



Full wwPDB EM Validation Report ⓘ

Jan 1, 2025 – 11:55 AM EST

PDB ID : 8TW2
EMDB ID : EMD-41657
Title : Acinetobacter phage AP205 T=4 VLP
Authors : Meng, R.; Xing, Z.; Zhang, J.
Deposited on : 2023-08-19
Resolution : 3.39 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

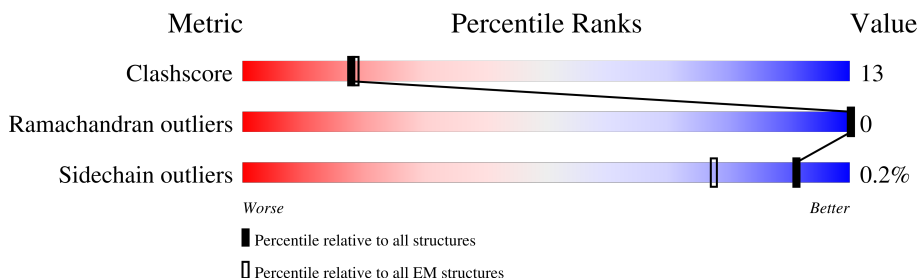
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.39 Å.

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









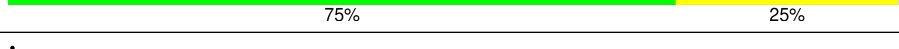
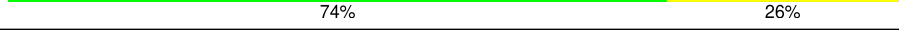
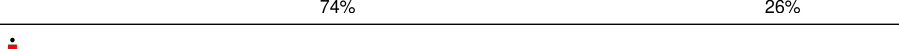
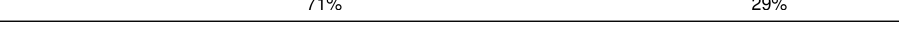
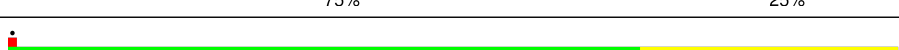

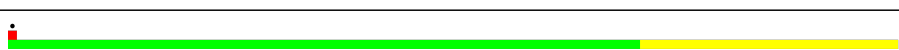

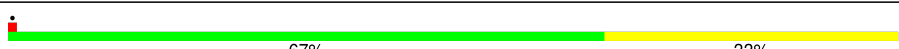





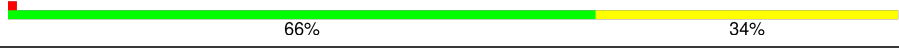
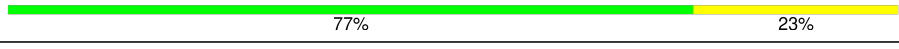



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	129	74% 26%
1	AB	129	65% 35%
1	AC	129	77% 23%
1	AD	129	64% 36%
1	AE	129	67% 33%
1	AF	129	68% 32%
1	AG	129	78% 22%
1	AH	129	67% 33%



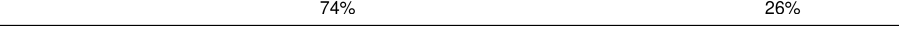
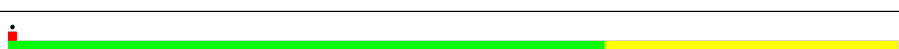



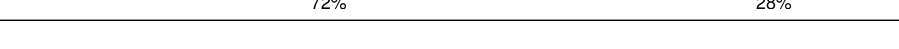



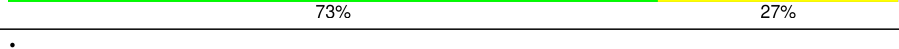

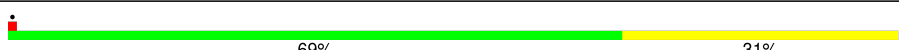


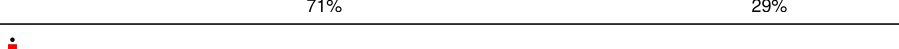







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Mol	Chain	Length	Quality of chain
1	AI	129	
1	AJ	129	
1	AK	129	
1	AL	129	
1	AM	129	
1	AN	129	
1	AO	129	
1	AP	129	
1	AQ	129	
1	AR	129	
1	AS	129	
1	AT	129	
1	AU	129	
1	AV	129	
1	AW	129	
1	AX	129	
1	AY	129	
1	AZ	129	
1	BA	129	
1	BB	129	
1	BC	129	
1	BD	129	
1	BE	129	
1	BF	129	
1	BG	129	



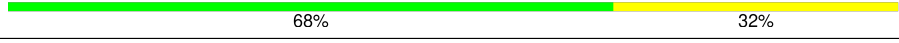
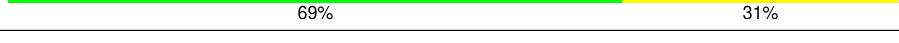
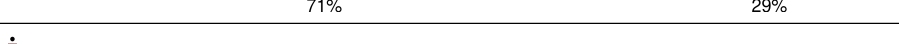
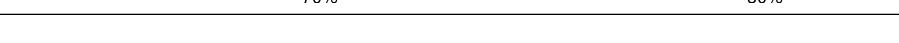






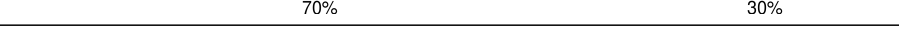

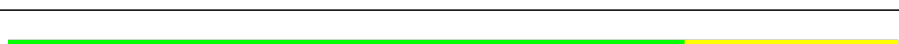






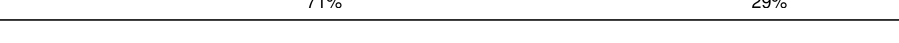



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Mol	Chain	Length	Quality of chain
1	BH	129	
1	BI	129	
1	BJ	129	
1	BK	129	
1	BL	129	
1	BM	129	
1	BN	129	
1	BO	129	
1	BP	129	
1	BQ	129	
1	BR	129	
1	BS	129	
1	BT	129	
1	BU	129	
1	BV	129	
1	BW	129	
1	BX	129	
1	BY	129	
1	BZ	129	
1	CA	129	
1	CB	129	
1	CC	129	
1	CD	129	
1	CE	129	
1	CF	129	



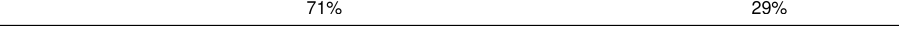
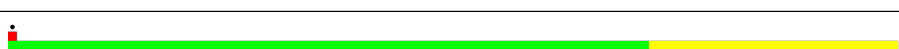



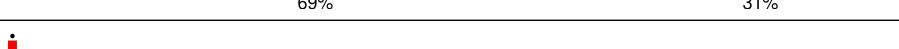



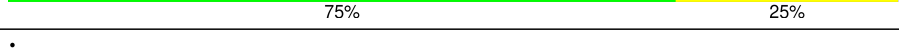

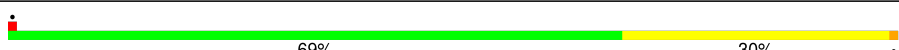


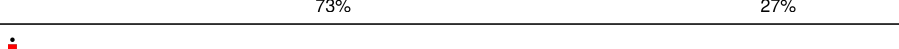







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Mol	Chain	Length	Quality of chain
1	CG	129	
1	CH	129	
1	CI	129	
1	CJ	129	
1	CK	129	
1	CL	129	
1	CM	129	
1	CN	129	
1	CO	129	
1	CP	129	
1	CQ	129	
1	CR	129	
1	CS	129	
1	CT	129	
1	CU	129	
1	CV	129	
1	CW	129	
1	CX	129	
1	CY	129	
1	CZ	129	
1	DA	129	
1	DB	129	
1	DC	129	
1	DE	129	
1	DF	129	

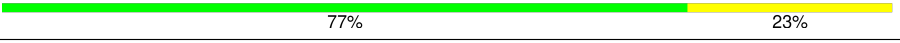










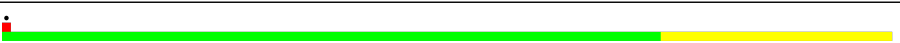




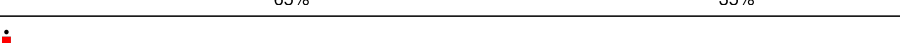
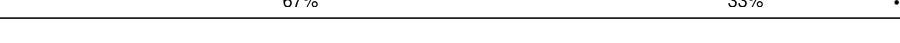



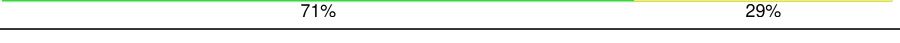



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Mol	Chain	Length	Quality of chain
1	DG	129	
1	DH	129	
1	DI	129	
1	DJ	129	
1	DK	129	
1	DL	129	
1	DM	129	
1	DN	129	
1	DO	129	
1	DP	129	
1	DQ	129	
1	DR	129	
1	DS	129	
1	DT	129	
1	DU	129	
1	DV	129	
1	DW	129	
1	DX	129	
1	DY	129	
1	DZ	129	
1	EA	129	
1	EB	129	
1	EC	129	
1	ED	129	
1	EE	129	


























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Mol	Chain	Length	Quality of chain
1	EF	129	
1	EG	129	
1	EH	129	
1	EI	129	
1	EJ	129	
1	EK	129	
1	EL	129	
1	EM	129	
1	EN	129	
1	EO	129	
1	EP	129	
1	EQ	129	
1	ER	129	
1	ES	129	
1	ET	129	
1	EU	129	
1	EV	129	
1	EW	129	
1	EX	129	
1	EY	129	
1	EZ	129	
1	FA	129	
1	FB	129	
1	FC	129	
1	FD	129	


























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Mol	Chain	Length	Quality of chain
1	FE	129	 80% 19%
1	FF	129	 71% 28%
1	FG	129	 73% 27%
1	FH	129	 66% 33%
1	FI	129	 77% 23%
1	FJ	129	 78% 22%
1	FK	129	 73% 27%
1	FL	129	 70% 30%
1	FM	129	 67% 32%
1	FN	129	 71% 29%
1	FO	129	 73% 27%
1	FP	129	 69% 30%
1	FQ	129	 74% 26%
1	FR	129	 72% 28%
1	FS	129	 70% 29%
1	FT	129	 70% 29%
1	FU	129	 74% 26%
1	FV	129	 74% 26%
1	FW	129	 63% 37%
1	FX	129	 74% 26%
1	FY	129	 70% 30%
1	FZ	129	 69% 30%
1	GA	129	 74% 26%
1	GB	129	 73% 27%
1	GC	129	 84% 16%


























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Mol	Chain	Length	Quality of chain
1	GD	129	
1	GE	129	
1	GF	129	
1	GG	129	
1	GH	129	
1	GI	129	
1	GK	129	
1	GL	129	
1	GM	129	
1	GN	129	
1	GO	129	
1	GP	129	
1	GQ	129	
1	GR	129	
1	GS	129	
1	GT	129	
1	GU	129	
1	GV	129	
1	GW	129	
1	GX	129	
1	GY	129	
1	GZ	129	
1	HA	129	
1	HB	129	
1	HC	129	



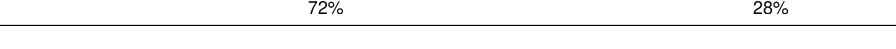
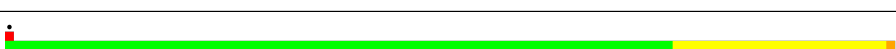



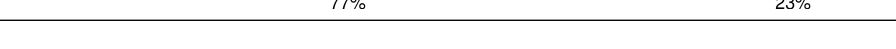



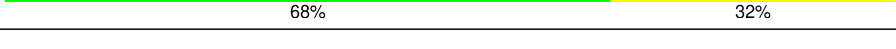

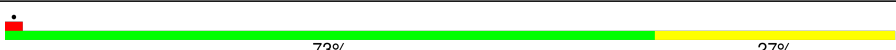


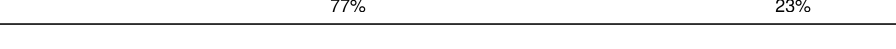







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Mol	Chain	Length	Quality of chain
1	HD	129	 74%26%
1	HE	129	 72%28%
1	HF	129	 75%25%
1	HG	129	 75%25%
1	HI	129	 66%34%
1	HJ	129	 72%28%
1	HK	129	 74%26%
1	HL	129	 73%27%
1	HM	129	 77%23%
1	HN	129	 74%26%
1	HO	129	 83%17%
1	HP	129	 78%22%
1	HQ	129	 72%28%
1	HR	129	 69%31%
1	HS	129	 70%30%
1	HT	129	 68%32%
1	HU	129	 73%27%
1	HV	129	 68%32%
1	HW	129	 72%28%
1	HX	129	 73%27%
1	HY	129	 78%22%
1	HZ	129	 65%35%
1	IA	129	 77%23%
1	IB	129	 71%29%
1	IC	129	 74%26%

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Mol	Chain	Length	Quality of chain
1	ID	129	
1	IE	129	
1	IF	129	
1	IG	129	
1	IH	129	
1	II	129	
1	IJ	129	
1	IK	129	
1	IL	129	
1	IM	129	
1	IN	129	
1	IO	129	
1	IP	129	
1	IQ	129	
1	IR	129	
1	IS	129	
1	IT	129	
1	IU	129	
1	IV	129	
1	IW	129	
1	IX	129	
1	IZ	129	
1	JA	129	
1	JB	129	
1	JC	129	

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Mol	Chain	Length	Quality of chain
1	JD	129	 71%29%
1	JE	129	 73%27%
1	JF	129	 66%34%
1	JG	129	 77%23%
1	JH	129	 74%26%
1	JI	129	 71%29%
1	JJ	129	 71%29%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 232320 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Coat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AQ	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BL	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CG	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DB	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DX	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	ED	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	ER	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	ES	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	ET	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FN	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	FO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GI	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	GK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HE	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	HF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	HZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IA	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	IB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	ID	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	II	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IV	129	Total 968	C 602	N 171	O 191	S 4	0	0

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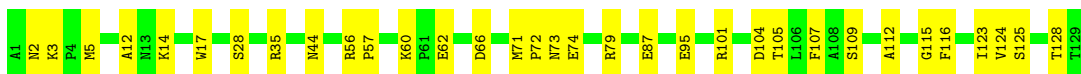
Mol	Chain	Residues	Atoms					AltConf	Trace
1	IW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	IZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	JJ	129	Total 968	C 602	N 171	O 191	S 4	0	0

3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

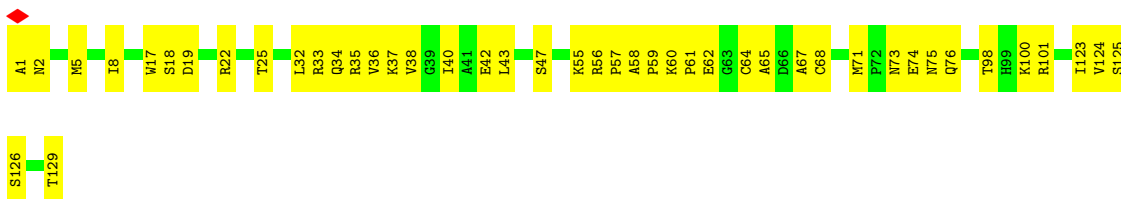
- Molecule 1: Coat protein

Chain AA:  74% 26%




- Molecule 1: Coat protein

Chain AB:  65% 35%



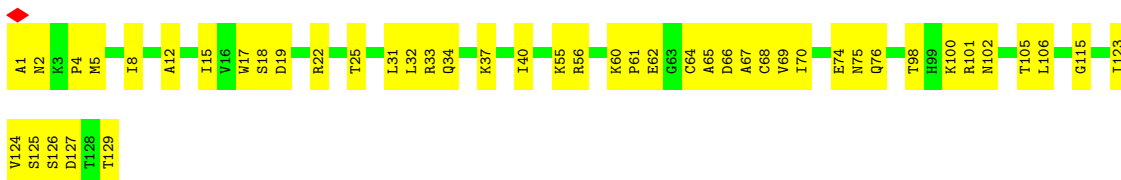
- Molecule 1: Coat protein

Chain AC:  77% 23%



- Molecule 1: Coat protein

Chain AD:  64% 36%



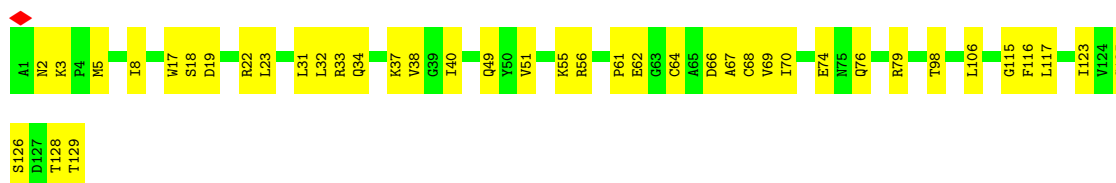
- Molecule 1: Coat protein

Chain AE:  67% 33%




- Molecule 1: Coat protein

Chain AF:  68% 32%



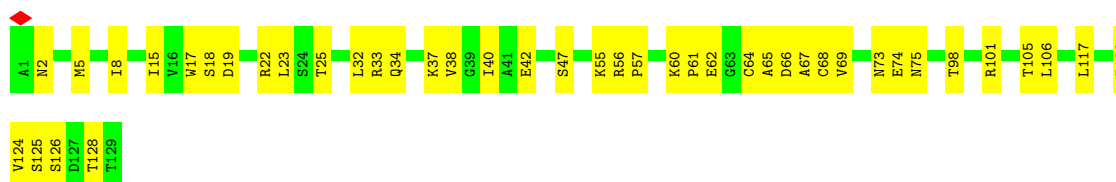
- Molecule 1: Coat protein

Chain AG:  78% 22%



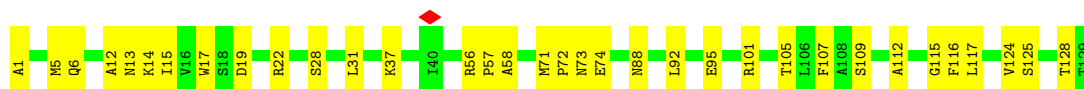
- Molecule 1: Coat protein

Chain AH:  67% 33%



- Molecule 1: Coat protein

Chain AI:  74% 26%




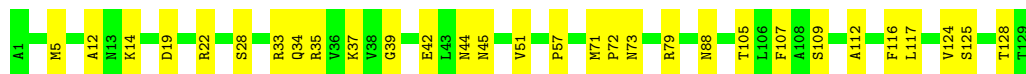
- Molecule 1: Coat protein

Chain AJ:  68% 32%



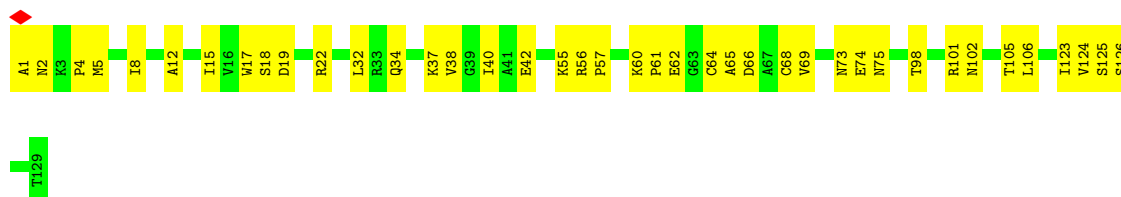
- Molecule 1: Coat protein

Chain AK:  77% 23%



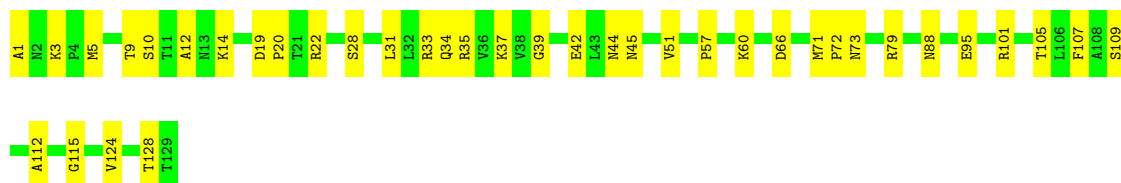
- Molecule 1: Coat protein

Chain AL:  69% 31%



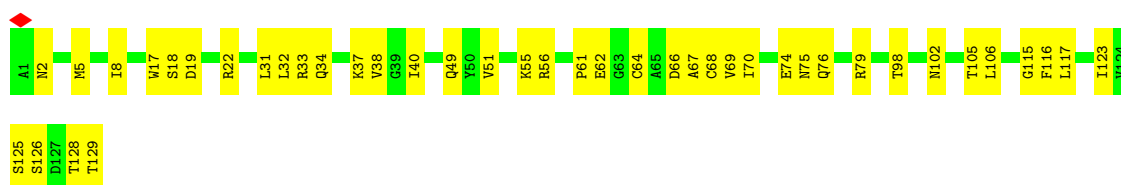
- Molecule 1: Coat protein

Chain AM:  71% 29%




- Molecule 1: Coat protein

Chain AN:  67% 33%



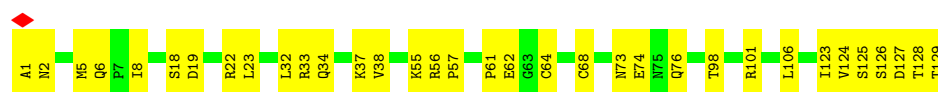
- Molecule 1: Coat protein

Chain AO:  75% 25%

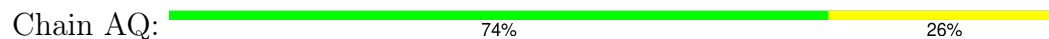


- Molecule 1: Coat protein

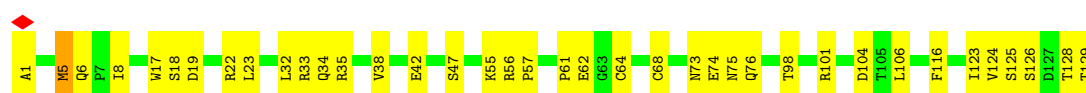
Chain AP:  74% 26%



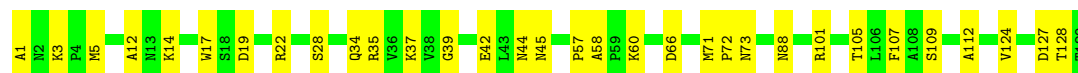
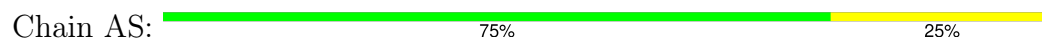
- Molecule 1: Coat protein



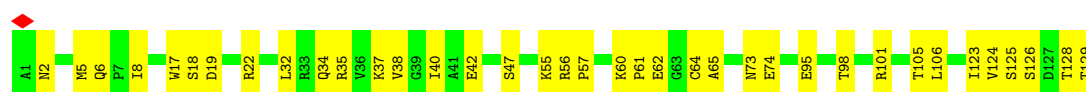
- Molecule 1: Coat protein



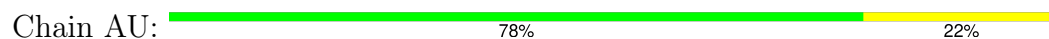
- Molecule 1: Coat protein



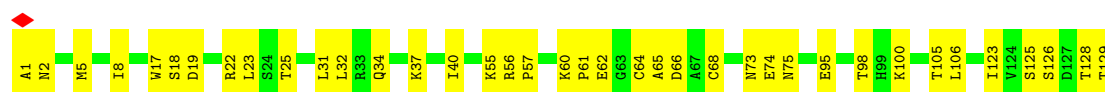
- Molecule 1: Coat protein




- Molecule 1: Coat protein



- Molecule 1: Coat protein



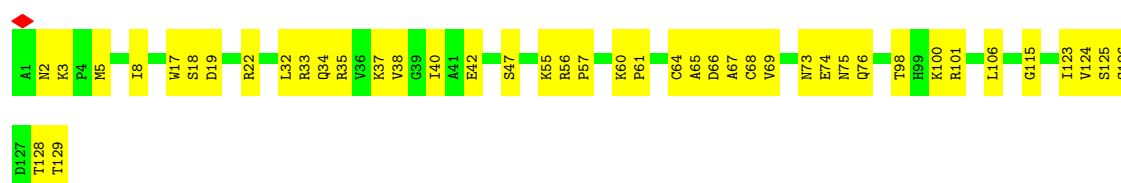
- Molecule 1: Coat protein

Chain AW:  77% 23%



- Molecule 1: Coat protein

Chain AX:  67% 33%



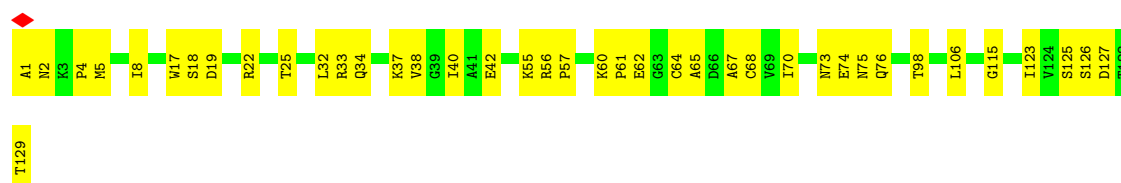
- Molecule 1: Coat protein

Chain AY:  74% 26%




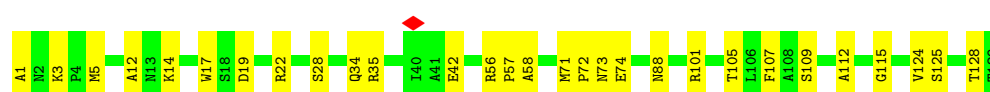
- Molecule 1: Coat protein

Chain AZ:  69% 31%



- Molecule 1: Coat protein

Chain BA:  78% 22%



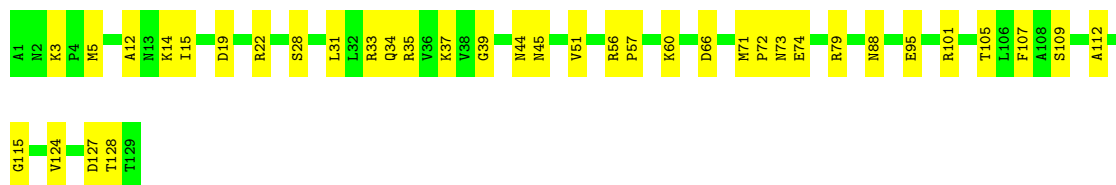
- Molecule 1: Coat protein

Chain BB:  71% 29%



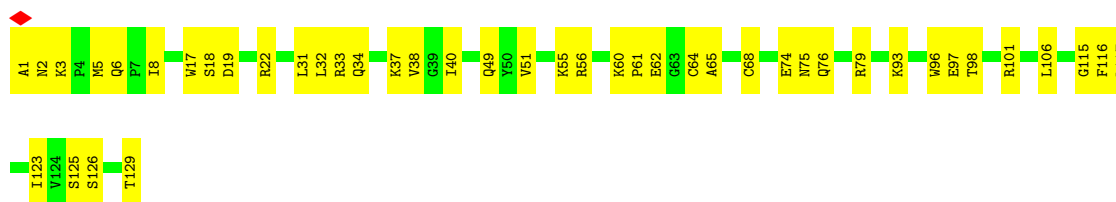
- Molecule 1: Coat protein

Chain BC:  71% 29%




- Molecule 1: Coat protein

Chain BD:  66% 34%



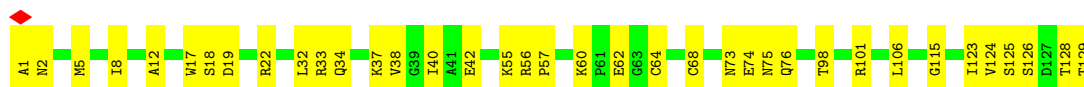
- Molecule 1: Coat protein

Chain BE:  77% 23%



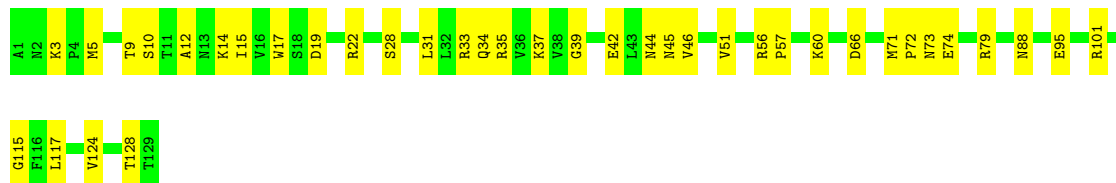
- Molecule 1: Coat protein

Chain BF:  71% 29%



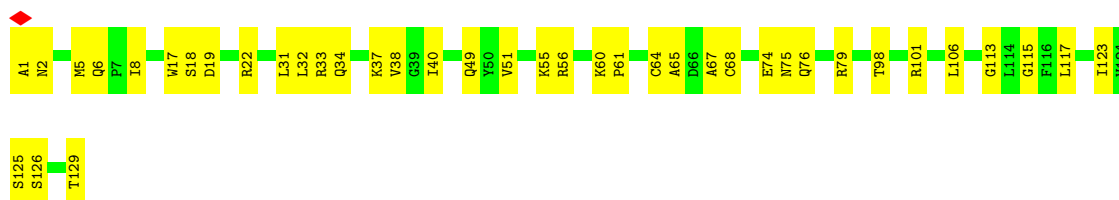
- Molecule 1: Coat protein

Chain BG:  71% 29%



- Molecule 1: Coat protein

Chain BH:  69% 31%



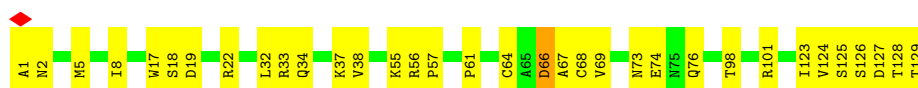
- Molecule 1: Coat protein

Chain BI: 75% 25%



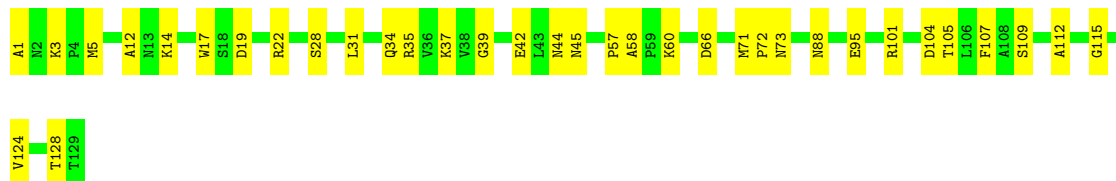
- Molecule 1: Coat protein

Chain BJ: 74% 26%



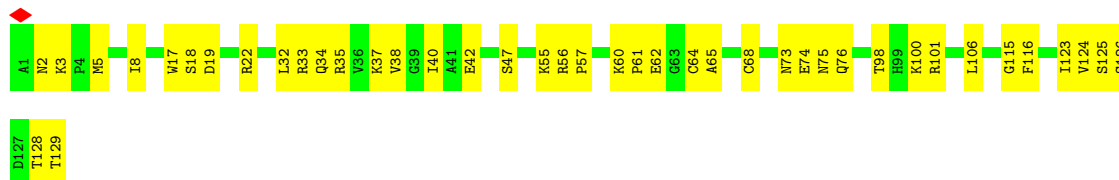
- Molecule 1: Coat protein

Chain BK: 73% 27%



- Molecule 1: Coat protein

Chain BL: 67% 33%



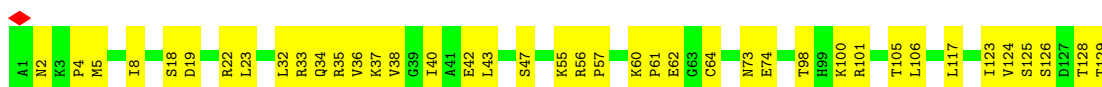
- Molecule 1: Coat protein

Chain BM: 71% 29%

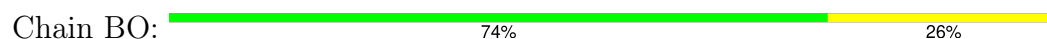




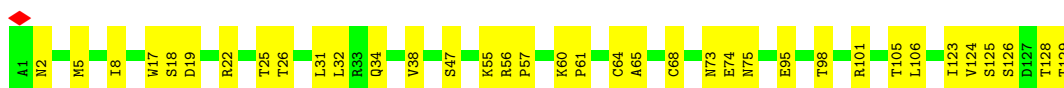
- Molecule 1: Coat protein



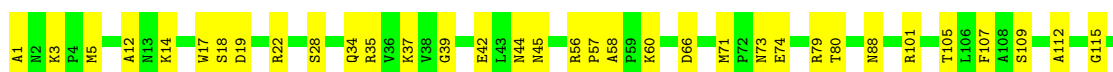
- Molecule 1: Coat protein



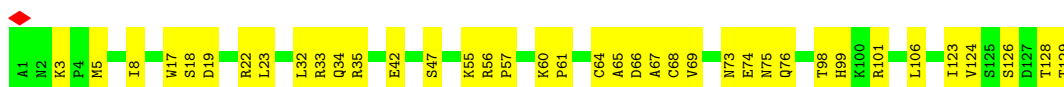
- Molecule 1: Coat protein



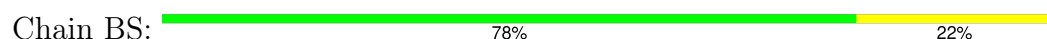
- Molecule 1: Coat protein



- Molecule 1: Coat protein

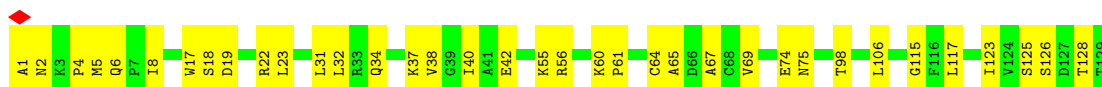
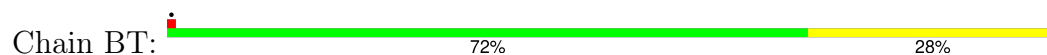


- Molecule 1: Coat protein





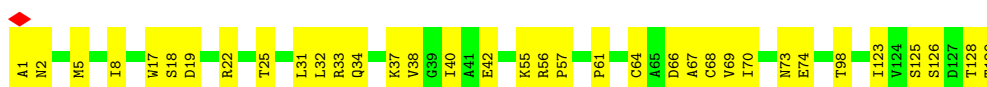
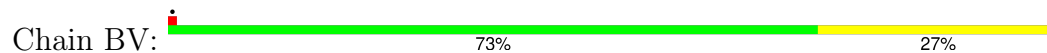
- Molecule 1: Coat protein



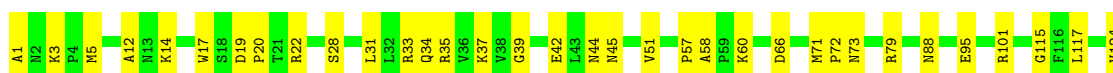
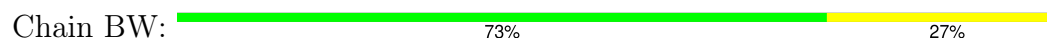
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein

