.34	0.40
1:AT:13:THR:O	1:AT:13:THR:HG22	2.21	0.40
1:AT:64:ARG:HD2	1:AT:89:GLN:NE2	2.37	0.40
1:AT:88:ILE:HD11	1:EZ:110:ALA:HB1	2.02	0.40
1:AX:65:ILE:HB	1:AX:90:VAL:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:112:ASP:HB2	1:AX:118:SER:HB3	2.04	0.40
1:BA:112:ASP:HB2	1:BA:118:SER:HB3	2.03	0.40
1:BE:130:PHE:N	1:BE:131:PRO:HD2	2.37	0.40
1:BI:13:THR:O	1:BI:14:LEU:HB2	2.20	0.40
1:BJ:99:ASN:HB2	1:BJ:102:MET:HG3	2.03	0.40
1:BK:130:PHE:N	1:BK:131:PRO:HD2	2.36	0.40
1:BM:99:ASN:HB2	1:BM:102:MET:HG3	2.03	0.40
1:BS:65:ILE:HB	1:BS:90:VAL:HB	2.03	0.40
1:BX:64:ARG:HD2	1:BX:89:GLN:NE2	2.37	0.40
1:BY:65:ILE:HB	1:BY:90:VAL:HB	2.03	0.40
1:BY:112:ASP:HB2	1:BY:118:SER:HB3	2.04	0.40
1:CD:117:THR:HB	1:CR:117:THR:O	2.22	0.40
1:CF:73:VAL:HG11	1:GN:97:ALA:O	2.21	0.40
1:CJ:105:SER:O	1:CJ:109:GLN:HG3	2.21	0.40
1:CK:99:ASN:HB2	1:CK:102:MET:HG3	2.03	0.40
1:CK:112:ASP:HB2	1:CK:118:SER:HB3	2.04	0.40
1:CL:130:PHE:N	1:CL:131:PRO:HD2	2.37	0.40
1:CM:64:ARG:HD2	1:CM:89:GLN:NE2	2.37	0.40
1:CS:13:THR:O	1:CS:13:THR:HG22	2.21	0.40
1:CU:130:PHE:N	1:CU:131:PRO:HD2	2.36	0.40
1:CY:64:ARG:HD2	1:CY:89:GLN:NE2	2.37	0.40
1:CZ:99:ASN:HB2	1:CZ:102:MET:HG3	2.03	0.40
1:DC:112:ASP:HB2	1:DC:118:SER:HB3	2.03	0.40
1:DC:118:SER:CB	1:GO:8:VAL:HB	2.49	0.40
1:DE:105:SER:O	1:DE:109:GLN:HG3	2.21	0.40
1:DQ:105:SER:O	1:DQ:109:GLN:HG3	2.21	0.40
1:DU:99:ASN:HB2	1:DU:102:MET:HG3	2.04	0.40
1:DV:19:VAL:HG21	1:GE:109:GLN:NE2	2.36	0.40
1:EM:65:ILE:HB	1:EM:90:VAL:HB	2.03	0.40
1:EM:99:ASN:HB2	1:EM:102:MET:HG3	2.03	0.40
1:EO:64:ARG:HD2	1:EO:89:GLN:NE2	2.37	0.40
1:EQ:54:ILE:HG12	1:FM:137:LEU:HD13	2.02	0.40
1:ER:105:SER:O	1:ER:109:GLN:HG3	2.21	0.40
1:EU:64:ARG:HD2	1:EU:89:GLN:NE2	2.37	0.40
1:EV:68:ASN:ND2	1:EV:70:ARG:HH11	2.18	0.40
1:EY:65:ILE:HB	1:EY:90:VAL:HB	2.03	0.40
1:FD:64:ARG:HD2	1:FD:89:GLN:NE2	2.37	0.40
1:FH:112:ASP:HB2	1:FH:118:SER:HB3	2.03	0.40
1:FL:130:PHE:N	1:FL:131:PRO:HD2	2.36	0.40
1:FN:99:ASN:HB2	1:FN:102:MET:HG3	2.04	0.40
1:FQ:99:ASN:HB2	1:FQ:102:MET:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FV:105:SER:O	1:FV:109:GLN:HG3	2.21	0.40
1:GA:130:PHE:N	1:GA:131:PRO:HD2	2.37	0.40
1:GB:105:SER:O	1:GB:109:GLN:HG3	2.21	0.40
1:GD:68:ASN:ND2	1:GD:70:ARG:HH11	2.18	0.40
1:GK:64:ARG:HD2	1:GK:89:GLN:NE2	2.37	0.40
1:GN:64:ARG:HD2	1:GN:89:GLN:NE2	2.37	0.40
1:AD:52:PHE:HD2	1:BC:139:PHE:CZ	2.39	0.40
1:AH:13:THR:O	1:AH:13:THR:HG22	2.21	0.40
1:AH:42:LEU:HD22	1:BF:137:LEU:HD12	2.02	0.40
1:AI:8:VAL:HB	1:DU:118:SER:HB2	2.02	0.40
1:AI:99:ASN:HB2	1:AI:102:MET:HG3	2.04	0.40
1:AO:112:ASP:HB2	1:AO:118:SER:HB3	2.04	0.40
1:AR:110:ALA:HB1	1:ED:88:ILE:HD11	2.03	0.40
1:AT:73:VAL:HG11	1:EZ:97:ALA:O	2.22	0.40
1:AU:65:ILE:HB	1:AU:90:VAL:HB	2.03	0.40
1:AW:24:ARG:HG3	1:EF:138:MET:HG2	2.02	0.40
1:BB:54:ILE:HG12	1:BR:137:LEU:HD13	2.04	0.40
1:BJ:112:ASP:HB2	1:BJ:118:SER:HB3	2.04	0.40
1:BP:65:ILE:HB	1:BP:90:VAL:HB	2.03	0.40
1:BP:87:THR:CG2	1:FB:89:GLN:HB3	2.52	0.40
1:BS:117:THR:OG1	1:FE:117:THR:OG1	2.30	0.40
1:BY:99:ASN:HB2	1:BY:102:MET:HG3	2.03	0.40
1:CA:64:ARG:HD2	1:CA:89:GLN:NE2	2.37	0.40
1:CB:99:ASN:HB2	1:CB:102:MET:HG3	2.03	0.40
1:CH:75:ASP:HA	1:FT:95:ASN:ND2	2.28	0.40
1:CJ:13:THR:O	1:CJ:13:THR:HG22	2.21	0.40
1:CK:65:ILE:HB	1:CK:90:VAL:HB	2.03	0.40
1:CS:27:ASN:CG	1:CS:28:GLY:N	2.76	0.40
1:CV:13:THR:O	1:CV:13:THR:HG22	2.21	0.40
1:CY:105:SER:O	1:CY:109:GLN:HG3	2.21	0.40
1:DO:112:ASP:HB2	1:DO:118:SER:HB3	2.04	0.40
1:DY:52:PHE:HE1	1:FY:137:LEU:HA	1.86	0.40
1:EE:52:PHE:HE1	1:EU:137:LEU:HA	1.85	0.40
1:FB:112:ASP:HB2	1:FB:118:SER:HB3	2.04	0.40
1:FJ:13:THR:O	1:FJ:13:THR:HG22	2.21	0.40
1:FP:88:ILE:HD11	1:GV:110:ALA:HB1	2.04	0.40
1:FS:13:THR:O	1:FS:13:THR:HG22	2.21	0.40
1:FS:52:PHE:CE1	1:GP:137:LEU:HD22	2.56	0.40
1:FV:13:THR:O	1:FV:13:THR:HG22	2.21	0.40
1:FX:130:PHE:N	1:FX:131:PRO:HD2	2.37	0.40
1:FZ:99:ASN:HB2	1:FZ:102:MET:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FZ:112:ASP:HB2	1:FZ:118:SER:HB3	2.04	0.40
1:GA:68:ASN:ND2	1:GA:70:ARG:HH11	2.18	0.40
1:GB:64:ARG:HD2	1:GB:89:GLN:NE2	2.37	0.40
1:GE:27:ASN:CG	1:GE:28:GLY:N	2.76	0.40
1:GK:13:THR:HG22	1:GK:13:THR:O	2.21	0.40
1:GN:13:THR:O	1:GN:14:LEU:HB2	2.20	0.40
1:GQ:13:THR:O	1:GQ:14:LEU:HB2	2.20	0.40
1:GR:99:ASN:HB2	1:GR:102:MET:HG3	2.03	0.40
1:AB:64:ARG:HD2	1:AB:89:GLN:NE2	2.37	0.40
1:AE:27:ASN:CG	1:AE:28:GLY:N	2.76	0.40
1:AF:99:ASN:HB2	1:AF:102:MET:HG3	2.03	0.40
1:AN:13:THR:O	1:AN:13:THR:HG22	2.21	0.40
1:AQ:13:THR:O	1:AQ:13:THR:HG22	2.21	0.40
1:AU:138:MET:SD	1:EE:22:SER:HB2	2.62	0.40
1:BC:13:THR:HG22	1:BC:13:THR:O	2.21	0.40
1:BH:24:ARG:NE	1:BH:34:VAL:HG21	2.37	0.40
1:BX:13:THR:O	1:BX:14:LEU:HB2	2.20	0.40
1:BY:75:ASP:HA	1:FK:95:ASN:ND2	2.28	0.40
1:CA:105:SER:O	1:CA:109:GLN:HG3	2.21	0.40
1:CB:73:VAL:HG11	1:FN:97:ALA:O	2.22	0.40
1:CG:52:PHE:CD1	1:CL:137:LEU:HD22	2.57	0.40
1:CJ:77:LYS:HG2	1:CP:79:ASN:ND2	2.36	0.40
1:CL:24:ARG:NE	1:CL:34:VAL:HG21	2.37	0.40
1:CN:65:ILE:HB	1:CN:90:VAL:HB	2.03	0.40
1:DC:99:ASN:HB2	1:DC:102:MET:HG3	2.04	0.40
1:DD:130:PHE:N	1:DD:131:PRO:HD2	2.36	0.40
1:DG:24:ARG:NE	1:DG:34:VAL:HG21	2.37	0.40
1:DH:64:ARG:HD2	1:DH:89:GLN:NE2	2.37	0.40
1:DI:112:ASP:HB2	1:DI:118:SER:HB3	2.04	0.40
1:DN:130:PHE:N	1:DN:131:PRO:HD2	2.37	0.40
1:DW:13:THR:HG22	1:DW:13:THR:O	2.21	0.40
1:EB:24:ARG:NE	1:EB:34:VAL:HG21	2.37	0.40
1:EJ:112:ASP:HB2	1:EJ:118:SER:HB3	2.04	0.40
1:EX:13:THR:O	1:EX:13:THR:HG22	2.21	0.40
1:EX:77:LYS:HG2	1:FJ:79:ASN:ND2	2.37	0.40
1:EY:99:ASN:HB2	1:EY:102:MET:HG3	2.03	0.40
1:FA:64:ARG:HD2	1:FA:89:GLN:NE2	2.36	0.40
1:FG:27:ASN:CG	1:FG:28:GLY:N	2.76	0.40
1:FG:64:ARG:HD2	1:FG:89:GLN:NE2	2.37	0.40
1:FS:64:ARG:HD2	1:FS:89:GLN:NE2	2.37	0.40
1:FW:112:ASP:HB2	1:FW:118:SER:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FY:13:THR:O	1:FY:13:THR:HG22	2.21	0.40
1:FZ:65:ILE:HB	1:FZ:90:VAL:HB	2.03	0.40
1:GI:65:ILE:HB	1:GI:90:VAL:HB	2.03	0.40
1:GJ:130:PHE:N	1:GJ:131:PRO:HD2	2.37	0.40
1:GK:13:THR:O	1:GK:14:LEU:HB2	2.21	0.40
1:GU:65:ILE:HB	1:GU:90:VAL:HB	2.03	0.40
1:GV:60:THR:HG23	1:GW:81:PRO:HG3	2.04	0.40

All (6) 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:DA:122:SER:OG	1:EU:13:THR:O[1_455]	1.10	1.10
1:EH:122:SER:OG	1:FU:120:THR:OG1[3_645]	1.39	0.81
1:AV:122:SER:OG	1:CS:13:THR:O[1_655]	2.13	0.07
1:DA:120:THR:O	1:EU:11:ASN:ND2[1_455]	2.17	0.03
1:BH:123:GLY:CA	1:CL:124:GLN:NE2[4_556]	2.19	0.01
1:BU:126:ASP:OD2	1:FJ:120:THR:CG2[3_655]	2.19	0.01

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AB	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AC	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	AD	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AE	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AF	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	AG	138/140 (99%)	136 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AH	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AI	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	AJ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AK	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AL	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	AM	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AO	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	AP	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AQ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AR	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	AS	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AT	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AU	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	AV	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AW	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AX	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	AY	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	AZ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BA	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	BB	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BC	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BD	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	BE	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BF	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BG	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	BH	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BI	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BJ	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	BK	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BL	138/140 (99%)	136 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BM	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	BN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BO	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BP	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	BQ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BR	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BS	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	BT	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BU	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BV	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	BW	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BX	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	BY	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	BZ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CA	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CB	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	CC	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CD	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CE	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	CF	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CG	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CH	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	CI	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CJ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CK	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	CL	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CM	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CN	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	CO	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CP	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CQ	138/140 (99%)	137 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CR	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CS	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CT	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	CU	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CV	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CW	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	CX	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CY	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	CZ	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	DA	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DB	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DC	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	DD	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DE	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DF	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	DG	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DH	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DI	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	DJ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DK	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DL	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	DM	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DO	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	DP	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DQ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DR	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	DS	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DT	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DU	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	DV	138/140 (99%)	136 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DW	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DX	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	DY	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	DZ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EA	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	EB	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EC	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	ED	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	EE	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EF	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EG	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	EH	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EI	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EJ	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	EK	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EL	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EM	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	EN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EO	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EP	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	EQ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	ER	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	ES	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	ET	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EU	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EV	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	EW	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EX	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	EY	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	EZ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FA	138/140 (99%)	136 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	FB	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	FC	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FD	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FE	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	FF	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FG	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FH	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	FI	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FJ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FK	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	FL	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FM	