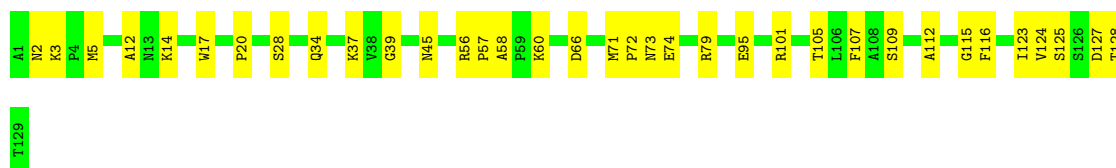


- Molecule 1: Coat protein



- Molecule 1: Coat protein





- Molecule 1: Coat protein



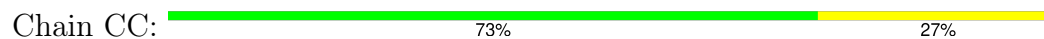
- Molecule 1: Coat protein



- Molecule 1: Coat protein

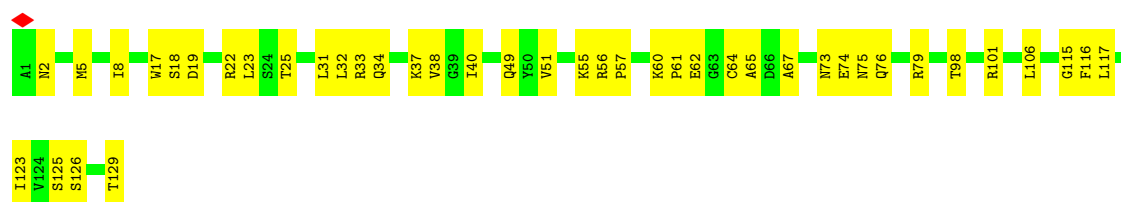


- Molecule 1: Coat protein



- Molecule 1: Coat protein





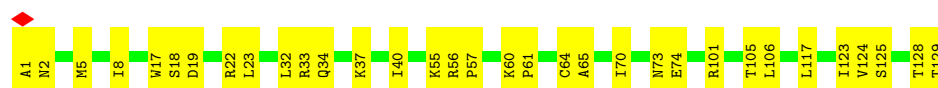
- Molecule 1: Coat protein

Chain CE: 75% 25%



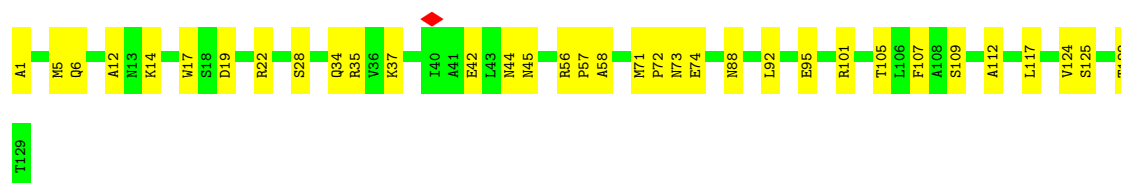
- Molecule 1: Coat protein

Chain CF: 74% 26%



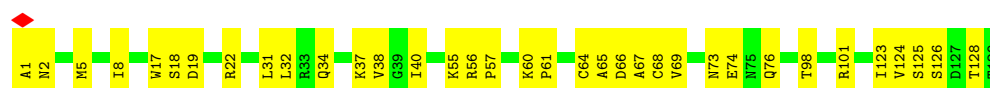
- Molecule 1: Coat protein

Chain CG: 74% 26%



- Molecule 1: Coat protein

Chain CH: 73% 27%

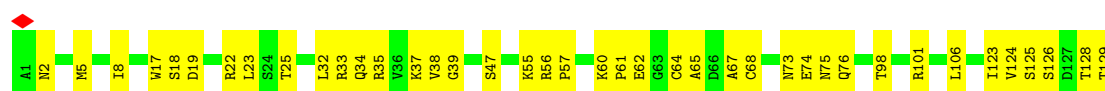


- Molecule 1: Coat protein

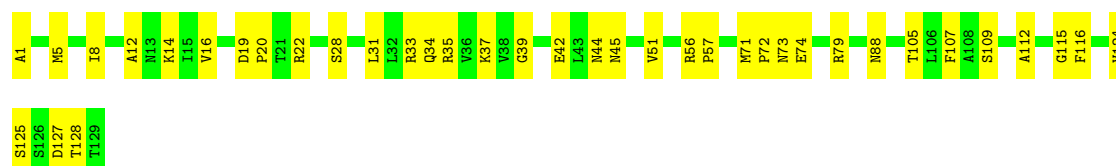
Chain CI: 68% 32%



- Molecule 1: Coat protein



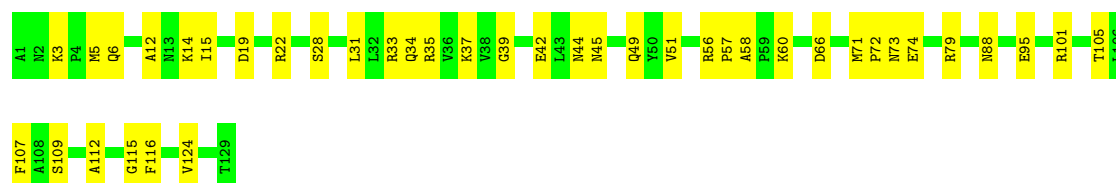
- Molecule 1: Coat protein



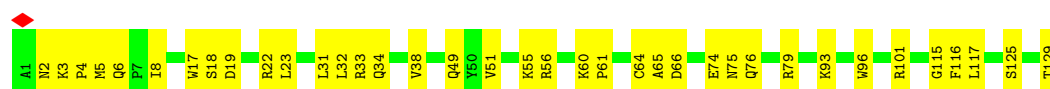
- Molecule 1: Coat protein



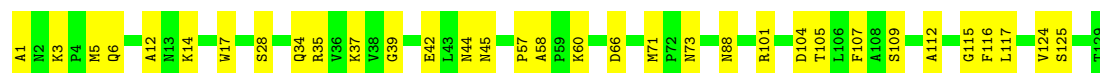
- Molecule 1: Coat protein



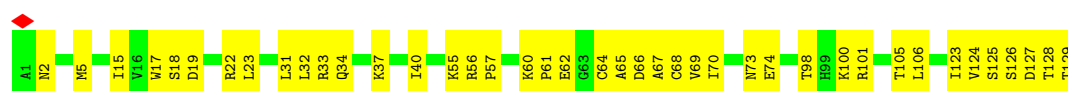
- Molecule 1: Coat protein



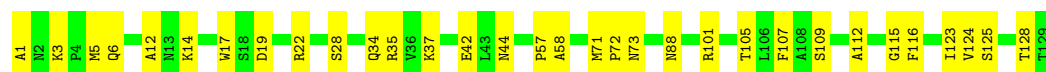
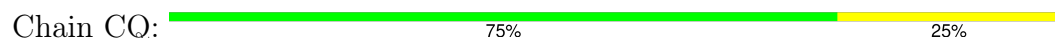
- Molecule 1: Coat protein



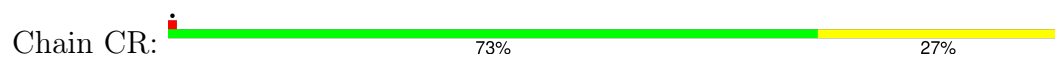
- Molecule 1: Coat protein



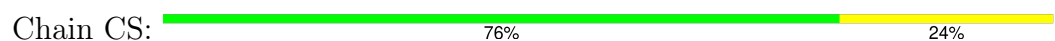
- Molecule 1: Coat protein



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- Molecule 1: Coat protein

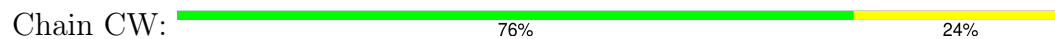


- Molecule 1: Coat protein

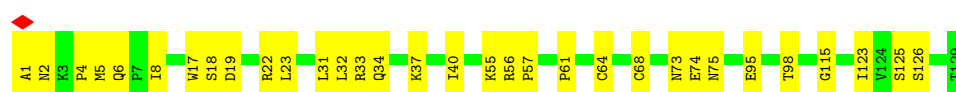
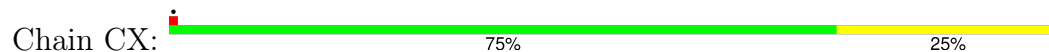




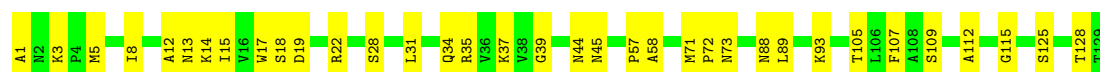
- Molecule 1: Coat protein



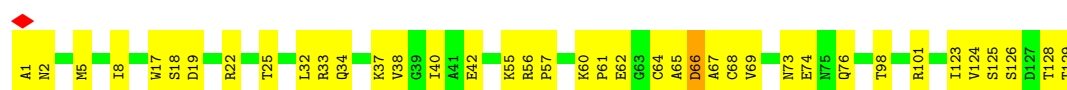
- Molecule 1: Coat protein



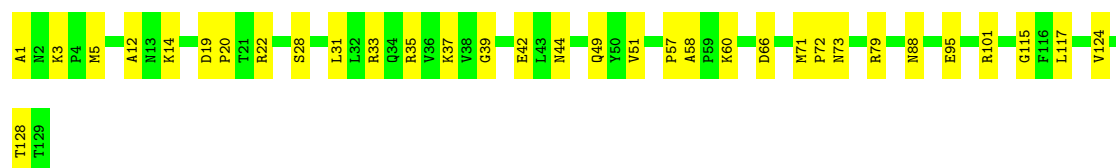
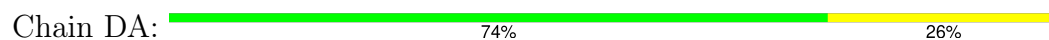
- Molecule 1: Coat protein



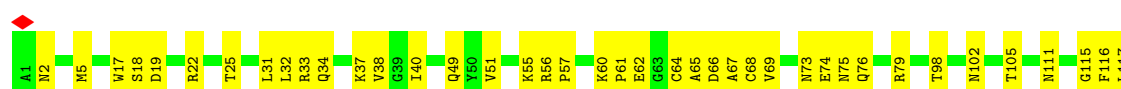
- Molecule 1: Coat protein



- Molecule 1: Coat protein



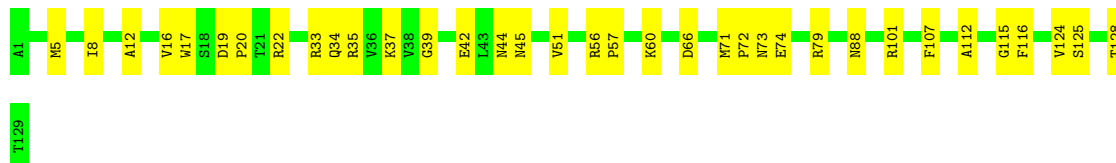
- Molecule 1: Coat protein





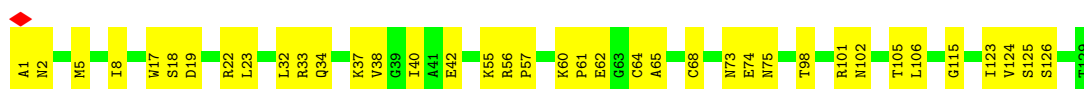
- Molecule 1: Coat protein

Chain DC: 73% 27%



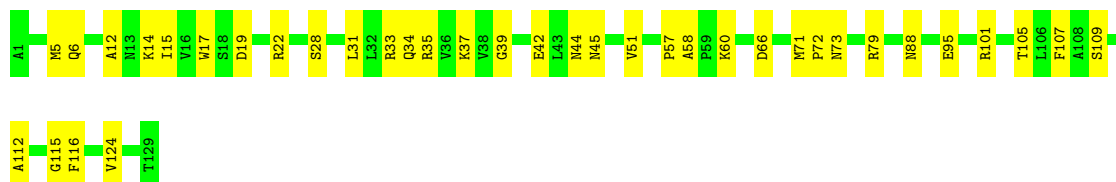
- Molecule 1: Coat protein

Chain DE: 71% 29%



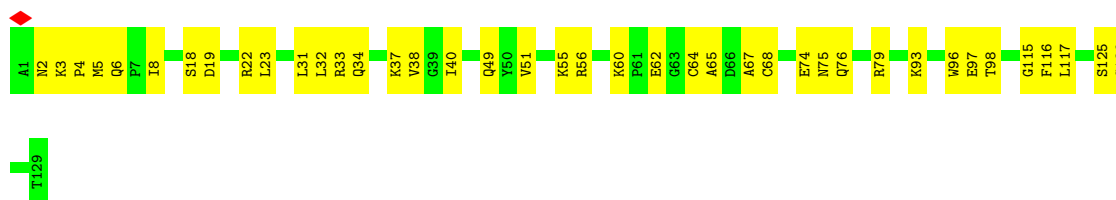
- Molecule 1: Coat protein

Chain DF: 71% 29%



- Molecule 1: Coat protein

Chain DG: 69% 31%



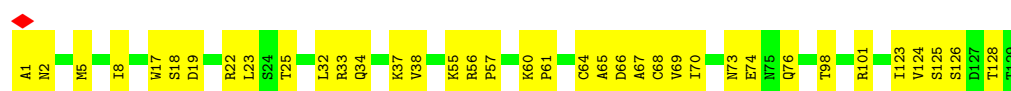
- Molecule 1: Coat protein

Chain DH: 76% 24%



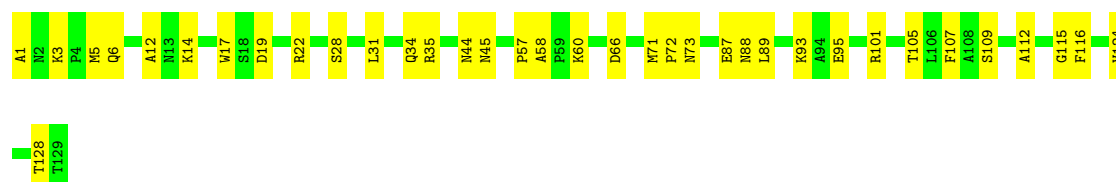
- Molecule 1: Coat protein

Chain DI:  71% 29%




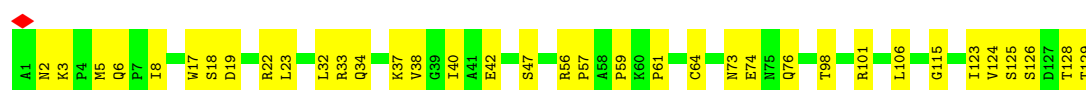
- Molecule 1: Coat protein

Chain DJ:  72% 28%




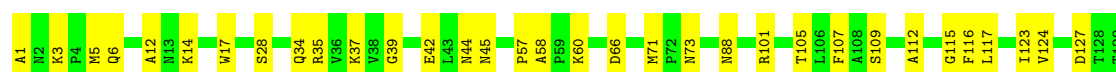
- Molecule 1: Coat protein

Chain DK:  72% 28%




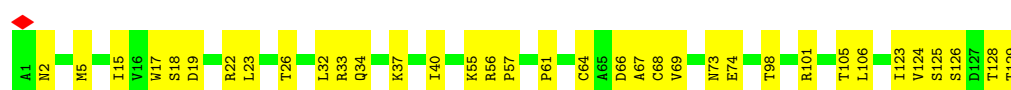
- Molecule 1: Coat protein

Chain DL:  74% 26%



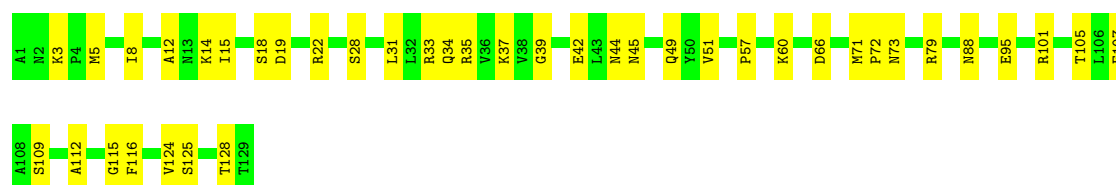
- Molecule 1: Coat protein

Chain DM:  73% 27%

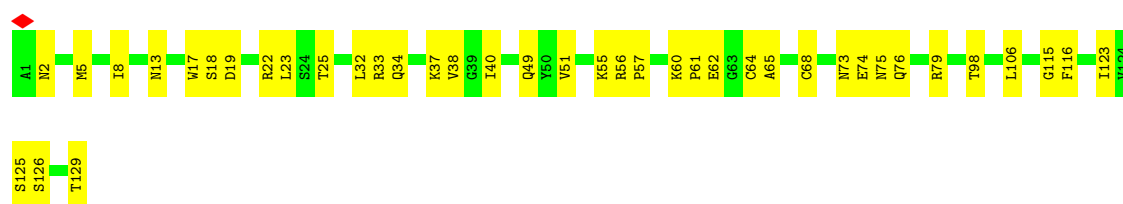


- Molecule 1: Coat protein

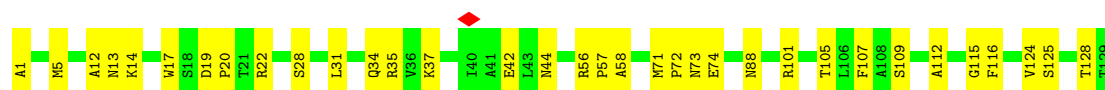
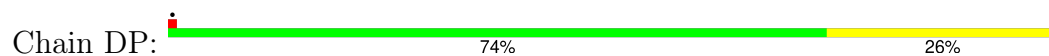
Chain DN:  69% 31%



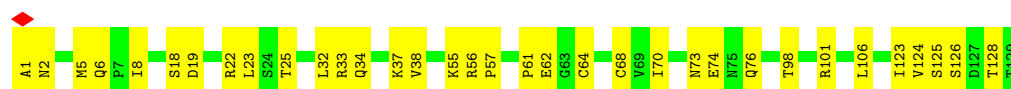
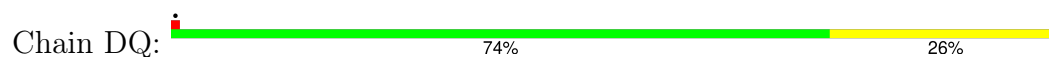
- Molecule 1: Coat protein



- Molecule 1: Coat protein



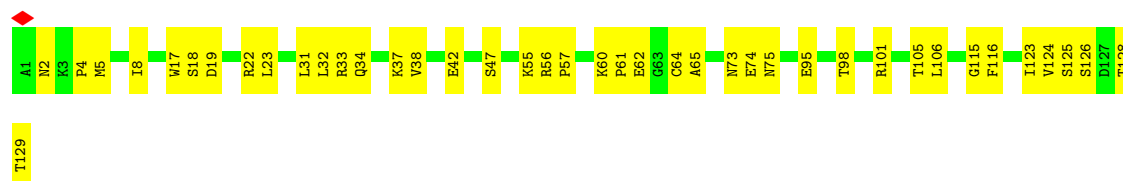
- Molecule 1: Coat protein



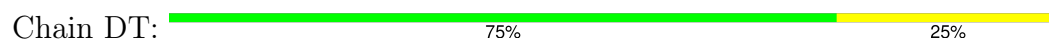
- Molecule 1: Coat protein



- Molecule 1: Coat protein

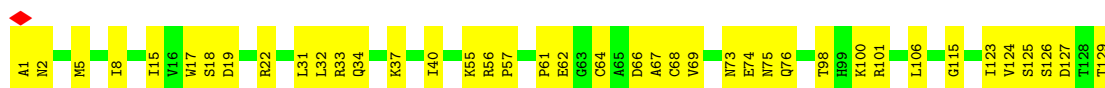


- Molecule 1: Coat protein

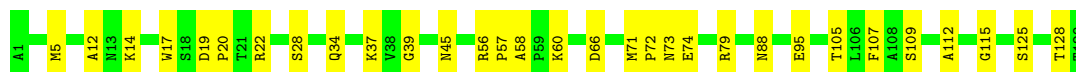
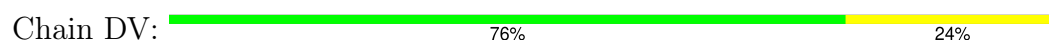




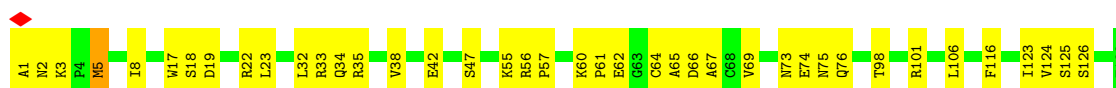
- Molecule 1: Coat protein



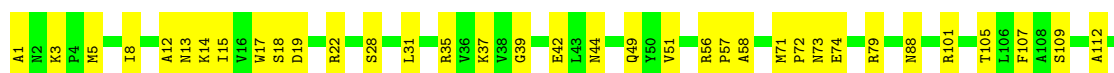
- Molecule 1: Coat protein



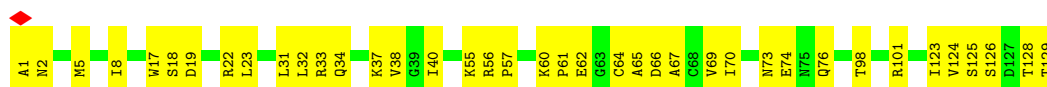
- Molecule 1: Coat protein



- Molecule 1: Coat protein

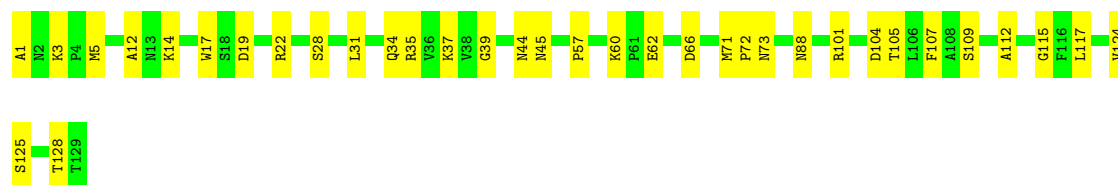


- Molecule 1: Coat protein

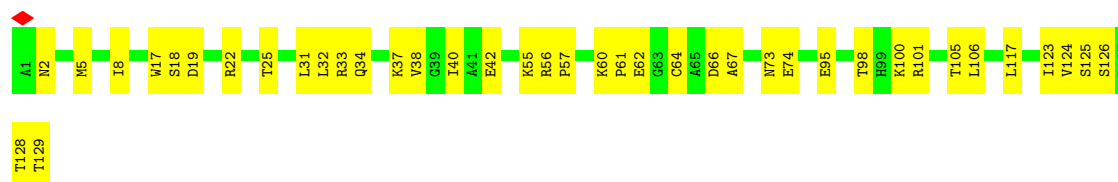


- Molecule 1: Coat protein

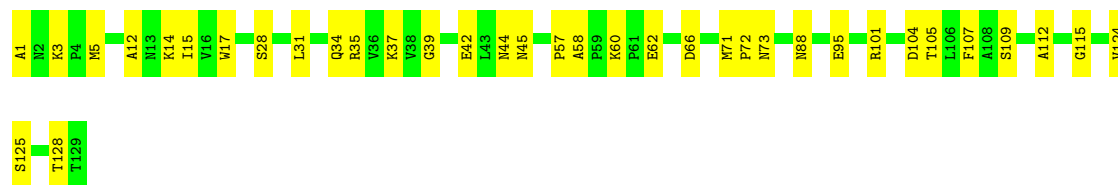




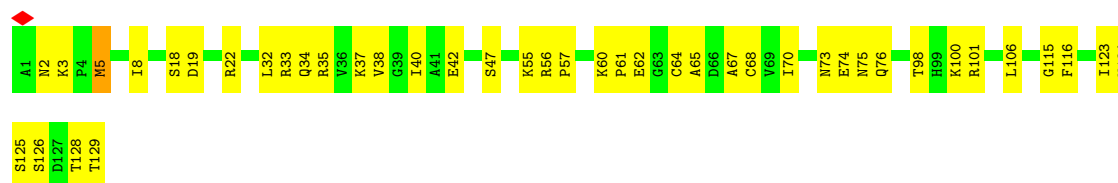
- Molecule 1: Coat protein



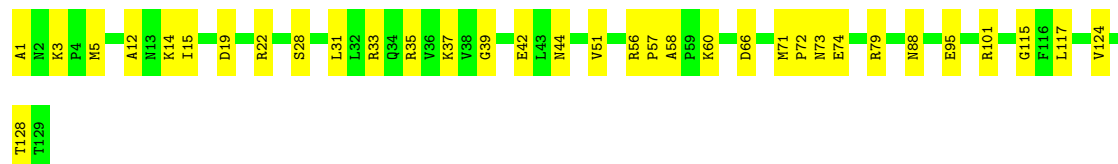
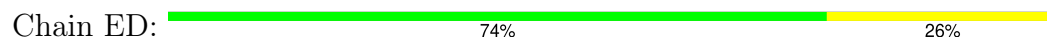
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein





- Molecule 1: Coat protein

Chain EF: 77% 23%



- Molecule 1: Coat protein

Chain EG: 69% 31%



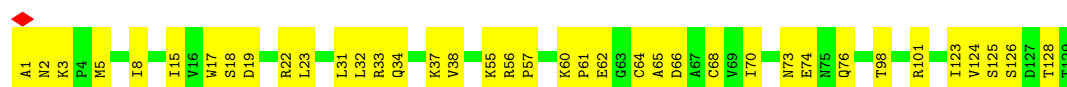
- Molecule 1: Coat protein

Chain EH: 77% 23%



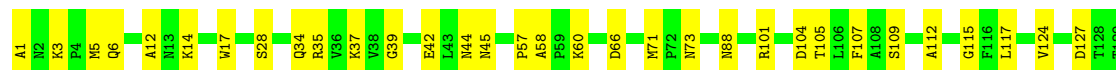
- Molecule 1: Coat protein

Chain EI: 71% 29%



- Molecule 1: Coat protein

Chain EJ: 75% 25%

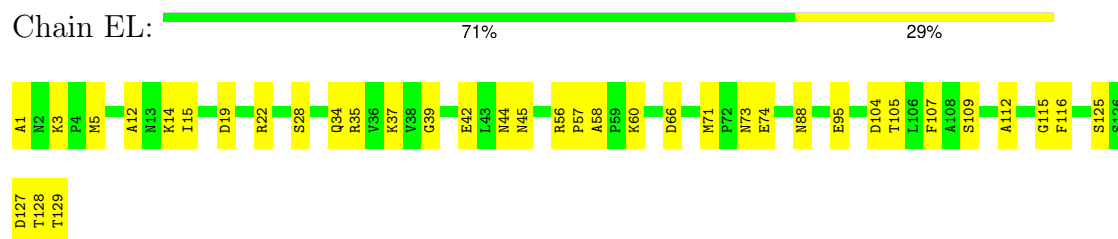


- Molecule 1: Coat protein

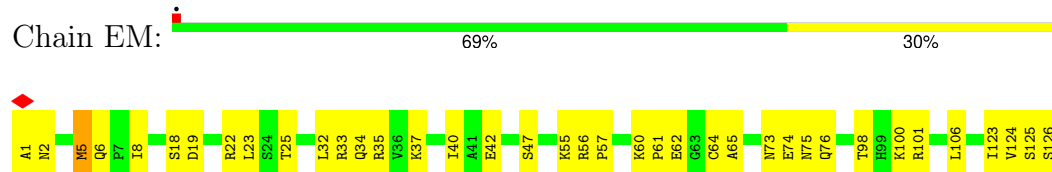
Chain EK: 71% 29%



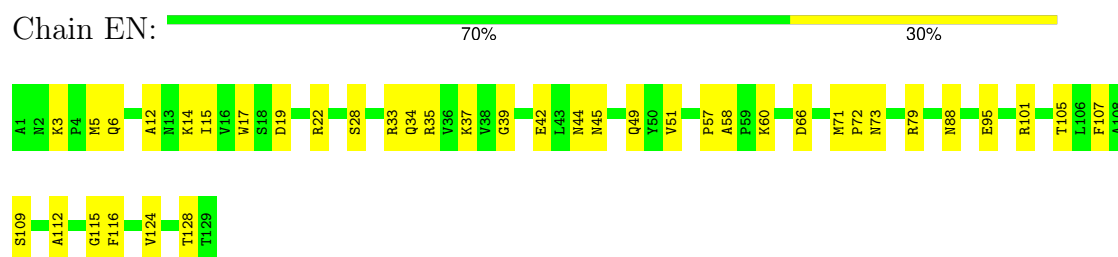
- Molecule 1: Coat protein



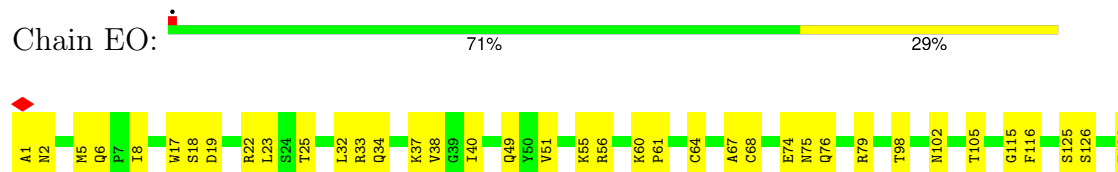
- Molecule 1: Coat protein



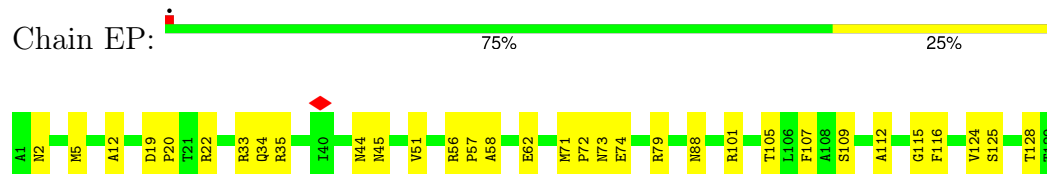
- Molecule 1: Coat protein



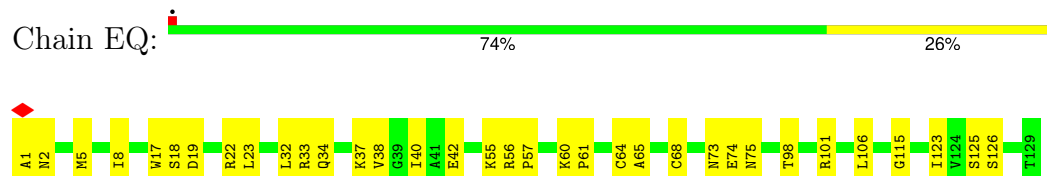
- Molecule 1: Coat protein



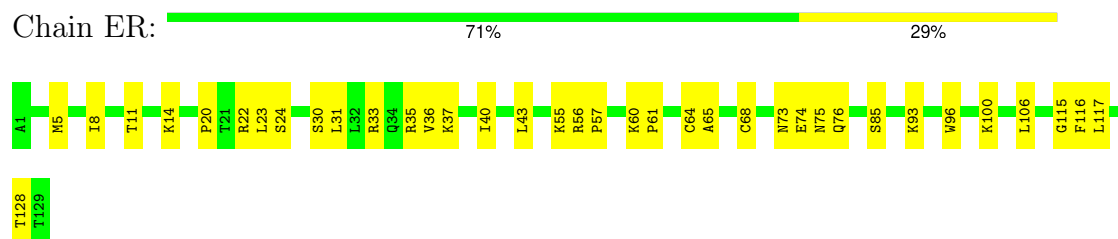
- Molecule 1: Coat protein



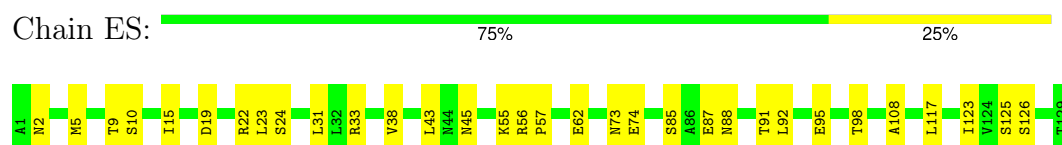
- Molecule 1: Coat protein



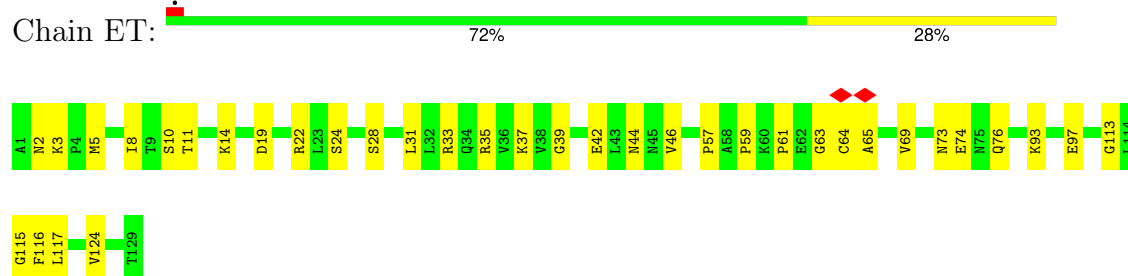
- Molecule 1: Coat protein



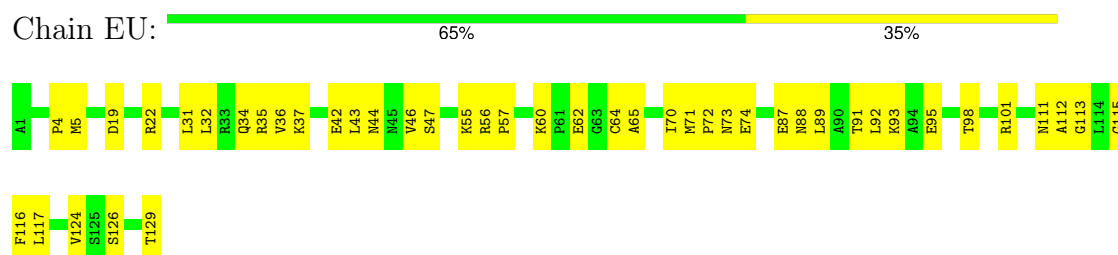
- Molecule 1: Coat protein



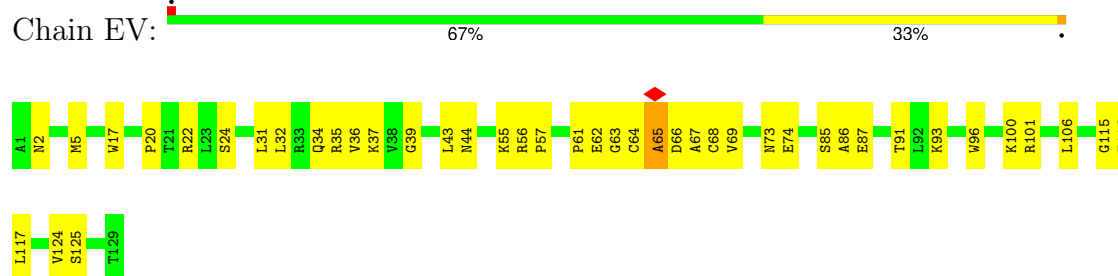
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein

Chain EW:  67% 33%




- Molecule 1: Coat protein

Chain EX:  72% 28%



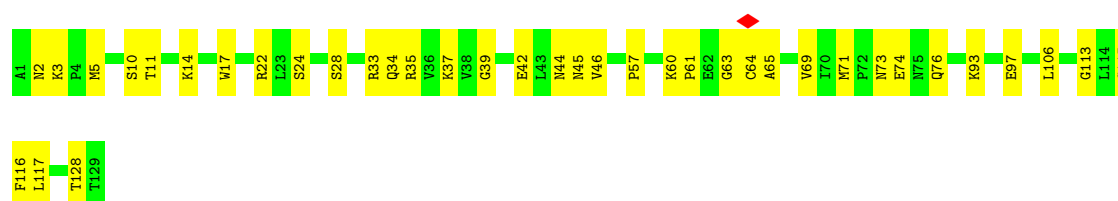
- Molecule 1: Coat protein

Chain EY:  77% 22%



- Molecule 1: Coat protein

Chain EZ:  71% 29%



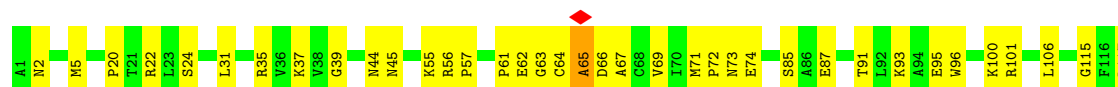
- Molecule 1: Coat protein

Chain FA:  71% 29%



- Molecule 1: Coat protein

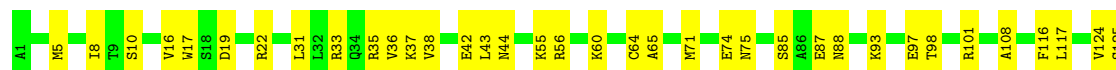
Chain FB:  70% 29%





- Molecule 1: Coat protein

Chain FC: 71% 29%



- Molecule 1: Coat protein

Chain FD: 72% 28%



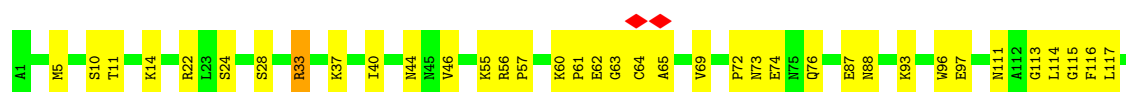
- Molecule 1: Coat protein

Chain FE: 80% 19%



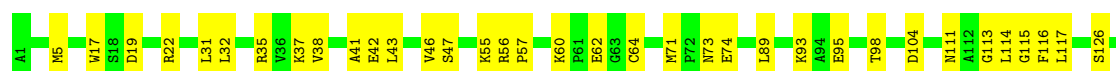
- Molecule 1: Coat protein

Chain FF: 71% 28%



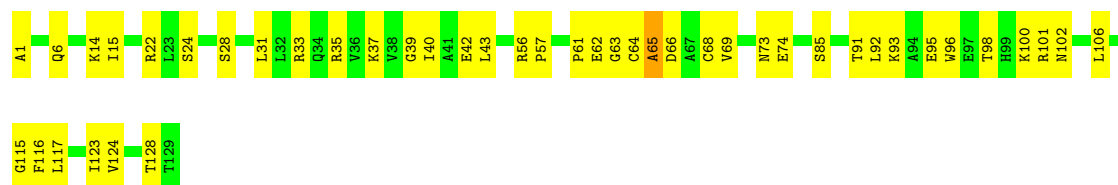
- Molecule 1: Coat protein

Chain FG: 73% 27%




- Molecule 1: Coat protein

Chain FH:  66% 33%




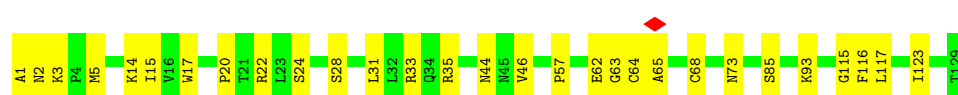
- Molecule 1: Coat protein

Chain FI:  77% 23%



- Molecule 1: Coat protein

Chain FJ:  78% 22%



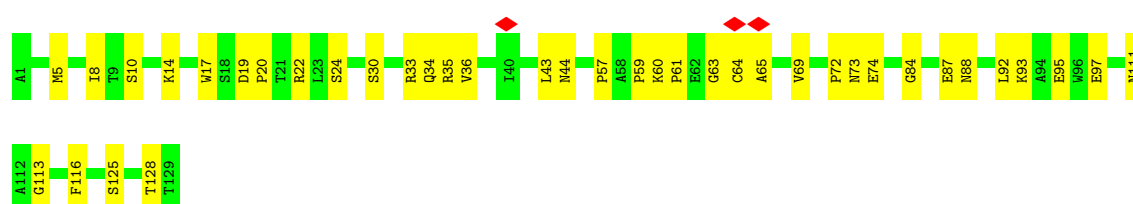
- Molecule 1: Coat protein

Chain FK:  73% 27%



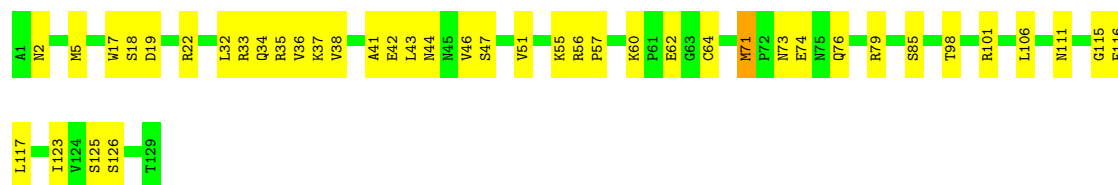
- Molecule 1: Coat protein

Chain FL:  70% 30%

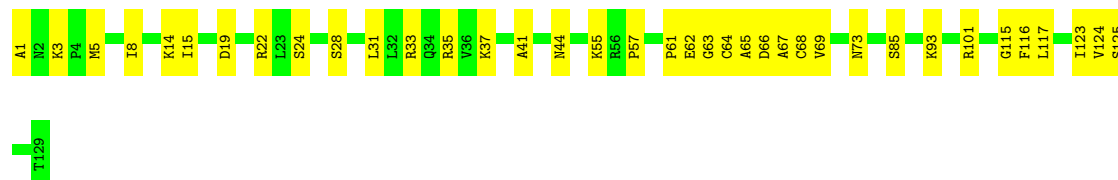


- Molecule 1: Coat protein

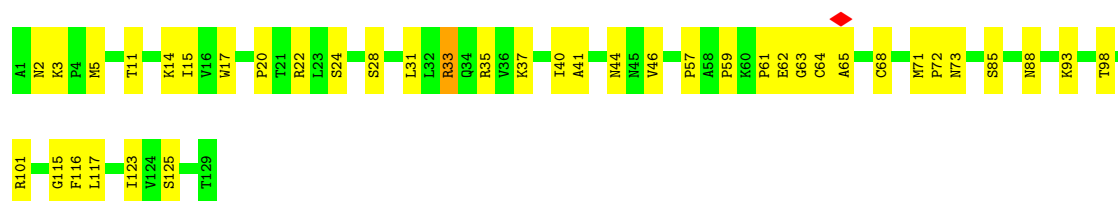
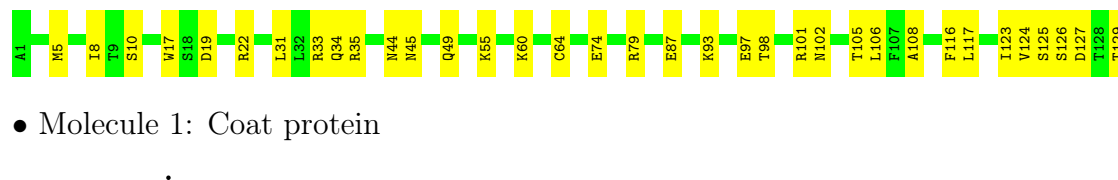
Chain FM:  67% 32%