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FN	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	FO	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FP	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FQ	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	FR	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FS	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FT	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	FU	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FV	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FW	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	FX	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FY	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	FZ	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	GA	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GB	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GC	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	GD	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GE	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GF	138/140 (99%)	137 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GG	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GH	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GI	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	GJ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GK	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GL	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	GM	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GO	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	GP	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GQ	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GR	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	GS	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GT	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GU	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
1	GV	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GW	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
1	GX	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
All	All	24840/25200 (99%)	24540 (99%)	300 (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	113/113 (100%)	113 (100%)	0	100	100
1	AB	113/113 (100%)	113 (100%)	0	100	100
1	AC	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AD	113/113 (100%)	113 (100%)	0	100	100
1	AE	113/113 (100%)	113 (100%)	0	100	100
1	AF	113/113 (100%)	113 (100%)	0	100	100
1	AG	113/113 (100%)	113 (100%)	0	100	100
1	AH	113/113 (100%)	113 (100%)	0	100	100
1	AI	113/113 (100%)	113 (100%)	0	100	100
1	AJ	113/113 (100%)	113 (100%)	0	100	100
1	AK	113/113 (100%)	113 (100%)	0	100	100
1	AL	113/113 (100%)	113 (100%)	0	100	100
1	AM	113/113 (100%)	113 (100%)	0	100	100
1	AN	113/113 (100%)	113 (100%)	0	100	100
1	AO	113/113 (100%)	113 (100%)	0	100	100
1	AP	113/113 (100%)	113 (100%)	0	100	100
1	AQ	113/113 (100%)	113 (100%)	0	100	100
1	AR	113/113 (100%)	113 (100%)	0	100	100
1	AS	113/113 (100%)	113 (100%)	0	100	100
1	AT	113/113 (100%)	113 (100%)	0	100	100
1	AU	113/113 (100%)	113 (100%)	0	100	100
1	AV	113/113 (100%)	113 (100%)	0	100	100
1	AW	113/113 (100%)	113 (100%)	0	100	100
1	AX	113/113 (100%)	113 (100%)	0	100	100
1	AY	113/113 (100%)	113 (100%)	0	100	100
1	AZ	113/113 (100%)	113 (100%)	0	100	100
1	BA	113/113 (100%)	113 (100%)	0	100	100
1	BB	113/113 (100%)	113 (100%)	0	100	100
1	BC	113/113 (100%)	113 (100%)	0	100	100
1	BD	113/113 (100%)	113 (100%)	0	100	100
1	BE	113/113 (100%)	113 (100%)	0	100	100
1	BF	113/113 (100%)	113 (100%)	0	100	100
1	BG	113/113 (100%)	113 (100%)	0	100	100
1	BH	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BI	113/113 (100%)	113 (100%)	0	100	100
1	BJ	113/113 (100%)	113 (100%)	0	100	100
1	BK	113/113 (100%)	113 (100%)	0	100	100
1	BL	113/113 (100%)	113 (100%)	0	100	100
1	BM	113/113 (100%)	113 (100%)	0	100	100
1	BN	113/113 (100%)	113 (100%)	0	100	100
1	BO	113/113 (100%)	113 (100%)	0	100	100
1	BP	113/113 (100%)	113 (100%)	0	100	100
1	BQ	113/113 (100%)	113 (100%)	0	100	100
1	BR	113/113 (100%)	113 (100%)	0	100	100
1	BS	113/113 (100%)	113 (100%)	0	100	100
1	BT	113/113 (100%)	113 (100%)	0	100	100
1	BU	113/113 (100%)	113 (100%)	0	100	100
1	BV	113/113 (100%)	113 (100%)	0	100	100
1	BW	113/113 (100%)	113 (100%)	0	100	100
1	BX	113/113 (100%)	113 (100%)	0	100	100
1	BY	113/113 (100%)	113 (100%)	0	100	100
1	BZ	113/113 (100%)	113 (100%)	0	100	100
1	CA	113/113 (100%)	113 (100%)	0	100	100
1	CB	113/113 (100%)	113 (100%)	0	100	100
1	CC	113/113 (100%)	113 (100%)	0	100	100
1	CD	113/113 (100%)	113 (100%)	0	100	100
1	CE	113/113 (100%)	113 (100%)	0	100	100
1	CF	113/113 (100%)	113 (100%)	0	100	100
1	CG	113/113 (100%)	113 (100%)	0	100	100
1	CH	113/113 (100%)	113 (100%)	0	100	100
1	CI	113/113 (100%)	113 (100%)	0	100	100
1	CJ	113/113 (100%)	113 (100%)	0	100	100
1	CK	113/113 (100%)	113 (100%)	0	100	100
1	CL	113/113 (100%)	113 (100%)	0	100	100
1	CM	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CN	113/113 (100%)	113 (100%)	0	100	100
1	CO	113/113 (100%)	113 (100%)	0	100	100
1	CP	113/113 (100%)	113 (100%)	0	100	100
1	CQ	113/113 (100%)	113 (100%)	0	100	100
1	CR	113/113 (100%)	113 (100%)	0	100	100
1	CS	113/113 (100%)	113 (100%)	0	100	100
1	CT	113/113 (100%)	113 (100%)	0	100	100
1	CU	113/113 (100%)	113 (100%)	0	100	100
1	CV	113/113 (100%)	113 (100%)	0	100	100
1	CW	113/113 (100%)	113 (100%)	0	100	100
1	CX	113/113 (100%)	113 (100%)	0	100	100
1	CY	113/113 (100%)	113 (100%)	0	100	100
1	CZ	113/113 (100%)	113 (100%)	0	100	100
1	DA	113/113 (100%)	113 (100%)	0	100	100
1	DB	113/113 (100%)	113 (100%)	0	100	100
1	DC	113/113 (100%)	113 (100%)	0	100	100
1	DD	113/113 (100%)	113 (100%)	0	100	100
1	DE	113/113 (100%)	113 (100%)	0	100	100
1	DF	113/113 (100%)	113 (100%)	0	100	100
1	DG	113/113 (100%)	113 (100%)	0	100	100
1	DH	113/113 (100%)	113 (100%)	0	100	100
1	DI	113/113 (100%)	113 (100%)	0	100	100
1	DJ	113/113 (100%)	113 (100%)	0	100	100
1	DK	113/113 (100%)	113 (100%)	0	100	100
1	DL	113/113 (100%)	113 (100%)	0	100	100
1	DM	113/113 (100%)	113 (100%)	0	100	100
1	DN	113/113 (100%)	113 (100%)	0	100	100
1	DO	113/113 (100%)	113 (100%)	0	100	100
1	DP	113/113 (100%)	113 (100%)	0	100	100
1	DQ	113/113 (100%)	113 (100%)	0	100	100
1	DR	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DS	113/113 (100%)	113 (100%)	0	100	100
1	DT	113/113 (100%)	113 (100%)	0	100	100
1	DU	113/113 (100%)	113 (100%)	0	100	100
1	DV	113/113 (100%)	113 (100%)	0	100	100
1	DW	113/113 (100%)	113 (100%)	0	100	100
1	DX	113/113 (100%)	113 (100%)	0	100	100
1	DY	113/113 (100%)	113 (100%)	0	100	100
1	DZ	113/113 (100%)	113 (100%)	0	100	100
1	EA	113/113 (100%)	113 (100%)	0	100	100
1	EB	113/113 (100%)	113 (100%)	0	100	100
1	EC	113/113 (100%)	113 (100%)	0	100	100
1	ED	113/113 (100%)	113 (100%)	0	100	100
1	EE	113/113 (100%)	113 (100%)	0	100	100
1	EF	113/113 (100%)	113 (100%)	0	100	100
1	EG	113/113 (100%)	113 (100%)	0	100	100
1	EH	113/113 (100%)	113 (100%)	0	100	100
1	EI	113/113 (100%)	113 (100%)	0	100	100
1	EJ	113/113 (100%)	113 (100%)	0	100	100
1	EK	113/113 (100%)	113 (100%)	0	100	100
1	EL	113/113 (100%)	113 (100%)	0	100	100