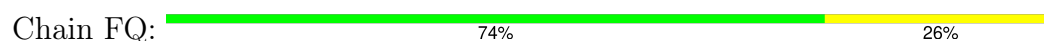
- Molecule 1: Coat protein



- Molecule 1: Coat protein

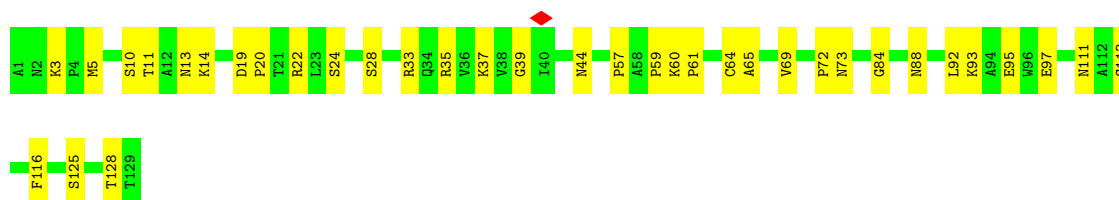


- Molecule 1: Coat protein



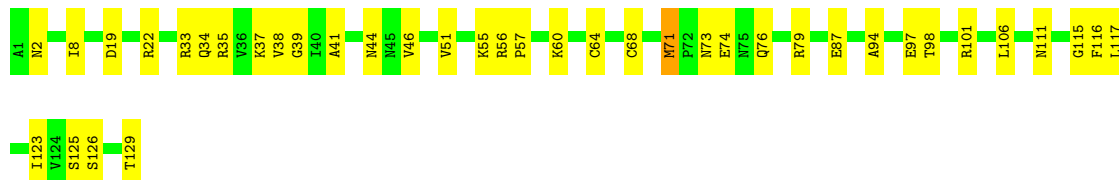
- Molecule 1: Coat protein





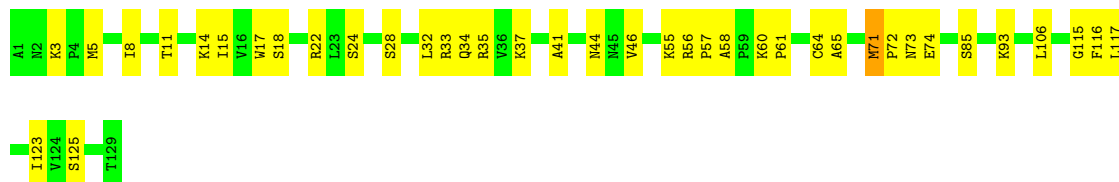
- Molecule 1: Coat protein

Chain FS: 70% 29%



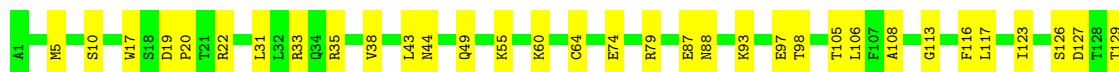
- Molecule 1: Coat protein

Chain FT: 70% 29%



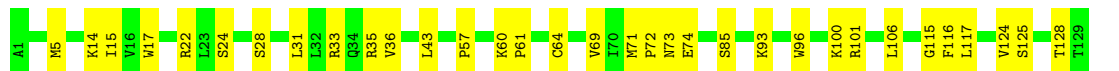
- Molecule 1: Coat protein

Chain FU: 74% 26%



- Molecule 1: Coat protein

Chain FV: 74% 26%



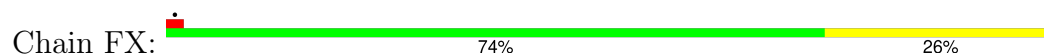
- Molecule 1: Coat protein

Chain FW: 63% 37%

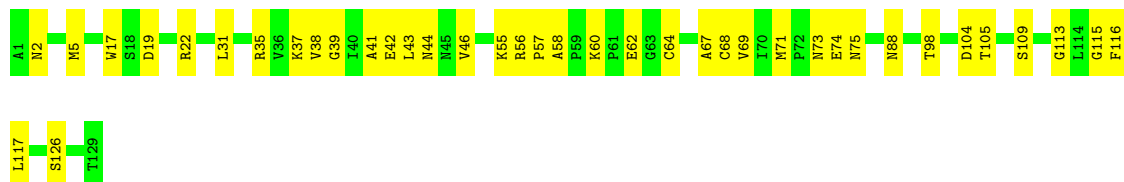




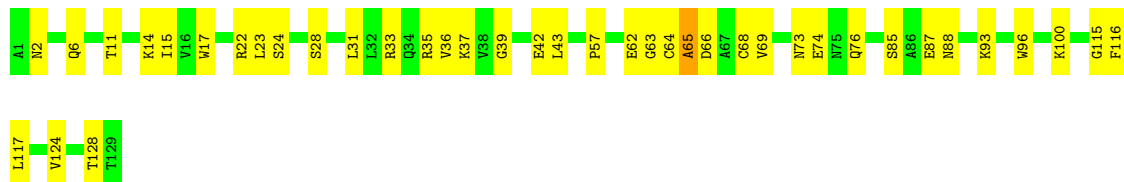
- Molecule 1: Coat protein



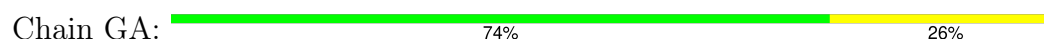
- Molecule 1: Coat protein



- Molecule 1: Coat protein




- Molecule 1: Coat protein



- Molecule 1: Coat protein




- Molecule 1: Coat protein

Chain GC:  84% 16%



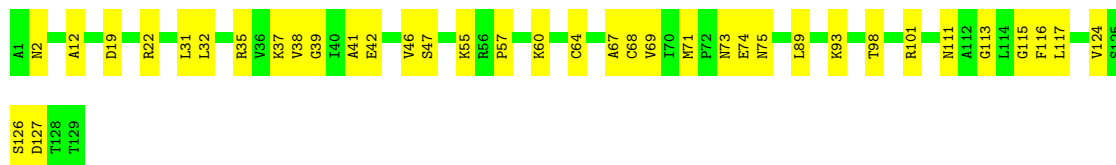
- Molecule 1: Coat protein

Chain GD:  74% 26%



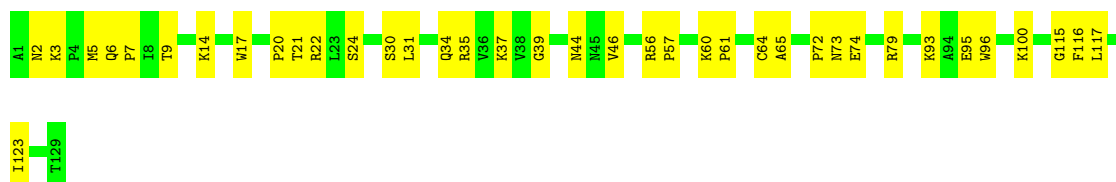
- Molecule 1: Coat protein

Chain GE:  71% 29%



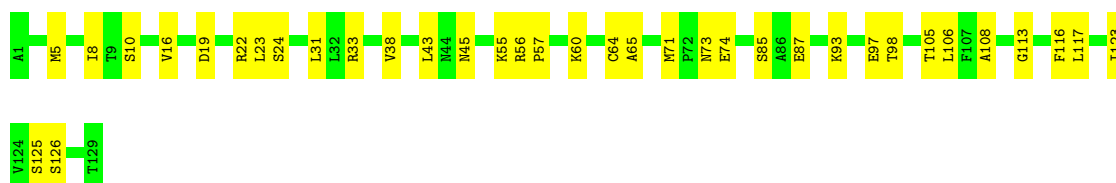
- Molecule 1: Coat protein

Chain GF:  71% 29%



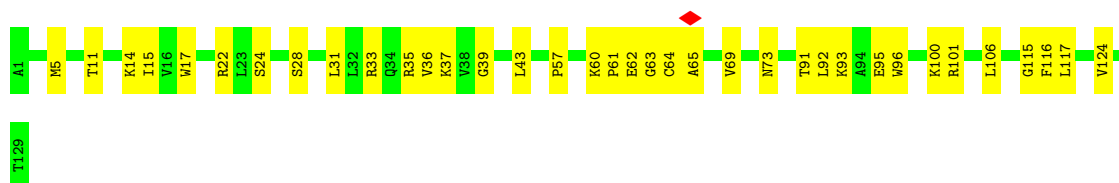
- Molecule 1: Coat protein

Chain GG:  72% 28%

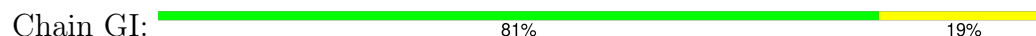


- Molecule 1: Coat protein

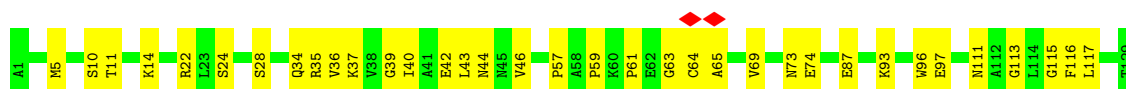
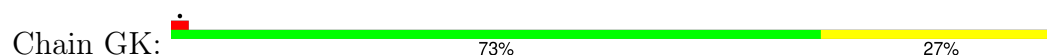
Chain GH:  72% 28%



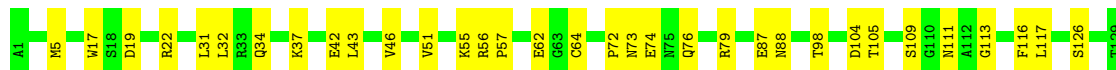
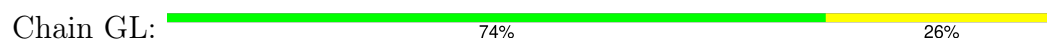
- Molecule 1: Coat protein



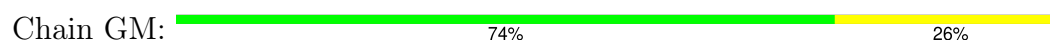
- Molecule 1: Coat protein



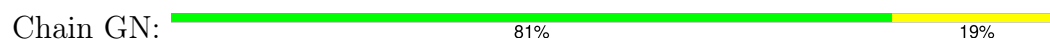
- Molecule 1: Coat protein



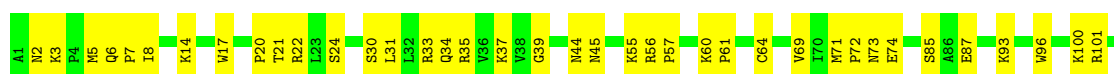
- Molecule 1: Coat protein

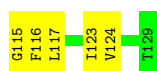


- Molecule 1: Coat protein



- Molecule 1: Coat protein





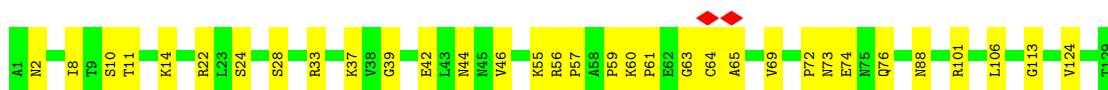
- Molecule 1: Coat protein

Chain GP: 68% 32%



- Molecule 1: Coat protein

Chain GQ: 74% 26%



- Molecule 1: Coat protein

Chain GR: 70% 30%



- Molecule 1: Coat protein

Chain GS: 77% 22%




- Molecule 1: Coat protein

Chain GT: 71% 29%



- Molecule 1: Coat protein

Chain GU:  74% 26%




- Molecule 1: Coat protein

Chain GV:  70% 30%



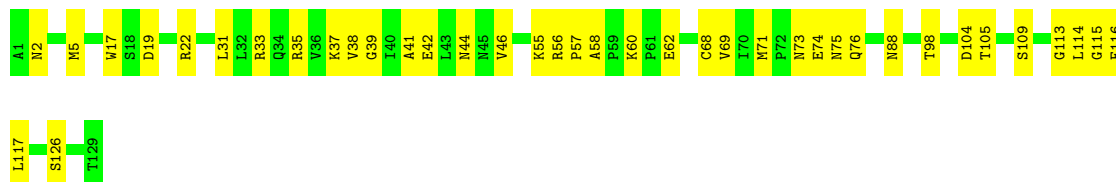
- Molecule 1: Coat protein

Chain GW:  74% 26%



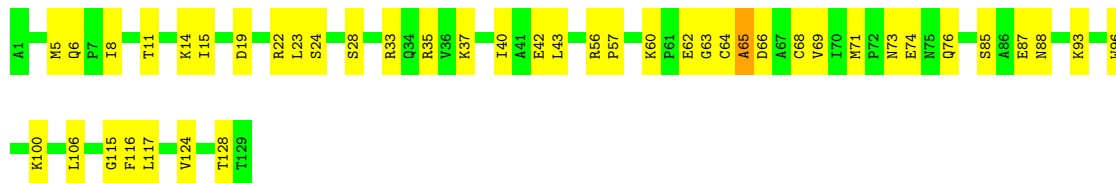
- Molecule 1: Coat protein

Chain GX:  70% 30%




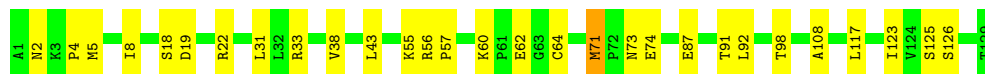
- Molecule 1: Coat protein

Chain GY:  67% 33%

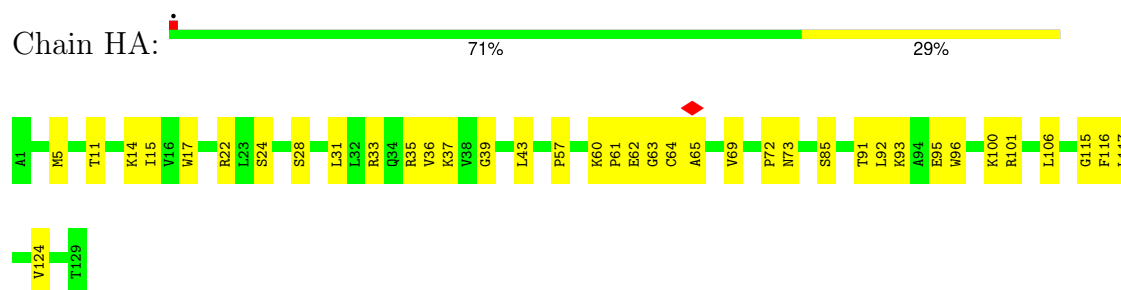


- Molecule 1: Coat protein

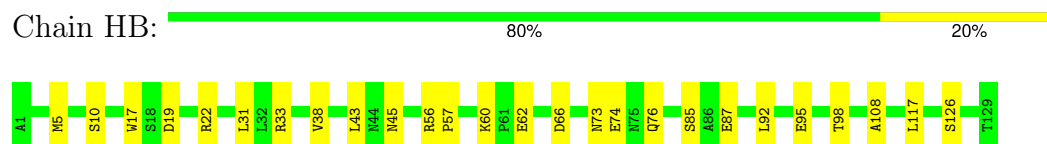
Chain GZ:  78% 22%



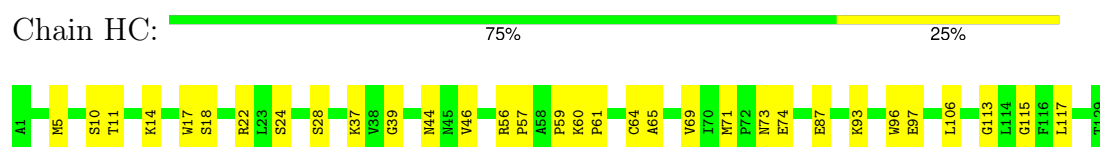
- Molecule 1: Coat protein



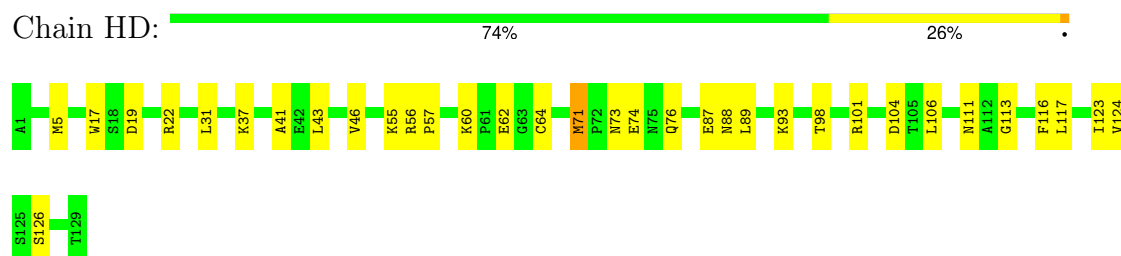
- Molecule 1: Coat protein



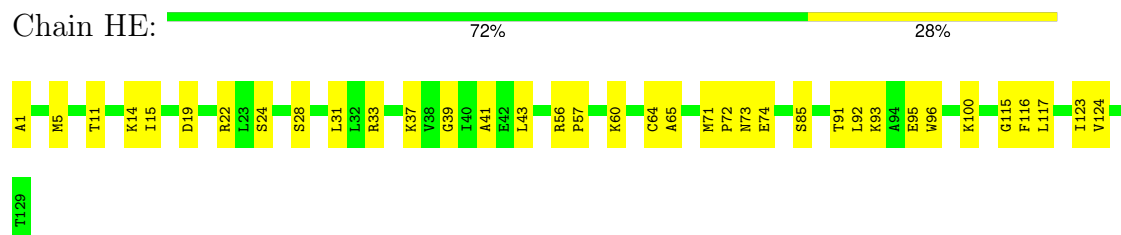
- Molecule 1: Coat protein



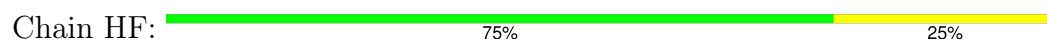
- Molecule 1: Coat protein

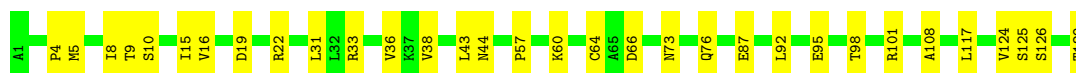


- Molecule 1: Coat protein

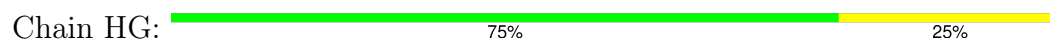


- Molecule 1: Coat protein

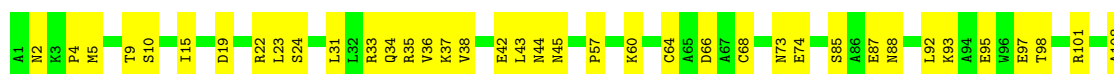




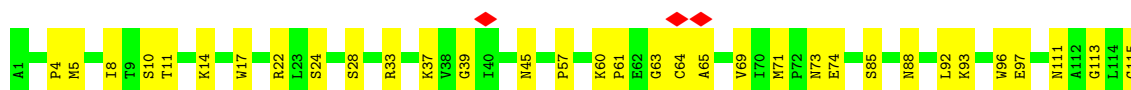
- Molecule 1: Coat protein



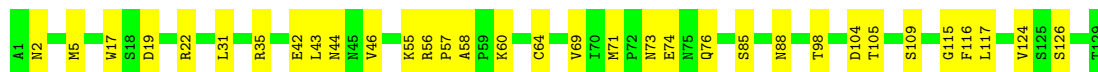
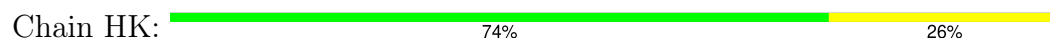
- Molecule 1: Coat protein



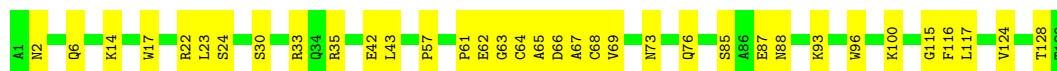
- Molecule 1: Coat protein



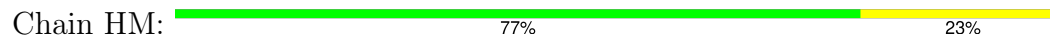
- Molecule 1: Coat protein



- Molecule 1: Coat protein

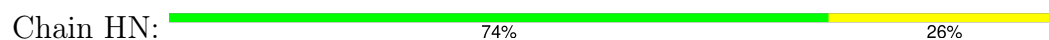


- Molecule 1: Coat protein

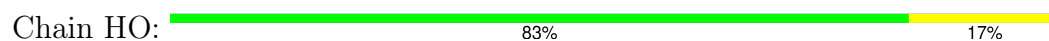




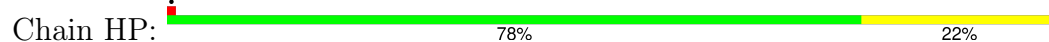
- Molecule 1: Coat protein



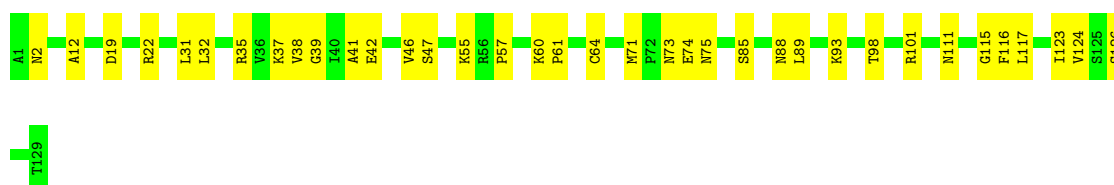
- Molecule 1: Coat protein



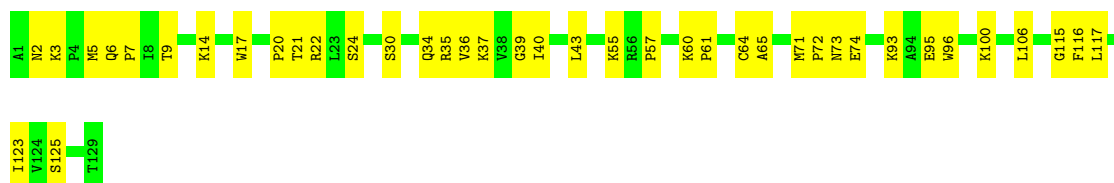
- Molecule 1: Coat protein



- Molecule 1: Coat protein

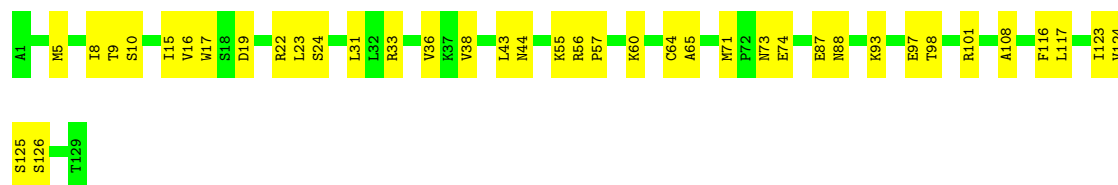


- Molecule 1: Coat protein



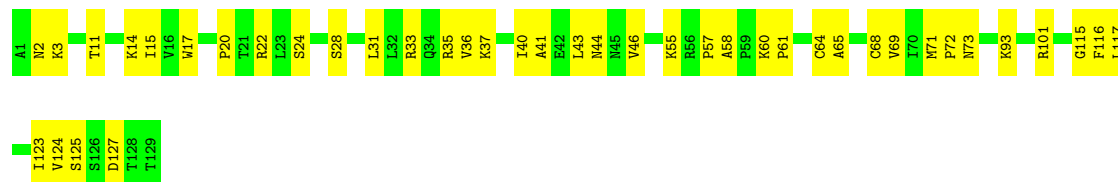
- Molecule 1: Coat protein





- Molecule 1: Coat protein

Chain HT: 68% 32%



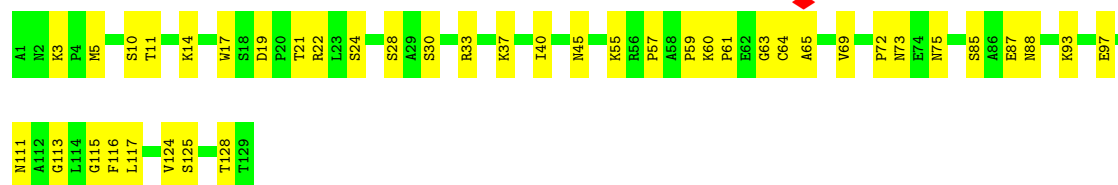
- Molecule 1: Coat protein

Chain HU: 73% 27%



- Molecule 1: Coat protein

Chain HV: 68% 32%



- Molecule 1: Coat protein

Chain HW: 72% 28%




- Molecule 1: Coat protein

Chain HX: 73% 27%



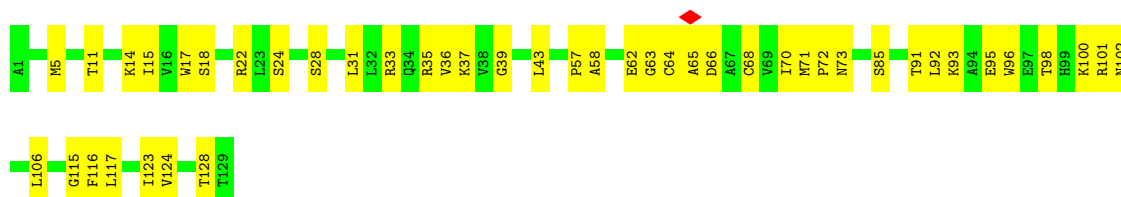
- Molecule 1: Coat protein

Chain HY:  78% 22%




- Molecule 1: Coat protein

Chain HZ:  65% 35%



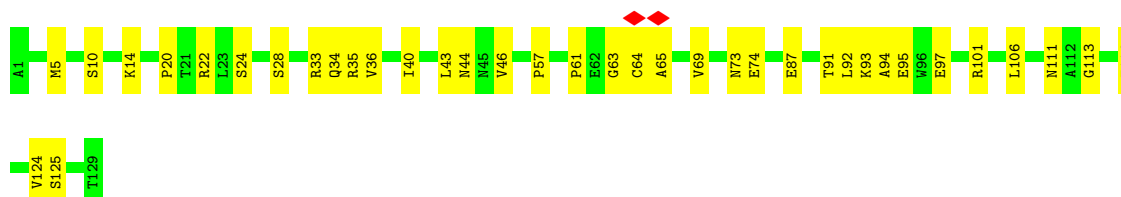
- Molecule 1: Coat protein

Chain IA:  77% 23%



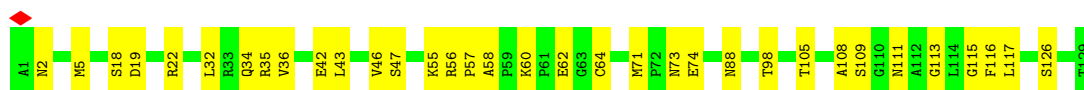
- Molecule 1: Coat protein

Chain IB:  71% 29%



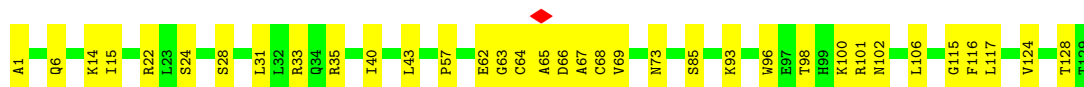
- Molecule 1: Coat protein

Chain IC:  74% 26%




- Molecule 1: Coat protein

Chain ID:  73% 27%



- Molecule 1: Coat protein

Chain IE:  78% 22%



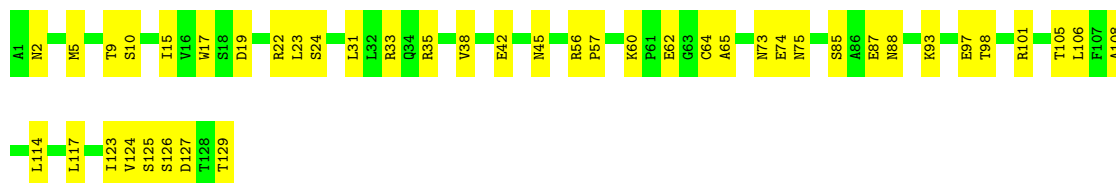
- Molecule 1: Coat protein

Chain IF:  72% 28%



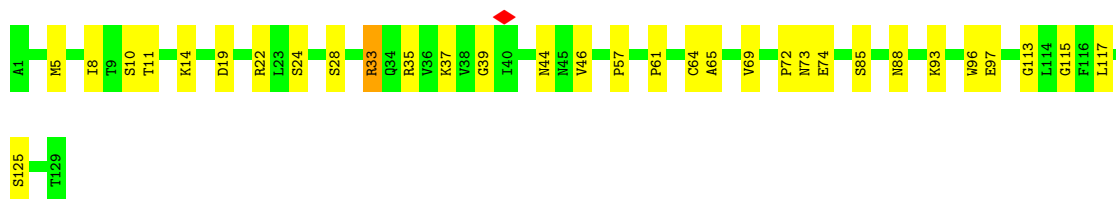
- Molecule 1: Coat protein

Chain IG:  67% 33%



- Molecule 1: Coat protein

Chain IH:  75% 24%



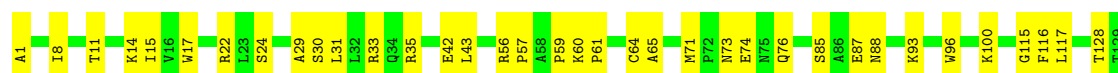
- Molecule 1: Coat protein

Chain II:  68% 32%




- Molecule 1: Coat protein

Chain IJ:  72% 28%




- Molecule 1: Coat protein

Chain IK:  78% 22%



- Molecule 1: Coat protein

Chain IL:  77% 23%



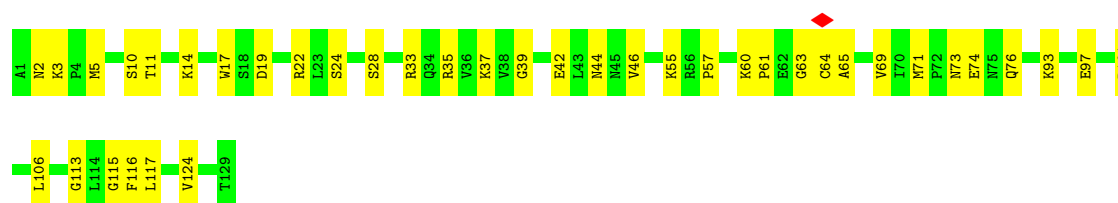
- Molecule 1: Coat protein

Chain IM:  73% 27%



- Molecule 1: Coat protein

Chain IN:  70% 30%



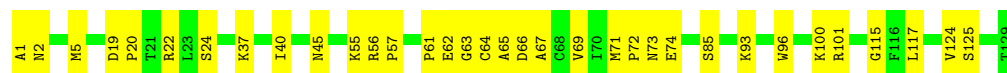
- Molecule 1: Coat protein

Chain IO:  74% 26%

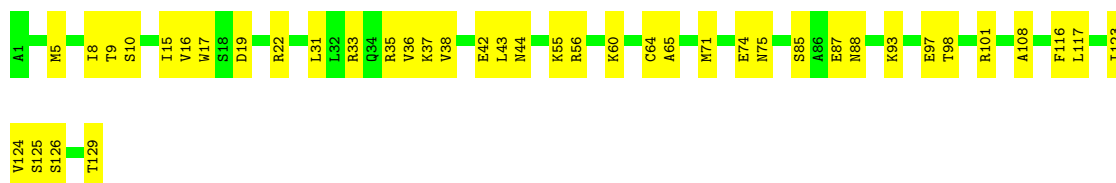


- Molecule 1: Coat protein

Chain IP:  74% 26%



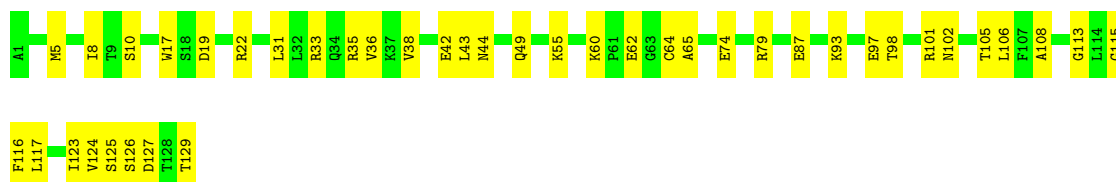
● Molecule 1: Coat protein

Chain IQ:  68% 32%

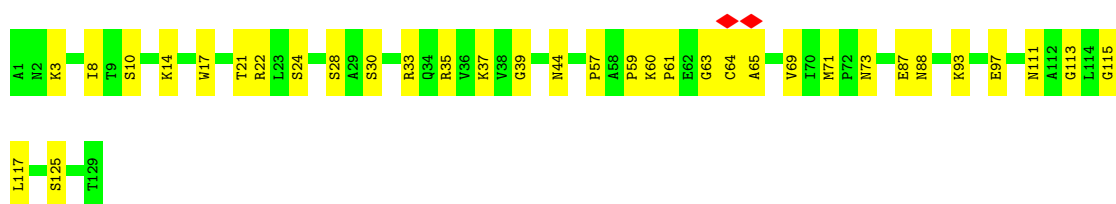
● Molecule 1: Coat protein

Chain IR:  67% 32% .

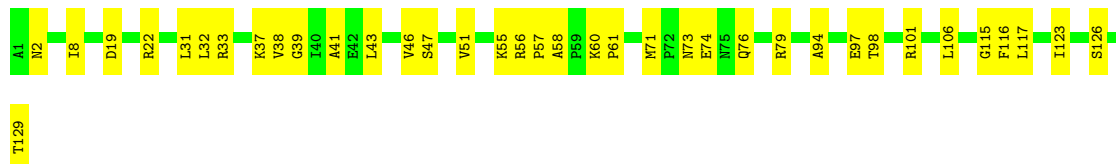
● Molecule 1: Coat protein

Chain IS:  68% 32%

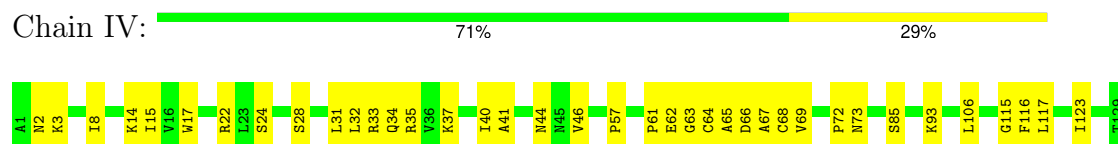
● Molecule 1: Coat protein

Chain IT:  73% 27%

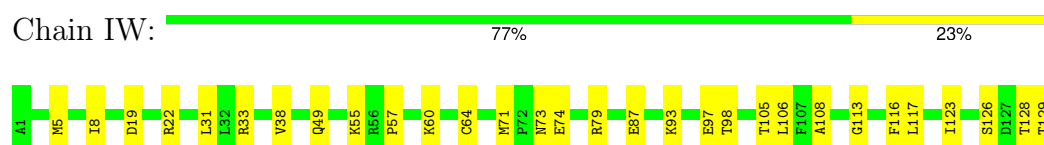
● Molecule 1: Coat protein

Chain IU:  71% 29%

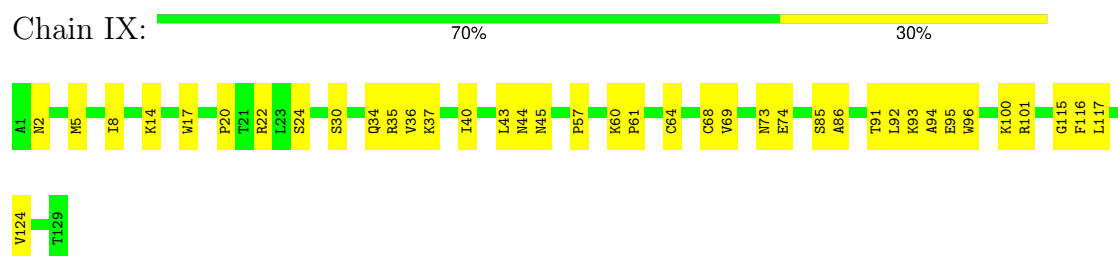
- Molecule 1: Coat protein



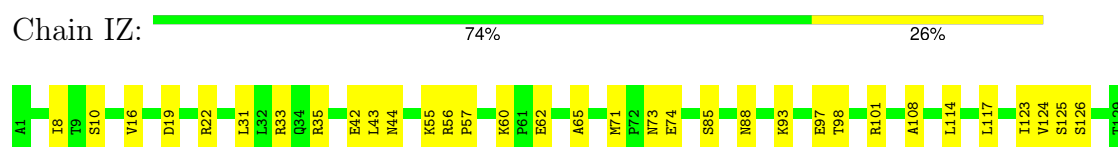
- Molecule 1: Coat protein



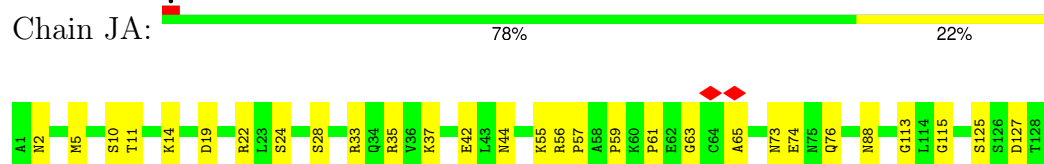
- Molecule 1: Coat protein



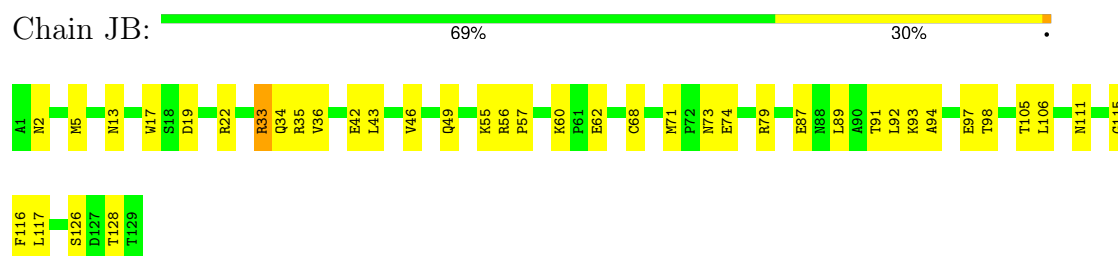
- Molecule 1: Coat protein




- Molecule 1: Coat protein

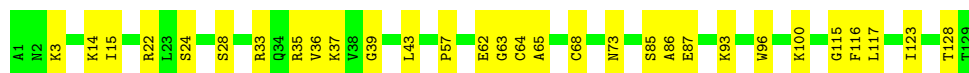


- Molecule 1: Coat protein



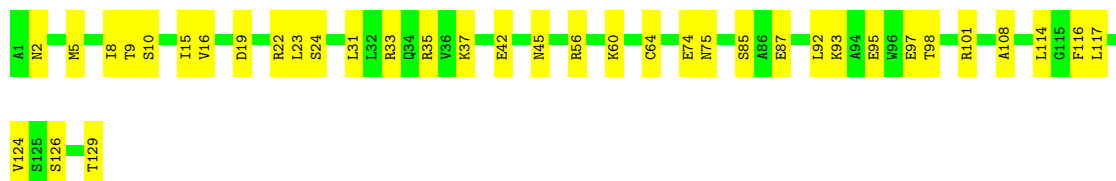
- Molecule 1: Coat protein

Chain JC:  77% 23%



- Molecule 1: Coat protein

Chain JD:  71% 29%



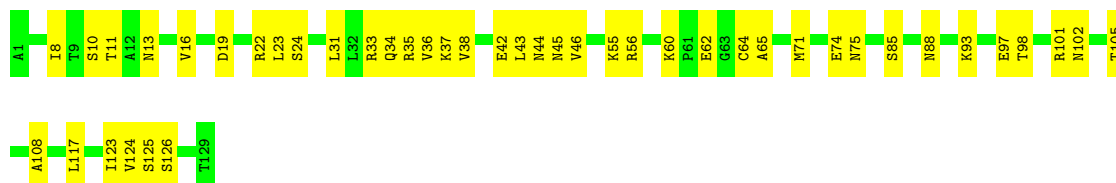
- Molecule 1: Coat protein

Chain JE:  73% 27%



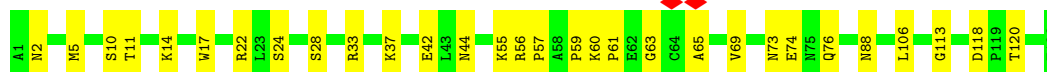
- Molecule 1: Coat protein

Chain JF:  66% 34%



- Molecule 1: Coat protein

Chain JG:  77% 23%

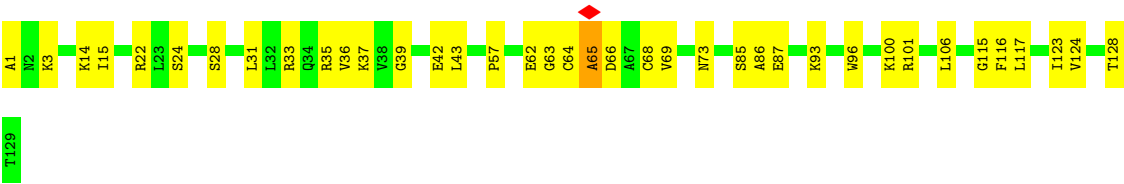


- Molecule 1: Coat protein

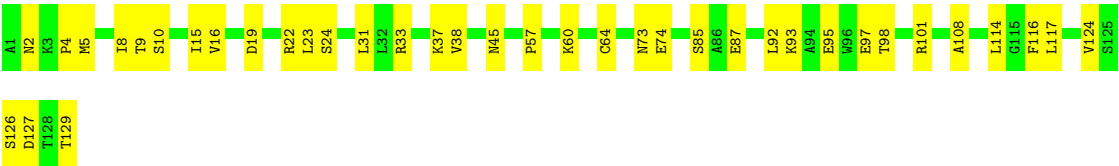
Chain JH:  74% 26%



- Molecule 1: Coat protein



● Molecule 1: Coat protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.039	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.012	Depositor
Map size (\AA)	457.91998, 457.91998, 457.91998	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

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	0.32	0/985	0.50	0/1342
1	AB	0.33	0/985	0.53	0/1342
1	AC	0.32	0/985	0.49	0/1342
1	AD	0.33	0/985	0.55	0/1342
1	AE	0.32	0/985	0.49	0/1342
1	AF	0.34	0/985	0.55	0/1342
1	AG	0.32	0/985	0.49	0/1342
1	AH	0.33	0/985	0.55	0/1342
1	AI	0.33	0/985	0.50	0/1342
1	AJ	0.33	0/985	0.56	0/1342
1	AK	0.32	0/985	0.49	0/1342
1	AL	0.33	0/985	0.56	0/1342
1	AM	0.32	0/985	0.49	0/1342
1	AN	0.34	0/985	0.56	0/1342
1	AO	0.32	0/985	0.50	0/1342
1	AP	0.34	0/985	0.52	0/1342
1	AQ	0.33	0/985	0.50	0/1342
1	AR	0.34	0/985	0.52	0/1342
1	AS	0.32	0/985	0.49	0/1342
1	AT	0.33	0/985	0.52	0/1342
1	AU	0.32	0/985	0.49	0/1342
1	AV	0.33	0/985	0.54	0/1342
1	AW	0.32	0/985	0.50	0/1342
1	AX	0.34	0/985	0.56	0/1342
1	AY	0.32	0/985	0.49	0/1342
1	AZ	0.33	0/985	0.53	0/1342
1	BA	0.32	0/985	0.50	0/1342
1	BB	0.34	0/985	0.53	0/1342
1	BC	0.32	0/985	0.49	0/1342
1	BD	0.35	0/985	0.53	0/1342
1	BE	0.32	0/985	0.48	0/1342
1	BF	0.34	0/985	0.54	0/1342
1	BG	0.32	0/985	0.50	0/1342
1	BH	0.33	0/985	0.52	0/1342

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.32	0/985	0.50	0/1342
1	BJ	0.33	0/985	0.57	0/1342
1	BK	0.33	0/985	0.50	0/1342
1	BL	0.33	0/985	0.53	0/1342
1	BM	0.32	0/985	0.49	0/1342
1	BN	0.33	0/985	0.52	0/1342
1	BO	0.32	0/985	0.49	0/1342
1	BP	0.33	0/985	0.54	0/1342
1	BQ	0.33	0/985	0.50	0/1342
1	BR	0.34	0/985	0.57	0/1342
1	BS	0.32	0/985	0.49	0/1342
1	BT	0.33	0/985	0.53	0/1342
1	BU	0.32	0/985	0.49	0/1342
1	BV	0.33	0/985	0.55	0/1342
1	BW	0.32	0/985	0.49	0/1342
1	BX	0.33	0/985	0.54	0/1342
1	BY	0.32	0/985	0.50	0/1342
1	BZ	0.33	0/985	0.53	0/1342
1	CA	0.32	0/985	0.50	0/1342
1	CB	0.33	0/985	0.56	0/1342
1	CC	0.32	0/985	0.49	0/1342
1	CD	0.33	0/985	0.52	0/1342
1	CE	0.32	0/985	0.49	0/1342
1	CF	0.33	0/985	0.54	0/1342
1	CG	0.32	0/985	0.50	0/1342
1	CH	0.33	0/985	0.55	0/1342
1	CI	0.32	0/985	0.50	0/1342
1	CJ	0.33	0/985	0.52	0/1342
1	CK	0.32	0/985	0.49	0/1342
1	CL	0.33	0/985	0.55	0/1342
1	CM	0.32	0/985	0.49	0/1342
1	CN	0.34	0/985	0.54	0/1342
1	CO	0.32	0/985	0.49	0/1342
1	CP	0.33	0/985	0.54	0/1342
1	CQ	0.32	0/985	0.49	0/1342
1	CR	0.34	0/985	0.52	0/1342
1	CS	0.32	0/985	0.48	0/1342
1	CT	0.34	0/985	0.54	0/1342
1	CU	0.32	0/985	0.51	0/1342
1	CV	0.33	0/985	0.56	0/1342
1	CW	0.32	0/985	0.49	0/1342
1	CX	0.34	0/985	0.54	0/1342
1	CY	0.32	0/985	0.49	0/1342

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CZ	0.33	0/985	0.56	0/1342
1	DA	0.32	0/985	0.49	0/1342
1	DB	0.33	0/985	0.52	0/1342
1	DC	0.32	0/985	0.48	0/1342
1	DE	0.33	0/985	0.53	0/1342
1	DF	0.32	0/985	0.49	0/1342
1	DG	0.34	0/985	0.53	0/1342
1	DH	0.32	0/985	0.49	0/1342
1	DI	0.33	0/985	0.55	0/1342
1	DJ	0.32	0/985	0.50	0/1342
1	DK	0.34	0/985	0.53	0/1342
1	DL	0.32	0/985	0.49	0/1342
1	DM	0.33	0/985	0.55	0/1342
1	DN	0.32	0/985	0.50	0/1342
1	DO	0.33	0/985	0.52	0/1342
1	DP	0.32	0/985	0.49	0/1342
1	DQ	0.34	0/985	0.53	0/1342
1	DR	0.32	0/985	0.49	0/1342
1	DS	0.33	0/985	0.53	0/1342
1	DT	0.32	0/985	0.49	0/1342
1	DU	0.33	0/985	0.55	0/1342
1	DV	0.32	0/985	0.50	0/1342
1	DW	0.35	0/985	0.54	0/1342
1	DX	0.32	0/985	0.49	0/1342
1	DY	0.33	0/985	0.53	0/1342
1	DZ	0.32	0/985	0.49	0/1342
1	EA	0.33	0/985	0.52	0/1342
1	EB	0.32	0/985	0.50	0/1342
1	EC	0.33	0/985	0.52	0/1342
1	ED	0.32	0/985	0.50	0/1342
1	EE	0.34	0/985	0.57	0/1342
1	EF	0.32	0/985	0.49	0/1342
1	EG	0.33	0/985	0.56	0/1342
1	EH	0.32	0/985	0.49	0/1342
1	EI	0.33	0/985	0.54	0/1342
1	EJ	0.32	0/985	0.49	0/1342
1	EK	0.33	0/985	0.55	0/1342
1	EL	0.32	0/985	0.50	0/1342
1	EM	0.33	0/985	0.53	0/1342
1	EN	0.32	0/985	0.49	0/1342
1	EO	0.33	0/985	0.53	0/1342
1	EP	0.32	0/985	0.49	0/1342
1	EQ	0.34	0/985	0.54	0/1342

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	ER	0.33	0/985	0.51	0/1342
1	ES	0.33	0/985	0.53	0/1342
1	ET	0.33	0/985	0.50	0/1342
1	EU	0.33	0/985	0.53	0/1342
1	EV	0.33	0/985	0.54	0/1342
1	EW	0.33	0/985	0.53	0/1342
1	EX	0.33	0/985	0.52	0/1342
1	EY	0.33	0/985	0.53	0/1342
1	EZ	0.32	0/985	0.50	0/1342
1	FA	0.33	0/985	0.53	0/1342
1	FB	0.34	0/985	0.53	0/1342
1	FC	0.32	0/985	0.53	0/1342
1	FD	0.33	0/985	0.51	0/1342
1	FE	0.33	0/985	0.54	0/1342
1	FF	0.33	0/985	0.51	0/1342
1	FG	0.34	0/985	0.53	0/1342
1	FH	0.34	0/985	0.54	0/1342
1	FI	0.33	0/985	0.52	0/1342
1	FJ	0.33	0/985	0.52	0/1342
1	FK	0.33	0/985	0.54	0/1342
1	FL	0.32	0/985	0.51	0/1342
1	FM	0.33	0/985	0.54	0/1342
1	FN	0.35	0/985	0.53	0/1342
1	FO	0.33	0/985	0.54	0/1342
1	FP	0.33	0/985	0.51	0/1342
1	FQ	0.33	0/985	0.54	0/1342
1	FR	0.32	0/985	0.52	0/1342
1	FS	0.34	0/985	0.53	0/1342
1	FT	0.32	0/985	0.51	0/1342
1	FU	0.33	0/985	0.52	0/1342
1	FV	0.33	0/985	0.52	0/1342
1	FW	0.33	0/985	0.53	0/1342
1	FX	0.32	0/985	0.50	0/1342
1	FY	0.33	0/985	0.53	0/1342
1	FZ	0.34	0/985	0.54	0/1342
1	GA	0.33	0/985	0.55	0/1342
1	GB	0.33	0/985	0.51	0/1342
1	GC	0.32	0/985	0.53	0/1342
1	GD	0.32	0/985	0.50	0/1342
1	GE	0.33	0/985	0.52	0/1342
1	GF	0.33	0/985	0.55	0/1342
1	GG	0.33	0/985	0.54	0/1342
1	GH	0.33	0/985	0.53	0/1342

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GI	0.33	0/985	0.54	0/1342
1	GK	0.33	0/985	0.51	0/1342
1	GL	0.34	0/985	0.54	0/1342
1	GM	0.34	0/985	0.54	0/1342
1	GN	0.32	0/985	0.54	0/1342
1	GO	0.32	0/985	0.53	0/1342
1	GP	0.33	0/985	0.54	0/1342
1	GQ	0.33	0/985	0.51	0/1342
1	GR	0.33	0/985	0.54	0/1342
1	GS	0.34	0/985	0.55	0/1342
1	GT	0.33	0/985	0.54	0/1342
1	GU	0.33	0/985	0.52	0/1342
1	GV	0.33	0/985	0.52	0/1342
1	GW	0.32	0/985	0.50	0/1342
1	GX	0.33	0/985	0.55	0/1342
1	GY	0.34	0/985	0.54	0/1342
1	GZ	0.32	0/985	0.54	0/1342
1	HA	0.33	0/985	0.53	0/1342
1	HB	0.33	0/985	0.55	0/1342
1	HC	0.33	0/985	0.50	0/1342
1	HD	0.34	0/985	0.54	0/1342
1	HE	0.33	0/985	0.51	0/1342
1	HF	0.33	0/985	0.54	0/1342
1	HG	0.33	0/985	0.52	0/1342
1	HI	0.33	0/985	0.53	0/1342
1	HJ	0.32	0/985	0.51	0/1342
1	HK	0.33	0/985	0.54	0/1342
1	HL	0.34	0/985	0.53	0/1342
1	HM	0.33	0/985	0.54	0/1342
1	HN	0.33	0/985	0.51	0/1342
1	HO	0.32	0/985	0.53	0/1342
1	HP	0.32	0/985	0.50	0/1342
1	HQ	0.34	0/985	0.52	0/1342
1	HR	0.33	0/985	0.53	0/1342
1	HS	0.32	0/985	0.53	0/1342
1	HT	0.33	0/985	0.51	0/1342
1	HU	0.33	0/985	0.55	0/1342
1	HV	0.33	0/985	0.51	0/1342
1	HW	0.34	0/985	0.53	0/1342
1	HX	0.34	0/985	0.53	0/1342
1	HY	0.34	0/985	0.54	0/1342
1	HZ	0.34	0/985	0.54	0/1342
1	IA	0.33	0/985	0.53	0/1342

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	IB	0.33	0/985	0.51	0/1342
1	IC	0.34	0/985	0.53	0/1342
1	ID	0.34	0/985	0.53	0/1342
1	IE	0.33	0/985	0.54	0/1342
1	IF	0.33	0/985	0.52	0/1342
1	IG	0.33	0/985	0.54	0/1342
1	IH	0.32	0/985	0.50	0/1342
1	II	0.34	0/985	0.55	0/1342
1	IJ	0.33	0/985	0.50	0/1342
1	IK	0.32	0/985	0.53	0/1342
1	IL	0.33	0/985	0.51	0/1342
1	IM	0.33	0/985	0.55	0/1342
1	IN	0.32	0/985	0.50	0/1342
1	IO	0.33	0/985	0.54	0/1342
1	IP	0.34	0/985	0.53	0/1342
1	IQ	0.33	0/985	0.54	0/1342
1	IR	0.33	0/985	0.51	0/1342
1	IS	0.33	0/985	0.55	0/1342
1	IT	0.33	0/985	0.51	0/1342
1	IU	0.34	0/985	0.52	0/1342
1	IV	0.34	0/985	0.53	0/1342
1	IW	0.33	0/985	0.53	0/1342
1	IX	0.33	0/985	0.52	0/1342
1	IZ	0.33	0/985	0.53	0/1342
1	JA	0.32	0/985	0.51	0/1342
1	JB	0.33	0/985	0.54	0/1342
1	JC	0.34	0/985	0.56	0/1342
1	JD	0.33	0/985	0.53	0/1342
1	JE	0.33	0/985	0.52	0/1342
1	JF	0.33	0/985	0.54	0/1342
1	JG	0.32	0/985	0.51	0/1342
1	JH	0.33	0/985	0.55	0/1342
1	JI	0.34	0/985	0.55	0/1342
1	JJ	0.33	0/985	0.52	0/1342
All	All	0.33	0/236400	0.52	0/322080

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AF	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	AN	0	1
1	BJ	0	1
1	CB	0	1
1	CZ	0	1
1	EV	0	1
1	FB	0	1
1	FH	0	1
1	FZ	0	1
1	GY	0	1
1	JI	0	1
All	All	0	11

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AF	66	ASP	Peptide
1	AN	66	ASP	Peptide
1	BJ	66	ASP	Peptide
1	CB	66	ASP	Peptide
1	CZ	66	ASP	Peptide
1	EV	65	ALA	Peptide
1	FB	65	ALA	Peptide
1	FH	65	ALA	Peptide
1	FZ	65	ALA	Peptide
1	GY	65	ALA	Peptide
1	JI	65	ALA	Peptide