1	EM	113/113 (100%)	113 (100%)	0	100	100
1	EN	113/113 (100%)	113 (100%)	0	100	100
1	EO	113/113 (100%)	113 (100%)	0	100	100
1	EP	113/113 (100%)	113 (100%)	0	100	100
1	EQ	113/113 (100%)	113 (100%)	0	100	100
1	ER	113/113 (100%)	113 (100%)	0	100	100
1	ES	113/113 (100%)	113 (100%)	0	100	100
1	ET	113/113 (100%)	113 (100%)	0	100	100
1	EU	113/113 (100%)	113 (100%)	0	100	100
1	EV	113/113 (100%)	113 (100%)	0	100	100
1	EW	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	EX	113/113 (100%)	113 (100%)	0	100	100
1	EY	113/113 (100%)	113 (100%)	0	100	100
1	EZ	113/113 (100%)	113 (100%)	0	100	100
1	FA	113/113 (100%)	113 (100%)	0	100	100
1	FB	113/113 (100%)	113 (100%)	0	100	100
1	FC	113/113 (100%)	113 (100%)	0	100	100
1	FD	113/113 (100%)	113 (100%)	0	100	100
1	FE	113/113 (100%)	113 (100%)	0	100	100
1	FF	113/113 (100%)	113 (100%)	0	100	100
1	FG	113/113 (100%)	113 (100%)	0	100	100
1	FH	113/113 (100%)	113 (100%)	0	100	100
1	FI	113/113 (100%)	113 (100%)	0	100	100
1	FJ	113/113 (100%)	113 (100%)	0	100	100
1	FK	113/113 (100%)	113 (100%)	0	100	100
1	FL	113/113 (100%)	113 (100%)	0	100	100
1	FM	113/113 (100%)	113 (100%)	0	100	100
1	FN	113/113 (100%)	113 (100%)	0	100	100
1	FO	113/113 (100%)	113 (100%)	0	100	100
1	FP	113/113 (100%)	113 (100%)	0	100	100
1	FQ	113/113 (100%)	113 (100%)	0	100	100
1	FR	113/113 (100%)	113 (100%)	0	100	100
1	FS	113/113 (100%)	113 (100%)	0	100	100
1	FT	113/113 (100%)	113 (100%)	0	100	100
1	FU	113/113 (100%)	113 (100%)	0	100	100
1	FV	113/113 (100%)	113 (100%)	0	100	100
1	FW	113/113 (100%)	113 (100%)	0	100	100
1	FX	113/113 (100%)	113 (100%)	0	100	100
1	FY	113/113 (100%)	113 (100%)	0	100	100
1	FZ	113/113 (100%)	113 (100%)	0	100	100
1	GA	113/113 (100%)	113 (100%)	0	100	100
1	GB	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	GC	113/113 (100%)	113 (100%)	0	100	100
1	GD	113/113 (100%)	113 (100%)	0	100	100
1	GE	113/113 (100%)	113 (100%)	0	100	100
1	GF	113/113 (100%)	113 (100%)	0	100	100
1	GG	113/113 (100%)	113 (100%)	0	100	100
1	GH	113/113 (100%)	113 (100%)	0	100	100
1	GI	113/113 (100%)	113 (100%)	0	100	100
1	GJ	113/113 (100%)	113 (100%)	0	100	100
1	GK	113/113 (100%)	113 (100%)	0	100	100
1	GL	113/113 (100%)	113 (100%)	0	100	100
1	GM	113/113 (100%)	113 (100%)	0	100	100
1	GN	113/113 (100%)	113 (100%)	0	100	100
1	GO	113/113 (100%)	113 (100%)	0	100	100
1	GP	113/113 (100%)	113 (100%)	0	100	100
1	GQ	113/113 (100%)	113 (100%)	0	100	100
1	GR	113/113 (100%)	113 (100%)	0	100	100
1	GS	113/113 (100%)	113 (100%)	0	100	100
1	GT	113/113 (100%)	113 (100%)	0	100	100
1	GU	113/113 (100%)	113 (100%)	0	100	100
1	GV	113/113 (100%)	113 (100%)	0	100	100
1	GW	113/113 (100%)	113 (100%)	0	100	100
1	GX	113/113 (100%)	113 (100%)	0	100	100
All	All	20340/20340 (100%)	20340 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (187) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	124	GLN
1	AB	89	GLN
1	AC	79	ASN
1	AC	89	GLN
1	AD	124	GLN

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Mol	Chain	Res	Type
1	AE	89	GLN
1	AE	109	GLN
1	AF	79	ASN
1	AF	89	GLN
1	AG	124	GLN
1	AH	89	GLN
1	AI	89	GLN
1	AJ	124	GLN
1	AK	89	GLN
1	AM	124	GLN
1	AN	89	GLN
1	AP	124	GLN
1	AQ	89	GLN
1	AR	89	GLN
1	AS	124	GLN
1	AT	89	GLN
1	AU	79	ASN
1	AU	89	GLN
1	AV	124	GLN
1	AX	89	GLN
1	AY	124	GLN
1	AZ	89	GLN
1	BA	89	GLN
1	BB	66	HIS
1	BB	89	GLN
1	BB	124	GLN
1	BC	89	GLN
1	BD	79	ASN
1	BD	89	GLN
1	BE	124	GLN
1	BF	89	GLN
1	BH	124	GLN
1	BJ	79	ASN
1	BJ	89	GLN
1	BK	124	GLN
1	BM	79	ASN
1	BM	89	GLN
1	BN	124	GLN
1	BP	89	GLN
1	BQ	124	GLN
1	BS	79	ASN
1	BT	124	GLN

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Mol	Chain	Res	Type
1	BU	89	GLN
1	BV	89	GLN
1	BW	124	GLN
1	BX	89	GLN
1	BY	79	ASN
1	BY	89	GLN
1	BZ	124	GLN
1	CA	89	GLN
1	CB	79	ASN
1	CB	89	GLN
1	CC	124	GLN
1	CD	89	GLN
1	CE	79	ASN
1	CE	89	GLN
1	CF	124	GLN
1	CI	124	GLN
1	CK	79	ASN
1	CK	89	GLN
1	CL	124	GLN
1	CM	89	GLN
1	CN	79	ASN
1	CO	124	GLN
1	CP	89	GLN
1	CQ	79	ASN
1	CQ	89	GLN
1	CR	124	GLN
1	CS	89	GLN
1	CT	89	GLN
1	CU	124	GLN
1	CV	89	GLN
1	CW	79	ASN
1	CW	89	GLN
1	CX	124	GLN
1	CY	89	GLN
1	CZ	79	ASN
1	DA	124	GLN
1	DB	89	GLN
1	DC	89	GLN
1	DD	124	GLN
1	DF	89	GLN
1	DG	124	GLN
1	DH	89	GLN

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Mol	Chain	Res	Type
1	DI	89	GLN
1	DJ	124	GLN
1	DK	89	GLN
1	DL	79	ASN
1	DL	89	GLN
1	DM	124	GLN
1	DN	89	GLN
1	DP	124	GLN
1	DQ	89	GLN
1	DR	89	GLN
1	DS	124	GLN
1	DT	89	GLN
1	DU	79	ASN
1	DV	124	GLN
1	DX	89	GLN
1	DY	124	GLN
1	DZ	89	GLN
1	EA	79	ASN
1	EA	89	GLN
1	EB	66	HIS
1	EB	89	GLN
1	EB	124	GLN
1	EC	89	GLN
1	ED	79	ASN
1	EE	124	GLN
1	EH	124	GLN
1	EJ	89	GLN
1	EK	124	GLN
1	EM	79	ASN
1	EM	89	GLN
1	EN	124	GLN
1	EO	89	GLN
1	EP	79	ASN
1	EP	89	GLN
1	EQ	124	GLN
1	ER	89	GLN
1	ES	89	GLN
1	ET	124	GLN
1	EU	89	GLN
1	EV	89	GLN
1	EW	124	GLN
1	EX	89	GLN

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Mol	Chain	Res	Type
1	EY	79	ASN
1	EY	89	GLN
1	EZ	124	GLN
1	FB	79	ASN
1	FB	89	GLN
1	FC	124	GLN
1	FD	89	GLN
1	FE	89	GLN
1	FF	124	GLN
1	FG	89	GLN
1	FH	79	ASN
1	FH	89	GLN
1	FI	124	GLN
1	FJ	89	GLN
1	FK	89	GLN
1	FL	124	GLN
1	FN	79	ASN
1	FN	89	GLN
1	FO	124	GLN
1	FP	89	GLN
1	FQ	89	GLN
1	FR	124	GLN
1	FS	89	GLN
1	FT	79	ASN
1	FT	89	GLN
1	FU	124	GLN
1	FX	124	GLN
1	FY	89	GLN
1	FZ	79	ASN
1	FZ	89	GLN
1	GA	124	GLN
1	GB	89	GLN
1	GC	79	ASN
1	GC	89	GLN
1	GD	124	GLN
1	GF	79	ASN
1	GF	89	GLN
1	GG	124	GLN
1	GH	89	GLN
1	GI	79	ASN
1	GJ	66	HIS
1	GJ	89	GLN

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Mol	Chain	Res	Type
1	GJ	124	GLN
1	GK	89	GLN
1	GM	66	HIS
1	GM	89	GLN
1	GM	124	GLN
1	GN	89	GLN
1	GO	79	ASN
1	GO	89	GLN
1	GP	124	GLN
1	GQ	89	GLN
1	GR	79	ASN
1	GS	124	GLN
1	GU	79	ASN
1	GV	124	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	140/140 (100%)	0.47	8 (5%) 29 19	17, 32, 64, 77	0
1	AB	140/140 (100%)	0.33	2 (1%) 73 54	17, 30, 53, 71	0
1	AC	140/140 (100%)	0.27	1 (0%) 84 69	18, 32, 55, 63	0
1	AD	140/140 (100%)	0.54	10 (7%) 22 14	17, 32, 64, 77	0
1	AE	140/140 (100%)	0.40	3 (2%) 63 43	17, 30, 53, 71	0
1	AF	140/140 (100%)	0.36	2 (1%) 73 54	18, 32, 55, 63	0
1	AG	140/140 (100%)	0.58	6 (4%) 40 24	17, 32, 64, 77	0
1	AH	140/140 (100%)	0.38	3 (2%) 63 43	17, 30, 53, 71	0
1	AI	140/140 (100%)	0.31	1 (0%) 84 69	18, 32, 55, 63	0
1	AJ	140/140 (100%)	0.41	7 (5%) 34 22	17, 32, 64, 77	0
1	AK	140/140 (100%)	0.35	4 (2%) 53 35	17, 30, 53, 71	0
1	AL	140/140 (100%)	0.39	4 (2%) 53 35	18, 32, 55, 63	0
1	AM	140/140 (100%)	0.68	13 (9%) 14 9	17, 32, 64, 77	0
1	AN	140/140 (100%)	0.61	8 (5%) 29 19	17, 30, 53, 71	0
1	AO	140/140 (100%)	0.47	7 (5%) 34 22	18, 32, 55, 63	0
1	AP	140/140 (100%)	0.88	16 (11%) 10 7	17, 32, 64, 77	0
1	AQ	140/140 (100%)	0.59	6 (4%) 40 24	17, 30, 53, 71	0
1	AR	140/140 (100%)	0.54	3 (2%) 63 43	18, 32, 55, 63	0
1	AS	140/140 (100%)	0.56	7 (5%) 34 22	17, 32, 64, 77	0
1	AT	140/140 (100%)	0.29	3 (2%) 63 43	17, 30, 53, 71	0
1	AU	140/140 (100%)	0.43	2 (1%) 73 54	18, 32, 55, 63	0
1	AV	140/140 (100%)	0.72	15 (10%) 11 7	17, 32, 64, 77	0
1	AW	140/140 (100%)	0.28	6 (4%) 40 24	17, 30, 53, 71	0
1	AX	140/140 (100%)	0.47	5 (3%) 46 28	18, 32, 55, 63	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	140/140 (100%)	0.38	9 (6%) 25 16	17, 32, 64, 77	0
1	AZ	140/140 (100%)	0.22	1 (0%) 84 69	17, 30, 53, 71	0
1	BA	140/140 (100%)	0.37	2 (1%) 73 54	18, 32, 55, 63	0
1	BB	140/140 (100%)	0.31	6 (4%) 40 24	17, 32, 64, 77	0
1	BC	140/140 (100%)	0.34	4 (2%) 53 35	17, 30, 53, 71	0
1	BD	140/140 (100%)	0.53	7 (5%) 34 22	18, 32, 55, 63	0
1	BE	140/140 (100%)	0.38	2 (1%) 73 54	17, 32, 64, 77	0
1	BF	140/140 (100%)	0.45	3 (2%) 63 43	17, 30, 53, 71	0
1	BG	140/140 (100%)	0.35	3 (2%) 63 43	18, 32, 55, 63	0
1	BH	140/140 (100%)	0.71	16 (11%) 10 7	17, 32, 64, 77	0
1	BI	140/140 (100%)	0.54	8 (5%) 29 19	17, 30, 53, 71	0
1	BJ	140/140 (100%)	0.60	9 (6%) 25 16	18, 32, 55, 63	0
1	BK	140/140 (100%)	0.35	4 (2%) 53 35	17, 32, 64, 77	0
1	BL	140/140 (100%)	0.37	2 (1%) 73 54	17, 30, 53, 71	0
1	BM	140/140 (100%)	0.41	4 (2%) 53 35	18, 32, 55, 63	0
1	BN	140/140 (100%)	0.46	8 (5%) 29 19	17, 32, 64, 77	0
1	BO	140/140 (100%)	0.59	6 (4%) 40 24	17, 30, 53, 71	0
1	BP	140/140 (100%)	0.65	7 (5%) 34 22	18, 32, 55, 63	0
1	BQ	140/140 (100%)	0.33	5 (3%) 46 28	17, 32, 64, 77	0
1	BR	140/140 (100%)	0.23	0 100 100	17, 30, 53, 71	0
1	BS	140/140 (100%)	0.50	8 (5%) 29 19	18, 32, 55, 63	0
1	BT	140/140 (100%)	0.52	12 (8%) 16 11	17, 32, 64, 77	0
1	BU	140/140 (100%)	0.53	7 (5%) 34 22	17, 30, 53, 71	0
1	BV	140/140 (100%)	0.36	6 (4%) 40 24	18, 32, 55, 63	0
1	BW	140/140 (100%)	0.44	7 (5%) 34 22	17, 32, 64, 77	0
1	BX	140/140 (100%)	0.47	3 (2%) 63 43	17, 30, 53, 71	0
1	BY	140/140 (100%)	0.40	5 (3%) 46 28	18, 32, 55, 63	0
1	BZ	140/140 (100%)	0.46	5 (3%) 46 28	17, 32, 64, 77	0
1	CA	140/140 (100%)	0.49	6 (4%) 40 24	17, 30, 53, 71	0
1	CB	140/140 (100%)	0.62	3 (2%) 63 43	18, 32, 55, 63	0
1	CC	140/140 (100%)	0.43	5 (3%) 46 28	17, 32, 64, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	CD	140/140 (100%)	0.44	4 (2%) 53 35	17, 30, 53, 71	0
1	CE	140/140 (100%)	0.40	3 (2%) 63 43	18, 32, 55, 63	0
1	CF	140/140 (100%)	0.48	10 (7%) 22 14	17, 32, 64, 77	0
1	CG	140/140 (100%)	0.59	5 (3%) 46 28	17, 30, 53, 71	0
1	CH	140/140 (100%)	0.59	11 (7%) 18 12	18, 32, 55, 63	0
1	CI	140/140 (100%)	0.52	14 (10%) 12 8	17, 32, 64, 77	0
1	CJ	140/140 (100%)	0.45	2 (1%) 73 54	17, 30, 53, 71	0
1	CK	140/140 (100%)	0.34	1 (0%) 84 69	18, 32, 55, 63	0
1	CL	140/140 (100%)	0.77	13 (9%) 14 9	17, 32, 64, 77	0
1	CM	140/140 (100%)	0.43	5 (3%) 46 28	17, 30, 53, 71	0
1	CN	140/140 (100%)	0.51	10 (7%) 22 14	18, 32, 55, 63	0
1	CO	140/140 (100%)	0.49	10 (7%) 22 14	17, 32, 64, 77	0
1	CP	140/140 (100%)	0.39	4 (2%) 53 35	17, 30, 53, 71	0
1	CQ	140/140 (100%)	0.66	11 (7%) 18 12	18, 32, 55, 63	0
1	CR	140/140 (100%)	0.51	4 (2%) 53 35	17, 32, 64, 77	0
1	CS	140/140 (100%)	0.70	12 (8%) 16 11	17, 30, 53, 71	0
1	CT	140/140 (100%)	0.32	1 (0%) 84 69	18, 32, 55, 63	0
1	CU	140/140 (100%)	0.94	16 (11%) 10 7	17, 32, 64, 77	0
1	CV	140/140 (100%)	0.29	1 (0%) 84 69	17, 30, 53, 71	0
1	CW	140/140 (100%)	0.56	9 (6%) 25 16	18, 32, 55, 63	0
1	CX	140/140 (100%)	0.38	4 (2%) 53 35	17, 32, 64, 77	0
1	CY	140/140 (100%)	0.31	4 (2%) 53 35	17, 30, 53, 71	0
1	CZ	140/140 (100%)	0.45	6 (4%) 40 24	18, 32, 55, 63	0
1	DA	140/140 (100%)	0.60	11 (7%) 18 12	17, 32, 64, 77	0
1	DB	140/140 (100%)	0.40	2 (1%) 73 54	17, 30, 53, 71	0
1	DC	140/140 (100%)	0.38	7 (5%) 34 22	18, 32, 55, 63	0
1	DD	140/140 (100%)	0.94	20 (14%) 6 5	17, 32, 64, 77	0
1	DE	140/140 (100%)	1.07	24 (17%) 4 3	17, 30, 53, 71	0
1	DF	140/140 (100%)	0.76	13 (9%) 14 9	18, 32, 55, 63	0
1	DG	140/140 (100%)	0.69	9 (6%) 25 16	17, 32, 64, 77	0
1	DH	140/140 (100%)	0.39	7 (5%) 34 22	17, 30, 53, 71	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	DI	140/140 (100%)	0.41	3 (2%) 63 43	18, 32, 55, 63	0
1	DJ	140/140 (100%)	0.55	11 (7%) 18 12	17, 32, 64, 77	0
1	DK	140/140 (100%)	0.23	1 (0%) 84 69	17, 30, 53, 71	0
1	DL	140/140 (100%)	0.44	3 (2%) 63 43	18, 32, 55, 63	0
1	DM	140/140 (100%)	0.51	5 (3%) 46 28	17, 32, 64, 77	0
1	DN	140/140 (100%)	0.37	3 (2%) 63 43	17, 30, 53, 71	0
1	DO	140/140 (100%)	0.31	2 (1%) 73 54	18, 32, 55, 63	0
1	DP	140/140 (100%)	0.36	4 (2%) 53 35	17, 32, 64, 77	0
1	DQ	140/140 (100%)	0.37	2 (1%) 73 54	17, 30, 53, 71	0
1	DR	140/140 (100%)	0.29	1 (0%) 84 69	18, 32, 55, 63	0
1	DS	140/140 (100%)	0.39	6 (4%) 40 24	17, 32, 64, 77	0
1	DT	140/140 (100%)	0.54	10 (7%) 22 14	17, 30, 53, 71	0
1	DU	140/140 (100%)	0.43	3 (2%) 63 43	18, 32, 55, 63	0
1	DV	140/140 (100%)	0.52	4 (2%) 53 35	17, 32, 64, 77	0
1	DW	140/140 (100%)	0.35	1 (0%) 84 69	17, 30, 53, 71	0
1	DX	140/140 (100%)	0.54	5 (3%) 46 28	18, 32, 55, 63	0
1	DY	140/140 (100%)	0.44	9 (6%) 25 16	17, 32, 64, 77	0
1	DZ	140/140 (100%)	0.29	1 (0%) 84 69	17, 30, 53, 71	0
1	EA	140/140 (100%)	0.36	4 (2%) 53 35	18, 32, 55, 63	0
1	EB	140/140 (100%)	0.54	9 (6%) 25 16	17, 32, 64, 77	0
1	EC	140/140 (100%)	0.27	1 (0%) 84 69	17, 30, 53, 71	0
1	ED	140/140 (100%)	0.59	9 (6%) 25 16	18, 32, 55, 63	0
1	EE	140/140 (100%)	0.92	20 (14%) 6 5	17, 32, 64, 77	0
1	EF	140/140 (100%)	0.90	19 (13%) 7 5	17, 30, 53, 71	0
1	EG	140/140 (100%)	0.62	8 (5%) 29 19	18, 32, 55, 63	0
1	EH	140/140 (100%)	0.48	8 (5%) 29 19	17, 32, 64, 77	0
1	EI	140/140 (100%)	0.24	3 (2%) 63 43	17, 30, 53, 71	0
1	EJ	140/140 (100%)	0.32	5 (3%) 46 28	18, 32, 55, 63	0
1	EK	140/140 (100%)	0.58	6 (4%) 40 24	17, 32, 64, 77	0
1	EL	140/140 (100%)	0.28	1 (0%) 84 69	17, 30, 53, 71	0
1	EM	140/140 (100%)	0.37	3 (2%) 63 43	18, 32, 55, 63	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	EN	140/140 (100%)	0.94	17 (12%) 8 6	17, 32, 64, 77	0
1	EO	140/140 (100%)	0.35	4 (2%) 53 35	17, 30, 53, 71	0
1	EP	140/140 (100%)	0.73	12 (8%) 16 11	18, 32, 55, 63	0
1	EQ	140/140 (100%)	0.73	11 (7%) 18 12	17, 32, 64, 77	0
1	ER	140/140 (100%)	0.50	5 (3%) 46 28	17, 30, 53, 71	0
1	ES	140/140 (100%)	0.47	3 (2%) 63 43	18, 32, 55, 63	0
1	ET	140/140 (100%)	0.45	5 (3%) 46 28	17, 32, 64, 77	0
1	EU	140/140 (100%)	0.77	18 (12%) 7 6	17, 30, 53, 71	0
1	EV	140/140 (100%)	0.40	4 (2%) 53 35	18, 32, 55, 63	0
1	EW	140/140 (100%)	0.43	5 (3%) 46 28	17, 32, 64, 77	0
1	EX	140/140 (100%)	0.31	3 (2%) 63 43	17, 30, 53, 71	0
1	EY	140/140 (100%)	0.30	2 (1%) 73 54	18, 32, 55, 63	0
1	EZ	140/140 (100%)	0.43	7 (5%) 34 22	17, 32, 64, 77	0
1	FA	140/140 (100%)	0.59	7 (5%) 34 22	17, 30, 53, 71	0
1	FB	140/140 (100%)	0.49	4 (2%) 53 35	18, 32, 55, 63	0
1	FC	140/140 (100%)	0.44	8 (5%) 29 19	17, 32, 64, 77	0
1	FD	140/140 (100%)	0.41	5 (3%) 46 28	17, 30, 53, 71	0
1	FE	140/140 (100%)	0.26	2 (1%) 73 54	18, 32, 55, 63	0
1	FF	140/140 (100%)	0.51	5 (3%) 46 28	17, 32, 64, 77	0
1	FG	140/140 (100%)	0.44	3 (2%) 63 43	17, 30, 53, 71	0
1	FH	140/140 (100%)	0.51	5 (3%) 46 28	18, 32, 55, 63	0
1	FI	140/140 (100%)	0.52	6 (4%) 40 24	17, 32, 64, 77	0
1	FJ	140/140 (100%)	0.53	10 (7%) 22 14	17, 30, 53, 71	0
1	FK	140/140 (100%)	0.39	1 (0%) 84 69	18, 32, 55, 63	0
1	FL	140/140 (100%)	0.64	7 (5%) 34 22	17, 32, 64, 77	0
1	FM	140/140 (100%)	0.47	6 (4%) 40 24	17, 30, 53, 71	0
1	FN	140/140 (100%)	0.84	11 (7%) 18 12	18, 32, 55, 63	0
1	FO	140/140 (100%)	0.53	9 (6%) 25 16	17, 32, 64, 77	0
1	FP	140/140 (100%)	0.42	4 (2%) 53 35	17, 30, 53, 71	0
1	FQ	140/140 (100%)	0.37	1 (0%) 84 69	18, 32, 55, 63	0
1	FR	140/140 (100%)	0.47	7 (5%) 34 22	17, 32, 64, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	FS	140/140 (100%)	0.23	2 (1%)	73 54	17, 30, 53, 71	0
1	FT	140/140 (100%)	0.45	7 (5%)	34 22	18, 32, 55, 63	0
1	FU	140/140 (100%)	0.57	9 (6%)	25 16	17, 32, 64, 77	0
1	FV	140/140 (100%)	0.38	4 (2%)	53 35	17, 30, 53, 71	0