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	968	0	975	28	0
1	AB	968	0	975	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AC	968	0	975	33	0
1	AD	968	0	975	60	0
1	AE	968	0	975	37	0
1	AF	968	0	975	48	0
1	AG	968	0	975	27	0
1	AH	968	0	975	48	0
1	AI	968	0	975	32	0
1	AJ	968	0	975	55	0
1	AK	968	0	975	24	0
1	AL	968	0	975	33	0
1	AM	968	0	975	34	0
1	AN	968	0	975	52	0
1	AO	968	0	975	30	0
1	AP	968	0	974	30	0
1	AQ	968	0	975	26	0
1	AR	968	0	974	31	0
1	AS	968	0	975	26	0
1	AT	968	0	974	29	0
1	AU	968	0	975	24	0
1	AV	968	0	975	36	0
1	AW	968	0	975	27	0
1	AX	968	0	975	50	0
1	AY	968	0	975	28	0
1	AZ	968	0	975	36	0
1	BA	968	0	975	25	0
1	BB	968	0	974	32	0
1	BC	968	0	975	31	0
1	BD	968	0	974	37	0
1	BE	968	0	975	23	0
1	BF	968	0	974	33	0
1	BG	968	0	975	32	0
1	BH	968	0	974	35	0
1	BI	968	0	975	28	0
1	BJ	968	0	975	46	0
1	BK	968	0	975	29	0
1	BL	968	0	975	36	0
1	BM	968	0	975	31	0
1	BN	968	0	974	32	0
1	BO	968	0	975	29	0
1	BP	968	0	975	33	0
1	BQ	968	0	975	27	0
1	BR	968	0	975	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BS	968	0	975	20	0
1	BT	968	0	974	30	0
1	BU	968	0	975	31	0
1	BV	968	0	975	50	0
1	BW	968	0	975	32	0
1	BX	968	0	975	54	0
1	BY	968	0	975	30	0
1	BZ	968	0	975	31	0
1	CA	968	0	975	39	0
1	CB	968	0	975	52	0
1	CC	968	0	975	29	0
1	CD	968	0	975	37	0
1	CE	968	0	975	27	0
1	CF	968	0	975	29	0
1	CG	968	0	975	27	0
1	CH	968	0	975	48	0
1	CI	968	0	975	36	0
1	CJ	968	0	975	36	0
1	CK	968	0	975	31	0
1	CL	968	0	975	51	0
1	CM	968	0	975	34	0
1	CN	968	0	974	32	0
1	CO	968	0	975	31	0
1	CP	968	0	975	52	0
1	CQ	968	0	975	28	0
1	CR	968	0	974	31	0
1	CS	968	0	975	25	0
1	CT	968	0	975	36	0
1	CU	968	0	975	28	0
1	CV	968	0	975	52	0
1	CW	968	0	975	24	0
1	CX	968	0	974	25	0
1	CY	968	0	975	27	0
1	CZ	968	0	975	56	0
1	DA	968	0	975	29	0
1	DB	968	0	975	39	0
1	DC	968	0	975	26	0
1	DE	968	0	975	30	0
1	DF	968	0	975	30	0
1	DG	968	0	974	32	0
1	DH	968	0	975	27	0
1	DI	968	0	975	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DJ	968	0	975	34	0
1	DK	968	0	974	32	0
1	DL	968	0	975	29	0
1	DM	968	0	975	47	0
1	DN	968	0	975	32	0
1	DO	968	0	975	36	0
1	DP	968	0	975	30	0
1	DQ	968	0	974	29	0
1	DR	968	0	975	39	0
1	DS	968	0	974	37	0
1	DT	968	0	975	31	0
1	DU	968	0	975	52	0
1	DV	968	0	975	25	0
1	DW	968	0	975	32	0
1	DX	968	0	975	31	0
1	DY	968	0	975	35	0
1	DZ	968	0	975	34	0
1	EA	968	0	974	36	0
1	EB	968	0	975	31	0
1	EC	968	0	975	37	0
1	ED	968	0	975	33	0
1	EE	968	0	975	55	0
1	EF	968	0	975	23	0
1	EG	968	0	975	52	0
1	EH	968	0	975	27	0
1	EI	968	0	975	36	0
1	EJ	968	0	975	27	0
1	EK	968	0	975	50	0
1	EL	968	0	975	31	0
1	EM	968	0	974	34	0
1	EN	968	0	975	33	0
1	EO	968	0	974	30	0
1	EP	968	0	975	25	0
1	EQ	968	0	974	28	0
1	ER	968	0	974	35	0
1	ES	968	0	975	28	0
1	ET	968	0	975	32	0
1	EU	968	0	974	41	0
1	EV	968	0	975	62	0
1	EW	968	0	974	40	0
1	EX	968	0	974	36	0
1	EY	968	0	975	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	EZ	968	0	975	32	0
1	FA	968	0	974	36	0
1	FB	968	0	975	54	0
1	FC	968	0	974	37	0
1	FD	968	0	974	33	0
1	FE	968	0	975	24	0
1	FF	968	0	975	35	0
1	FG	968	0	974	29	0
1	FH	968	0	975	56	0
1	FI	968	0	974	28	0
1	FJ	968	0	974	40	0
1	FK	968	0	975	32	0
1	FL	968	0	975	35	0
1	FM	968	0	974	45	0
1	FN	968	0	975	53	0
1	FO	968	0	974	33	0
1	FP	968	0	974	54	0
1	FQ	968	0	975	35	0
1	FR	968	0	975	36	0
1	FS	968	0	974	42	0
1	FT	968	0	975	37	0
1	FU	968	0	974	32	0
1	FV	968	0	974	31	0
1	FW	968	0	975	41	0
1	FX	968	0	975	30	0
1	FY	968	0	974	34	0
1	FZ	968	0	975	56	0
1	GA	968	0	974	30	0
1	GB	968	0	974	31	0
1	GC	968	0	975	19	0
1	GD	968	0	975	26	0
1	GE	968	0	974	33	0
1	GF	968	0	975	30	0
1	GG	968	0	974	31	0
1	GH	968	0	974	43	0
1	GI	968	0	975	19	0
1	GK	968	0	975	29	0
1	GL	968	0	974	26	0
1	GM	968	0	975	48	0
1	GN	968	0	974	22	0
1	GO	968	0	974	43	0
1	GP	968	0	975	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GQ	968	0	975	29	0
1	GR	968	0	974	30	0
1	GS	968	0	975	32	0
1	GT	968	0	974	33	0
1	GU	968	0	974	48	0
1	GV	968	0	975	29	0
1	GW	968	0	975	31	0
1	GX	968	0	974	34	0
1	GY	968	0	975	56	0
1	GZ	968	0	974	26	0
1	HA	968	0	974	47	0
1	HB	968	0	975	23	0
1	HC	968	0	975	26	0
1	HD	968	0	974	30	0
1	HE	968	0	975	28	0
1	HF	968	0	974	29	0
1	HG	968	0	974	32	0
1	HI	968	0	975	35	0
1	HJ	968	0	975	32	0
1	HK	968	0	974	33	0
1	HL	968	0	975	53	0
1	HM	968	0	974	28	0
1	HN	968	0	974	31	0
1	HO	968	0	975	20	0
1	HP	968	0	975	23	0
1	HQ	968	0	974	29	0
1	HR	968	0	975	36	0
1	HS	968	0	974	34	0
1	HT	968	0	974	41	0
1	HU	968	0	975	34	0
1	HV	968	0	975	36	0
1	HW	968	0	974	33	0
1	HX	968	0	975	51	0
1	HY	968	0	974	26	0
1	HZ	968	0	974	59	0
1	IA	968	0	975	27	0
1	IB	968	0	975	29	0
1	IC	968	0	974	28	0
1	ID	968	0	975	50	0
1	IE	968	0	974	25	0
1	IF	968	0	974	36	0
1	IG	968	0	975	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	IH	968	0	975	28	0
1	II	968	0	974	38	0
1	IJ	968	0	975	36	0
1	IK	968	0	974	27	0
1	IL	968	0	974	30	0
1	IM	968	0	975	30	0
1	IN	968	0	975	35	0
1	IO	968	0	974	31	0
1	IP	968	0	975	48	0
1	IQ	968	0	974	39	0
1	IR	968	0	974	40	0
1	IS	968	0	975	38	0
1	IT	968	0	975	28	0
1	IU	968	0	974	32	0
1	IV	968	0	975	50	0
1	IW	968	0	974	28	0
1	IX	968	0	974	32	0
1	IZ	968	0	975	31	0
1	JA	968	0	975	27	0
1	JB	968	0	974	33	0
1	JC	968	0	975	43	0
1	JD	968	0	974	32	0
1	JE	968	0	974	44	0
1	JF	968	0	975	39	0
1	JG	968	0	975	26	0
1	JH	968	0	974	27	0
1	JI	968	0	975	55	0
1	JJ	968	0	974	36	0
All	All	232320	0	233920	6106	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (6106) 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:EG:68:CYS:H	1:HX:64:CYS:H	1.07	1.00
1:AD:68:CYS:H	1:IV:64:CYS:H	1.08	1.00
1:CL:68:CYS:H	1:FN:64:CYS:H	1.07	1.00
1:DI:68:CYS:H	1:FH:64:CYS:H	1.10	0.96
1:CP:68:CYS:H	1:IP:64:CYS:H	1.09	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:68:CYS:H	1:FZ:64:CYS:H	1.01	0.96
1:AJ:68:CYS:H	1:GM:64:CYS:N	1.64	0.95
1:AJ:68:CYS:H	1:GM:64:CYS:H	1.01	0.95
1:AX:68:CYS:H	1:GY:64:CYS:H	1.02	0.94
1:CV:68:CYS:H	1:HL:64:CYS:N	1.63	0.94
1:AD:68:CYS:H	1:IV:64:CYS:N	1.65	0.94
1:AX:68:CYS:H	1:GY:64:CYS:N	1.65	0.94
1:BX:32:LEU:HB3	1:BX:34:GLN:HE22	1.33	0.94
1:CL:68:CYS:H	1:FN:64:CYS:N	1.65	0.94
1:BR:68:CYS:H	1:FZ:64:CYS:N	1.65	0.93
1:EG:68:CYS:H	1:HX:64:CYS:N	1.65	0.93
1:DB:32:LEU:HB3	1:DB:34:GLN:HE22	1.32	0.93
1:AD:32:LEU:HB3	1:AD:34:GLN:HE22	1.32	0.92
1:CX:32:LEU:HB3	1:CX:34:GLN:HE22	1.32	0.92
1:BH:32:LEU:HB3	1:BH:34:GLN:HE22	1.32	0.92
1:DI:68:CYS:H	1:FH:64:CYS:N	1.67	0.92
1:FM:35:ARG:HH12	1:FM:44:ASN:HA	1.33	0.92
1:AJ:67:ALA:HA	1:GM:63:GLY:H	1.36	0.91
1:CP:68:CYS:H	1:IP:64:CYS:N	1.68	0.91
1:CV:68:CYS:H	1:HL:64:CYS:H	1.07	0.91
1:EE:32:LEU:HB3	1:EE:34:GLN:HE22	1.33	0.91
1:BR:67:ALA:HA	1:FZ:63:GLY:H	1.36	0.90
1:CP:32:LEU:HB3	1:CP:34:GLN:HE22	1.35	0.90
1:CF:32:LEU:HB3	1:CF:34:GLN:HE22	1.34	0.90
1:AV:32:LEU:HB3	1:AV:34:GLN:HE22	1.36	0.90
1:AN:68:CYS:HB3	1:JC:65:ALA:HB2	1.53	0.90
1:BV:68:CYS:H	1:GH:64:CYS:H	1.10	0.90
1:BV:68:CYS:H	1:GH:64:CYS:N	1.68	0.89
1:EK:32:LEU:HB3	1:EK:34:GLN:HE22	1.36	0.89
1:CZ:68:CYS:H	1:ID:64:CYS:N	1.69	0.88
1:AX:67:ALA:HA	1:GY:63:GLY:H	1.37	0.88
1:DM:32:LEU:HB3	1:DM:34:GLN:HE22	1.36	0.88
1:CZ:68:CYS:H	1:ID:64:CYS:H	1.15	0.88
1:DU:32:LEU:HB3	1:DU:34:GLN:HE22	1.37	0.87
1:EI:32:LEU:HB3	1:EI:34:GLN:HE22	1.40	0.87
1:CL:32:LEU:HB3	1:CL:34:GLN:HE22	1.39	0.87
1:DI:32:LEU:HB3	1:DI:34:GLN:HE22	1.39	0.87
1:DY:32:LEU:HB3	1:DY:34:GLN:HE22	1.40	0.87
1:IM:35:ARG:NH2	1:IM:36:VAL:O	2.06	0.87
1:CH:32:LEU:HB3	1:CH:34:GLN:HE22	1.39	0.87
1:DI:67:ALA:HA	1:FH:63:GLY:H	1.39	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EW:35:ARG:NH2	1:EW:36:VAL:O	2.07	0.86
1:CZ:67:ALA:HA	1:ID:63:GLY:H	1.39	0.86
1:AN:67:ALA:HA	1:JC:63:GLY:H	1.37	0.86
1:DM:67:ALA:HA	1:FB:63:GLY:H	1.42	0.85
1:IQ:35:ARG:NH2	1:IQ:36:VAL:O	2.10	0.85
1:BB:32:LEU:HB3	1:BB:34:GLN:HE22	1.41	0.85
1:BJ:32:LEU:HB3	1:BJ:34:GLN:HE22	1.40	0.85
1:DO:32:LEU:HB3	1:DO:34:GLN:HE22	1.42	0.85
1:JF:35:ARG:NH2	1:JF:36:VAL:O	2.08	0.85
1:AX:68:CYS:N	1:GY:64:CYS:H	1.74	0.84
1:BR:68:CYS:N	1:FZ:64:CYS:H	1.74	0.84
1:AJ:68:CYS:N	1:GM:64:CYS:H	1.75	0.84
1:CL:67:ALA:HA	1:FN:63:GLY:H	1.42	0.84
1:EG:67:ALA:HA	1:HX:63:GLY:H	1.43	0.84
1:DS:32:LEU:HB3	1:DS:34:GLN:HE22	1.41	0.84
1:AD:67:ALA:HA	1:IV:63:GLY:H	1.42	0.84
1:GA:35:ARG:NH2	1:GA:36:VAL:O	2.10	0.84
1:AP:32:LEU:HB3	1:AP:34:GLN:HE22	1.40	0.84
1:CV:67:ALA:HA	1:HL:63:GLY:H	1.41	0.84
1:HM:35:ARG:NH2	1:HM:36:VAL:O	2.09	0.84
1:DU:67:ALA:HA	1:FP:63:GLY:H	1.43	0.83
1:EK:67:ALA:HA	1:EV:63:GLY:H	1.41	0.83
1:FC:35:ARG:NH2	1:FC:36:VAL:O	2.10	0.83
1:AF:67:ALA:HA	1:GS:63:GLY:H	1.42	0.83
1:DQ:32:LEU:HB3	1:DQ:34:GLN:HE22	1.41	0.83
1:CT:32:LEU:HB3	1:CT:34:GLN:HE22	1.43	0.83
1:BV:32:LEU:HB3	1:BV:34:GLN:HE22	1.44	0.82
1:BV:67:ALA:HA	1:GH:63:GLY:H	1.44	0.82
1:DQ:23:LEU:HD13	1:IB:44:ASN:HD21	1.44	0.82
1:FW:35:ARG:NH2	1:FW:36:VAL:O	2.11	0.82
1:CZ:32:LEU:HB3	1:CZ:34:GLN:HE22	1.44	0.82
1:HI:35:ARG:NH2	1:HI:36:VAL:O	2.11	0.82
1:AN:68:CYS:H	1:JC:64:CYS:H	1.24	0.82
1:BP:32:LEU:HB3	1:BP:34:GLN:HE22	1.44	0.82
1:DP:12:ALA:HB2	1:FW:10:SER:H	1.43	0.82
1:CR:23:LEU:HD13	1:FF:44:ASN:HD21	1.44	0.81
1:II:35:ARG:NH1	1:II:44:ASN:OD1	2.12	0.81
1:BV:69:VAL:HG13	1:GH:64:CYS:SG	2.20	0.81
1:CP:67:ALA:HA	1:IP:63:GLY:H	1.44	0.81
1:CR:32:LEU:HB3	1:CR:34:GLN:HE22	1.45	0.81
1:EA:32:LEU:HB3	1:EA:34:GLN:HE22	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:32:LEU:HB3	1:AH:34:GLN:HE22	1.44	0.81
1:CB:32:LEU:HB3	1:CB:34:GLN:HE22	1.45	0.81
1:BT:32:LEU:HB3	1:BT:34:GLN:HE22	1.46	0.81
1:CL:68:CYS:N	1:FN:64:CYS:H	1.79	0.81
1:EK:68:CYS:H	1:EV:64:CYS:H	1.28	0.81
1:BF:32:LEU:HB3	1:BF:34:GLN:HE22	1.46	0.81
1:EG:32:LEU:HB3	1:EG:34:GLN:HE22	1.46	0.81
1:AP:23:LEU:HD13	1:HC:44:ASN:HD21	1.46	0.81
1:JH:55:LYS:NZ	1:JH:75:ASN:OD1	2.14	0.81
1:CA:12:ALA:HB2	1:ES:10:SER:H	1.46	0.80
1:EQ:32:LEU:HB3	1:EQ:34:GLN:HE22	1.46	0.80
1:AZ:32:LEU:HB3	1:AZ:34:GLN:HE22	1.46	0.80
1:BR:69:VAL:HG22	1:FZ:64:CYS:HB3	1.63	0.80
1:GK:63:GLY:HA2	1:GM:68:CYS:HA	1.62	0.80
1:CH:68:CYS:H	1:HA:64:CYS:N	1.79	0.80
1:DU:68:CYS:H	1:FP:64:CYS:N	1.79	0.80
1:AL:32:LEU:HB3	1:AL:34:GLN:HE22	1.47	0.80
1:DF:14:LYS:HZ1	1:DF:28:SER:HB2	1.47	0.80
1:BX:67:ALA:HA	1:JI:63:GLY:H	1.46	0.80
1:DM:68:CYS:H	1:FB:64:CYS:N	1.79	0.80
1:HV:88:ASN:HD21	1:HW:56:ARG:HD2	1.44	0.79
1:AJ:32:LEU:HB3	1:AJ:34:GLN:HE22	1.45	0.79
1:EG:68:CYS:N	1:HX:64:CYS:H	1.79	0.79
1:CV:68:CYS:N	1:HL:64:CYS:H	1.79	0.79
1:AD:68:CYS:N	1:IV:64:CYS:H	1.80	0.79
1:CB:67:ALA:HA	1:FJ:63:GLY:H	1.47	0.79
1:CH:68:CYS:H	1:HA:64:CYS:H	1.28	0.79
1:EE:68:CYS:H	1:GU:64:CYS:N	1.81	0.79
1:JG:76:GLN:HE21	1:JH:92:LEU:HD22	1.47	0.79
1:CJ:5:MET:HG3	1:CJ:17:TRP:HB3	1.65	0.79
1:EU:35:ARG:HH12	1:EU:44:ASN:HA	1.48	0.79
1:BZ:5:MET:HG3	1:BZ:17:TRP:HB3	1.64	0.78
1:EK:68:CYS:H	1:EV:64:CYS:N	1.79	0.78
1:JI:101:ARG:HH22	1:JI:124:VAL:HG23	1.46	0.78
1:BA:14:LYS:HZ1	1:BA:28:SER:HB2	1.48	0.78
1:DS:23:LEU:HD13	1:IH:44:ASN:HD21	1.47	0.78
1:DN:14:LYS:HZ1	1:DN:28:SER:HB2	1.48	0.78
1:AB:5:MET:HG3	1:AB:17:TRP:HB3	1.65	0.78
1:CP:68:CYS:N	1:IP:64:CYS:H	1.81	0.78
1:DE:32:LEU:HB3	1:DE:34:GLN:HE22	1.46	0.78
1:DM:68:CYS:H	1:FB:64:CYS:H	1.28	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:14:LYS:HZ1	1:AM:28:SER:HB2	1.47	0.78
1:CX:23:LEU:HD13	1:FL:44:ASN:HD21	1.47	0.78
1:EH:14:LYS:HZ1	1:EH:28:SER:HB2	1.49	0.78
1:CL:69:VAL:HG22	1:FN:64:CYS:HB3	1.66	0.78
1:DU:68:CYS:H	1:FP:64:CYS:H	1.30	0.78
1:JA:76:GLN:HE21	1:JB:92:LEU:HD22	1.49	0.77
1:CG:14:LYS:HZ1	1:CG:28:SER:HB2	1.48	0.77
1:AN:68:CYS:H	1:JC:64:CYS:N	1.82	0.77
1:FS:35:ARG:NH2	1:FS:44:ASN:HA	1.99	0.77
1:GE:35:ARG:NH1	1:GE:42:GLU:OE1	2.18	0.77
1:AH:67:ALA:HA	1:JE:63:GLY:H	1.48	0.77
1:BV:68:CYS:N	1:GH:64:CYS:H	1.83	0.77
1:DP:14:LYS:HZ1	1:DP:28:SER:HB2	1.50	0.77
1:ED:14:LYS:HZ1	1:ED:28:SER:HB2	1.49	0.77
1:FX:88:ASN:HD21	1:FY:56:ARG:HD2	1.50	0.77
1:BC:14:LYS:HZ1	1:BC:28:SER:HB2	1.50	0.77
1:BC:33:ARG:NH2	1:BD:115:GLY:O	2.18	0.77
1:FT:57:PRO:HA	1:FT:73:ASN:HA	1.65	0.77
1:HB:5:MET:HG2	1:HB:17:TRP:HB3	1.65	0.77
1:BX:67:ALA:HB1	1:JI:62:GLU:HG3	1.67	0.77
1:HQ:35:ARG:NH1	1:HQ:42:GLU:OE1	2.18	0.77
1:CG:12:ALA:HB2	1:HI:10:SER:H	1.50	0.76
1:DF:33:ARG:NH2	1:DG:115:GLY:O	2.18	0.76
1:FD:101:ARG:HH21	1:FD:124:VAL:HG21	1.50	0.76
1:DH:14:LYS:HZ1	1:DH:28:SER:HB2	1.51	0.76
1:AX:69:VAL:HG22	1:GY:64:CYS:HB3	1.65	0.76
1:DI:68:CYS:N	1:FH:64:CYS:H	1.82	0.76
1:CM:14:LYS:HZ1	1:CM:28:SER:HB2	1.49	0.76
1:GQ:76:GLN:HE21	1:GR:92:LEU:HD22	1.48	0.76
1:CZ:67:ALA:HB1	1:ID:62:GLU:HG3	1.66	0.76
1:DJ:12:ALA:HB2	1:FC:10:SER:H	1.51	0.76
1:AI:14:LYS:HZ1	1:AI:28:SER:HB2	1.51	0.76
1:EE:68:CYS:H	1:GU:64:CYS:H	1.34	0.76
1:FF:63:GLY:HA2	1:FH:68:CYS:HA	1.68	0.76
1:BG:14:LYS:HZ1	1:BG:28:SER:HB2	1.49	0.76
1:CY:14:LYS:HZ1	1:CY:28:SER:HB2	1.51	0.76
1:EJ:12:ALA:HB2	1:FE:10:SER:H	1.51	0.76
1:BB:5:MET:HG3	1:BB:17:TRP:HB3	1.68	0.75
1:GW:88:ASN:HD21	1:GX:56:ARG:HD2	1.51	0.75
1:CB:68:CYS:SG	1:FJ:65:ALA:HA	2.26	0.75
1:FZ:35:ARG:NH1	1:FZ:43:LEU:O	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:12:ALA:HB2	1:GI:10:SER:H	1.50	0.75
1:BY:12:ALA:HB2	1:IZ:10:SER:H	1.51	0.75
1:DL:12:ALA:HB2	1:FI:10:SER:H	1.51	0.75
1:EG:69:VAL:HG22	1:HX:64:CYS:HB3	1.67	0.75
1:EL:12:ALA:HB2	1:EW:10:SER:H	1.50	0.75
1:BT:23:LEU:HD13	1:FR:44:ASN:HD21	1.49	0.75
1:FA:60:LYS:HG2	1:FA:71:MET:HE1	1.67	0.75
1:HI:101:ARG:HH21	1:HI:124:VAL:HG21	1.52	0.75
1:DX:14:LYS:HZ1	1:DX:28:SER:HB2	1.52	0.75
1:CQ:14:LYS:HZ1	1:CQ:28:SER:HB2	1.51	0.74
1:EX:57:PRO:HA	1:EX:73:ASN:HA	1.69	0.74
1:BP:5:MET:HG3	1:BP:17:TRP:HB3	1.69	0.74
1:DM:5:MET:HG3	1:DM:17:TRP:HB3	1.69	0.74
1:CH:67:ALA:HA	1:HA:63:GLY:H	1.51	0.74
1:AK:51:VAL:HG22	1:AK:79:ARG:HG2	1.69	0.74
1:IM:35:ARG:HH22	1:IM:43:LEU:N	1.85	0.74
1:JA:14:LYS:HZ1	1:JA:28:SER:HB2	1.53	0.74
1:CZ:68:CYS:N	1:ID:64:CYS:H	1.84	0.74
1:EU:98:THR:HG21	1:EU:126:SER:HA	1.69	0.74
1:BF:60:LYS:NZ	1:BF:64:CYS:SG	2.59	0.74
1:CT:5:MET:HG3	1:CT:17:TRP:HB3	1.68	0.74
1:FN:57:PRO:HA	1:FN:73:ASN:HA	1.68	0.74
1:JA:88:ASN:HD21	1:JB:56:ARG:HD2	1.52	0.74
1:JI:35:ARG:NH2	1:JI:36:VAL:O	2.21	0.74
1:BG:33:ARG:NH1	1:BH:115:GLY:O	2.20	0.74
1:JA:63:GLY:HA2	1:JC:68:CYS:HA	1.69	0.74
1:BM:12:ALA:HB2	1:IA:10:SER:H	1.52	0.74
1:DI:67:ALA:HB1	1:FH:62:GLU:HG3	1.69	0.74
1:EE:67:ALA:HA	1:GU:63:GLY:H	1.52	0.74
1:BC:12:ALA:HB2	1:HU:10:SER:H	1.53	0.74
1:CZ:68:CYS:SG	1:ID:65:ALA:HA	2.28	0.74
1:DK:5:MET:HG3	1:DK:17:TRP:HB3	1.68	0.73
1:IR:57:PRO:HA	1:IR:73:ASN:HA	1.68	0.73
1:DF:12:ALA:HB2	1:FU:10:SER:H	1.52	0.73
1:HA:35:ARG:NH2	1:HA:36:VAL:O	2.19	0.73
1:BU:14:LYS:HZ1	1:BU:28:SER:HB2	1.53	0.73
1:IH:88:ASN:HD21	1:II:56:ARG:HD2	1.52	0.73
1:CK:12:ALA:HB2	1:IK:10:SER:H	1.51	0.73
1:DM:68:CYS:SG	1:FB:65:ALA:HA	2.28	0.73
1:GF:57:PRO:HA	1:GF:73:ASN:HA	1.70	0.73
1:IC:60:LYS:HG2	1:IC:71:MET:HE1	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IT:88:ASN:ND2	1:IU:74:GLU:OE2	2.21	0.73
1:AG:12:ALA:HB2	1:GN:10:SER:H	1.53	0.73
1:BJ:67:ALA:HA	1:HZ:63:GLY:H	1.53	0.73
1:DA:33:ARG:NH2	1:DB:115:GLY:O	2.21	0.73
1:DI:67:ALA:N	1:FH:65:ALA:H	1.85	0.73
1:HZ:35:ARG:NH2	1:HZ:36:VAL:O	2.19	0.73
1:JG:88:ASN:HD21	1:JH:56:ARG:HD2	1.52	0.73
1:BY:14:LYS:HZ1	1:BY:28:SER:HB2	1.53	0.73
1:CE:12:ALA:HB2	1:HB:10:SER:H	1.54	0.73
1:AA:12:ALA:HB2	1:JF:10:SER:H	1.53	0.73
1:DQ:6:GLN:HE22	1:IC:111:ASN:HB2	1.54	0.73
1:EK:68:CYS:SG	1:EV:65:ALA:HA	2.28	0.73
1:FD:35:ARG:NH2	1:FD:36:VAL:O	2.18	0.73
1:IB:125:SER:O	1:IC:2:ASN:ND2	2.21	0.73
1:JC:35:ARG:NH2	1:JC:36:VAL:O	2.21	0.73
1:AW:12:ALA:HB2	1:GP:10:SER:H	1.53	0.73
1:CU:14:LYS:HZ1	1:CU:28:SER:HB2	1.54	0.73
1:GO:57:PRO:HA	1:GO:73:ASN:HA	1.70	0.73
1:GY:76:GLN:HE21	1:GZ:92:LEU:HD22	1.54	0.73
1:IP:57:PRO:HA	1:IP:73:ASN:HA	1.71	0.73
1:BA:12:ALA:HB2	1:GD:10:SER:H	1.54	0.72
1:BC:60:LYS:NZ	1:BC:66:ASP:O	2.21	0.72
1:EB:14:LYS:HZ1	1:EB:28:SER:HB2	1.53	0.72
1:FW:101:ARG:HH21	1:FW:124:VAL:HG21	1.52	0.72
1:II:57:PRO:HA	1:II:73:ASN:HA	1.70	0.72
1:IV:57:PRO:HA	1:IV:73:ASN:HA	1.71	0.72
1:AM:12:ALA:HB2	1:IS:10:SER:H	1.54	0.72
1:BJ:68:CYS:H	1:HZ:64:CYS:N	1.86	0.72
1:IL:35:ARG:NH2	1:IL:36:VAL:O	2.17	0.72
1:CW:117:LEU:HD21	1:CX:31:LEU:HD13	1.72	0.72
1:HT:57:PRO:HA	1:HT:73:ASN:HA	1.69	0.72
1:DJ:60:LYS:NZ	1:DJ:66:ASP:O	2.20	0.72
1:GE:98:THR:HG21	1:GE:126:SER:HA	1.71	0.72
1:AO:14:LYS:HZ1	1:AO:28:SER:HB2	1.52	0.72
1:DA:60:LYS:NZ	1:DA:66:ASP:O	2.21	0.72
1:DK:23:LEU:HD13	1:JG:44:ASN:HD21	1.55	0.72
1:FM:57:PRO:HA	1:FM:73:ASN:HA	1.71	0.72
1:GH:35:ARG:NH2	1:GH:36:VAL:O	2.21	0.72
1:IF:57:PRO:HA	1:IF:73:ASN:HA	1.71	0.72
1:JG:63:GLY:HA2	1:JI:68:CYS:HA	1.70	0.72
1:IO:98:THR:HG21	1:IO:126:SER:HA	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:69:VAL:HG13	1:HA:64:CYS:HB2	1.72	0.72
1:CS:12:ALA:HB2	1:IE:10:SER:H	1.53	0.72
1:GY:60:LYS:HD2	1:GY:71:MET:HE1	1.71	0.72
1:HJ:14:LYS:HZ1	1:HJ:28:SER:HB2	1.55	0.72
1:JJ:101:ARG:HH21	1:JJ:124:VAL:HG21	1.53	0.72
1:CP:69:VAL:HG22	1:IP:64:CYS:HB3	1.70	0.72
1:GS:57:PRO:HA	1:GS:73:ASN:HA	1.71	0.72
1:HM:35:ARG:HH22	1:HM:43:LEU:N	1.87	0.72
1:CV:69:VAL:HG22	1:HL:64:CYS:HB3	1.71	0.72
1:IH:14:LYS:HZ1	1:IH:28:SER:HB2	1.55	0.72
1:BH:98:THR:HG21	1:BH:126:SER:HA	1.71	0.71
1:CC:14:LYS:HZ1	1:CC:28:SER:HB2	1.54	0.71
1:HD:57:PRO:HA	1:HD:73:ASN:HA	1.72	0.71
1:HV:61:PRO:HG2	1:HV:64:CYS:SG	2.31	0.71
1:AJ:69:VAL:O	1:GM:63:GLY:HA3	1.89	0.71
1:DJ:14:LYS:HZ1	1:DJ:28:SER:HB2	1.55	0.71
1:EN:14:LYS:HZ1	1:EN:28:SER:HB2	1.53	0.71
1:FS:56:ARG:O	1:FS:74:GLU:N	2.21	0.71
1:AA:14:LYS:HZ1	1:AA:28:SER:HB2	1.53	0.71
1:BK:60:LYS:NZ	1:BK:66:ASP:O	2.20	0.71
1:BQ:12:ALA:HB2	1:GG:10:SER:H	1.53	0.71
1:HR:57:PRO:HA	1:HR:73:ASN:HA	1.73	0.71
1:AC:51:VAL:HG22	1:AC:79:ARG:HG2	1.73	0.71
1:CO:12:ALA:HB2	1:FF:10:SER:H	1.56	0.71
1:CU:12:ALA:HB2	1:HS:10:SER:H	1.53	0.71
1:GQ:88:ASN:HD21	1:GR:56:ARG:HD2	1.54	0.71
1:BK:14:LYS:HZ1	1:BK:28:SER:HB2	1.55	0.71
1:CI:12:ALA:HB2	1:IQ:10:SER:H	1.52	0.71
1:IG:101:ARG:HH21	1:IG:124:VAL:HG21	1.55	0.71
1:EH:12:ALA:HB2	1:EZ:10:SER:H	1.54	0.71
1:BG:12:ALA:HB2	1:HV:10:SER:H	1.55	0.71
1:BV:98:THR:HG21	1:BV:126:SER:HA	1.72	0.71
1:BW:14:LYS:HZ1	1:BW:28:SER:HB2	1.54	0.71
1:EN:12:ALA:HB2	1:IT:10:SER:H	1.55	0.71
1:DI:67:ALA:H	1:FH:65:ALA:H	1.36	0.71
1:FB:57:PRO:HA	1:FB:73:ASN:HA	1.71	0.71
1:IX:57:PRO:HA	1:IX:73:ASN:HA	1.72	0.71
1:AE:14:LYS:HZ1	1:AE:28:SER:HB2	1.56	0.71
1:AK:12:ALA:HB2	1:GQ:10:SER:H	1.55	0.71
1:BX:98:THR:HG21	1:BX:126:SER:HA	1.72	0.71
1:AJ:69:VAL:HG13	1:GM:64:CYS:SG	2.31	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:69:VAL:O	1:FZ:63:GLY:HA3	1.91	0.70
1:CE:3:LYS:NZ	1:CF:129:THR:OG1	2.22	0.70
1:DH:12:ALA:HB2	1:IN:10:SER:H	1.55	0.70
1:IF:115:GLY:O	1:IG:33:ARG:NH1	2.25	0.70
1:CA:51:VAL:HG22	1:CA:79:ARG:HG2	1.71	0.70
1:EE:66:ASP:OD1	1:GU:64:CYS:HA	1.92	0.70
1:FH:57:PRO:HA	1:FH:73:ASN:HA	1.73	0.70
1:FY:35:ARG:NH1	1:FY:42:GLU:HG3	2.06	0.70
1:CZ:69:VAL:O	1:ID:63:GLY:HA3	1.92	0.70
1:DC:51:VAL:HG22	1:DC:79:ARG:HG2	1.74	0.70
1:DM:66:ASP:OD1	1:FB:64:CYS:HA	1.91	0.70
1:FS:57:PRO:HA	1:FS:73:ASN:HA	1.74	0.70
1:HU:98:THR:HG21	1:HU:126:SER:HA	1.74	0.70
1:HY:98:THR:HG21	1:HY:126:SER:HA	1.74	0.70
1:AU:12:ALA:HB2	1:GK:10:SER:H	1.56	0.70
1:EG:67:ALA:HB1	1:HX:62:GLU:HG3	1.73	0.70
1:EV:57:PRO:HA	1:EV:73:ASN:HA	1.74	0.70
1:HG:57:PRO:HA	1:HG:73:ASN:HA	1.71	0.70
1:AR:23:LEU:HD13	1:GQ:44:ASN:HD21	1.55	0.70
1:AW:14:LYS:HZ1	1:AW:28:SER:HB2	1.54	0.70
1:AH:68:CYS:H	1:JE:64:CYS:N	1.90	0.70
1:BJ:68:CYS:H	1:HZ:64:CYS:H	1.37	0.70
1:CK:51:VAL:HG22	1:CK:79:ARG:HG2	1.71	0.70
1:DA:14:LYS:HZ1	1:DA:28:SER:HB2	1.55	0.70
1:GX:35:ARG:NH1	1:GX:42:GLU:HG3	2.06	0.70
1:JD:60:LYS:HD3	1:JD:64:CYS:HB3	1.74	0.70
1:DT:51:VAL:HG22	1:DT:79:ARG:HG2	1.74	0.70
1:HD:101:ARG:HH12	1:HD:124:VAL:HG21	1.57	0.70
1:HG:115:GLY:O	1:HI:33:ARG:NH1	2.25	0.70
1:AP:98:THR:HG21	1:AP:126:SER:HA	1.74	0.70
1:CW:51:VAL:HG22	1:CW:79:ARG:HG2	1.74	0.70
1:FR:14:LYS:HZ1	1:FR:28:SER:HB2	1.56	0.70
1:AY:51:VAL:HG22	1:AY:79:ARG:HG2	1.72	0.70
1:EO:60:LYS:NZ	1:EO:64:CYS:SG	2.61	0.70
1:FV:115:GLY:O	1:FW:33:ARG:NH1	2.24	0.70
1:FX:14:LYS:HZ1	1:FX:28:SER:HB2	1.57	0.70
1:CL:69:VAL:O	1:FN:63:GLY:HA3	1.92	0.70
1:DR:12:ALA:HB2	1:IB:10:SER:H	1.57	0.70
1:EF:51:VAL:HG22	1:EF:79:ARG:HG2	1.74	0.70
1:JE:85:SER:N	1:JF:74:GLU:OE2	2.22	0.70
1:AD:69:VAL:O	1:IV:63:GLY:HA3	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:12:ALA:HB2	1:FX:10:SER:H	1.57	0.69
1:BQ:14:LYS:HZ1	1:BQ:28:SER:HB2	1.55	0.69
1:EM:98:THR:HG21	1:EM:126:SER:HA	1.73	0.69
1:IZ:60:LYS:NZ	1:IZ:65:ALA:O	2.25	0.69
1:AD:69:VAL:HG22	1:IV:64:CYS:HB3	1.75	0.69
1:AQ:14:LYS:HZ1	1:AQ:28:SER:HB2	1.55	0.69
1:BX:68:CYS:H	1:JI:64:CYS:H	1.39	0.69
1:DZ:12:ALA:HB2	1:HF:10:SER:H	1.56	0.69
1:JF:35:ARG:HH22	1:JF:43:LEU:N	1.90	0.69
1:EQ:23:LEU:HD13	1:IT:44:ASN:HD21	1.55	0.69
1:EW:60:LYS:NZ	1:EW:65:ALA:O	2.25	0.69
1:FA:98:THR:HG21	1:FA:126:SER:HA	1.72	0.69
1:FW:35:ARG:HH22	1:FW:43:LEU:N	1.90	0.69
1:FY:57:PRO:HA	1:FY:73:ASN:HA	1.73	0.69
1:GT:60:LYS:HD3	1:GT:64:CYS:HB3	1.73	0.69
1:BJ:67:ALA:HB1	1:HZ:62:GLU:HG3	1.74	0.69
1:CZ:98:THR:HG21	1:CZ:126:SER:HA	1.74	0.69
1:HV:60:LYS:HE2	1:HV:65:ALA:HB3	1.74	0.69
1:JG:14:LYS:HZ1	1:JG:28:SER:HB2	1.58	0.69
1:AD:67:ALA:HB1	1:IV:62:GLU:HG3	1.74	0.69
1:AX:69:VAL:O	1:GY:63:GLY:HA3	1.92	0.69
1:DG:67:ALA:HB3	1:IO:64:CYS:HA	1.73	0.69
1:EK:66:ASP:OD1	1:EV:64:CYS:HA	1.91	0.69