1	FW	140/140 (100%)	0.51	1 (0%)	84 69	18, 32, 55, 63	0
1	FX	140/140 (100%)	0.53	8 (5%)	29 19	17, 32, 64, 77	0
1	FY	140/140 (100%)	0.43	5 (3%)	46 28	17, 30, 53, 71	0
1	FZ	140/140 (100%)	0.57	12 (8%)	16 11	18, 32, 55, 63	0
1	GA	140/140 (100%)	0.61	7 (5%)	34 22	17, 32, 64, 77	0
1	GB	140/140 (100%)	0.43	3 (2%)	63 43	17, 30, 53, 71	0
1	GC	140/140 (100%)	0.61	6 (4%)	40 24	18, 32, 55, 63	0
1	GD	140/140 (100%)	0.53	11 (7%)	18 12	17, 32, 64, 77	0
1	GE	140/140 (100%)	0.36	3 (2%)	63 43	17, 30, 53, 71	0
1	GF	140/140 (100%)	0.38	6 (4%)	40 24	18, 32, 55, 63	0
1	GG	140/140 (100%)	0.33	6 (4%)	40 24	17, 32, 64, 77	0
1	GH	140/140 (100%)	0.38	5 (3%)	46 28	17, 30, 53, 71	0
1	GI	140/140 (100%)	0.51	4 (2%)	53 35	18, 32, 55, 63	0
1	GJ	140/140 (100%)	0.42	9 (6%)	25 16	17, 32, 64, 77	0
1	GK	140/140 (100%)	0.32	4 (2%)	53 35	17, 30, 53, 71	0
1	GL	140/140 (100%)	0.32	5 (3%)	46 28	18, 32, 55, 63	0
1	GM	140/140 (100%)	0.67	10 (7%)	22 14	17, 32, 64, 77	0
1	GN	140/140 (100%)	0.44	5 (3%)	46 28	17, 30, 53, 71	0
1	GO	140/140 (100%)	0.52	6 (4%)	40 24	18, 32, 55, 63	0
1	GP	140/140 (100%)	0.46	9 (6%)	25 16	17, 32, 64, 77	0
1	GQ	140/140 (100%)	0.29	2 (1%)	73 54	17, 30, 53, 71	0
1	GR	140/140 (100%)	0.46	8 (5%)	29 19	18, 32, 55, 63	0
1	GS	140/140 (100%)	0.45	6 (4%)	40 24	17, 32, 64, 77	0
1	GT	140/140 (100%)	0.42	2 (1%)	73 54	17, 30, 53, 71	0
1	GU	140/140 (100%)	0.51	4 (2%)	53 35	18, 32, 55, 63	0
1	GV	140/140 (100%)	0.50	8 (5%)	29 19	17, 32, 64, 77	0
1	GW	140/140 (100%)	0.34	2 (1%)	73 54	17, 30, 53, 71	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	GX	140/140 (100%)	0.49	4 (2%) 53 35	18, 32, 55, 63	0
All	All	25200/25200 (100%)	0.48	1118 (4%) 39 24	17, 32, 59, 77	0

All (1118) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	ED	136	GLY	6.2
1	AN	122	SER	5.5
1	BQ	28	GLY	5.4
1	AV	122	SER	5.4
1	EU	13	THR	5.3
1	CS	15	ALA	5.3
1	AM	28	GLY	4.9
1	DA	122	SER	4.8
1	DM	89	GLN	4.7
1	GM	58	GLY	4.7
1	CF	39	ASP	4.5
1	CS	13	THR	4.4
1	FJ	120	THR	4.4
1	EH	58	GLY	4.4
1	CL	27	ASN	4.4
1	BT	27	ASN	4.4
1	AA	28	GLY	4.4
1	DG	28	GLY	4.4
1	DE	27	ASN	4.4
1	DA	28	GLY	4.4
1	AP	60	THR	4.3
1	FU	39	ASP	4.3
1	CF	60	THR	4.3
1	DJ	60	THR	4.2
1	DA	60	THR	4.2
1	DA	27	ASN	4.2
1	AE	122	SER	4.1
1	GM	60	THR	4.1
1	GJ	27	ASN	4.1
1	EU	15	ALA	4.1
1	BU	117	THR	4.1
1	BT	39	ASP	4.0
1	AA	39	ASP	4.0
1	ER	122	SER	4.0
1	EZ	60	THR	4.0
1	AA	27	ASN	4.0

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Mol	Chain	Res	Type	RSRZ
1	GV	56	ALA	4.0
1	EU	12	SER	4.0
1	CN	122	SER	3.9
1	CU	60	THR	3.9
1	EE	27	ASN	3.9
1	GR	136	GLY	3.9
1	AD	28	GLY	3.8
1	FR	28	GLY	3.8
1	BQ	39	ASP	3.8
1	DE	126	ASP	3.8
1	BE	59	ILE	3.8
1	GM	28	GLY	3.8
1	EB	28	GLY	3.8
1	BH	27	ASN	3.8
1	FH	89	GLN	3.8
1	DV	39	ASP	3.8
1	EQ	39	ASP	3.8
1	GJ	60	THR	3.8
1	AX	53	ASP	3.7
1	FX	39	ASP	3.7
1	DP	60	THR	3.7
1	AV	58	GLY	3.7
1	BZ	89	GLN	3.7
1	AG	60	THR	3.7
1	FR	60	THR	3.7
1	FU	122	SER	3.7
1	AN	76	GLU	3.7
1	EF	6	ALA	3.7
1	FU	60	THR	3.7
1	EQ	28	GLY	3.7
1	FX	28	GLY	3.7
1	EQ	27	ASN	3.6
1	BU	53	ASP	3.6
1	EE	126	ASP	3.6
1	EF	53	ASP	3.6
1	DD	60	THR	3.6
1	FU	28	GLY	3.6
1	EE	39	ASP	3.6
1	DG	59	ILE	3.6
1	GJ	66	HIS	3.6
1	DD	58	GLY	3.6
1	DJ	58	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	FL	28	GLY	3.6
1	EU	16	SER	3.6
1	EB	39	ASP	3.6
1	EU	14	LEU	3.5
1	DG	27	ASN	3.5
1	FR	27	ASN	3.5
1	BU	122	SER	3.5
1	CH	53	ASP	3.5
1	FT	53	ASP	3.5
1	DJ	28	GLY	3.5
1	AS	77	LYS	3.5
1	EE	119	ALA	3.5
1	AM	27	ASN	3.5
1	EK	27	ASN	3.5
1	FO	60	THR	3.5
1	AJ	89	GLN	3.5
1	DN	122	SER	3.5
1	BH	123	GLY	3.5
1	DE	53	ASP	3.5
1	GM	136	GLY	3.5
1	EF	27	ASN	3.5
1	EE	89	GLN	3.5
1	DC	29	ASN	3.5
1	CL	60	THR	3.5
1	DY	59	ILE	3.5
1	DD	123	GLY	3.4
1	FN	117	THR	3.4
1	CC	89	GLN	3.4
1	CY	122	SER	3.4
1	DF	122	SER	3.4
1	CW	53	ASP	3.4
1	CX	28	GLY	3.4
1	BB	60	THR	3.4
1	BT	60	THR	3.4
1	CM	122	SER	3.4
1	DY	60	THR	3.4
1	AS	39	ASP	3.4
1	EF	39	ASP	3.4
1	GG	39	ASP	3.4
1	CF	58	GLY	3.4
1	GS	28	GLY	3.4
1	AV	60	THR	3.4

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Mol	Chain	Res	Type	RSRZ
1	CC	59	ILE	3.4
1	DD	117	THR	3.4
1	DD	120	THR	3.4
1	FO	39	ASP	3.4
1	FL	77	LYS	3.4
1	BN	89	GLN	3.4
1	BH	122	SER	3.3
1	DE	25	SER	3.3
1	DG	53	ASP	3.3
1	GP	39	ASP	3.3
1	AV	27	ASN	3.3
1	BN	27	ASN	3.3
1	CU	25	SER	3.3
1	AS	28	GLY	3.3
1	DG	89	GLN	3.3
1	FX	27	ASN	3.3
1	FC	28	GLY	3.3
1	BB	39	ASP	3.3
1	EZ	58	GLY	3.3
1	DE	4	SER	3.3
1	DH	122	SER	3.3
1	AG	39	ASP	3.3
1	CS	39	ASP	3.3
1	EN	39	ASP	3.3
1	CR	89	GLN	3.3
1	EQ	60	THR	3.3
1	BT	77	LYS	3.3
1	EP	55	LYS	3.3
1	FP	122	SER	3.2
1	EK	60	THR	3.2
1	FY	27	ASN	3.2
1	EQ	136	GLY	3.2
1	DY	89	GLN	3.2
1	EP	126	ASP	3.2
1	EW	39	ASP	3.2
1	FJ	117	THR	3.2
1	FY	60	THR	3.2
1	EY	27	ASN	3.2
1	CS	16	SER	3.2
1	EH	89	GLN	3.2
1	BW	39	ASP	3.2
1	FD	39	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	CO	58	GLY	3.2
1	DD	28	GLY	3.2
1	FO	28	GLY	3.2
1	DE	76	GLU	3.2
1	BS	30	ASN	3.2
1	CF	27	ASN	3.2
1	CT	29	ASN	3.2
1	GM	77	LYS	3.2
1	BK	39	ASP	3.2
1	AD	27	ASN	3.2
1	FC	27	ASN	3.2
1	GA	27	ASN	3.2
1	AK	39	ASP	3.1
1	GS	39	ASP	3.1
1	AJ	28	GLY	3.1
1	FR	58	GLY	3.1
1	GD	28	GLY	3.1
1	AV	121	VAL	3.1
1	DG	66	HIS	3.1
1	FI	89	GLN	3.1
1	AP	117	THR	3.1
1	CU	39	ASP	3.1
1	DM	27	ASN	3.1
1	FN	29	ASN	3.1
1	DE	6	ALA	3.1
1	EB	89	GLN	3.1
1	CG	117	THR	3.1
1	BI	118	SER	3.1
1	DJ	39	ASP	3.1
1	GL	53	ASP	3.1
1	BJ	29	ASN	3.1
1	DJ	59	ILE	3.1
1	GD	66	HIS	3.1
1	AM	60	THR	3.1
1	FJ	118	SER	3.1
1	DD	27	ASN	3.1
1	EE	124	GLN	3.1
1	FJ	126	ASP	3.1
1	FM	27	ASN	3.0
1	GJ	28	GLY	3.0
1	AD	60	THR	3.0
1	EH	60	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	DR	55	LYS	3.0
1	BO	76	GLU	3.0
1	FM	122	SER	3.0
1	FV	122	SER	3.0
1	DI	53	ASP	3.0
1	BS	27	ASN	3.0
1	FZ	27	ASN	3.0
1	GP	28	GLY	3.0
1	GS	77	LYS	3.0
1	AP	39	ASP	3.0
1	GM	39	ASP	3.0
1	AK	27	ASN	3.0
1	AN	27	ASN	3.0
1	AX	62	ASN	3.0
1	BB	27	ASN	3.0
1	CN	29	ASN	3.0
1	FO	58	GLY	3.0
1	CI	60	THR	3.0
1	AM	77	LYS	3.0
1	BI	124	GLN	3.0
1	BK	58	GLY	3.0
1	DS	89	GLN	3.0
1	CX	27	ASN	3.0
1	GM	27	ASN	3.0
1	GS	27	ASN	3.0
1	BH	120	THR	3.0
1	BO	122	SER	3.0
1	CL	122	SER	3.0
1	EF	122	SER	3.0
1	FR	39	ASP	3.0
1	BH	89	GLN	3.0
1	BJ	95	ASN	3.0
1	EN	27	ASN	3.0
1	CO	77	LYS	2.9
1	BT	28	GLY	2.9
1	ER	121	VAL	2.9
1	CU	126	ASP	2.9
1	DY	39	ASP	2.9
1	GP	59	ILE	2.9
1	FL	27	ASN	2.9
1	EF	13	THR	2.9
1	EM	96	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	GS	58	GLY	2.9
1	AY	53	ASP	2.9
1	FG	89	GLN	2.9
1	GA	39	ASP	2.9
1	CS	14	LEU	2.9
1	BK	77	LYS	2.9
1	CG	27	ASN	2.9
1	DX	77	LYS	2.9
1	EW	27	ASN	2.9
1	GH	117	THR	2.9
1	GR	135	ALA	2.9
1	CA	123	GLY	2.9
1	DD	89	GLN	2.9
1	DD	126	ASP	2.9
1	FU	77	LYS	2.9
1	GV	39	ASP	2.9
1	AV	120	THR	2.9
1	CN	27	ASN	2.9
1	ED	13	THR	2.9
1	DE	3	PRO	2.9
1	FN	99	ASN	2.9
1	FD	122	SER	2.9
1	FI	66	HIS	2.9
1	FZ	122	SER	2.9
1	DV	77	LYS	2.9
1	GF	51	LYS	2.9
1	CR	39	ASP	2.9
1	EY	53	ASP	2.9
1	CS	117	THR	2.9
1	BK	27	ASN	2.9
1	BV	29	ASN	2.9
1	DD	29	ASN	2.9
1	GF	29	ASN	2.9
1	BD	136	GLY	2.9
1	AP	59	ILE	2.9
1	AV	77	LYS	2.9
1	EE	138	MET	2.9
1	DT	122	SER	2.8
1	AL	53	ASP	2.8
1	CC	39	ASP	2.8
1	FK	53	ASP	2.8
1	GJ	39	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	BP	117	THR	2.8
1	CI	27	ASN	2.8
1	EE	121	VAL	2.8
1	BD	53	ASP	2.8
1	BP	30	ASN	2.8
1	DX	55	LYS	2.8
1	GH	99	ASN	2.8
1	AM	58	GLY	2.8
1	ET	58	GLY	2.8
1	GU	124	GLN	2.8
1	DE	119	ALA	2.8
1	ED	122	SER	2.8
1	EU	10	ALA	2.8
1	FD	16	SER	2.8
1	AA	60	THR	2.8
1	AQ	76	GLU	2.8
1	BX	117	THR	2.8
1	CM	53	ASP	2.8
1	DD	125	THR	2.8
1	DX	53	ASP	2.8
1	EX	53	ASP	2.8
1	BH	58	GLY	2.8
1	DN	99	ASN	2.8
1	FQ	27	ASN	2.8
1	AV	89	GLN	2.8
1	CD	89	GLN	2.8
1	FT	89	GLN	2.8
1	DT	76	GLU	2.8
1	EF	18	LEU	2.8
1	EF	76	GLU	2.8
1	AU	136	GLY	2.8
1	EQ	58	GLY	2.8
1	AQ	27	ASN	2.8
1	BW	27	ASN	2.8
1	EB	27	ASN	2.8
1	CI	89	GLN	2.8
1	EN	89	GLN	2.8
1	AQ	122	SER	2.8
1	AS	122	SER	2.8
1	EN	40	SER	2.8
1	DE	13	THR	2.8
1	GA	60	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	BH	39	ASP	2.7
1	BN	39	ASP	2.7
1	BU	39	ASP	2.7
1	DL	136	GLY	2.7
1	GI	53	ASP	2.7
1	DL	49	ASN	2.7
1	EI	68	ASN	2.7
1	DJ	89	GLN	2.7
1	BL	76	GLU	2.7
1	BU	76	GLU	2.7
1	GW	122	SER	2.7
1	CP	126	ASP	2.7
1	BJ	30	ASN	2.7
1	BM	27	ASN	2.7
1	EC	99	ASN	2.7
1	FT	27	ASN	2.7
1	GN	99	ASN	2.7
1	AP	119	ALA	2.7
1	DC	89	GLN	2.7
1	EW	89	GLN	2.7
1	AJ	60	THR	2.7
1	CA	122	SER	2.7
1	CL	28	GLY	2.7
1	CQ	122	SER	2.7
1	DF	128	SER	2.7
1	EF	4	SER	2.7
1	EI	122	SER	2.7
1	AT	53	ASP	2.7
1	CI	39	ASP	2.7
1	ED	135	ALA	2.7
1	CN	121	VAL	2.7
1	AM	59	ILE	2.7
1	CQ	123	GLY	2.7
1	DM	28	GLY	2.7
1	GN	76	GLU	2.7
1	AQ	25	SER	2.7
1	BZ	77	LYS	2.7
1	AP	126	ASP	2.7
1	BH	119	ALA	2.7
1	BX	53	ASP	2.7
1	DE	39	ASP	2.7
1	CF	62	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	EJ	29	ASN	2.7
1	BB	89	GLN	2.7
1	CL	89	GLN	2.7
1	GG	89	GLN	2.7
1	EG	76	GLU	2.7
1	DE	117	THR	2.7
1	CN	118	SER	2.7
1	CQ	118	SER	2.7
1	DE	40	SER	2.7
1	GO	122	SER	2.7
1	BT	66	HIS	2.7
1	AR	99	ASN	2.7
1	AY	27	ASN	2.7
1	BJ	99	ASN	2.7
1	AS	58	GLY	2.6
1	BB	28	GLY	2.6
1	EE	117	THR	2.6
1	ER	117	THR	2.6
1	FC	60	THR	2.6
1	FU	120	THR	2.6
1	CL	118	SER	2.6
1	CW	118	SER	2.6
1	FC	40	SER	2.6
1	BF	39	ASP	2.6
1	BZ	39	ASP	2.6
1	FF	39	ASP	2.6
1	GU	29	ASN	2.6
1	BW	28	GLY	2.6
1	EW	28	GLY	2.6
1	BW	77	LYS	2.6
1	EK	77	LYS	2.6
1	BS	29	ASN	2.6
1	EU	11	ASN	2.6
1	FF	89	GLN	2.6
1	GB	99	ASN	2.6
1	BN	58	GLY	2.6
1	EK	28	GLY	2.6
1	GA	61	GLY	2.6
1	FN	76	GLU	2.6
1	AD	56	ALA	2.6
1	BE	60	THR	2.6
1	BO	117	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	CO	60	THR	2.6
1	EI	83	THR	2.6
1	GW	117	THR	2.6
1	GL	55	LYS	2.6
1	AA	53	ASP	2.6
1	AD	53	ASP	2.6
1	DA	39	ASP	2.6
1	DQ	89	GLN	2.6
1	FC	53	ASP	2.6
1	CB	29	ASN	2.6
1	FT	99	ASN	2.6
1	GD	61	GLY	2.6
1	BF	76	GLU	2.6
1	CS	10	ALA	2.6
1	FX	60	THR	2.6
1	CC	77	LYS	2.6
1	EB	77	LYS	2.6
1	CU	66	HIS	2.6
1	DE	33	TYR	2.6
1	BH	118	SER	2.6
1	CW	122	SER	2.6
1	AW	39	ASP	2.6
1	CL	39	ASP	2.6
1	CU	58	GLY	2.6
1	DD	39	ASP	2.6
1	EU	84	GLY	2.6
1	EH	27	ASN	2.6
1	ES	27	ASN	2.6
1	EV	53	ASP	2.6
1	GD	39	ASP	2.6
1	DY	76	GLU	2.6
1	DD	119	ALA	2.6
1	EA	77	LYS	2.6
1	FF	60	THR	2.6
1	FI	120	THR	2.6
1	FP	117	THR	2.6
1	GT	120	THR	2.6
1	AS	59	ILE	2.5
1	FY	122	SER	2.5
1	FZ	16	SER	2.5
1	AA	58	GLY	2.5
1	EN	26	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	AD	77	LYS	2.5
1	BJ	51	LYS	2.5
1	BU	27	ASN	2.5
1	CQ	30	ASN	2.5
1	DA	121	VAL	2.5
1	DF	27	ASN	2.5
1	EF	126	ASP	2.5
1	EG	29	ASN	2.5
1	FM	53	ASP	2.5
1	GD	27	ASN	2.5
1	EP	119	ALA	2.5
1	FN	1	ALA	2.5
1	FZ	76	GLU	2.5
1	GG	77	LYS	2.5
1	AY	60	THR	2.5
1	DV	120	THR	2.5
1	DE	130	PHE	2.5
1	FL	66	HIS	2.5
1	AO	122	SER	2.5
1	DP	58	GLY	2.5
1	EH	122	SER	2.5
1	EX	122	SER	2.5
1	GC	122	SER	2.5
1	DE	89	GLN	2.5
1	FL	89	GLN	2.5
1	GI	89	GLN	2.5
1	AB	27	ASN	2.5
1	BT	76	GLU	2.5
1	FN	119	ALA	2.5
1	GO	53	ASP	2.5
1	DD	59	ILE	2.5
1	AM	13	THR	2.5
1	BH	60	THR	2.5
1	DD	127	THR	2.5
1	FZ	13	THR	2.5
1	FZ	117	THR	2.5
1	CW	55	LYS	2.5
1	ED	137	LEU	2.5
1	DS	58	GLY	2.5
1	EG	55	LYS	2.5
1	GP	77	LYS	2.5
1	DF	76	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	FJ	76	GLU	2.5
1	DJ	27	ASN	2.5
1	DS	27	ASN	2.5
1	DY	53	ASP	2.5
1	FI	27	ASN	2.5
1	FM	29	ASN	2.5
1	FO	27	ASN	2.5
1	FU	59	ILE	2.5
1	GC	30	ASN	2.5
1	GE	27	ASN	2.5
1	AP	120	THR	2.5
1	BL	60	THR	2.5
1	CB	117	THR	2.5
1	DF	117	THR	2.5
1	BG	55	LYS	2.5
1	EZ	77	LYS	2.5
1	BB	58	GLY	2.5
1	FN	25	SER	2.5
1	GQ	118	SER	2.5
1	FV	76	GLU	2.5
1	GM	59	ILE	2.5
1	BF	68	ASN	2.5
1	BS	53	ASP	2.5
1	CA	53	ASP	2.5
1	CC	27	ASN	2.5
1	CM	39	ASP	2.5
1	CU	27	ASN	2.5
1	CX	39	ASP	2.5
1	CZ	53	ASP	2.5
1	EL	99	ASN	2.5
1	EP	29	ASN	2.5
1	GL	30	ASN	2.5
1	AH	117	THR	2.5
1	CQ	77	LYS	2.5
1	DM	64	ARG	2.5
1	FC	66	HIS	2.5
1	AM	136	GLY	2.5
1	DD	26	GLN	2.5
1	AW	40	SER	2.4
1	CS	12	SER	2.4
1	EF	40	SER	2.4
1	EQ	59	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	FO	59	ILE	2.4
1	AP	27	ASN	2.4
1	BJ	27	ASN	2.4
1	CO	27	ASN	2.4
1	ET	39	ASP	2.4
1	FX	77	LYS	2.4
1	FZ	62	ASN	2.4
1	GO	55	LYS	2.4
1	BN	117	THR	2.4
1	BQ	117	THR	2.4
1	CA	120	THR	2.4
1	CY	60	THR	2.4
1	EU	87	THR	2.4
1	EE	140	PRO	2.4
1	AD	136	GLY	2.4
1	FL	58	GLY	2.4
1	GA	28	GLY	2.4
1	AH	89	GLN	2.4
1	AY	89	GLN	2.4
1	CU	89	GLN	2.4
1	CI	59	ILE	2.4
1	AL	122	SER	2.4
1	FR	77	LYS	2.4
1	BH	117	THR	2.4
1	BP	99	ASN	2.4
1	CU	120	THR	2.4
1	DC	27	ASN	2.4
1	DT	53	ASP	2.4
1	EN	60	THR	2.4
1	FH	117	THR	2.4
1	FL	60	THR	2.4
1	FZ	49	ASN	2.4
1	GF	27	ASN	2.4
1	BP	53	ASP	2.4
1	GM	57	PRO	2.4
1	AV	66	HIS	2.4
1	CI	58	GLY	2.4
1	AW	89	GLN	2.4
1	BW	59	ILE	2.4
1	EH	77	LYS	2.4
1	AH	76	GLU	2.4
1	AJ	27	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	CH	30	ASN	2.4
1	CH	117	THR	2.4
1	DF	140	PRO	2.4
1	EF	3	PRO	2.4
1	EU	68	ASN	2.4
1	FN	3	PRO	2.4
1	CG	126	ASP	2.4
1	DC	53	ASP	2.4
1	EQ	53	ASP	2.4
1	FC	39	ASP	2.4
1	GO	136	GLY	2.4
1	BT	59	ILE	2.4
1	CU	59	ILE	2.4
1	AG	89	GLN	2.4
1	AV	124	GLN	2.4
1	DE	124	GLN	2.4
1	AP	128	SER	2.4
1	AW	122	SER	2.4
1	CB	118	SER	2.4
1	DE	122	SER	2.4
1	CU	127	THR	2.4
1	EQ	120	THR	2.4
1	AX	29	ASN	2.4
1	BU	99	ASN	2.4
1	GR	27	ASN	2.4
1	AQ	126	ASP	2.4
1	BX	39	ASP	2.4
1	DT	39	ASP	2.4
1	DJ	56	ALA	2.4
1	DU	77	LYS	2.4
1	GV	77	LYS	2.4
1	EP	124	GLN	2.4
1	EU	89	GLN	2.4
1	DH	76	GLU	2.4
1	BP	12	SER	2.4
1	DE	128	SER	2.4
1	EP	122	SER	2.4
1	EQ	82	SER	2.4
1	FJ	122	SER	2.4
1	GA	40	SER	2.4
1	GD	122	SER	2.4
1	DY	58	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	EB	117	THR	2.3
1	EU	17	THR	2.3
1	FZ	87	THR	2.3
1	BG	77	LYS	2.3
1	BV	27	ASN	2.3
1	DF	119	ALA	2.3
1	DJ	77	LYS	2.3
1	DV	56	ALA	2.3
1	EA	30	ASN	2.3
1	EP	51	LYS	2.3
1	GC	55	LYS	2.3
1	GN	68	ASN	2.3
1	GP	27	ASN	2.3
1	GP	95	ASN	2.3
1	CQ	53	ASP	2.3
1	EJ	53	ASP	2.3
1	EN	124	GLN	2.3
1	AT	122	SER	2.3
1	EF	128	SER	2.3
1	EJ	122	SER	2.3
1	EN	122	SER	2.3
1	GH	118	SER	2.3
1	AD	117	THR	2.3
1	AP	77	LYS	2.3
1	BI	117	THR	2.3
1	CL	58	GLY	2.3
1	DT	117	THR	2.3
1	EG	117	THR	2.3
1	AM	56	ALA	2.3
1	CO	66	HIS	2.3
1	FT	95	ASN	2.3
1	GR	138	MET	2.3
1	AJ	39	ASP	2.3
1	CP	39	ASP	2.3
1	EU	53	ASP	2.3
1	CH	89	GLN	2.3
1	DA	89	GLN	2.3
1	GX	124	GLN	2.3
1	CM	76	GLU	2.3
1	AG	77	LYS	2.3
1	CH	51	LYS	2.3
1	CK	77	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	FC	77	LYS	2.3
1	DO	96	PRO	2.3
1	AG	28	GLY	2.3
1	AY	59	ILE	2.3
1	AW	83	THR	2.3
1	BI	120	THR	2.3
1	BI	122	SER	2.3
1	BM	118	SER	2.3
1	CS	84	GLY	2.3
1	DB	122	SER	2.3
1	EE	58	GLY	2.3
1	FF	59	ILE	2.3
1	DT	120	THR	2.3
1	EE	125	THR	2.3
1	EN	12	SER	2.3
1	EN	58	GLY	2.3
1	FA	122	SER	2.3
1	GN	117	THR	2.3
1	AL	27	ASN	2.3
1	EO	29	ASN	2.3
1	FB	29	ASN	2.3
1	GU	30	ASN	2.3
1	DF	126	ASP	2.3
1	DS	39	ASP	2.3
1	EM	53	ASP	2.3
1	GM	89	GLN	2.3
1	EX	76	GLU	2.3
1	CI	77	LYS	2.3
1	GC	77	LYS	2.3
1	DD	140	PRO	2.3
1	AY	58	GLY	2.3
1	CI	136	GLY	2.3
1	DA	58	GLY	2.3
1	EG	123	GLY	2.3
1	FR	59	ILE	2.3
1	FZ	136	GLY	2.3
1	GG	28	GLY	2.3
1	GV	58	GLY	2.3
1	CQ	50	ALA	2.3
1	ES	50	ALA	2.3
1	FX	56	ALA	2.3
1	AE	117	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	DG	60	THR	2.3
1	DU	118	SER	2.3