1:AE:33:ARG:NH2	1:AF:115:GLY:O	2.25	0.69
1:AN:98:THR:HG21	1:AN:126:SER:HA	1.73	0.69
1:AP:6:GLN:HE22	1:HD:111:ASN:HB2	1.57	0.69
1:BB:98:THR:HG21	1:BB:126:SER:HA	1.74	0.69
1:CB:98:THR:HG21	1:CB:126:SER:HA	1.73	0.69
1:CP:69:VAL:O	1:IP:63:GLY:HA3	1.93	0.69
1:DK:98:THR:HG21	1:DK:126:SER:HA	1.74	0.69
1:AJ:67:ALA:HB1	1:GM:62:GLU:HG3	1.75	0.69
1:AP:68:CYS:N	1:HD:64:CYS:SG	2.64	0.69
1:DU:98:THR:HG21	1:DU:126:SER:HA	1.75	0.69
1:EB:12:ALA:HB2	1:HJ:10:SER:H	1.58	0.69
1:EW:35:ARG:HH22	1:EW:43:LEU:N	1.91	0.69
1:CM:12:ALA:HB2	1:FO:10:SER:H	1.56	0.69
1:CQ:12:ALA:HB2	1:ET:10:SER:H	1.56	0.69
1:DB:98:THR:HG21	1:DB:126:SER:HA	1.74	0.69
1:DV:12:ALA:HB2	1:IH:10:SER:H	1.57	0.69
1:IU:22:ARG:NH2	1:IU:55:LYS:O	2.26	0.69
1:AF:68:CYS:HB3	1:GS:65:ALA:HB3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FR:88:ASN:HD21	1:FS:56:ARG:HD2	1.58	0.69
1:GQ:14:LYS:HZ1	1:GQ:28:SER:HB2	1.58	0.69
1:HD:55:LYS:NZ	1:HD:73:ASN:HB2	2.08	0.69
1:II:22:ARG:NH2	1:II:55:LYS:O	2.26	0.69
1:IN:76:GLN:HE21	1:IO:92:LEU:HD22	1.58	0.69
1:BJ:68:CYS:SG	1:HZ:65:ALA:HA	2.33	0.69
1:FW:98:THR:HG21	1:FW:126:SER:HA	1.75	0.69
1:BS:117:LEU:HD21	1:BT:31:LEU:HD13	1.74	0.68
1:BW:12:ALA:HB2	1:FR:10:SER:H	1.57	0.68
1:DT:115:GLY:O	1:DU:33:ARG:NH1	2.24	0.68
1:DV:14:LYS:HZ1	1:DV:28:SER:HB2	1.56	0.68
1:HI:35:ARG:HH22	1:HI:43:LEU:N	1.91	0.68
1:JE:74:GLU:OE2	1:JF:88:ASN:ND2	2.26	0.68
1:CV:69:VAL:O	1:HL:63:GLY:HA3	1.92	0.68
1:DC:12:ALA:HB2	1:JG:10:SER:H	1.58	0.68
1:DT:12:ALA:HB2	1:IM:10:SER:H	1.57	0.68
1:ER:35:ARG:NH2	1:ER:36:VAL:O	2.20	0.68
1:FA:57:PRO:HA	1:FA:73:ASN:HA	1.76	0.68
1:FO:98:THR:HG21	1:FO:126:SER:HA	1.73	0.68
1:FZ:76:GLN:HE21	1:GA:92:LEU:HD22	1.57	0.68
1:HQ:35:ARG:HH22	1:HQ:42:GLU:HB3	1.58	0.68
1:IS:98:THR:HG21	1:IS:126:SER:HA	1.75	0.68
1:AD:98:THR:HG21	1:AD:126:SER:HA	1.75	0.68
1:AP:22:ARG:NH2	1:AP:55:LYS:O	2.25	0.68
1:EL:14:LYS:HZ1	1:EL:28:SER:HB2	1.58	0.68
1:BE:51:VAL:HG22	1:BE:79:ARG:HG2	1.74	0.68
1:DI:68:CYS:SG	1:FH:65:ALA:HA	2.34	0.68
1:EA:60:LYS:NZ	1:EA:64:CYS:SG	2.60	0.68
1:EN:33:ARG:NH1	1:EO:115:GLY:O	2.27	0.68
1:EP:12:ALA:HB2	1:JA:10:SER:H	1.58	0.68
1:FY:22:ARG:NH2	1:FY:55:LYS:O	2.27	0.68
1:GA:35:ARG:HH22	1:GA:43:LEU:N	1.90	0.68
1:GU:57:PRO:HA	1:GU:73:ASN:HA	1.76	0.68
1:AR:98:THR:HG21	1:AR:126:SER:HA	1.76	0.68
1:FM:56:ARG:O	1:FM:74:GLU:N	2.19	0.68
1:HK:22:ARG:NH2	1:HK:55:LYS:O	2.26	0.68
1:AQ:12:ALA:HB2	1:GW:10:SER:H	1.58	0.68
1:BJ:98:THR:HG21	1:BJ:126:SER:HA	1.75	0.68
1:EG:69:VAL:O	1:HX:63:GLY:HA3	1.93	0.68
1:EZ:74:GLU:OE2	1:FA:88:ASN:ND2	2.27	0.68
1:BI:12:ALA:HB2	1:HP:10:SER:H	1.56	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:67:ALA:HB1	1:FN:62:GLU:HG3	1.74	0.68
1:EM:6:GLN:HE22	1:JB:111:ASN:HB2	1.59	0.68
1:GG:60:LYS:NZ	1:GG:65:ALA:O	2.26	0.68
1:IC:98:THR:HG21	1:IC:126:SER:HA	1.76	0.68
1:AC:12:ALA:HB2	1:EY:10:SER:H	1.56	0.68
1:AD:66:ASP:OD1	1:IV:64:CYS:HA	1.93	0.68
1:BV:55:LYS:NZ	1:BV:73:ASN:OD1	2.27	0.68
1:CC:33:ARG:NH2	1:CD:115:GLY:O	2.25	0.68
1:DA:3:LYS:HZ2	1:DB:129:THR:HG23	1.56	0.68
1:DP:13:ASN:ND2	1:DP:31:LEU:O	2.26	0.68
1:EP:51:VAL:HG22	1:EP:79:ARG:HG2	1.74	0.68
1:FR:125:SER:O	1:FS:2:ASN:ND2	2.27	0.68
1:BN:60:LYS:NZ	1:BN:64:CYS:SG	2.62	0.68
1:BS:51:VAL:HG22	1:BS:79:ARG:HG2	1.74	0.68
1:DK:6:GLN:HE22	1:JH:111:ASN:HB2	1.58	0.68
1:FY:56:ARG:O	1:FY:74:GLU:N	2.27	0.68
1:GW:45:ASN:HA	1:GW:85:SER:HA	1.76	0.68
1:HK:60:LYS:NZ	1:HK:69:VAL:O	2.27	0.68
1:CJ:98:THR:HG21	1:CJ:126:SER:HA	1.75	0.68
1:EZ:76:GLN:HE21	1:FA:92:LEU:HD22	1.58	0.68
1:IO:22:ARG:NH2	1:IO:55:LYS:O	2.27	0.68
1:AM:33:ARG:NH2	1:AN:115:GLY:O	2.25	0.67
1:CI:14:LYS:HZ1	1:CI:28:SER:HB2	1.57	0.67
1:GE:35:ARG:HH22	1:GE:42:GLU:HB3	1.58	0.67
1:HC:14:LYS:HZ1	1:HC:28:SER:HB2	1.57	0.67
1:IF:85:SER:N	1:IG:74:GLU:OE1	2.27	0.67
1:AO:12:ALA:HB2	1:JD:10:SER:H	1.59	0.67
1:EC:98:THR:HG21	1:EC:126:SER:HA	1.76	0.67
1:GW:117:LEU:HD21	1:GX:31:LEU:HD13	1.75	0.67
1:IG:98:THR:HG21	1:IG:126:SER:HA	1.76	0.67
1:FL:65:ALA:HB1	1:FL:69:VAL:HB	1.76	0.67
1:HX:57:PRO:HA	1:HX:73:ASN:HA	1.74	0.67
1:ID:101:ARG:NH2	1:ID:124:VAL:O	2.26	0.67
1:IO:57:PRO:HA	1:IO:73:ASN:HA	1.75	0.67
1:BX:68:CYS:H	1:JI:64:CYS:N	1.93	0.67
1:EG:66:ASP:OD1	1:HX:64:CYS:HA	1.95	0.67
1:GP:64:CYS:HA	1:GR:67:ALA:HB3	1.77	0.67
1:BB:68:CYS:N	1:GL:64:CYS:SG	2.65	0.67
1:EJ:60:LYS:HZ1	1:EJ:66:ASP:H	1.43	0.67
1:GN:5:MET:HG2	1:GN:17:TRP:HB3	1.75	0.67
1:HV:125:SER:O	1:HW:2:ASN:ND2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IN:74:GLU:OE2	1:IO:88:ASN:ND2	2.27	0.67
1:IT:61:PRO:HG2	1:IT:64:CYS:SG	2.34	0.67
1:JJ:60:LYS:HD3	1:JJ:64:CYS:HB3	1.77	0.67
1:AU:37:LYS:HG3	1:AU:39:GLY:H	1.60	0.67
1:BG:115:GLY:O	1:BH:33:ARG:NH1	2.24	0.67
1:CW:88:ASN:ND2	1:CX:74:GLU:OE2	2.26	0.67
1:FA:22:ARG:NH2	1:FA:55:LYS:O	2.28	0.67
1:IT:117:LEU:HD21	1:IU:31:LEU:HD13	1.76	0.67
1:JC:85:SER:N	1:JD:74:GLU:OE1	2.27	0.67
1:DT:117:LEU:HD21	1:DU:31:LEU:HD13	1.77	0.67
1:ET:61:PRO:HG2	1:ET:64:CYS:SG	2.35	0.67
1:EU:22:ARG:NH2	1:EU:55:LYS:O	2.27	0.67
1:EV:85:SER:N	1:EW:74:GLU:OE2	2.26	0.67
1:EV:115:GLY:O	1:EW:33:ARG:NH1	2.28	0.67
1:FS:22:ARG:NH2	1:FS:55:LYS:O	2.27	0.67
1:GW:33:ARG:NH2	1:GX:115:GLY:O	2.28	0.67
1:HI:98:THR:HG21	1:HI:126:SER:HA	1.76	0.67
1:AH:68:CYS:H	1:JE:64:CYS:H	1.41	0.67
1:BR:67:ALA:N	1:FZ:65:ALA:H	1.92	0.67
1:CR:22:ARG:NH2	1:CR:55:LYS:O	2.28	0.67
1:CV:66:ASP:OD2	1:HL:64:CYS:HA	1.95	0.67
1:EU:57:PRO:HA	1:EU:73:ASN:HA	1.75	0.67
1:IJ:76:GLN:HE21	1:IK:92:LEU:HD22	1.59	0.67
1:BC:3:LYS:HZ2	1:BD:129:THR:HG23	1.60	0.67
1:FZ:35:ARG:NH2	1:FZ:42:GLU:OE1	2.27	0.67
1:GD:14:LYS:HZ1	1:GD:28:SER:HB2	1.60	0.67
1:GT:35:ARG:HH22	1:GT:42:GLU:HB3	1.59	0.67
1:HE:57:PRO:HA	1:HE:73:ASN:HA	1.77	0.67
1:AJ:67:ALA:N	1:GM:65:ALA:H	1.93	0.67
1:BQ:60:LYS:NZ	1:BQ:66:ASP:O	2.20	0.67
1:CA:117:LEU:HD21	1:CB:31:LEU:HD13	1.77	0.67
1:CH:55:LYS:NZ	1:CH:73:ASN:OD1	2.27	0.67
1:CM:33:ARG:NH2	1:CN:115:GLY:O	2.25	0.67
1:CU:60:LYS:NZ	1:CU:66:ASP:O	2.21	0.67
1:DM:69:VAL:O	1:FB:63:GLY:HA3	1.95	0.67
1:ED:115:GLY:O	1:EE:33:ARG:NH1	2.24	0.67
1:EL:60:LYS:NZ	1:EL:66:ASP:O	2.23	0.67
1:GH:5:MET:HG2	1:GH:17:TRP:HB3	1.76	0.67
1:AF:68:CYS:H	1:GS:64:CYS:H	1.43	0.66
1:CH:68:CYS:SG	1:HA:65:ALA:HA	2.36	0.66
1:JF:60:LYS:NZ	1:JF:65:ALA:O	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JJ:98:THR:HG21	1:JJ:126:SER:HA	1.78	0.66
1:CI:60:LYS:NZ	1:CI:66:ASP:O	2.22	0.66
1:CZ:55:LYS:NZ	1:CZ:73:ASN:OD1	2.27	0.66
1:DN:12:ALA:HB2	1:FQ:10:SER:H	1.58	0.66
1:CP:67:ALA:HB1	1:IP:62:GLU:HG3	1.76	0.66
1:EB:60:LYS:NZ	1:EB:66:ASP:O	2.22	0.66
1:FV:60:LYS:NZ	1:FV:69:VAL:O	2.27	0.66
1:IU:32:LEU:HB3	1:IU:47:SER:HB3	1.77	0.66
1:BJ:22:ARG:NH2	1:BJ:55:LYS:O	2.28	0.66
1:DA:115:GLY:O	1:DB:33:ARG:NH1	2.24	0.66
1:HD:60:LYS:HG2	1:HD:71:MET:HE1	1.78	0.66
1:IP:37:LYS:NZ	1:IP:40:ILE:O	2.28	0.66
1:IT:37:LYS:NZ	1:IT:39:GLY:O	2.29	0.66
1:BB:22:ARG:NH2	1:BB:55:LYS:O	2.28	0.66
1:CV:67:ALA:HB1	1:HL:62:GLU:HG3	1.76	0.66
1:CZ:69:VAL:HG22	1:ID:64:CYS:HB3	1.76	0.66
1:GK:14:LYS:HZ1	1:GK:28:SER:HB2	1.61	0.66
1:HK:56:ARG:O	1:HK:74:GLU:N	2.28	0.66
1:IN:14:LYS:HZ1	1:IN:28:SER:HB2	1.61	0.66
1:IQ:60:LYS:NZ	1:IQ:65:ALA:O	2.27	0.66
1:AF:69:VAL:O	1:GS:63:GLY:HA3	1.96	0.66
1:AR:6:GLN:HE22	1:GR:111:ASN:HB2	1.60	0.66
1:AX:98:THR:HG21	1:AX:126:SER:HA	1.77	0.66
1:HZ:91:THR:OG1	1:IA:76:GLN:NE2	2.28	0.66
1:IX:85:SER:N	1:IZ:74:GLU:OE2	2.21	0.66
1:AK:88:ASN:ND2	1:AL:74:GLU:OE2	2.26	0.66
1:CS:37:LYS:HG3	1:CS:39:GLY:H	1.61	0.66
1:EK:69:VAL:O	1:EV:63:GLY:HA3	1.96	0.66
1:FU:98:THR:HG21	1:FU:126:SER:HA	1.77	0.66
1:HZ:5:MET:N	1:HZ:5:MET:SD	2.69	0.66
1:IB:65:ALA:HB1	1:IB:69:VAL:HB	1.77	0.66
1:JE:115:GLY:O	1:JF:33:ARG:NH1	2.28	0.66
1:AJ:69:VAL:HG22	1:GM:64:CYS:HB3	1.78	0.66
1:AS:12:ALA:HB2	1:HC:10:SER:H	1.59	0.66
1:BJ:69:VAL:H	1:HZ:64:CYS:H	1.44	0.66
1:DA:12:ALA:HB2	1:FL:10:SER:H	1.61	0.66
1:DI:69:VAL:HG22	1:FH:64:CYS:HB3	1.77	0.66
1:DJ:88:ASN:ND2	1:DK:74:GLU:OE2	2.29	0.66
1:ET:76:GLN:HE21	1:EU:92:LEU:HD22	1.61	0.66
1:FB:74:GLU:OE2	1:FC:88:ASN:ND2	2.29	0.66
1:FK:98:THR:HG21	1:FK:126:SER:HA	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GS:115:GLY:O	1:GT:33:ARG:NH1	2.29	0.66
1:HC:117:LEU:HD21	1:HD:31:LEU:HD13	1.78	0.66
1:HD:98:THR:HG21	1:HD:126:SER:HA	1.77	0.66
1:HV:5:MET:HB2	1:HW:123:ILE:HB	1.77	0.66
1:BL:98:THR:HG21	1:BL:126:SER:HA	1.77	0.66
1:DM:68:CYS:N	1:FB:64:CYS:H	1.94	0.66
1:FB:115:GLY:O	1:FC:33:ARG:NH1	2.28	0.66
1:HV:65:ALA:HB1	1:HV:69:VAL:HB	1.77	0.66
1:IH:117:LEU:HD21	1:IL:31:LEU:HD13	1.76	0.66
1:IR:115:GLY:O	1:IS:33:ARG:NH1	2.29	0.66
1:EK:67:ALA:HB1	1:EV:62:GLU:HG3	1.77	0.66
1:EK:68:CYS:N	1:EV:64:CYS:H	1.94	0.66
1:GL:98:THR:HG21	1:GL:126:SER:HA	1.77	0.66
1:HJ:117:LEU:HD21	1:HK:31:LEU:HD13	1.78	0.66
1:AC:117:LEU:HD21	1:AD:31:LEU:HD13	1.77	0.65
1:CL:66:ASP:OD1	1:FN:64:CYS:HA	1.95	0.65
1:EX:55:LYS:NZ	1:EX:73:ASN:HB2	2.11	0.65
1:AC:115:GLY:O	1:AD:33:ARG:NH1	2.24	0.65
1:FL:33:ARG:NH1	1:FM:115:GLY:O	2.29	0.65
1:IL:74:GLU:OE2	1:IM:88:ASN:ND2	2.29	0.65
1:IP:115:GLY:O	1:IQ:33:ARG:NH1	2.28	0.65
1:AJ:67:ALA:H	1:GM:65:ALA:H	1.45	0.65
1:AM:5:MET:HE1	1:AN:123:ILE:HG22	1.79	0.65
1:ED:12:ALA:HB2	1:HY:10:SER:H	1.60	0.65
1:FB:85:SER:N	1:FC:74:GLU:OE2	2.24	0.65
1:GU:35:ARG:HH12	1:GU:42:GLU:HB3	1.62	0.65
1:GW:14:LYS:HZ1	1:GW:28:SER:HB2	1.61	0.65
1:HS:60:LYS:NZ	1:HS:65:ALA:O	2.26	0.65
1:IL:115:GLY:O	1:IM:33:ARG:NH1	2.29	0.65
1:IN:33:ARG:NH1	1:IO:115:GLY:O	2.30	0.65
1:AC:88:ASN:ND2	1:AD:74:GLU:OE2	2.28	0.65
1:BV:67:ALA:HB1	1:GH:62:GLU:HG3	1.77	0.65
1:DI:69:VAL:O	1:FH:63:GLY:HA3	1.95	0.65
1:DQ:68:CYS:N	1:IC:64:CYS:SG	2.70	0.65
1:EM:23:LEU:HD13	1:JA:44:ASN:HD21	1.61	0.65
1:ER:76:GLN:HE21	1:ES:92:LEU:HD22	1.61	0.65
1:AE:51:VAL:HG22	1:AE:79:ARG:HG2	1.78	0.65
1:AW:60:LYS:NZ	1:AW:66:ASP:O	2.23	0.65
1:BS:88:ASN:ND2	1:BT:74:GLU:OE2	2.26	0.65
1:DO:106:LEU:HD21	1:DO:123:ILE:HD11	1.79	0.65
1:EI:22:ARG:NH2	1:EI:55:LYS:O	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GX:22:ARG:NH2	1:GX:55:LYS:O	2.29	0.65
1:IP:74:GLU:OE2	1:IQ:88:ASN:ND2	2.29	0.65
1:AX:67:ALA:N	1:GY:65:ALA:H	1.95	0.65
1:FB:101:ARG:HH12	1:FB:124:VAL:HG21	1.61	0.65
1:FV:74:GLU:OE2	1:FW:88:ASN:ND2	2.30	0.65
1:HQ:60:LYS:HA	1:HQ:71:MET:HE3	1.78	0.65
1:IE:60:LYS:NZ	1:IE:66:ASP:O	2.30	0.65
1:IP:85:SER:N	1:IQ:74:GLU:OE2	2.24	0.65
1:IP:101:ARG:HH12	1:IP:124:VAL:HG21	1.62	0.65
1:AM:51:VAL:HG22	1:AM:79:ARG:HG2	1.79	0.65
1:AX:66:ASP:OD1	1:GY:64:CYS:HA	1.96	0.65
1:DZ:60:LYS:HZ1	1:DZ:66:ASP:H	1.43	0.65
1:EV:74:GLU:OE2	1:EW:88:ASN:ND2	2.29	0.65
1:FL:88:ASN:HD21	1:FM:56:ARG:HD2	1.61	0.65
1:IT:125:SER:O	1:IU:2:ASN:ND2	2.29	0.65
1:AM:60:LYS:NZ	1:AM:66:ASP:O	2.23	0.65
1:EG:98:THR:HG21	1:EG:126:SER:HA	1.79	0.65
1:EZ:33:ARG:NH1	1:FA:115:GLY:O	2.29	0.65
1:FF:14:LYS:HZ1	1:FF:28:SER:HB2	1.62	0.65
1:BO:37:LYS:HG3	1:BO:39:GLY:H	1.61	0.65
1:DV:57:PRO:HA	1:DV:73:ASN:HA	1.79	0.65
1:EE:68:CYS:SG	1:GU:65:ALA:HA	2.37	0.65
1:IQ:35:ARG:HH22	1:IQ:43:LEU:N	1.95	0.65
1:AZ:98:THR:HG21	1:AZ:126:SER:HA	1.77	0.65
1:CV:98:THR:HG21	1:CV:126:SER:HA	1.79	0.65
1:DA:51:VAL:HG22	1:DA:79:ARG:HG2	1.78	0.65
1:ED:33:ARG:NH2	1:EE:115:GLY:O	2.25	0.65
1:EX:35:ARG:NH2	1:EX:36:VAL:O	2.23	0.65
1:EX:76:GLN:HE21	1:EY:92:LEU:HD22	1.60	0.65
1:HJ:65:ALA:HB1	1:HJ:69:VAL:HB	1.78	0.65
1:BC:51:VAL:HG22	1:BC:79:ARG:HG2	1.79	0.64
1:BX:69:VAL:O	1:JI:63:GLY:HA3	1.98	0.64
1:CG:125:SER:O	1:CH:2:ASN:ND2	2.28	0.64
1:CM:51:VAL:HG22	1:CM:79:ARG:HG2	1.79	0.64
1:AI:101:ARG:HH21	1:AI:124:VAL:HG21	1.61	0.64
1:BI:35:ARG:NH1	1:BI:44:ASN:OD1	2.30	0.64
1:CD:22:ARG:NH2	1:CD:55:LYS:O	2.28	0.64
1:DN:60:LYS:NZ	1:DN:66:ASP:O	2.23	0.64
1:EE:69:VAL:H	1:GU:64:CYS:H	1.44	0.64
1:FH:101:ARG:NH1	1:FH:102:ASN:OD1	2.30	0.64
1:FM:22:ARG:NH2	1:FM:55:LYS:O	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FZ:115:GLY:O	1:GA:33:ARG:NH1	2.29	0.64
1:HK:98:THR:HG21	1:HK:126:SER:HA	1.80	0.64
1:BG:60:LYS:NZ	1:BG:66:ASP:O	2.23	0.64
1:BJ:69:VAL:H	1:HZ:64:CYS:N	1.96	0.64
1:BZ:57:PRO:HA	1:BZ:73:ASN:HA	1.80	0.64
1:DL:60:LYS:HZ1	1:DL:66:ASP:H	1.45	0.64
1:DN:35:ARG:NH1	1:DN:44:ASN:OD1	2.30	0.64
1:DN:51:VAL:HG22	1:DN:79:ARG:HG2	1.79	0.64
1:EL:57:PRO:HA	1:EL:73:ASN:HA	1.79	0.64
1:HK:57:PRO:HA	1:HK:73:ASN:HA	1.78	0.64
1:IC:57:PRO:HA	1:IC:73:ASN:HA	1.80	0.64
1:IW:98:THR:HG21	1:IW:126:SER:HA	1.79	0.64
1:JF:98:THR:HG21	1:JF:126:SER:HA	1.80	0.64
1:AJ:66:ASP:OD1	1:GM:64:CYS:HA	1.97	0.64
1:AJ:67:ALA:CA	1:GM:63:GLY:H	2.08	0.64
1:AT:32:LEU:HB3	1:AT:47:SER:HB3	1.80	0.64
1:BY:95:GLU:OE2	1:BZ:76:GLN:NE2	2.30	0.64
1:CZ:67:ALA:CA	1:ID:63:GLY:H	2.10	0.64
1:EQ:22:ARG:NH2	1:EQ:55:LYS:O	2.30	0.64
1:FQ:98:THR:HG21	1:FQ:126:SER:HA	1.78	0.64
1:IJ:74:GLU:OE2	1:IK:88:ASN:ND2	2.30	0.64
1:IL:57:PRO:HA	1:IL:73:ASN:HA	1.78	0.64
1:JD:101:ARG:HH21	1:JD:124:VAL:HG21	1.61	0.64
1:BT:22:ARG:NH2	1:BT:55:LYS:O	2.31	0.64
1:CH:69:VAL:H	1:HA:64:CYS:N	1.96	0.64
1:CI:57:PRO:HA	1:CI:73:ASN:HA	1.79	0.64
1:DJ:95:GLU:OE2	1:DK:76:GLN:NE2	2.30	0.64
1:DZ:117:LEU:HD21	1:EA:31:LEU:HD13	1.78	0.64
1:FG:98:THR:HG21	1:FG:126:SER:HA	1.77	0.64
1:FZ:74:GLU:OE2	1:GA:88:ASN:ND2	2.29	0.64
1:GV:98:THR:HG21	1:GV:126:SER:HA	1.78	0.64
1:HD:55:LYS:HZ2	1:HD:73:ASN:HB2	1.61	0.64
1:AA:95:GLU:OE2	1:AB:76:GLN:NE2	2.30	0.64
1:BQ:57:PRO:HA	1:BQ:73:ASN:HA	1.79	0.64
1:CC:60:LYS:NZ	1:CC:66:ASP:O	2.24	0.64
1:DE:22:ARG:NH2	1:DE:55:LYS:O	2.31	0.64
1:DM:67:ALA:HB1	1:FB:62:GLU:HG3	1.79	0.64
1:FB:2:ASN:ND2	1:FC:125:SER:O	2.30	0.64
1:FH:101:ARG:NH2	1:FH:124:VAL:O	2.28	0.64
1:FT:3:LYS:HZ3	1:FU:127:ASP:HB3	1.61	0.64
1:GB:56:ARG:NH2	1:GC:95:GLU:OE2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HA:101:ARG:HH21	1:HA:124:VAL:HG21	1.62	0.64
1:AH:68:CYS:SG	1:JE:65:ALA:HA	2.37	0.64
1:CB:69:VAL:H	1:FJ:64:CYS:H	1.46	0.64
1:DM:67:ALA:CA	1:FB:63:GLY:H	2.10	0.64
1:DU:68:CYS:SG	1:FP:65:ALA:HA	2.38	0.64
1:EV:101:ARG:HH12	1:EV:124:VAL:HG21	1.61	0.64
1:FC:35:ARG:HH22	1:FC:43:LEU:N	1.95	0.64
1:HG:74:GLU:OE2	1:HI:88:ASN:ND2	2.29	0.64
1:HW:57:PRO:HA	1:HW:73:ASN:HA	1.80	0.64
1:HZ:101:ARG:NH1	1:HZ:102:ASN:OD1	2.29	0.64
1:IT:65:ALA:HB1	1:IT:69:VAL:HB	1.78	0.64
1:AC:35:ARG:NH1	1:AC:44:ASN:OD1	2.31	0.64
1:CP:67:ALA:N	1:IP:65:ALA:H	1.96	0.64
1:CU:95:GLU:OE2	1:CV:76:GLN:NE2	2.31	0.64
1:DK:106:LEU:HD21	1:DK:123:ILE:HD11	1.79	0.64
1:DY:98:THR:HG21	1:DY:126:SER:HA	1.80	0.64
1:HL:115:GLY:O	1:HM:33:ARG:NH1	2.30	0.64
1:HV:33:ARG:NH1	1:HW:115:GLY:O	2.31	0.64
1:IU:57:PRO:HA	1:IU:73:ASN:HA	1.79	0.64
1:BV:67:ALA:N	1:GH:65:ALA:H	1.95	0.64
1:FX:117:LEU:HD21	1:FY:31:LEU:HD13	1.80	0.64
1:GQ:63:GLY:HA2	1:GS:68:CYS:HA	1.80	0.64
1:AF:106:LEU:HD21	1:AF:123:ILE:HD11	1.79	0.64
1:BD:98:THR:HG21	1:BD:126:SER:HA	1.79	0.64
1:CH:22:ARG:NH2	1:CH:55:LYS:O	2.31	0.64
1:GW:91:THR:OG1	1:GX:76:GLN:NE2	2.29	0.64
1:AB:22:ARG:NH2	1:AB:55:LYS:O	2.30	0.63
1:AI:117:LEU:HD21	1:AJ:31:LEU:HD13	1.80	0.63
1:AQ:95:GLU:OE2	1:AR:76:GLN:NE2	2.31	0.63
1:BC:35:ARG:NH1	1:BC:44:ASN:OD1	2.31	0.63
1:BD:51:VAL:HG22	1:BD:79:ARG:HG2	1.80	0.63
1:BF:98:THR:HG21	1:BF:126:SER:HA	1.80	0.63
1:BW:115:GLY:O	1:BX:33:ARG:NH1	2.24	0.63
1:EH:20:PRO:HB3	1:EN:116:PHE:HE2	1.63	0.63
1:GW:65:ALA:N	1:GY:68:CYS:SG	2.72	0.63
1:BS:35:ARG:NH1	1:BS:44:ASN:OD1	2.31	0.63
1:BX:68:CYS:SG	1:JI:65:ALA:HA	2.38	0.63
1:CU:57:PRO:HA	1:CU:73:ASN:HA	1.79	0.63
1:DT:88:ASN:ND2	1:DU:74:GLU:OE2	2.28	0.63
1:GT:98:THR:HG21	1:GT:126:SER:HA	1.80	0.63
1:AD:55:LYS:NZ	1:AD:75:ASN:OD1	2.27	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:57:PRO:HA	1:AQ:73:ASN:HA	1.81	0.63
1:CW:35:ARG:NH1	1:CW:44:ASN:OD1	2.31	0.63
1:DW:22:ARG:NH2	1:DW:55:LYS:O	2.29	0.63
1:EE:57:PRO:HA	1:EE:73:ASN:HA	1.80	0.63
1:EO:22:ARG:NH2	1:EO:55:LYS:O	2.30	0.63
1:HA:91:THR:OG1	1:HB:76:GLN:NE2	2.30	0.63
1:IA:101:ARG:HH21	1:IA:124:VAL:HG21	1.63	0.63
1:AF:51:VAL:HG22	1:AF:79:ARG:HG2	1.80	0.63
1:CB:69:VAL:O	1:FJ:63:GLY:HA3	1.99	0.63
1:CC:35:ARG:NH1	1:CC:44:ASN:OD1	2.31	0.63
1:CD:106:LEU:HD21	1:CD:123:ILE:HD11	1.81	0.63
1:DG:22:ARG:NH2	1:DG:55:LYS:O	2.30	0.63
1:DM:67:ALA:N	1:FB:65:ALA:H	1.95	0.63
1:FV:35:ARG:NH2	1:FV:43:LEU:O	2.32	0.63
1:JE:57:PRO:HA	1:JE:73:ASN:HA	1.80	0.63
1:BY:57:PRO:HA	1:BY:73:ASN:HA	1.79	0.63
1:CI:95:GLU:OE2	1:CJ:76:GLN:NE2	2.31	0.63
1:CT:22:ARG:NH2	1:CT:55:LYS:O	2.32	0.63
1:DA:35:ARG:NH1	1:DA:44:ASN:OD1	2.32	0.63
1:EB:95:GLU:OE2	1:EC:76:GLN:NE2	2.32	0.63
1:EK:67:ALA:N	1:EV:65:ALA:H	1.95	0.63
1:FD:115:GLY:O	1:FE:33:ARG:NH1	2.31	0.63
1:FE:98:THR:HG21	1:FE:126:SER:HA	1.80	0.63
1:GC:98:THR:HG21	1:GC:126:SER:HA	1.81	0.63
1:GH:60:LYS:NZ	1:GH:69:VAL:O	2.31	0.63
1:AH:69:VAL:H	1:JE:64:CYS:H	1.46	0.63
1:BZ:22:ARG:NH2	1:BZ:55:LYS:O	2.31	0.63
1:EE:51:VAL:HG22	1:EE:79:ARG:HG2	1.81	0.63
1:FX:65:ALA:N	1:FZ:68:CYS:SG	2.72	0.63
1:IC:35:ARG:NH1	1:IC:43:LEU:O	2.31	0.63
1:ID:101:ARG:NH1	1:ID:102:ASN:OD1	2.31	0.63
1:AE:35:ARG:NH1	1:AE:44:ASN:OD1	2.32	0.63
1:AG:60:LYS:HG2	1:AG:71:MET:HE1	1.80	0.63
1:AX:67:ALA:HB1	1:GY:62:GLU:HG3	1.81	0.63
1:CP:66:ASP:OD1	1:IP:64:CYS:HA	1.98	0.63
1:DB:51:VAL:HG22	1:DB:79:ARG:HG2	1.81	0.63
1:DV:88:ASN:ND2	1:DW:74:GLU:OE2	2.31	0.63
1:IQ:98:THR:HG21	1:IQ:126:SER:HA	1.81	0.63
1:AN:106:LEU:HD21	1:AN:123:ILE:HD11	1.80	0.63
1:BN:32:LEU:HB3	1:BN:47:SER:HB3	1.80	0.63
1:FR:5:MET:HG3	1:FR:19:ASP:HA	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FV:57:PRO:HA	1:FV:73:ASN:HA	1.80	0.63
1:GZ:98:THR:HG21	1:GZ:126:SER:HA	1.81	0.63
1:JE:37:LYS:NZ	1:JE:40:ILE:O	2.30	0.63
1:CB:67:ALA:HB1	1:FJ:62:GLU:HG3	1.81	0.63
1:CH:66:ASP:OD1	1:HA:64:CYS:HA	1.98	0.63
1:CN:51:VAL:HG22	1:CN:79:ARG:HG2	1.81	0.63
1:DI:67:ALA:CA	1:FH:63:GLY:H	2.09	0.63
1:EN:35:ARG:NH1	1:EN:44:ASN:OD1	2.32	0.63
1:GB:57:PRO:HA	1:GB:73:ASN:HA	1.79	0.63
1:HE:115:GLY:O	1:HF:33:ARG:NH1	2.32	0.63
1:HJ:33:ARG:NH1	1:HK:115:GLY:O	2.31	0.63
1:IR:60:LYS:NZ	1:IR:69:VAL:O	2.32	0.63
1:AF:68:CYS:H	1:GS:64:CYS:N	1.97	0.62
1:AN:51:VAL:HG22	1:AN:79:ARG:HG2	1.80	0.62
1:BK:115:GLY:O	1:BL:33:ARG:NH1	2.32	0.62
1:BY:37:LYS:HG3	1:BY:39:GLY:H	1.63	0.62
1:DY:22:ARG:NH2	1:DY:55:LYS:O	2.28	0.62
1:EK:22:ARG:NH2	1:EK:55:LYS:O	2.31	0.62
1:FF:24:SER:HB2	1:FF:55:LYS:HG3	1.81	0.62
1:FH:115:GLY:O	1:FI:33:ARG:NH1	2.32	0.62
1:FS:35:ARG:HA	1:FS:35:ARG:NE	2.14	0.62
1:GM:35:ARG:NH2	1:GM:43:LEU:O	2.32	0.62
1:GR:22:ARG:NH2	1:GR:55:LYS:O	2.32	0.62
1:IN:117:LEU:HD21	1:IO:31:LEU:HD13	1.81	0.62
1:IO:32:LEU:HB3	1:IO:47:SER:HB3	1.80	0.62
1:IP:2:ASN:ND2	1:IQ:125:SER:O	2.30	0.62
1:CN:22:ARG:NH2	1:CN:55:LYS:O	2.30	0.62
1:DS:56:ARG:O	1:DS:74:GLU:N	2.32	0.62
1:EE:106:LEU:HD21	1:EE:123:ILE:HD11	1.80	0.62
1:GL:22:ARG:NH2	1:GL:55:LYS:O	2.31	0.62
1:GM:101:ARG:HH21	1:GM:124:VAL:HG21	1.63	0.62
1:HO:38:VAL:HG21	1:HO:43:LEU:HD22	1.81	0.62
1:IC:22:ARG:NH2	1:IC:55:LYS:O	2.32	0.62
1:AA:57:PRO:HA	1:AA:73:ASN:HA	1.80	0.62
1:AK:37:LYS:HG3	1:AK:39:GLY:H	1.63	0.62
1:AM:35:ARG:NH1	1:AM:44:ASN:OD1	2.32	0.62
1:BL:61:PRO:HB2	1:BL:64:CYS:HB3	1.81	0.62
1:BR:98:THR:HG21	1:BR:126:SER:HA	1.79	0.62
1:CM:35:ARG:NH1	1:CM:44:ASN:OD1	2.32	0.62
1:GO:60:LYS:NZ	1:GO:69:VAL:O	2.29	0.62
1:HL:88:ASN:ND2	1:HM:74:GLU:OE2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HP:117:LEU:HD21	1:HQ:31:LEU:HD13	1.80	0.62
1:IH:85:SER:N	1:II:74:GLU:OE2	2.27	0.62
1:IJ:57:PRO:HA	1:IJ:73:ASN:HA	1.80	0.62
1:CE:37:LYS:HG3	1:CE:39:GLY:H	1.64	0.62
1:CJ:22:ARG:NH2	1:CJ:55:LYS:O	2.30	0.62
1:CX:61:PRO:HB2	1:CX:64:CYS:HB3	1.82	0.62
1:DM:22:ARG:NH2	1:DM:55:LYS:O	2.32	0.62
1:DV:95:GLU:OE2	1:DW:76:GLN:NE2	2.31	0.62
1:EO:51:VAL:HG22	1:EO:79:ARG:HG2	1.81	0.62
1:EX:35:ARG:NH2	1:EX:43:LEU:O	2.32	0.62
1:EZ:61:PRO:HG2	1:EZ:64:CYS:HB2	1.81	0.62
1:HW:22:ARG:NH2	1:HW:55:LYS:O	2.32	0.62
1:HZ:124:VAL:HA	1:IA:4:PRO:HA	1.81	0.62
1:AB:57:PRO:HA	1:AB:73:ASN:HA	1.81	0.62
1:AD:67:ALA:N	1:IV:65:ALA:H	1.97	0.62
1:AZ:55:LYS:NZ	1:AZ:75:ASN:OD1	2.27	0.62
1:BW:33:ARG:NH1	1:BX:115:GLY:O	2.33	0.62
1:DA:37:LYS:HG3	1:DA:39:GLY:H	1.64	0.62
1:DQ:22:ARG:NH2	1:DQ:55:LYS:O	2.28	0.62
1:DV:37:LYS:HG3	1:DV:39:GLY:H	1.65	0.62
1:EL:95:GLU:OE2	1:EM:76:GLN:NE2	2.31	0.62
1:ER:57:PRO:HA	1:ER:73:ASN:HA	1.80	0.62
1:ET:65:ALA:HB1	1:ET:69:VAL:HB	1.80	0.62
1:FN:14:LYS:HZ1	1:FN:28:SER:HB2	1.64	0.62
1:GD:117:LEU:HD21	1:GE:31:LEU:HD13	1.80	0.62
1:HC:65:ALA:HB1	1:HC:69:VAL:HB	1.82	0.62
1:HN:88:ASN:ND2	1:HO:74:GLU:OE2	2.30	0.62
1:HT:125:SER:HB2	1:HU:5:MET:HE1	1.82	0.62
1:IT:33:ARG:NH1	1:IU:115:GLY:O	2.33	0.62
1:AR:56:ARG:O	1:AR:74:GLU:N	2.29	0.62
1:BH:106:LEU:HD21	1:BH:123:ILE:HD11	1.81	0.62
1:BR:67:ALA:HB1	1:FZ:62:GLU:HG3	1.80	0.62
1:BV:67:ALA:CA	1:GH:63:GLY:H	2.12	0.62
1:BX:51:VAL:HG22	1:BX:79:ARG:HG2	1.81	0.62
1:DO:51:VAL:HG22	1:DO:79:ARG:HG2	1.81	0.62
1:DU:69:VAL:H	1:FP:64:CYS:H	1.47	0.62
1:GF:2:ASN:ND2	1:GG:125:SER:O	2.33	0.62
1:GM:115:GLY:O	1:GN:33:ARG:NH1	2.32	0.62
1:GQ:33:ARG:NH1	1:GR:115:GLY:O	2.32	0.62
1:HS:5:MET:HB3	1:HS:17:TRP:HB3	1.81	0.62
1:IB:33:ARG:NH1	1:IC:115:GLY:O	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:II:56:ARG:O	1:II:74:GLU:N	2.31	0.62
1:IN:63:GLY:HA2	1:IP:67:ALA:O	2.00	0.62
1:JH:22:ARG:NH2	1:JH:55:LYS:O	2.33	0.62
1:AY:35:ARG:NH1	1:AY:44:ASN:OD1	2.33	0.62
1:BR:67:ALA:CA	1:FZ:63:GLY:H	2.10	0.62
1:CJ:56:ARG:O	1:CJ:74:GLU:N	2.31	0.62
1:DE:23:LEU:HD13	1:FU:44:ASN:HD21	1.64	0.62
1:DS:32:LEU:HB2	1:DS:47:SER:HB3	1.81	0.62
1:DT:37:LYS:HG3	1:DT:39:GLY:H	1.64	0.62
1:EE:69:VAL:H	1:GU:64:CYS:N	1.98	0.62
1:FA:32:LEU:HB3	1:FA:47:SER:HB3	1.82	0.62
1:FX:63:GLY:HA2	1:FZ:68:CYS:HA	1.81	0.62
1:GD:65:ALA:HB1	1:GD:69:VAL:HB	1.82	0.62
1:GM:91:THR:OG1	1:GN:76:GLN:NE2	2.30	0.62
1:GX:98:THR:HG21	1:GX:126:SER:HA	1.80	0.62
1:IX:74:GLU:OE2	1:IZ:88:ASN:ND2	2.33	0.62
1:AB:55:LYS:NZ	1:AB:75:ASN:OD1	2.27	0.62
1:BE:88:ASN:ND2	1:BF:74:GLU:OE2	2.29	0.62
1:CU:115:GLY:O	1:CV:33:ARG:NH1	2.33	0.62
1:DC:35:ARG:NH1	1:DC:44:ASN:OD1	2.33	0.62
1:DG:51:VAL:HG22	1:DG:79:ARG:HG2	1.81	0.62
1:EF:33:ARG:NH1	1:EG:115:GLY:O	2.33	0.62
1:ET:117:LEU:HD21	1:EU:31:LEU:HD13	1.82	0.62
1:FD:57:PRO:HA	1:FD:73:ASN:HA	1.82	0.62
1:FG:22:ARG:NH2	1:FG:55:LYS:O	2.33	0.62
1:GF:34:GLN:NE2	1:GF:35:ARG:O	2.33	0.62
1:HZ:115:GLY:O	1:IA:33:ARG:NH1	2.33	0.62
1:AO:13:ASN:ND2	1:AO:31:LEU:O	2.32	0.62
1:AR:61:PRO:HB2	1:AR:64:CYS:HB3	1.82	0.62
1:BR:66:ASP:OD2	1:FZ:64:CYS:HA	2.00	0.62
1:BV:56:ARG:O	1:BV:74:GLU:N	2.32	0.62
1:CI:37:LYS:HG3	1:CI:39:GLY:H	1.65	0.62
1:FH:124:VAL:HA	1:FI:4:PRO:HA	1.81	0.62
1:FP:57:PRO:HA	1:FP:73:ASN:HA	1.82	0.62
1:FR:33:ARG:NH1	1:FS:115:GLY:O	2.33	0.62
1:AJ:22:ARG:NH2	1:AJ:55:LYS:O	2.32	0.62
1:AZ:22:ARG:NH2	1:AZ:55:LYS:O	2.31	0.62
1:BK:37:LYS:HG3	1:BK:39:GLY:H	1.64	0.62
1:BZ:98:THR:HG21	1:BZ:126:SER:HA	1.80	0.62
1:EE:98:THR:HG21	1:EE:126:SER:HA	1.81	0.62
1:EM:22:ARG:NH2	1:EM:55:LYS:O	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FY:98:THR:HG21	1:FY:126:SER:HA	1.80	0.62
1:HQ:22:ARG:NH2	1:HQ:55:LYS:O	2.33	0.62
1:HR:93:LYS:NZ	1:HS:108:ALA:O	2.33	0.62
1:ID:115:GLY:O	1:IE:33:ARG:NH1	2.32	0.62
1:BK:95:GLU:OE2	1:BL:76:GLN:NE2	2.32	0.61
1:CK:71:MET:N	1:CK:71:MET:SD	2.73	0.61
1:CY:37:LYS:HG3	1:CY:39:GLY:H	1.63	0.61
1:DB:61:PRO:HB2	1:DB:64:CYS:HB3	1.82	0.61
1:DN:33:ARG:NH1	1:DO:115:GLY:O	2.32	0.61
1:EB:115:GLY:O	1:EC:33:ARG:NH1	2.33	0.61
1:EF:35:ARG:NH1	1:EF:44:ASN:OD1	2.33	0.61
1:EW:5:MET:HB3	1:EW:17:TRP:HB3	1.82	0.61
1:FG:35:ARG:NH1	1:FG:43:LEU:O	2.33	0.61
1:FG:57:PRO:HA	1:FG:73:ASN:HA	1.80	0.61
1:FL:128:THR:HA	1:FM:2:ASN:HA	1.82	0.61
1:FX:33:ARG:NH1	1:FY:115:GLY:O	2.32	0.61
1:GP:106:LEU:HD11	1:GP:123:ILE:HD11	1.82	0.61
1:HP:11:THR:HB	1:HP:14:LYS:H	1.65	0.61
1:II:98:THR:HG21	1:II:126:SER:HA	1.80	0.61
1:AU:35:ARG:NH1	1:AU:44:ASN:OD1	2.33	0.61
1:BC:88:ASN:ND2	1:BD:74:GLU:OE2	2.27	0.61
1:CB:22:ARG:NH2	1:CB:55:LYS:O	2.33	0.61
1:ED:117:LEU:HD21	1:EE:31:LEU:HD13	1.82	0.61
1:EZ:37:LYS:NZ	1:EZ:39:GLY:O	2.33	0.61
1:FC:98:THR:HG21	1:FC:126:SER:HA	1.81	0.61
1:HV:5:MET:HB3	1:HV:17:TRP:HB3	1.82	0.61
1:ID:124:VAL:HA	1:IE:4:PRO:HA	1.80	0.61
1:IN:11:THR:HB	1:IN:14:LYS:H	1.65	0.61
1:JA:76:GLN:NE2	1:JB:91:THR:OG1	2.34	0.61
1:AB:98:THR:HG21	1:AB:126:SER:HA	1.81	0.61
1:AK:35:ARG:NH1	1:AK:44:ASN:OD1	2.33	0.61
1:BD:22:ARG:NH2	1:BD:55:LYS:O	2.31	0.61
1:BE:35:ARG:NH1	1:BE:44:ASN:OD1	2.33	0.61
1:BN:56:ARG:O	1:BN:74:GLU:N	2.33	0.61
1:BR:69:VAL:HG13	1:FZ:64:CYS:SG	2.41	0.61
1:BW:37:LYS:HG3	1:BW:39:GLY:H	1.65	0.61
1:CC:37:LYS:HG3	1:CC:39:GLY:H	1.64	0.61
1:CP:22:ARG:NH2	1:CP:55:LYS:O	2.33	0.61
1:CX:22:ARG:NH2	1:CX:55:LYS:O	2.31	0.61
1:EZ:117:LEU:HD21	1:FA:31:LEU:HD13	1.82	0.61
1:FP:5:MET:HG2	1:FP:17:TRP:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GO:115:GLY:O	1:GP:33:ARG:NH1	2.32	0.61
1:GT:101:ARG:HH21	1:GT:124:VAL:HG21	1.66	0.61
1:GY:14:LYS:HZ1	1:GY:28:SER:HB2	1.65	0.61
1:HX:14:LYS:HZ1	1:HX:28:SER:HB2	1.66	0.61
1:IJ:128:THR:HA	1:IK:2:ASN:HA	1.83	0.61
1:IM:98:THR:HG21	1:IM:126:SER:HA	1.81	0.61
1:AI:13:ASN:ND2	1:AI:31:LEU:O	2.33	0.61
1:CL:22:ARG:NH2	1:CL:55:LYS:O	2.32	0.61
1:DN:5:MET:HE1	1:DO:123:ILE:HG22	1.82	0.61
1:DU:69:VAL:H	1:FP:64:CYS:N	1.98	0.61
1:DU:69:VAL:O	1:FP:63:GLY:HA3	1.99	0.61
1:EC:22:ARG:NH2	1:EC:55:LYS:O	2.30	0.61
1:EF:71:MET:N	1:EF:71:MET:SD	2.74	0.61
1:EU:32:LEU:HB3	1:EU:47:SER:HB3	1.81	0.61
1:FZ:35:ARG:NH1	1:FZ:36:VAL:O	2.32	0.61
1:AV:22:ARG:NH2	1:AV:55:LYS:O	2.32	0.61
1:BC:95:GLU:OE2	1:BD:76:GLN:NE2	2.33	0.61
1:BG:95:GLU:OE2	1:BH:76:GLN:NE2	2.33	0.61
1:BN:22:ARG:NH2	1:BN:55:LYS:O	2.30	0.61
1:CH:68:CYS:N	1:HA:64:CYS:H	1.98	0.61
1:FC:5:MET:HB3	1:FC:17:TRP:HB3	1.82	0.61
1:GC:38:VAL:HG21	1:GC:43:LEU:HD22	1.82	0.61
1:GD:57:PRO:HA	1:GD:73:ASN:HA	1.83	0.61
1:GT:37:LYS:NZ	1:GT:38:VAL:O	2.27	0.61
1:IS:35:ARG:HD2	1:IS:44:ASN:HB3	1.82	0.61
1:JB:22:ARG:NH2	1:JB:55:LYS:O	2.32	0.61
1:BJ:69:VAL:HG13	1:HZ:64:CYS:HB2	1.83	0.61
1:BV:22:ARG:NH2	1:BV:55:LYS:O	2.33	0.61
1:CB:68:CYS:H	1:FJ:64:CYS:H	1.46	0.61
1:DU:68:CYS:N	1:FP:64:CYS:H	1.98	0.61
1:DW:98:THR:HG21	1:DW:126:SER:HA	1.82	0.61
1:EJ:37:LYS:HG3	1:EJ:39:GLY:H	1.66	0.61
1:FJ:57:PRO:HA	1:FJ:73:ASN:HA	1.83	0.61
1:GQ:76:GLN:NE2	1:GR:91:THR:OG1	2.33	0.61
1:HB:38:VAL:HG21	1:HB:43:LEU:HD22	1.82	0.61
1:HN:76:GLN:HE21	1:HO:92:LEU:HD22	1.65	0.61
1:HO:98:THR:HG21	1:HO:126:SER:HA	1.83	0.61
1:BC:57:PRO:HA	1:BC:73:ASN:HA	1.82	0.61
1:BD:106:LEU:HD21	1:BD:123:ILE:HD11	1.81	0.61
1:BG:117:LEU:HD21	1:BH:31:LEU:HD13	1.81	0.61
1:CC:95:GLU:OE2	1:CD:76:GLN:NE2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:51:VAL:HG22	1:CD:79:ARG:HG2	1.81	0.61
1:ED:37:LYS:HG3	1:ED:39:GLY:H	1.65	0.61
1:EY:98:THR:HG21	1:EY:126:SER:HA	1.82	0.61
1:FJ:5:MET:HG2	1:FJ:17:TRP:HB3	1.82	0.61
1:GG:106:LEU:HD11	1:GG:123:ILE:HD11	1.82	0.61
1:GH:115:GLY:O	1:GI:33:ARG:NH1	2.33	0.61
1:ID:35:ARG:NH2	1:ID:43:LEU:O	2.34	0.61
1:IX:93:LYS:NZ	1:IZ:108:ALA:O	2.33	0.61
1:BH:51:VAL:HG22	1:BH:79:ARG:HG2	1.80	0.61
1:BQ:115:GLY:O	1:BR:33:ARG:NH1	2.33	0.61
1:BW:35:ARG:NH1	1:BW:44:ASN:OD1	2.34	0.61
1:CC:5:MET:HE1	1:CD:123:ILE:HG22	1.81	0.61
1:CH:69:VAL:H	1:HA:64:CYS:H	1.48	0.61
1:CZ:56:ARG:O	1:CZ:74:GLU:N	2.32	0.61
1:EA:56:ARG:O	1:EA:74:GLU:N	2.32	0.61
1:ES:98:THR:HG21	1:ES:126:SER:HA	1.82	0.61
1:FH:56:ARG:NH2	1:FI:95:GLU:OE2	2.30	0.61
1:GI:101:ARG:HH21	1:GI:124:VAL:HG21	1.65	0.61
1:GO:2:ASN:ND2	1:GP:125:SER:O	2.33	0.61
1:GO:74:GLU:OE2	1:GP:88:ASN:ND2	2.34	0.61
1:HA:115:GLY:O	1:HB:33:ARG:NH1	2.34	0.61
1:HQ:98:THR:HG21	1:HQ:126:SER:HA	1.80	0.61
1:IB:74:GLU:OE2	1:IC:88:ASN:ND2	2.34	0.61
1:IN:37:LYS:NZ	1:IN:39:GLY:O	2.34	0.61
1:JI:57:PRO:HA	1:JI:73:ASN:HA	1.83	0.61
1:AZ:106:LEU:HD21	1:AZ:123:ILE:HD11	1.82	0.61
1:CD:49:GLN:OE1	1:CD:79:ARG:NH2	2.32	0.61
1:CX:56:ARG:O	1:CX:74:GLU:N	2.33	0.61
1:DS:22:ARG:NH2	1:DS:55:LYS:O	2.29	0.61
1:EE:22:ARG:NH2	1:EE:55:LYS:O	2.31	0.61
1:EG:67:ALA:N	1:HX:65:ALA:H	1.99	0.61
1:EK:67:ALA:CA	1:EV:63:GLY:H	2.10	0.61
1:GD:61:PRO:HG2	1:GD:64:CYS:SG	2.40	0.61
1:HR:74:GLU:OE2	1:HS:88:ASN:ND2	2.34	0.61
1:HT:115:GLY:O	1:HU:33:ARG:NH1	2.34	0.61
1:IC:56:ARG:O	1:IC:74:GLU:N	2.25	0.61
1:IH:61:PRO:HG2	1:IH:64:CYS:SG	2.41	0.61
1:IN:3:LYS:HZ1	1:IO:129:THR:HG23	1.65	0.61
1:CA:125:SER:O	1:CB:2:ASN:ND2	2.28	0.61
1:CE:35:ARG:NH1	1:CE:44:ASN:OD1	2.34	0.61
1:CZ:22:ARG:NH2	1:CZ:55:LYS:O	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DN:37:LYS:HG3	1:DN:39:GLY:H	1.66	0.61
1:EB:37:LYS:HG3	1:EB:39:GLY:H	1.65	0.61
1:EM:56:ARG:O	1:EM:74:GLU:N	2.31	0.61
1:ET:74:GLU:OE2	1:EU:88:ASN:ND2	2.26	0.61
1:GW:63:GLY:HA2	1:GY:68:CYS:HA	1.82	0.61
1:AD:22:ARG:NH2	1:AD:55:LYS:O	2.34	0.60
1:AJ:61:PRO:HB2	1:AJ:64:CYS:HB3	1.83	0.60
1:AN:22:ARG:NH2	1:AN:55:LYS:O	2.32	0.60
1:AV:56:ARG:O	1:AV:74:GLU:N	2.32	0.60
1:AX:67:ALA:CA	1:GY:63:GLY:H	2.10	0.60
1:AX:69:VAL:HG13	1:GY:64:CYS:SG	2.41	0.60
1:AY:37:LYS:HG3	1:AY:39:GLY:H	1.65	0.60
1:BJ:57:PRO:HA	1:BJ:73:ASN:HA	1.83	0.60
1:BO:35:ARG:NH1	1:BO:44:ASN:OD1	2.33	0.60
1:BS:60:LYS:NZ	1:BS:66:ASP:O	2.24	0.60
1:CB:68:CYS:H	1:FJ:64:CYS:N	1.99	0.60
1:CK:35:ARG:NH1	1:CK:44:ASN:OD1	2.34	0.60
1:CL:67:ALA:CA	1:FN:63:GLY:H	2.13	0.60
1:CM:88:ASN:ND2	1:CN:74:GLU:OE2	2.28	0.60
1:CO:35:ARG:NH1	1:CO:44:ASN:OD1	2.34	0.60
1:DB:22:ARG:NH2	1:DB:55:LYS:O	2.31	0.60
1:EC:61:PRO:HB2	1:EC:64:CYS:HB3	1.83	0.60
1:GM:57:PRO:HA	1:GM:73:ASN:HA	1.83	0.60
1:GO:45:ASN:HA	1:GO:85:SER:HA	1.81	0.60
1:HA:35:ARG:HH22	1:HA:43:LEU:N	1.99	0.60
1:HT:117:LEU:HD11	1:HU:31:LEU:HB2	1.83	0.60
1:JD:98:THR:HG21	1:JD:126:SER:HA	1.82	0.60
1:AH:22:ARG:NH2	1:AH:55:LYS:O	2.33	0.60
1:AI:57:PRO:HA	1:AI:73:ASN:HA	1.83	0.60
1:AU:117:LEU:HD21	1:AV:31:LEU:HD13	1.82	0.60
1:BB:8:ILE:HA	1:GL:116:PHE:HB2	1.83	0.60
1:BG:37:LYS:HG3	1:BG:39:GLY:H	1.66	0.60
1:CA:35:ARG:NH1	1:CA:44:ASN:OD1	2.33	0.60
1:CS:35:ARG:NH1	1:CS:44:ASN:OD1	2.33	0.60
1:CT:56:ARG:O	1:CT:74:GLU:N	2.31	0.60
1:DK:8:ILE:HA	1:JH:116:PHE:HB2	1.83	0.60
1:EJ:35:ARG:NH1	1:EJ:44:ASN:OD1	2.33	0.60
1:FM:5:MET:HB3	1:FM:17:TRP:HB3	1.83	0.60
1:FT:5:MET:HG2	1:FT:17:TRP:HB3	1.82	0.60
1:HC:74:GLU:OE2	1:HD:88:ASN:ND2	2.34	0.60
1:HF:98:THR:HG21	1:HF:126:SER:HA	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IH:37:LYS:NZ	1:IH:39:GLY:O	2.34	0.60
1:AF:22:ARG:NH2	1:AF:55:LYS:O	2.34	0.60
1:BP:22:ARG:NH2	1:BP:55:LYS:O	2.30	0.60
1:CH:55:LYS:NZ	1:CH:73:ASN:O	2.35	0.60
1:DU:67:ALA:CA	1:FP:63:GLY:H	2.12	0.60
1:EF:37:LYS:HG3	1:EF:39:GLY:H	1.66	0.60
1:AC:71:MET:N	1:AC:71:MET:SD	2.73	0.60
1:CG:57:PRO:HA	1:CG:73:ASN:HA	1.83	0.60
1:DC:88:ASN:ND2	1:DE:74:GLU:OE2	2.27	0.60
1:EL:37:LYS:HG3	1:EL:39:GLY:H	1.65	0.60
1:EM:106:LEU:HD21	1:EM:123:ILE:HD11	1.84	0.60
1:HG:93:LYS:NZ	1:HI:108:ALA:O	2.34	0.60
1:HX:117:LEU:HD11	1:HY:31:LEU:HB2	1.84	0.60
1:JI:35:ARG:HH22	1:JI:43:LEU:N	1.98	0.60
1:AG:35:ARG:NH1	1:AG:44:ASN:OD1	2.34	0.60
1:AG:37:LYS:HG3	1:AG:39:GLY:H	1.65	0.60
1:AN:68:CYS:N	1:JC:64:CYS:H	1.99	0.60
1:AY:88:ASN:ND2	1:AZ:74:GLU:OE2	2.30	0.60
1:BM:35:ARG:NH1	1:BM:44:ASN:OD1	2.34	0.60
1:BU:37:LYS:NZ	1:BU:39:GLY:O	2.34	0.60
1:DY:23:LEU:HD13	1:HF:44:ASN:HD21	1.66	0.60
1:EN:95:GLU:OE2	1:EO:76:GLN:NE2	2.35	0.60
1:EQ:56:ARG:O	1:EQ:74:GLU:N	2.34	0.60
1:FJ:115:GLY:O	1:FK:33:ARG:NH1	2.34	0.60
1:GE:22:ARG:NH2	1:GE:55:LYS:O	2.35	0.60
1:GF:115:GLY:O	1:GG:33:ARG:NH1	2.34	0.60
1:IN:61:PRO:HG2	1:IN:64:CYS:HB2	1.81	0.60
1:IU:106:LEU:HD11	1:IU:123:ILE:HD11	1.83	0.60
1:JI:93:LYS:NZ	1:JJ:108:ALA:O	2.35	0.60
1:AW:37:LYS:HG3	1:AW:39:GLY:H	1.66	0.60
1:CV:67:ALA:CA	1:HL:63:GLY:H	2.12	0.60
1:DF:95:GLU:OE2	1:DG:76:GLN:NE2	2.35	0.60
1:DR:35:ARG:NH1	1:DR:44:ASN:OD1	2.35	0.60
1:DT:35:ARG:NH1	1:DT:44:ASN:OD1	2.34	0.60
1:HC:61:PRO:HG2	1:HC:64:CYS:SG	2.41	0.60
1:IG:5:MET:HB3	1:IG:17:TRP:HB3	1.83	0.60
1:JG:33:ARG:NH1	1:JH:115:GLY:O	2.35	0.60
1:AM:37:LYS:HG3	1:AM:39:GLY:H	1.66	0.60
1:AW:115:GLY:O	1:AX:33:ARG:NH1	2.33	0.60
1:BR:56:ARG:O	1:BR:74:GLU:N	2.31	0.60
1:BV:68:CYS:SG	1:GH:65:ALA:HA	2.41	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:37:LYS:HG3	1:CK:39:GLY:H	1.66	0.60
1:CQ:88:ASN:ND2	1:CR:74:GLU:OE2	2.31	0.60
1:DU:67:ALA:HB1	1:FP:62:GLU:HG3	1.83	0.60
1:FW:5:MET:HB3	1:FW:17:TRP:HB3	1.84	0.60
1:HJ:88:ASN:HD21	1:HK:56:ARG:HD2	1.65	0.60
1:JC:57:PRO:HA	1:JC:73:ASN:HA	1.84	0.60
1:AE:95:GLU:OE2	1:AF:76:GLN:NE2	2.35	0.60
1:AQ:115:GLY:O	1:AR:33:ARG:NH1	2.34	0.60
1:BH:55:LYS:NZ	1:BH:75:ASN:OD1	2.27	0.60
1:BW:95:GLU:OE2	1:BX:76:GLN:NE2	2.35	0.60
1:CH:61:PRO:HB2	1:CH:64:CYS:HB3	1.84	0.60
1:DL:35:ARG:NH1	1:DL:44:ASN:OD1	2.34	0.60
1:DU:66:ASP:OD1	1:FP:64:CYS:HA	2.02	0.60
1:GD:11:THR:HB	1:GD:14:LYS:H	1.67	0.60
1:GX:33:ARG:HH12	1:GY:8:ILE:HG23	1.67	0.60
1:GY:56:ARG:O	1:GY:74:GLU:N	2.33	0.60
1:AF:32:LEU:HB3	1:AF:34:GLN:HE22	1.66	0.60
1:BQ:37:LYS:HG3	1:BQ:39:GLY:H	1.66	0.60
1:BX:69:VAL:H	1:JI:64:CYS:H	1.50	0.60
1:CP:56:ARG:O	1:CP:74:GLU:N	2.32	0.60
1:CP:98:THR:HG21	1:CP:126:SER:HA	1.84	0.60
1:CW:116:PHE:HE2	1:DA:20:PRO:HB3	1.67	0.60
1:DC:37:LYS:HG3	1:DC:39:GLY:H	1.65	0.60
1:EV:56:ARG:NH2	1:EW:95:GLU:OE2	2.35	0.60
1:FD:35:ARG:HH22	1:FD:43:LEU:N	1.99	0.60
1:HD:5:MET:HG2	1:HD:17:TRP:HB3	1.83	0.60
1:HR:115:GLY:O	1:HS:33:ARG:NH1	2.35	0.60
1:HZ:35:ARG:NH2	1:HZ:43:LEU:O	2.35	0.60
1:IL:93:LYS:NZ	1:IM:108:ALA:O	2.35	0.60
1:JG:57:PRO:HA	1:JG:73:ASN:HA	1.84	0.60
1:AS:35:ARG:NH1	1:AS:44:ASN:OD1	2.35	0.60
1:BH:22:ARG:NH2	1:BH:55:LYS:O	2.31	0.60
1:BM:37:LYS:HG3	1:BM:39:GLY:H	1.66	0.60
1:BM:60:LYS:HZ1	1:BM:66:ASP:H	1.48	0.60
1:CA:37:LYS:HG3	1:CA:39:GLY:H	1.65	0.60
1:CM:95:GLU:OE2	1:CN:76:GLN:NE2	2.35	0.60
1:DG:32:LEU:HB3	1:DG:34:GLN:HE22	1.66	0.60
1:DI:22:ARG:NH2	1:DI:55:LYS:O	2.30	0.60
1:DZ:35:ARG:NH1	1:DZ:44:ASN:OD1	2.34	0.60
1:FE:71:MET:N	1:FE:71:MET:SD	2.75	0.60
1:FN:117:LEU:HD11	1:FO:31:LEU:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FP:115:GLY:O	1:FQ:33:ARG:NH1	2.35	0.60
1:FT:117:LEU:HD11	1:FU:31:LEU:HB2	1.84	0.60
1:GH:35:ARG:HH22	1:GH:43:LEU:N	1.99	0.60
1:GK:39:GLY:HA3	1:GL:72:PRO:HG2	1.82	0.60
1:IF:93:LYS:NZ	1:IG:108:ALA:O	2.35	0.60
1:IL:35:ARG:NH2	1:IL:43:LEU:O	2.35	0.60
1:AN:32:LEU:HB3	1:AN:34:GLN:HE22	1.67	0.59
1:BG:57:PRO:HA	1:BG:73:ASN:HA	1.84	0.59
1:EO:32:LEU:HB3	1:EO:34:GLN:HE22	1.67	0.59
1:EO:67:ALA:HB3	1:FA:64:CYS:HA	1.84	0.59
1:EZ:11:THR:HB	1:EZ:14:LYS:H	1.65	0.59
1:FD:35:ARG:NH2	1:FD:43:LEU:O	2.35	0.59
1:HN:2:ASN:ND2	1:HO:125:SER:O	2.35	0.59
1:HZ:57:PRO:HA	1:HZ:73:ASN:HA	1.84	0.59
1:IV:14:LYS:HZ1	1:IV:28:SER:HB2	1.66	0.59
1:JC:35:ARG:HH22	1:JC:43:LEU:N	2.00	0.59
1:AE:57:PRO:HA	1:AE:73:ASN:HA	1.84	0.59
1:BE:37:LYS:HG3	1:BE:39:GLY:H	1.65	0.59
1:BW:117:LEU:HD21	1:BX:31:LEU:HD13	1.82	0.59
1:BX:106:LEU:HD21	1:BX:123:ILE:HD11	1.84	0.59
1:CC:57:PRO:HA	1:CC:73:ASN:HA	1.84	0.59
1:CZ:55:LYS:NZ	1:CZ:73:ASN:O	2.35	0.59
1:DN:125:SER:O	1:DO:2:ASN:ND2	2.33	0.59
1:DR:57:PRO:HA	1:DR:73:ASN:HA	1.84	0.59
1:DZ:37:LYS:HG3	1:DZ:39:GLY:H	1.67	0.59
1:EI:61:PRO:HB2	1:EI:64:CYS:HB3	1.85	0.59
1:EZ:65:ALA:HB1	1:EZ:69:VAL:HB	1.84	0.59
1:FN:125:SER:HB2	1:FO:5:MET:HE1	1.84	0.59
1:GB:115:GLY:O	1:GC:33:ARG:NH1	2.35	0.59
1:GH:35:ARG:NH2	1:GH:43:LEU:O	2.35	0.59
1:GX:58:ALA:HB3	1:GX:71:MET:HG3	1.85	0.59
1:HE:14:LYS:NZ	1:HE:15:ILE:O	2.35	0.59
1:HN:115:GLY:O	1:HO:33:ARG:NH1	2.35	0.59
1:HQ:35:ARG:HH12	1:HQ:42:GLU:HB3	1.67	0.59
1:HT:14:LYS:HZ1	1:HT:28:SER:HB2	1.68	0.59
1:HZ:35:ARG:HH22	1:HZ:43:LEU:N	1.99	0.59
1:IB:63:GLY:HA2	1:ID:67:ALA:O	2.02	0.59
1:IL:88:ASN:ND2	1:IM:74:GLU:OE2	2.30	0.59
1:IN:65:ALA:HB1	1:IN:69:VAL:HB	1.84	0.59
1:JA:33:ARG:NH1	1:JB:115:GLY:O	2.34	0.59
1:AN:69:VAL:O	1:JC:63:GLY:HA3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:37:LYS:HG3	1:AS:39:GLY:H	1.66	0.59
1:AY:33:ARG:NH1	1:AZ:115:GLY:O	2.35	0.59
1:CB:69:VAL:H	1:FJ:64:CYS:N	2.00	0.59
1:CD:32:LEU:HB3	1:CD:34:GLN:HE22	1.66	0.59
1:DE:56:ARG:O	1:DE:74:GLU:N	2.32	0.59
1:DP:57:PRO:HA	1:DP:73:ASN:HA	1.83	0.59
1:DR:37:LYS:HG3	1:DR:39:GLY:H	1.66	0.59
1:EN:57:PRO:HA	1:EN:73:ASN:HA	1.83	0.59
1:EX:93:LYS:NZ	1:EY:108:ALA:O	2.35	0.59
1:FM:98:THR:HG21	1:FM:126:SER:HA	1.84	0.59
1:GW:74:GLU:OE2	1:GX:88:ASN:ND2	2.28	0.59
1:BH:56:ARG:O	1:BH:74:GLU:N	2.35	0.59
1:BI:57:PRO:HA	1:BI:73:ASN:HA	1.84	0.59
1:BI:125:SER:O	1:BJ:2:ASN:ND2	2.33	0.59
1:BS:33:ARG:NH1	1:BT:115:GLY:O	2.35	0.59
1:CA:115:GLY:O	1:CB:33:ARG:NH1	2.26	0.59
1:CK:57:PRO:HA	1:CK:73:ASN:HA	1.84	0.59
1:CL:106:LEU:HD21	1:CL:123:ILE:HD11	1.83	0.59
1:CM:57:PRO:HA	1:CM:73:ASN:HA	1.83	0.59
1:CQ:37:LYS:HD2	1:CQ:42:GLU:HG2	1.84	0.59
1:CT:61:PRO:HB2	1:CT:64:CYS:HB3	1.84	0.59
1:DF:115:GLY:O	1:DG:33:ARG:NH1	2.35	0.59
1:DX:57:PRO:HA	1:DX:73:ASN:HA	1.83	0.59
1:EM:55:LYS:NZ	1:EM:75:ASN:OD1	2.28	0.59
1:EX:88:ASN:ND2	1:EY:74:GLU:OE2	2.29	0.59
1:FH:91:THR:OG1	1:FI:76:GLN:NE2	2.33	0.59
1:GM:14:LYS:NZ	1:GM:15:ILE:O	2.35	0.59
1:GP:35:ARG:HH22	1:GP:42:GLU:HB3	1.67	0.59
1:AH:61:PRO:HB2	1:AH:64:CYS:HB3	1.85	0.59
1:AQ:60:LYS:NZ	1:AQ:66:ASP:O	2.23	0.59
1:BA:57:PRO:HA	1:BA:73:ASN:HA	1.84	0.59
1:BT:60:LYS:NZ	1:BT:64:CYS:SG	2.63	0.59
1:CG:37:LYS:NZ	1:CG:42:GLU:OE2	2.27	0.59
1:CZ:61:PRO:HB2	1:CZ:64:CYS:HB3	1.84	0.59
1:DI:61:PRO:HB2	1:DI:64:CYS:HB3	1.85	0.59
1:DM:69:VAL:H	1:FB:64:CYS:N	2.00	0.59
1:ED:57:PRO:HA	1:ED:73:ASN:HA	1.84	0.59
1:FI:98:THR:HG21	1:FI:126:SER:HA	1.85	0.59
1:FJ:117:LEU:HD11	1:FK:31:LEU:HB2	1.84	0.59
1:FN:55:LYS:NZ	1:FN:73:ASN:HB2	2.17	0.59
1:JC:93:LYS:NZ	1:JD:108:ALA:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JH:57:PRO:HA	1:JH:73:ASN:HA	1.85	0.59
1:JI:14:LYS:HZ1	1:JI:28:SER:HB2	1.67	0.59
1:AL:56:ARG:O	1:AL:74:GLU:N	2.32	0.59
1:AR:8:ILE:HA	1:GR:116:PHE:HB2	1.85	0.59
1:BM:57:PRO:HA	1:BM:73:ASN:HA	1.85	0.59
1:BW:88:ASN:ND2	1:BX:74:GLU:OE2	2.28	0.59
1:CL:67:ALA:N	1:FN:65:ALA:H	2.00	0.59
1:CN:60:LYS:HZ1	1:CN:65:ALA:H	1.50	0.59
1:CV:67:ALA:N	1:HL:65:ALA:H	2.01	0.59
1:CX:55:LYS:NZ	1:CX:75:ASN:OD1	2.27	0.59
1:DF:57:PRO:HA	1:DF:73:ASN:HA	1.85	0.59
1:DM:69:VAL:HG13	1:FB:64:CYS:HB2	1.83	0.59
1:EK:69:VAL:HG13	1:EV:64:CYS:HB2	1.84	0.59
1:EY:71:MET:N	1:EY:71:MET:SD	2.76	0.59
1:GY:93:LYS:NZ	1:GZ:108:ALA:O	2.34	0.59
1:HA:60:LYS:NZ	1:HA:69:VAL:O	2.35	0.59
1:IH:125:SER:O	1:II:2:ASN:ND2	2.29	0.59
1:AC:117:LEU:HD13	1:AD:15:ILE:HG13	1.85	0.59
1:AN:56:ARG:O	1:AN:74:GLU:N	2.34	0.59
1:BS:5:MET:SD	1:BT:125:SER:HB2	2.43	0.59
1:CO:37:LYS:HG3	1:CO:39:GLY:H	1.66	0.59
1:CO:88:ASN:ND2	1:CP:74:GLU:OE2	2.28	0.59
1:DN:57:PRO:HA	1:DN:73:ASN:HA	1.85	0.59
1:HD:56:ARG:O	1:HD:74:GLU:N	2.23	0.59
1:HN:57:PRO:HA	1:HN:73:ASN:HA	1.83	0.59
1:AE:88:ASN:ND2	1:AF:74:GLU:OE2	2.27	0.59
1:AK:33:ARG:HH12	1:GQ:8:ILE:HG23	1.67	0.59
1:AL:22:ARG:NH2	1:AL:55:LYS:O	2.32	0.59
1:BQ:128:THR:O	1:BR:3:LYS:NZ	2.35	0.59
1:CW:56:ARG:NH2	1:CX:95:GLU:OE2	2.29	0.59
1:DC:57:PRO:HA	1:DC:73:ASN:HA	1.83	0.59
1:EK:61:PRO:HB2	1:EK:64:CYS:HB3	1.85	0.59
1:FO:35:ARG:HD2	1:FO:44:ASN:HB3	1.85	0.59
1:FX:125:SER:O	1:FY:2:ASN:ND2	2.28	0.59
1:FZ:93:LYS:NZ	1:GA:108:ALA:O	2.36	0.59
1:GY:115:GLY:O	1:GZ:33:ARG:NH1	2.36	0.59
1:IQ:5:MET:HB3	1:IQ:17:TRP:HB3	1.83	0.59
1:IT:57:PRO:HA	1:IT:73:ASN:HA	1.84	0.59
1:JB:5:MET:HG2	1:JB:17:TRP:HB3	1.84	0.59
1:AM:57:PRO:HA	1:AM:73:ASN:HA	1.85	0.59
1:AV:60:LYS:NZ	1:AV:65:ALA:H	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:34:GLN:NE2	1:BN:35:ARG:O	2.35	0.59
1:CD:55:LYS:NZ	1:CD:75:ASN:OD1	2.28	0.59
1:CM:37:LYS:HG3	1:CM:39:GLY:H	1.68	0.59
1:EE:49:GLN:OE1	1:EE:79:ARG:NH2	2.33	0.59
1:EM:8:ILE:HA	1:JB:116:PHE:HB2	1.84	0.59
1:EN:37:LYS:HG3	1:EN:39:GLY:H	1.68	0.59
1:ER:35:ARG:HH22	1:ER:43:LEU:N	2.00	0.59
1:AH:69:VAL:H	1:JE:64:CYS:N	2.01	0.59
1:AX:56:ARG:O	1:AX:74:GLU:N	2.34	0.59
1:BV:67:ALA:H	1:GH:65:ALA:H	1.51	0.59
1:BX:22:ARG:NH2	1:BX:55:LYS:O	2.33	0.59
1:DL:37:LYS:HG3	1:DL:39:GLY:H	1.66	0.59
1:DM:98:THR:HG21	1:DM:126:SER:HA	1.84	0.59
1:DO:22:ARG:NH2	1:DO:55:LYS:O	2.29	0.59
1:DR:116:PHE:HE2	1:DV:20:PRO:HB3	1.68	0.59
1:DW:57:PRO:HA	1:DW:73:ASN:HA	1.85	0.59
1:GX:5:MET:HG2	1:GX:17:TRP:HB3	1.85	0.59
1:HY:60:LYS:HD3	1:HY:64:CYS:HB3	1.85	0.59
1:HZ:101:ARG:NH2	1:HZ:124:VAL:O	2.27	0.59
1:IA:45:ASN:HA	1:IA:85:SER:HA	1.85	0.59
1:AA:60:LYS:NZ	1:AA:66:ASP:O	2.23	0.58
1:AJ:60:LYS:HZ1	1:AJ:65:ALA:HB3	1.68	0.58
1:AM:95:GLU:OE2	1:AN:76:GLN:NE2	2.35	0.58
1:BZ:56:ARG:O	1:BZ:74:GLU:N	2.30	0.58
1:DA:95:GLU:OE2	1:DB:76:GLN:NE2	2.35	0.58
1:DB:60:LYS:HZ1	1:DB:65:ALA:H	1.51	0.58
1:FH:35:ARG:NH2	1:FH:43:LEU:O	2.36	0.58
1:FY:5:MET:HG2	1:FY:17:TRP:HB3	1.85	0.58
1:HP:61:PRO:HG2	1:HP:64:CYS:SG	2.43	0.58
1:IH:65:ALA:HB1	1:IH:69:VAL:HB	1.85	0.58
1:IQ:56:ARG:O	1:IQ:74:GLU:N	2.28	0.58
1:IV:117:LEU:HD11	1:IW:31:LEU:HB2	1.85	0.58
1:AB:56:ARG:O	1:AB:74:GLU:N	2.32	0.58
1:BA:88:ASN:ND2	1:BB:74:GLU:OE2	2.30	0.58
1:BF:22:ARG:NH2	1:BF:55:LYS:O	2.33	0.58
1:BL:56:ARG:O	1:BL:74:GLU:N	2.30	0.58
1:DC:5:MET:SD	1:DE:125:SER:HB2	2.43	0.58
1:DF:37:LYS:HG3	1:DF:39:GLY:H	1.67	0.58
1:DQ:8:ILE:HA	1:IC:116:PHE:HB2	1.84	0.58
1:DV:60:LYS:NZ	1:DV:66:ASP:O	2.23	0.58
1:EK:98:THR:HG21	1:EK:126:SER:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FF:111:ASN:HB2	1:FF:116:PHE:HB2	1.83	0.58
1:FH:93:LYS:NZ	1:FI:108:ALA:O	2.35	0.58
1:FN:115:GLY:O	1:FO:33:ARG:NH1	2.36	0.58
1:FR:128:THR:HA	1:FS:2:ASN:HA	1.84	0.58
1:GH:14:LYS:NZ	1:GH:15:ILE:O	2.36	0.58
1:HA:57:PRO:HA	1:HA:73:ASN:HA	1.86	0.58
1:HP:33:ARG:NH1	1:HQ:115:GLY:O	2.36	0.58
1:HP:45:ASN:HA	1:HP:85:SER:HA	1.86	0.58
1:IH:74:GLU:OE2	1:II:88:ASN:ND2	2.36	0.58
1:AF:68:CYS:N	1:GS:65:ALA:H	2.01	0.58
1:AS:57:PRO:HA	1:AS:73:ASN:HA	1.85	0.58
1:AY:3:LYS:HZ2	1:AZ:129:THR:HG23	1.68	0.58
1:BD:32:LEU:HB3	1:BD:34:GLN:HE22	1.67	0.58
1:BS:116:PHE:HE2	1:BW:20:PRO:HB3	1.69	0.58
1:CH:56:ARG:O	1:CH:74:GLU:N	2.30	0.58
1:CH:67:ALA:HB1	1:HA:62:GLU:HG3	1.85	0.58
1:DF:60:LYS:NZ	1:DF:66:ASP:O	2.32	0.58
1:DW:60:LYS:NZ	1:DW:65:ALA:H	2.01	0.58
1:DX:37:LYS:HG3	1:DX:39:GLY:H	1.67	0.58
1:EP:35:ARG:NH1	1:EP:44:ASN:OD1	2.35	0.58
1:EV:93:LYS:NZ	1:EW:108:ALA:O	2.35	0.58
1:FJ:14:LYS:HZ1	1:FJ:28:SER:HB2	1.68	0.58
1:FP:117:LEU:HD11	1:FQ:31:LEU:HB2	1.84	0.58
1:IT:14:LYS:HD3	1:IT:30:SER:HB2	1.84	0.58
1:IX:5:MET:HG2	1:IX:17:TRP:HB3	1.85	0.58
1:JC:14:LYS:HZ1	1:JC:28:SER:HB2	1.68	0.58
1:JF:37:LYS:NZ	1:JF:38:VAL:O	2.34	0.58
1:JG:65:ALA:HB1	1:JG:69:VAL:HB	1.84	0.58
1:AH:67:ALA:HB1	1:JE:62:GLU:HG3	1.86	0.58
1:BO:57:PRO:HA	1:BO:73:ASN:HA	1.84	0.58
1:BS:57:PRO:HA	1:BS:73:ASN:HA	1.85	0.58
1:CQ:128:THR:OG1	1:CR:1:ALA:O	2.21	0.58
1:DM:61:PRO:HB2	1:DM:64:CYS:HB3	1.85	0.58
1:EN:60:LYS:NZ	1:EN:66:ASP:O	2.31	0.58
1:FG:35:ARG:NH2	1:FG:42:GLU:OE1	2.37	0.58
1:GN:5:MET:CG	1:GN:17:TRP:HB3	2.33	0.58
1:HV:14:LYS:HD3	1:HV:30:SER:HB2	1.85	0.58
1:IB:57:PRO:HA	1:IB:73:ASN:HA	1.85	0.58
1:IJ:88:ASN:ND2	1:IK:74:GLU:OE2	2.33	0.58
1:AB:61:PRO:HB2	1:AB:64:CYS:HB3	1.86	0.58
1:AO:115:GLY:O	1:AP:33:ARG:NH1	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:57:PRO:HA	1:AV:73:ASN:HA	1.86	0.58