1	FT	122	SER	2.3
1	GK	122	SER	2.3
1	BD	27	ASN	2.3
1	BI	27	ASN	2.3
1	EG	27	ASN	2.3
1	FG	99	ASN	2.3
1	GB	68	ASN	2.3
1	AI	53	ASP	2.3
1	BY	89	GLN	2.3
1	ED	53	ASP	2.3
1	AY	77	LYS	2.3
1	DI	64	ARG	2.3
1	AP	28	GLY	2.3
1	AV	28	GLY	2.3
1	BH	28	GLY	2.3
1	CI	28	GLY	2.3
1	DW	58	GLY	2.3
1	FA	117	THR	2.3
1	FM	117	THR	2.3
1	FS	60	THR	2.3
1	GD	60	THR	2.3
1	GR	117	THR	2.3
1	GV	66	HIS	2.3
1	CZ	122	SER	2.3
1	EE	130	PHE	2.3
1	EF	25	SER	2.3
1	FO	40	SER	2.3
1	BM	29	ASN	2.3
1	CH	29	ASN	2.3
1	CI	62	ASN	2.3
1	EE	30	ASN	2.3
1	FH	77	LYS	2.3
1	GJ	68	ASN	2.3
1	FU	89	GLN	2.3
1	FX	89	GLN	2.3
1	GJ	89	GLN	2.3
1	BI	53	ASP	2.3
1	EF	121	VAL	2.3
1	AG	61	GLY	2.2
1	AJ	58	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	AM	61	GLY	2.2
1	BM	129	GLY	2.2
1	DI	96	PRO	2.2
1	DS	28	GLY	2.2
1	DY	57	PRO	2.2
1	EN	3	PRO	2.2
1	BW	117	THR	2.2
1	EF	36	THR	2.2
1	EN	120	THR	2.2
1	AV	118	SER	2.2
1	BD	122	SER	2.2
1	CE	55	LYS	2.2
1	CF	40	SER	2.2
1	FE	25	SER	2.2
1	AO	29	ASN	2.2
1	BV	89	GLN	2.2
1	DC	62	ASN	2.2
1	EA	62	ASN	2.2
1	EJ	99	ASN	2.2
1	ES	29	ASN	2.2
1	AO	53	ASP	2.2
1	BS	126	ASP	2.2
1	CG	76	GLU	2.2
1	FZ	39	ASP	2.2
1	AV	59	ILE	2.2
1	BN	28	GLY	2.2
1	CF	28	GLY	2.2
1	CQ	3	PRO	2.2
1	CU	28	GLY	2.2
1	AN	117	THR	2.2
1	AO	51	LYS	2.2
1	BV	51	LYS	2.2
1	ED	139	PHE	2.2
1	CH	87	THR	2.2
1	EH	66	HIS	2.2
1	FD	117	THR	2.2
1	GP	60	THR	2.2
1	BD	12	SER	2.2
1	BY	101	SER	2.2
1	DK	122	SER	2.2
1	FA	118	SER	2.2
1	GV	4	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	FA	121	VAL	2.2
1	CP	89	GLN	2.2
1	CX	89	GLN	2.2
1	DH	124	GLN	2.2
1	EK	89	GLN	2.2
1	EP	89	GLN	2.2
1	FJ	124	GLN	2.2
1	FP	89	GLN	2.2
1	AC	29	ASN	2.2
1	AS	27	ASN	2.2
1	CZ	30	ASN	2.2
1	DF	29	ASN	2.2
1	DO	99	ASN	2.2
1	DY	27	ASN	2.2
1	AZ	76	GLU	2.2
1	CL	59	ILE	2.2
1	BC	53	ASP	2.2
1	DG	39	ASP	2.2
1	FV	53	ASP	2.2
1	AP	3	PRO	2.2
1	AY	28	GLY	2.2
1	CW	119	ALA	2.2
1	DE	140	PRO	2.2
1	DH	96	PRO	2.2
1	FJ	119	ALA	2.2
1	DA	77	LYS	2.2
1	FO	77	LYS	2.2
1	CA	117	THR	2.2
1	CL	83	THR	2.2
1	EN	13	THR	2.2
1	FA	125	THR	2.2
1	GD	117	THR	2.2
1	BO	12	SER	2.2
1	EG	122	SER	2.2
1	FM	12	SER	2.2
1	GC	118	SER	2.2
1	CM	89	GLN	2.2
1	EZ	89	GLN	2.2
1	GO	89	GLN	2.2
1	EW	59	ILE	2.2
1	GG	59	ILE	2.2
1	AB	76	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	AL	29	ASN	2.2
1	CW	29	ASN	2.2
1	DE	18	LEU	2.2
1	AJ	61	GLY	2.2
1	BS	136	GLY	2.2
1	AF	77	LYS	2.2
1	CR	55	LYS	2.2
1	DM	39	ASP	2.2
1	DS	77	LYS	2.2
1	EN	77	LYS	2.2
1	DT	83	THR	2.2
1	EB	60	THR	2.2
1	ET	87	THR	2.2
1	FZ	17	THR	2.2
1	GB	117	THR	2.2
1	GK	13	THR	2.2
1	BH	59	ILE	2.2
1	BO	124	GLN	2.2
1	CJ	122	SER	2.2
1	CO	89	GLN	2.2
1	CQ	25	SER	2.2
1	DD	118	SER	2.2
1	ER	118	SER	2.2
1	GP	122	SER	2.2
1	AR	20	ASN	2.2
1	BQ	77	LYS	2.2
1	BV	30	ASN	2.2
1	DH	27	ASN	2.2
1	FA	76	GLU	2.2
1	FY	76	GLU	2.2
1	EM	77	LYS	2.2
1	GL	29	ASN	2.2
1	GQ	99	ASN	2.2
1	GR	99	ASN	2.2
1	EP	123	GLY	2.2
1	EU	9	GLY	2.2
1	GP	58	GLY	2.2
1	AD	39	ASP	2.2
1	BC	39	ASP	2.2
1	CO	39	ASP	2.2
1	EA	39	ASP	2.2
1	EZ	39	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	FI	39	ASP	2.2
1	BH	66	HIS	2.2
1	BD	13	THR	2.1
1	DA	117	THR	2.1
1	EE	60	THR	2.1
1	EJ	87	THR	2.1
1	EU	117	THR	2.1
1	CO	59	ILE	2.1
1	DA	59	ILE	2.1
1	AX	89	GLN	2.1
1	DT	89	GLN	2.1
1	AO	55	LYS	2.1
1	AX	55	LYS	2.1
1	BY	55	LYS	2.1
1	CH	119	ALA	2.1
1	CH	122	SER	2.1
1	DB	40	SER	2.1
1	DZ	12	SER	2.1
1	EE	128	SER	2.1
1	ET	77	LYS	2.1
1	EO	67	ALA	2.1
1	FJ	128	SER	2.1
1	GD	55	LYS	2.1
1	AM	30	ASN	2.1
1	BN	62	ASN	2.1
1	BZ	27	ASN	2.1
1	CN	30	ASN	2.1
1	CS	62	ASN	2.1
1	CW	27	ASN	2.1
1	DE	29	ASN	2.1
1	DU	96	PRO	2.1
1	ED	140	PRO	2.1
1	ET	27	ASN	2.1
1	FJ	99	ASN	2.1
1	GG	27	ASN	2.1
1	GT	27	ASN	2.1
1	BG	53	ASP	2.1
1	DH	39	ASP	2.1
1	FH	53	ASP	2.1
1	DD	66	HIS	2.1
1	CI	117	THR	2.1
1	CP	117	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	CU	117	THR	2.1
1	DP	117	THR	2.1
1	AA	59	ILE	2.1
1	BN	59	ILE	2.1
1	FX	59	ILE	2.1
1	GO	77	LYS	2.1
1	BA	89	GLN	2.1
1	DF	1	ALA	2.1
1	GX	119	ALA	2.1
1	AF	122	SER	2.1
1	BO	96	PRO	2.1
1	CH	118	SER	2.1
1	CH	128	SER	2.1
1	CO	28	GLY	2.1
1	CQ	22	SER	2.1
1	CW	61	GLY	2.1
1	DJ	76	GLU	2.1
1	EO	76	GLU	2.1
1	EU	76	GLU	2.1
1	FS	76	GLU	2.1
1	FT	96	PRO	2.1
1	AQ	29	ASN	2.1
1	AW	27	ASN	2.1
1	CW	30	ASN	2.1
1	DX	29	ASN	2.1
1	EP	30	ASN	2.1
1	AM	39	ASP	2.1
1	CD	53	ASP	2.1
1	EB	126	ASP	2.1
1	FP	39	ASP	2.1
1	FV	39	ASP	2.1
1	FO	66	HIS	2.1
1	CO	51	LYS	2.1
1	EB	120	THR	2.1
1	EZ	59	ILE	2.1
1	GR	51	LYS	2.1
1	DJ	64	ARG	2.1
1	ED	138	MET	2.1
1	BS	1	ALA	2.1
1	CN	124	GLN	2.1
1	CQ	10	ALA	2.1
1	CY	76	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	EF	140	PRO	2.1
1	FU	58	GLY	2.1
1	GC	116	GLY	2.1
1	GU	96	PRO	2.1
1	AM	25	SER	2.1
1	AR	122	SER	2.1
1	BY	4	SER	2.1
1	CI	12	SER	2.1
1	CU	40	SER	2.1
1	DE	16	SER	2.1
1	EN	25	SER	2.1
1	EU	82	SER	2.1
1	AD	62	ASN	2.1
1	AO	27	ASN	2.1
1	CA	29	ASN	2.1
1	DD	30	ASN	2.1
1	EV	29	ASN	2.1
1	BI	39	ASP	2.1
1	CI	53	ASP	2.1
1	CS	53	ASP	2.1
1	CZ	77	LYS	2.1
1	DP	39	ASP	2.1
1	EE	59	ILE	2.1
1	FA	53	ASP	2.1
1	FG	53	ASP	2.1
1	FN	77	LYS	2.1
1	GD	77	LYS	2.1
1	GE	39	ASP	2.1
1	GI	55	LYS	2.1
1	GJ	77	LYS	2.1
1	GS	51	LYS	2.1
1	AN	60	THR	2.1
1	AT	60	THR	2.1
1	BJ	125	THR	2.1
1	DF	127	THR	2.1
1	DQ	60	THR	2.1
1	EN	117	THR	2.1
1	FE	87	THR	2.1
1	GJ	117	THR	2.1
1	CL	1	ALA	2.1
1	EN	15	ALA	2.1
1	GX	100	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	AN	89	GLN	2.1
1	AP	89	GLN	2.1
1	AV	109	GLN	2.1
1	GK	89	GLN	2.1
1	AN	123	GLY	2.1
1	CF	61	GLY	2.1
1	CD	38	PRO	2.1
1	CI	76	GLU	2.1
1	DT	140	PRO	2.1
1	GI	96	PRO	2.1
1	AA	40	SER	2.1
1	AU	118	SER	2.1
1	BY	122	SER	2.1
1	CZ	118	SER	2.1
1	EE	118	SER	2.1
1	GN	122	SER	2.1
1	AP	30	ASN	2.1
1	CF	77	LYS	2.1
1	CN	49	ASN	2.1
1	CZ	27	ASN	2.1
1	DC	30	ASN	2.1
1	DL	30	ASN	2.1
1	EQ	77	LYS	2.1
1	EV	55	LYS	2.1
1	EZ	79	ASN	2.1
1	FB	99	ASN	2.1
1	FH	30	ASN	2.1
1	GF	49	ASN	2.1
1	BH	64	ARG	2.1
1	EK	64	ARG	2.1
1	AP	53	ASP	2.1
1	CV	39	ASP	2.1
1	DT	138	MET	2.1
1	EF	37	ASP	2.1
1	GF	53	ASP	2.1
1	BW	60	THR	2.1
1	CR	60	THR	2.1
1	DX	13	THR	2.1
1	GV	117	THR	2.1
1	CS	6	ALA	2.1
1	BD	129	GLY	2.1
1	BT	89	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	DF	123	GLY	2.1
1	EE	28	GLY	2.1
1	CU	57	PRO	2.1
1	GL	76	GLU	2.1
1	BT	51	LYS	2.0
1	DF	77	LYS	2.0
1	FF	77	LYS	2.0
1	FN	55	LYS	2.0
1	AK	40	SER	2.0
1	AY	40	SER	2.0
1	BJ	122	SER	2.0
1	BQ	40	SER	2.0
1	CG	118	SER	2.0
1	AP	29	ASN	2.0
1	BC	99	ASN	2.0
1	GF	64	ARG	2.0
1	BZ	66	HIS	2.0
1	CL	66	HIS	2.0
1	EE	66	HIS	2.0
1	BA	13	THR	2.0
1	BV	53	ASP	2.0
1	EH	39	ASP	2.0
1	EO	83	THR	2.0
1	EP	112	ASP	2.0
1	FB	53	ASP	2.0
1	GH	60	THR	2.0
1	GR	120	THR	2.0
1	GV	60	THR	2.0
1	GX	125	THR	2.0
1	AE	130	PHE	2.0
1	BJ	123	GLY	2.0
1	BP	124	GLN	2.0
1	CF	89	GLN	2.0
1	EG	124	GLN	2.0
1	EP	52	PHE	2.0
1	AK	76	GLU	2.0
1	CD	76	GLU	2.0
1	GA	77	LYS	2.0
1	CU	128	SER	2.0
1	DC	122	SER	2.0
1	AO	62	ASN	2.0
1	BT	49	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	EF	20	ASN	2.0
1	EV	30	ASN	2.0
1	FN	30	ASN	2.0
1	GK	27	ASN	2.0
1	AN	87	THR	2.0
1	AV	117	THR	2.0
1	BC	60	THR	2.0
1	BT	87	THR	2.0
1	CJ	120	THR	2.0
1	CN	60	THR	2.0
1	CY	117	THR	2.0
1	DE	50	ALA	2.0
1	FB	60	THR	2.0
1	FY	83	THR	2.0
1	BP	126	ASP	2.0
1	CE	53	ASP	2.0
1	FW	53	ASP	2.0
1	GH	53	ASP	2.0
1	DN	61	GLY	2.0
1	EU	123	GLY	2.0
1	FD	9	GLY	2.0
1	BH	77	LYS	2.0
1	BS	55	LYS	2.0
1	CL	77	LYS	2.0
1	DG	51	LYS	2.0
1	DH	89	GLN	2.0
1	FI	51	LYS	2.0
1	GD	89	GLN	2.0
1	ER	76	GLU	2.0
1	GE	76	GLU	2.0
1	CE	64	ARG	2.0
1	CN	64	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.