1:BT:106:LEU:HD21	1:BT:123:ILE:HD11	1.84	0.58
1:BU:125:SER:O	1:BV:2:ASN:ND2	2.29	0.58
1:CN:32:LEU:HB3	1:CN:34:GLN:HE22	1.67	0.58
1:DB:55:LYS:NZ	1:DB:75:ASN:OD1	2.28	0.58
1:DM:67:ALA:H	1:FB:65:ALA:H	1.50	0.58
1:FF:60:LYS:NZ	1:FF:62:GLU:OE2	2.36	0.58
1:GB:2:ASN:ND2	1:GC:125:SER:O	2.35	0.58
1:GD:33:ARG:NH1	1:GE:115:GLY:O	2.36	0.58
1:GY:14:LYS:NZ	1:GY:15:ILE:O	2.37	0.58
1:HL:93:LYS:NZ	1:HM:108:ALA:O	2.35	0.58
1:IR:117:LEU:HD11	1:IS:31:LEU:HB2	1.84	0.58
1:AD:61:PRO:HB2	1:AD:64:CYS:HB3	1.86	0.58
1:AF:67:ALA:HB1	1:GS:62:GLU:HG3	1.86	0.58
1:AG:20:PRO:HB3	1:AI:116:PHE:HE2	1.69	0.58
1:AX:61:PRO:HB2	1:AX:64:CYS:HB3	1.84	0.58
1:DB:49:GLN:OE1	1:DB:79:ARG:NH2	2.33	0.58
1:DK:101:ARG:HH12	1:DK:124:VAL:HG21	1.69	0.58
1:DM:69:VAL:H	1:FB:64:CYS:H	1.52	0.58
1:EQ:60:LYS:NZ	1:EQ:64:CYS:SG	2.62	0.58
1:FV:14:LYS:HZ1	1:FV:28:SER:HB2	1.69	0.58
1:GT:105:THR:HG23	1:GT:106:LEU:HD12	1.84	0.58
1:HK:35:ARG:NH1	1:HK:42:GLU:OE2	2.37	0.58
1:HP:57:PRO:HA	1:HP:73:ASN:HA	1.86	0.58
1:HP:65:ALA:HB1	1:HP:69:VAL:HB	1.85	0.58
1:HW:5:MET:HG2	1:HW:18:SER:C	2.24	0.58
1:AD:67:ALA:CA	1:IV:63:GLY:H	2.13	0.58
1:AJ:23:LEU:HD13	1:GN:44:ASN:HD21	1.68	0.58
1:BC:37:LYS:HG3	1:BC:39:GLY:H	1.67	0.58
1:BS:124:VAL:HA	1:BT:4:PRO:HA	1.86	0.58
1:CA:57:PRO:HA	1:CA:73:ASN:HA	1.86	0.58
1:DA:57:PRO:HA	1:DA:73:ASN:HA	1.85	0.58
1:DL:57:PRO:HA	1:DL:73:ASN:HA	1.85	0.58
1:EP:5:MET:SD	1:EQ:125:SER:HB2	2.44	0.58
1:EX:55:LYS:HZ3	1:EX:73:ASN:HB2	1.67	0.58
1:FD:123:ILE:HG22	1:FE:5:MET:HE2	1.86	0.58
1:FH:14:LYS:NZ	1:FH:15:ILE:O	2.37	0.58
1:FZ:88:ASN:ND2	1:GA:74:GLU:OE2	2.31	0.58
1:ID:57:PRO:HA	1:ID:73:ASN:HA	1.86	0.58
1:IF:14:LYS:NZ	1:IF:15:ILE:O	2.36	0.58
1:JB:60:LYS:HA	1:JB:71:MET:HE1	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:5:MET:HE1	1:AZ:123:ILE:HG22	1.84	0.58
1:BF:55:LYS:NZ	1:BF:75:ASN:OD1	2.26	0.58
1:BP:56:ARG:O	1:BP:74:GLU:N	2.32	0.58
1:BV:55:LYS:NZ	1:BV:73:ASN:O	2.37	0.58
1:BZ:61:PRO:HB2	1:BZ:64:CYS:HB3	1.85	0.58
1:CO:57:PRO:HA	1:CO:73:ASN:HA	1.85	0.58
1:DN:95:GLU:OE2	1:DO:76:GLN:NE2	2.36	0.58
1:DU:56:ARG:O	1:DU:74:GLU:N	2.32	0.58
1:DZ:60:LYS:NZ	1:DZ:66:ASP:O	2.35	0.58
1:ED:95:GLU:OE2	1:EE:76:GLN:NE2	2.35	0.58
1:EE:67:ALA:HB1	1:GU:62:GLU:HG3	1.84	0.58
1:EG:22:ARG:NH2	1:EG:55:LYS:O	2.35	0.58
1:EP:57:PRO:HA	1:EP:73:ASN:HA	1.85	0.58
1:ER:35:ARG:NH2	1:ER:43:LEU:O	2.37	0.58
1:GW:85:SER:N	1:GX:74:GLU:OE2	2.23	0.58
1:HE:56:ARG:O	1:HE:74:GLU:N	2.30	0.58
1:IB:14:LYS:HZ1	1:IB:28:SER:HB2	1.68	0.58
1:ID:101:ARG:HH12	1:ID:124:VAL:H	1.52	0.58
1:IN:76:GLN:NE2	1:IO:91:THR:OG1	2.37	0.58
1:AT:60:LYS:HZ1	1:AT:65:ALA:H	1.52	0.58
1:BU:35:ARG:NH1	1:BU:44:ASN:OD1	2.36	0.58
1:CD:57:PRO:HA	1:CD:73:ASN:HA	1.86	0.58
1:CP:61:PRO:HB2	1:CP:64:CYS:HB3	1.84	0.58
1:CV:56:ARG:O	1:CV:74:GLU:N	2.31	0.58
1:CW:71:MET:SD	1:CW:71:MET:N	2.77	0.58
1:CY:35:ARG:NH1	1:CY:44:ASN:OD1	2.37	0.58
1:EB:57:PRO:HA	1:EB:73:ASN:HA	1.85	0.58
1:EF:57:PRO:HA	1:EF:73:ASN:HA	1.85	0.58
1:ET:76:GLN:NE2	1:EU:91:THR:OG1	2.37	0.58
1:EZ:76:GLN:NE2	1:FA:91:THR:OG1	2.37	0.58
1:FA:111:ASN:HB3	1:FA:114:LEU:HD12	1.86	0.58
1:FR:37:LYS:NZ	1:FR:39:GLY:O	2.37	0.58
1:FV:117:LEU:HD21	1:FW:31:LEU:HD13	1.86	0.58
1:FZ:14:LYS:HZ1	1:FZ:28:SER:HB2	1.68	0.58
1:GH:91:THR:OG1	1:GI:76:GLN:NE2	2.34	0.58
1:HK:5:MET:HG2	1:HK:17:TRP:HB3	1.85	0.58
1:HR:2:ASN:ND2	1:HS:125:SER:O	2.35	0.58
1:HZ:71:MET:HG3	1:HZ:72:PRO:HD2	1.84	0.58
1:IO:111:ASN:HB3	1:IO:114:LEU:HD12	1.86	0.58
1:JI:101:ARG:HH22	1:JI:124:VAL:CG2	2.15	0.58
1:AH:69:VAL:O	1:JE:63:GLY:HA3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:37:LYS:HG3	1:AO:39:GLY:H	1.69	0.58
1:AT:22:ARG:NH2	1:AT:55:LYS:O	2.32	0.58
1:BA:34:GLN:NE2	1:BA:35:ARG:O	2.37	0.58
1:BI:115:GLY:O	1:BJ:33:ARG:NH1	2.37	0.58
1:BP:57:PRO:HA	1:BP:73:ASN:HA	1.86	0.58
1:CC:115:GLY:O	1:CD:33:ARG:NH1	2.37	0.58
1:CL:61:PRO:HB2	1:CL:64:CYS:HB3	1.85	0.58
1:CT:23:LEU:HD22	1:HS:44:ASN:ND2	2.19	0.58
1:DH:125:SER:O	1:DI:2:ASN:ND2	2.35	0.58
1:DT:117:LEU:HD13	1:DU:15:ILE:HG13	1.85	0.58
1:DZ:57:PRO:HA	1:DZ:73:ASN:HA	1.86	0.58
1:EJ:57:PRO:HA	1:EJ:73:ASN:HA	1.85	0.58
1:GB:14:LYS:NZ	1:GB:15:ILE:O	2.36	0.58
1:GH:93:LYS:NZ	1:GI:108:ALA:O	2.34	0.58
1:HT:55:LYS:NZ	1:HT:73:ASN:HB2	2.18	0.58
1:HY:101:ARG:HE	1:HY:124:VAL:HG21	1.69	0.58
1:IL:35:ARG:HH22	1:IL:43:LEU:N	2.02	0.58
1:IM:37:LYS:NZ	1:IM:38:VAL:O	2.30	0.58
1:JG:76:GLN:NE2	1:JH:91:THR:OG1	2.35	0.58
1:AY:57:PRO:HA	1:AY:73:ASN:HA	1.86	0.57
1:BE:57:PRO:HA	1:BE:73:ASN:HA	1.86	0.57
1:CJ:61:PRO:HB2	1:CJ:64:CYS:HB3	1.85	0.57
1:CX:8:ILE:HA	1:FM:116:PHE:HB2	1.85	0.57
1:DJ:57:PRO:HA	1:DJ:73:ASN:HA	1.85	0.57
1:DK:61:PRO:HB2	1:DK:64:CYS:HB3	1.86	0.57
1:EC:56:ARG:O	1:EC:74:GLU:N	2.31	0.57
1:EI:23:LEU:HD13	1:FE:44:ASN:HD21	1.69	0.57
1:FD:14:LYS:NZ	1:FD:15:ILE:O	2.37	0.57
1:FT:14:LYS:HZ1	1:FT:28:SER:HB2	1.68	0.57
1:FV:93:LYS:NZ	1:FW:108:ALA:O	2.37	0.57
1:HA:14:LYS:HZ1	1:HA:28:SER:HB2	1.69	0.57
1:HG:14:LYS:NZ	1:HG:15:ILE:O	2.37	0.57
1:HJ:57:PRO:HA	1:HJ:73:ASN:HA	1.86	0.57
1:HZ:5:MET:HG2	1:HZ:17:TRP:HB3	1.85	0.57
1:IA:98:THR:HG21	1:IA:126:SER:HA	1.86	0.57
1:IJ:60:LYS:HB3	1:IJ:65:ALA:HB2	1.85	0.57
1:JG:65:ALA:N	1:JI:68:CYS:SG	2.77	0.57
1:AE:60:LYS:NZ	1:AE:66:ASP:O	2.32	0.57
1:AE:125:SER:O	1:AF:2:ASN:ND2	2.33	0.57
1:AK:125:SER:O	1:AL:2:ASN:ND2	2.34	0.57
1:AP:57:PRO:HA	1:AP:73:ASN:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:60:LYS:HZ1	1:AS:66:ASP:H	1.52	0.57
1:AX:67:ALA:C	1:GY:62:GLU:HA	2.25	0.57
1:CM:115:GLY:O	1:CN:33:ARG:NH1	2.37	0.57
1:CQ:34:GLN:NE2	1:CQ:35:ARG:O	2.37	0.57
1:DF:88:ASN:ND2	1:DG:74:GLU:OE2	2.28	0.57
1:DH:34:GLN:NE2	1:DH:35:ARG:O	2.37	0.57
1:DO:61:PRO:HB2	1:DO:64:CYS:HB3	1.85	0.57
1:DT:57:PRO:HA	1:DT:73:ASN:HA	1.85	0.57
1:EO:49:GLN:OE1	1:EO:79:ARG:NH2	2.33	0.57
1:FD:72:PRO:HG2	1:FE:38:VAL:HG12	1.86	0.57
1:FN:93:LYS:NZ	1:FO:108:ALA:O	2.37	0.57
1:FU:105:THR:HG23	1:FU:106:LEU:HD12	1.86	0.57
1:GU:93:LYS:NZ	1:GV:108:ALA:O	2.37	0.57
1:JI:35:ARG:NH2	1:JI:43:LEU:O	2.37	0.57
1:AE:37:LYS:HG3	1:AE:39:GLY:H	1.69	0.57
1:AI:125:SER:O	1:AJ:2:ASN:ND2	2.37	0.57
1:CD:56:ARG:O	1:CD:74:GLU:N	2.30	0.57
1:CE:125:SER:O	1:CF:2:ASN:ND2	2.33	0.57
1:CN:23:LEU:HD13	1:ET:44:ASN:HD21	1.69	0.57
1:CZ:69:VAL:H	1:ID:64:CYS:N	2.02	0.57
1:DJ:5:MET:SD	1:DK:125:SER:HB2	2.44	0.57
1:DY:57:PRO:HA	1:DY:73:ASN:HA	1.86	0.57
1:ER:115:GLY:O	1:ES:33:ARG:NH1	2.37	0.57
1:FE:87:GLU:N	1:FE:87:GLU:OE1	2.37	0.57
1:FR:3:LYS:NZ	1:FS:129:THR:OG1	2.38	0.57
1:GI:87:GLU:N	1:GI:87:GLU:OE1	2.37	0.57
1:HL:35:ARG:NH1	1:HL:43:LEU:O	2.38	0.57
1:HP:14:LYS:HZ1	1:HP:28:SER:HB2	1.69	0.57
1:BB:56:ARG:O	1:BB:74:GLU:N	2.35	0.57
1:CD:61:PRO:HB2	1:CD:64:CYS:HB3	1.86	0.57
1:CL:56:ARG:O	1:CL:74:GLU:N	2.35	0.57
1:DR:49:GLN:OE1	1:DR:79:ARG:NH2	2.31	0.57
1:EG:67:ALA:C	1:HX:62:GLU:HA	2.25	0.57
1:EG:67:ALA:CA	1:HX:63:GLY:H	2.13	0.57
1:EK:67:ALA:H	1:EV:65:ALA:H	1.50	0.57
1:EV:35:ARG:HH22	1:EV:44:ASN:HA	1.68	0.57
1:EX:115:GLY:O	1:EY:33:ARG:NH1	2.36	0.57
1:EZ:128:THR:HA	1:FA:2:ASN:HA	1.86	0.57
1:GK:117:LEU:HD21	1:GL:31:LEU:HD13	1.86	0.57
1:HZ:14:LYS:NZ	1:HZ:15:ILE:O	2.37	0.57
1:JE:5:MET:HG2	1:JE:17:TRP:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:56:ARG:O	1:AD:74:GLU:N	2.35	0.57
1:AK:57:PRO:HA	1:AK:73:ASN:HA	1.86	0.57
1:BO:60:LYS:NZ	1:BO:66:ASP:O	2.36	0.57
1:BP:61:PRO:HB2	1:BP:64:CYS:HB3	1.86	0.57
1:BR:67:ALA:C	1:FZ:62:GLU:HA	2.25	0.57
1:BS:71:MET:N	1:BS:71:MET:SD	2.77	0.57
1:BU:13:ASN:ND2	1:BU:31:LEU:O	2.37	0.57
1:BX:69:VAL:H	1:JI:64:CYS:N	2.02	0.57
1:DA:88:ASN:ND2	1:DB:74:GLU:OE2	2.30	0.57
1:EA:22:ARG:NH2	1:EA:55:LYS:O	2.32	0.57
1:EG:55:LYS:NZ	1:EG:75:ASN:OD1	2.28	0.57
1:EH:125:SER:O	1:EI:2:ASN:ND2	2.30	0.57
1:FH:101:ARG:HH12	1:FH:124:VAL:H	1.52	0.57
1:HG:117:LEU:HD21	1:HI:31:LEU:HD13	1.86	0.57
1:HN:93:LYS:NZ	1:HO:108:ALA:O	2.35	0.57
1:IJ:115:GLY:O	1:IK:33:ARG:NH1	2.38	0.57
1:IX:115:GLY:O	1:IZ:33:ARG:NH1	2.37	0.57
1:JC:35:ARG:NH2	1:JC:43:LEU:O	2.38	0.57
1:AE:115:GLY:O	1:AF:33:ARG:NH1	2.37	0.57
1:AF:49:GLN:OE1	1:AF:79:ARG:NH2	2.33	0.57
1:AX:67:ALA:H	1:GY:65:ALA:H	1.53	0.57
1:CP:67:ALA:C	1:IP:62:GLU:HA	2.25	0.57
1:CU:3:LYS:HZ2	1:CV:129:THR:HG23	1.70	0.57
1:CX:68:CYS:HB2	1:FM:64:CYS:HA	1.86	0.57
1:EG:37:LYS:HA	1:EG:42:GLU:HA	1.87	0.57
1:FR:84:GLY:HA3	1:FR:92:LEU:HD11	1.87	0.57
1:FT:14:LYS:NZ	1:FT:15:ILE:O	2.37	0.57
1:GF:95:GLU:OE2	1:GG:56:ARG:NH2	2.37	0.57
1:GO:85:SER:N	1:GP:74:GLU:OE2	2.24	0.57
1:IW:60:LYS:HE2	1:IW:64:CYS:HB3	1.85	0.57
1:IX:37:LYS:NZ	1:IX:40:ILE:O	2.36	0.57
1:AB:37:LYS:HA	1:AB:42:GLU:HA	1.87	0.57
1:AE:5:MET:HE1	1:AF:123:ILE:HG22	1.87	0.57
1:BR:61:PRO:HB2	1:BR:64:CYS:HB3	1.86	0.57
1:BX:49:GLN:OE1	1:BX:79:ARG:NH2	2.33	0.57
1:CE:57:PRO:HA	1:CE:73:ASN:HA	1.87	0.57
1:CF:57:PRO:HA	1:CF:73:ASN:HA	1.86	0.57
1:CS:5:MET:SD	1:CT:125:SER:HB2	2.45	0.57
1:DL:88:ASN:ND2	1:DM:74:GLU:OE2	2.29	0.57
1:FF:117:LEU:HD21	1:FG:31:LEU:HD13	1.85	0.57
1:FL:14:LYS:HD3	1:FL:30:SER:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FO:101:ARG:HE	1:FO:124:VAL:HG21	1.69	0.57
1:GB:14:LYS:HZ1	1:GB:28:SER:HB2	1.69	0.57
1:GW:125:SER:O	1:GX:2:ASN:ND2	2.37	0.57
1:HE:14:LYS:HZ1	1:HE:28:SER:HB2	1.70	0.57
1:HP:116:PHE:HE2	1:HR:20:PRO:HB3	1.69	0.57
1:AD:67:ALA:C	1:IV:62:GLU:HA	2.25	0.57
1:AJ:67:ALA:C	1:GM:62:GLU:HA	2.25	0.57
1:AM:115:GLY:O	1:AN:33:ARG:NH1	2.38	0.57
1:AZ:61:PRO:HB2	1:AZ:64:CYS:HB3	1.87	0.57
1:CA:117:LEU:HD13	1:CB:15:ILE:HG13	1.86	0.57
1:CD:60:LYS:NZ	1:CD:65:ALA:H	2.03	0.57
1:CF:61:PRO:HB2	1:CF:64:CYS:HB3	1.85	0.57
1:CK:88:ASN:ND2	1:CL:74:GLU:OE2	2.26	0.57
1:CK:115:GLY:O	1:CL:33:ARG:NH1	2.38	0.57
1:CP:67:ALA:CA	1:IP:63:GLY:H	2.14	0.57
1:DK:56:ARG:O	1:DK:74:GLU:N	2.34	0.57
1:DP:34:GLN:NE2	1:DP:35:ARG:O	2.37	0.57
1:EK:69:VAL:H	1:EV:64:CYS:N	2.02	0.57
1:EV:5:MET:HG2	1:EV:17:TRP:HB3	1.87	0.57
1:FL:60:LYS:HE2	1:FL:65:ALA:HB3	1.85	0.57
1:FQ:105:THR:HG23	1:FQ:106:LEU:HD12	1.87	0.57
1:GW:92:LEU:HD22	1:GX:76:GLN:HE21	1.69	0.57
1:HA:35:ARG:NH2	1:HA:43:LEU:O	2.38	0.57
1:HV:57:PRO:HA	1:HV:73:ASN:HA	1.86	0.57
1:JI:124:VAL:HA	1:JJ:4:PRO:HA	1.87	0.57
1:AI:124:VAL:HA	1:AJ:4:PRO:HA	1.87	0.57
1:AU:57:PRO:HA	1:AU:73:ASN:HA	1.87	0.57
1:BT:8:ILE:HA	1:FS:116:PHE:HB2	1.86	0.57
1:CV:67:ALA:C	1:HL:62:GLU:HA	2.25	0.57
1:DH:37:LYS:HD2	1:DH:42:GLU:HG2	1.85	0.57
1:DU:69:VAL:HG13	1:FP:64:CYS:HB2	1.85	0.57
1:EC:60:LYS:NZ	1:EC:65:ALA:H	2.02	0.57
1:EO:23:LEU:HD13	1:EZ:44:ASN:HD21	1.70	0.57
1:EO:55:LYS:NZ	1:EO:75:ASN:OD1	2.28	0.57
1:EU:35:ARG:NH1	1:EU:44:ASN:OD1	2.37	0.57
1:FL:92:LEU:HD22	1:FM:76:GLN:HE21	1.70	0.57
1:GE:35:ARG:HH12	1:GE:42:GLU:HB3	1.68	0.57
1:GK:61:PRO:HG2	1:GK:64:CYS:SG	2.45	0.57
1:GL:57:PRO:HA	1:GL:73:ASN:HA	1.86	0.57
1:GN:38:VAL:HG21	1:GN:43:LEU:HD22	1.86	0.57
1:HB:98:THR:HG21	1:HB:126:SER:HA	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ID:14:LYS:NZ	1:ID:15:ILE:O	2.38	0.57
1:IG:19:ASP:HB3	1:IG:22:ARG:O	2.04	0.57
1:AF:61:PRO:HB2	1:AF:64:CYS:HB3	1.87	0.57
1:AK:116:PHE:HE2	1:AM:20:PRO:HB3	1.69	0.57
1:AZ:37:LYS:HA	1:AZ:42:GLU:HA	1.87	0.57
1:BW:57:PRO:HA	1:BW:73:ASN:HA	1.86	0.57
1:CR:6:GLN:HE21	1:FG:114:LEU:HD22	1.69	0.57
1:CR:56:ARG:O	1:CR:74:GLU:N	2.37	0.57
1:DS:60:LYS:HZ1	1:DS:65:ALA:H	1.53	0.57
1:DW:116:PHE:CE1	1:IH:8:ILE:HD11	2.40	0.57
1:ET:57:PRO:HA	1:ET:73:ASN:HA	1.86	0.57
1:EW:56:ARG:O	1:EW:74:GLU:N	2.26	0.57
1:FL:72:PRO:HG2	1:FM:38:VAL:HG22	1.87	0.57
1:FV:35:ARG:HH22	1:FV:43:LEU:N	2.03	0.57
1:FX:74:GLU:OE2	1:FY:88:ASN:ND2	2.33	0.57
1:GH:57:PRO:HA	1:GH:73:ASN:HA	1.86	0.57
1:GS:37:LYS:NZ	1:GS:40:ILE:O	2.37	0.57
1:HC:57:PRO:HA	1:HC:73:ASN:HA	1.86	0.57
1:HU:106:LEU:HD11	1:HU:123:ILE:HD11	1.87	0.57
1:IG:105:THR:HG23	1:IG:106:LEU:HD12	1.87	0.57
1:AZ:57:PRO:HA	1:AZ:73:ASN:HA	1.86	0.56
1:BE:5:MET:SD	1:BF:125:SER:HB2	2.45	0.56
1:CB:67:ALA:CA	1:FJ:63:GLY:H	2.18	0.56
1:CQ:72:PRO:HG2	1:CR:38:VAL:HG22	1.87	0.56
1:DE:98:THR:HG21	1:DE:126:SER:HA	1.87	0.56
1:DO:23:LEU:HD13	1:FW:44:ASN:HD21	1.69	0.56
1:EI:98:THR:HG21	1:EI:126:SER:HA	1.87	0.56
1:EV:125:SER:HB2	1:EW:5:MET:HE1	1.87	0.56
1:EZ:63:GLY:HA2	1:FB:67:ALA:O	2.05	0.56
1:FH:22:ARG:NH1	1:FH:24:SER:OG	2.38	0.56
1:FM:5:MET:HG2	1:FM:18:SER:C	2.25	0.56
1:FN:14:LYS:NZ	1:FN:15:ILE:O	2.37	0.56
1:GB:93:LYS:NZ	1:GC:108:ALA:O	2.36	0.56
1:GD:116:PHE:HE2	1:GF:20:PRO:HB3	1.69	0.56
1:GQ:11:THR:HB	1:GQ:14:LYS:H	1.70	0.56
1:HZ:14:LYS:HZ1	1:HZ:28:SER:HB2	1.70	0.56
1:IB:111:ASN:HB2	1:IB:116:PHE:HB2	1.86	0.56
1:IF:128:THR:HA	1:IG:2:ASN:HA	1.87	0.56
1:IO:56:ARG:O	1:IO:74:GLU:N	2.26	0.56
1:JB:57:PRO:HA	1:JB:73:ASN:HA	1.86	0.56
1:JI:128:THR:HA	1:JJ:2:ASN:HA	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:60:LYS:NZ	1:AB:65:ALA:H	2.03	0.56
1:AI:88:ASN:ND2	1:AJ:74:GLU:OE2	2.30	0.56
1:AM:5:MET:SD	1:AN:125:SER:HB2	2.45	0.56
1:CA:101:ARG:HH22	1:CB:2:ASN:HD22	1.53	0.56
1:DE:37:LYS:NZ	1:DE:40:ILE:O	2.38	0.56
1:DR:117:LEU:HD21	1:DS:31:LEU:HD13	1.86	0.56
1:DV:115:GLY:O	1:DW:33:ARG:NH1	2.38	0.56
1:EX:56:ARG:O	1:EX:74:GLU:N	2.30	0.56
1:FP:3:LYS:HZ1	1:FQ:129:THR:HG23	1.70	0.56
1:FR:65:ALA:HB1	1:FR:69:VAL:HB	1.87	0.56
1:GI:98:THR:HG21	1:GI:126:SER:HA	1.87	0.56
1:GO:55:LYS:NZ	1:GO:73:ASN:HB2	2.20	0.56
1:GP:60:LYS:HE3	1:GP:64:CYS:HB3	1.88	0.56
1:GU:14:LYS:NZ	1:GU:15:ILE:O	2.37	0.56
1:GZ:71:MET:N	1:GZ:71:MET:SD	2.77	0.56
1:IL:117:LEU:HD21	1:IM:31:LEU:HD13	1.87	0.56
1:AC:33:ARG:NH1	1:AD:115:GLY:O	2.39	0.56
1:AG:57:PRO:HA	1:AG:73:ASN:HA	1.86	0.56
1:AL:60:LYS:NZ	1:AL:65:ALA:H	2.02	0.56
1:BA:125:SER:O	1:BB:2:ASN:ND2	2.35	0.56
1:BM:5:MET:SD	1:BN:125:SER:HB2	2.46	0.56
1:CB:57:PRO:HA	1:CB:73:ASN:HA	1.88	0.56
1:CN:56:ARG:O	1:CN:74:GLU:N	2.34	0.56
1:CR:68:CYS:N	1:FG:64:CYS:SG	2.78	0.56
1:CS:57:PRO:HA	1:CS:73:ASN:HA	1.87	0.56
1:CT:60:LYS:NZ	1:CT:65:ALA:H	2.04	0.56
1:CV:61:PRO:HB2	1:CV:64:CYS:HB3	1.85	0.56
1:CW:57:PRO:HA	1:CW:73:ASN:HA	1.87	0.56
1:DE:60:LYS:NZ	1:DE:65:ALA:H	2.04	0.56
1:DG:49:GLN:OE1	1:DG:79:ARG:NH2	2.33	0.56
1:DN:5:MET:SD	1:DO:125:SER:HB2	2.45	0.56
1:EE:61:PRO:HB2	1:EE:64:CYS:HB3	1.88	0.56
1:EK:57:PRO:HA	1:EK:73:ASN:HA	1.87	0.56
1:FD:22:ARG:NH1	1:FD:24:SER:OG	2.39	0.56
1:FG:60:LYS:HA	1:FG:71:MET:HE1	1.87	0.56
1:GY:35:ARG:NH1	1:GY:43:LEU:O	2.36	0.56
1:HG:14:LYS:HZ1	1:HG:28:SER:HB2	1.71	0.56
1:HG:61:PRO:HD3	1:HG:71:MET:HE1	1.87	0.56
1:HL:117:LEU:HD21	1:HM:31:LEU:HD13	1.86	0.56
1:II:33:ARG:HH12	1:IJ:8:ILE:HG23	1.70	0.56
1:IJ:93:LYS:NZ	1:IK:108:ALA:O	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IR:125:SER:HB2	1:IS:5:MET:HE1	1.87	0.56
1:JB:56:ARG:O	1:JB:74:GLU:N	2.25	0.56
1:JI:14:LYS:NZ	1:JI:15:ILE:O	2.39	0.56
1:AC:57:PRO:HA	1:AC:73:ASN:HA	1.86	0.56
1:AF:67:ALA:CA	1:GS:63:GLY:H	2.18	0.56
1:AN:68:CYS:CB	1:JC:65:ALA:HB2	2.30	0.56
1:BU:115:GLY:O	1:BV:33:ARG:NH1	2.38	0.56
1:CK:33:ARG:NH1	1:CL:115:GLY:O	2.38	0.56
1:CL:69:VAL:H	1:FN:64:CYS:N	2.04	0.56
1:DG:60:LYS:HZ1	1:DG:65:ALA:H	1.54	0.56
1:DO:60:LYS:NZ	1:DO:65:ALA:H	2.04	0.56
1:DT:125:SER:O	1:DU:2:ASN:ND2	2.34	0.56
1:EV:117:LEU:HD21	1:EW:31:LEU:HD13	1.88	0.56
1:EW:98:THR:HG21	1:EW:126:SER:HA	1.87	0.56
1:GU:2:ASN:ND2	1:GV:125:SER:O	2.38	0.56
1:IX:60:LYS:NZ	1:IX:69:VAL:O	2.34	0.56
1:IZ:98:THR:HG21	1:IZ:126:SER:HA	1.87	0.56
1:JB:35:ARG:HH11	1:JB:42:GLU:HG2	1.70	0.56
1:AK:5:MET:SD	1:AL:125:SER:HB2	2.45	0.56
1:AV:61:PRO:HB2	1:AV:64:CYS:HB3	1.87	0.56
1:AX:106:LEU:HD21	1:AX:123:ILE:HD11	1.88	0.56
1:BE:33:ARG:NH1	1:BF:115:GLY:O	2.38	0.56
1:BV:61:PRO:HB2	1:BV:64:CYS:HB3	1.88	0.56
1:CF:37:LYS:NZ	1:CF:40:ILE:O	2.39	0.56
1:DP:128:THR:OG1	1:DQ:1:ALA:O	2.23	0.56
1:DR:51:VAL:HG22	1:DR:79:ARG:HG2	1.88	0.56
1:EI:60:LYS:NZ	1:EI:65:ALA:H	2.02	0.56
1:EP:88:ASN:ND2	1:EQ:74:GLU:OE2	2.27	0.56
1:EQ:106:LEU:HD21	1:EQ:123:ILE:HD11	1.88	0.56
1:FF:57:PRO:HA	1:FF:73:ASN:HA	1.86	0.56
1:FM:55:LYS:NZ	1:FM:73:ASN:HB2	2.19	0.56
1:FP:93:LYS:NZ	1:FQ:108:ALA:O	2.38	0.56
1:GA:98:THR:HG21	1:GA:126:SER:HA	1.87	0.56
1:GE:60:LYS:HA	1:GE:71:MET:HE1	1.87	0.56
1:HE:72:PRO:HG2	1:HF:38:VAL:HG12	1.87	0.56
1:HJ:74:GLU:OE2	1:HK:88:ASN:ND2	2.29	0.56
1:JC:14:LYS:NZ	1:JC:15:ILE:O	2.38	0.56
1:AZ:70:ILE:HG13	1:AZ:70:ILE:O	2.06	0.56
1:BH:60:LYS:NZ	1:BH:64:CYS:SG	2.65	0.56
1:BJ:61:PRO:HB2	1:BJ:64:CYS:HB3	1.87	0.56
1:BR:67:ALA:H	1:FZ:65:ALA:H	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:5:MET:SD	1:BZ:125:SER:HB2	2.46	0.56
1:CD:23:LEU:HD13	1:HI:44:ASN:HD21	1.70	0.56
1:CF:60:LYS:NZ	1:CF:65:ALA:H	2.03	0.56
1:CL:67:ALA:C	1:FN:62:GLU:HA	2.25	0.56
1:CO:115:GLY:O	1:CP:33:ARG:NH1	2.38	0.56
1:DG:23:LEU:HD13	1:IN:44:ASN:HD21	1.70	0.56
1:DQ:56:ARG:O	1:DQ:74:GLU:N	2.38	0.56
1:EG:61:PRO:HB2	1:EG:64:CYS:HB3	1.86	0.56
1:EH:57:PRO:HA	1:EH:73:ASN:HA	1.88	0.56
1:EH:88:ASN:ND2	1:EI:74:GLU:OE2	2.34	0.56
1:EX:87:GLU:OE1	1:EX:87:GLU:N	2.34	0.56
1:FJ:3:LYS:HZ3	1:FK:127:ASP:HB3	1.70	0.56
1:GP:98:THR:HG21	1:GP:126:SER:HA	1.87	0.56
1:HW:5:MET:HB3	1:HW:17:TRP:HB3	1.88	0.56
1:II:37:LYS:NZ	1:II:38:VAL:O	2.36	0.56
1:IR:60:LYS:HA	1:IR:71:MET:HE1	1.87	0.56
1:AE:5:MET:SD	1:AF:125:SER:HB2	2.46	0.56
1:AR:106:LEU:HD21	1:AR:123:ILE:HD11	1.87	0.56
1:AT:56:ARG:O	1:AT:74:GLU:N	2.33	0.56
1:BF:8:ILE:HA	1:HW:116:PHE:HB2	1.87	0.56
1:BU:57:PRO:HA	1:BU:73:ASN:HA	1.88	0.56
1:CT:57:PRO:HA	1:CT:73:ASN:HA	1.86	0.56
1:DH:5:MET:SD	1:DI:125:SER:HB2	2.46	0.56
1:DW:61:PRO:HB2	1:DW:64:CYS:HB3	1.88	0.56
1:EC:106:LEU:HD21	1:EC:123:ILE:HD11	1.87	0.56
1:EQ:37:LYS:NZ	1:EQ:40:ILE:O	2.38	0.56
1:ES:38:VAL:HG21	1:ES:43:LEU:HD22	1.88	0.56
1:FC:60:LYS:NZ	1:FC:65:ALA:O	2.37	0.56
1:FZ:31:LEU:HD12	1:GA:117:LEU:HD22	1.87	0.56
1:FZ:117:LEU:HD21	1:GA:31:LEU:HD13	1.87	0.56
1:GF:93:LYS:NZ	1:GG:108:ALA:O	2.39	0.56
1:GY:128:THR:HA	1:GZ:2:ASN:HA	1.88	0.56
1:HA:14:LYS:NZ	1:HA:15:ILE:O	2.38	0.56
1:HF:60:LYS:HE2	1:HF:64:CYS:HB3	1.88	0.56
1:JJ:57:PRO:HA	1:JJ:73:ASN:HA	1.88	0.56
1:BB:23:LEU:HD13	1:GK:44:ASN:HD21	1.71	0.56
1:BT:67:ALA:HB3	1:FS:64:CYS:HA	1.87	0.56
1:CB:37:LYS:NZ	1:CB:40:ILE:O	2.39	0.56
1:CF:23:LEU:HD22	1:IZ:44:ASN:ND2	2.21	0.56
1:CQ:5:MET:SD	1:CR:125:SER:HB2	2.46	0.56
1:EB:3:LYS:HZ2	1:EC:129:THR:HG23	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ED:3:LYS:HZ2	1:EE:129:THR:HG23	1.70	0.56
1:EG:69:VAL:H	1:HX:64:CYS:N	2.04	0.56
1:EN:115:GLY:O	1:EO:33:ARG:NH1	2.39	0.56
1:EU:64:CYS:SG	1:EU:65:ALA:N	2.79	0.56
1:FD:5:MET:HG2	1:FD:17:TRP:HB3	1.86	0.56
1:GD:37:LYS:NZ	1:GD:39:GLY:O	2.39	0.56
1:GS:93:LYS:NZ	1:GT:108:ALA:O	2.36	0.56
1:GW:65:ALA:HB1	1:GW:69:VAL:HB	1.86	0.56
1:GX:57:PRO:HA	1:GX:73:ASN:HA	1.86	0.56
1:GZ:87:GLU:N	1:GZ:87:GLU:OE1	2.39	0.56
1:HM:98:THR:HG21	1:HM:126:SER:HA	1.88	0.56
1:HR:95:GLU:OE2	1:HS:56:ARG:NH2	2.38	0.56
1:IH:57:PRO:HA	1:IH:73:ASN:HA	1.88	0.56
1:AG:60:LYS:HZ1	1:AG:66:ASP:H	1.53	0.56
1:AH:37:LYS:NZ	1:AH:40:ILE:O	2.39	0.56
1:BF:37:LYS:HA	1:BF:42:GLU:HA	1.88	0.56
1:BW:60:LYS:NZ	1:BW:66:ASP:O	2.32	0.56
1:BX:67:ALA:C	1:JI:65:ALA:HB2	2.25	0.56
1:CF:106:LEU:HD11	1:CF:123:ILE:HD11	1.87	0.56
1:CJ:34:GLN:NE2	1:CJ:35:ARG:O	2.38	0.56
1:CN:6:GLN:HE22	1:EU:111:ASN:HB2	1.70	0.56
1:DP:125:SER:O	1:DQ:2:ASN:ND2	2.36	0.56
1:DU:22:ARG:NH2	1:DU:55:LYS:O	2.36	0.56
1:DX:128:THR:OG1	1:DY:1:ALA:O	2.24	0.56
1:DY:60:LYS:NZ	1:DY:65:ALA:H	2.03	0.56
1:EC:116:PHE:CE1	1:HJ:8:ILE:HD11	2.40	0.56
1:EG:37:LYS:NZ	1:EG:40:ILE:O	2.39	0.56
1:EI:70:ILE:O	1:EI:70:ILE:HG13	2.06	0.56
1:EJ:60:LYS:NZ	1:EJ:66:ASP:H	2.03	0.56
1:EL:5:MET:SD	1:EM:125:SER:HB2	2.45	0.56
1:FT:115:GLY:O	1:FU:33:ARG:NH1	2.38	0.56
1:GQ:57:PRO:HA	1:GQ:73:ASN:HA	1.88	0.56
1:IB:34:GLN:NE2	1:IB:35:ARG:O	2.38	0.56
1:ID:14:LYS:HZ1	1:ID:28:SER:HB2	1.71	0.56
1:ID:85:SER:OG	1:IE:74:GLU:OE1	2.17	0.56
1:IE:101:ARG:HH21	1:IE:124:VAL:HG21	1.70	0.56
1:IW:105:THR:HG23	1:IW:106:LEU:HD12	1.87	0.56
1:BI:5:MET:SD	1:BJ:125:SER:HB2	2.45	0.56
1:CW:5:MET:HE1	1:CX:123:ILE:HG22	1.87	0.56
1:CW:124:VAL:HA	1:CX:4:PRO:HA	1.87	0.56
1:DH:35:ARG:NH1	1:DH:44:ASN:OD1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DH:88:ASN:ND2	1:DI:74:GLU:OE2	2.32	0.56
1:DL:115:GLY:O	1:DM:33:ARG:NH1	2.39	0.56
1:EK:56:ARG:O	1:EK:74:GLU:N	2.34	0.56
1:GS:14:LYS:HZ1	1:GS:28:SER:HB2	1.71	0.56
1:GT:87:GLU:OE1	1:GT:87:GLU:N	2.38	0.56
1:JE:93:LYS:NZ	1:JF:108:ALA:O	2.38	0.56
1:AJ:68:CYS:SG	1:GM:65:ALA:HA	2.46	0.55
1:AN:61:PRO:HB2	1:AN:64:CYS:HB3	1.88	0.55
1:AP:106:LEU:HD21	1:AP:123:ILE:HD11	1.88	0.55
1:BD:56:ARG:O	1:BD:74:GLU:N	2.35	0.55
1:BE:125:SER:O	1:BF:2:ASN:ND2	2.34	0.55
1:BH:8:ILE:HA	1:HQ:116:PHE:HB2	1.88	0.55
1:BP:60:LYS:NZ	1:BP:65:ALA:H	2.04	0.55
1:BZ:37:LYS:HA	1:BZ:42:GLU:HA	1.87	0.55
1:CH:67:ALA:CA	1:HA:63:GLY:H	2.18	0.55
1:CQ:57:PRO:HA	1:CQ:73:ASN:HA	1.88	0.55
1:CV:69:VAL:H	1:HL:64:CYS:N	2.04	0.55
1:CZ:69:VAL:HG13	1:ID:64:CYS:SG	2.47	0.55
1:DY:61:PRO:HB2	1:DY:64:CYS:HB3	1.88	0.55
1:EG:57:PRO:HA	1:EG:73:ASN:HA	1.89	0.55
1:ET:3:LYS:NZ	1:EU:129:THR:HG23	2.20	0.55
1:FJ:14:LYS:NZ	1:FJ:15:ILE:O	2.39	0.55
1:FQ:5:MET:HB3	1:FQ:17:TRP:HB3	1.86	0.55
1:HE:91:THR:OG1	1:HF:76:GLN:NE2	2.32	0.55
1:HI:60:LYS:HD3	1:HI:64:CYS:HB3	1.88	0.55
1:AI:5:MET:SD	1:AJ:125:SER:HB2	2.46	0.55
1:AL:55:LYS:NZ	1:AL:75:ASN:OD1	2.29	0.55
1:BF:56:ARG:O	1:BF:74:GLU:N	2.37	0.55
1:BG:51:VAL:HG22	1:BG:79:ARG:HG2	1.88	0.55
1:BL:106:LEU:HD21	1:BL:123:ILE:HD11	1.88	0.55
1:BL:116:PHE:CE1	1:FX:8:ILE:HD11	2.40	0.55
1:CB:37:LYS:HA	1:CB:42:GLU:HA	1.88	0.55
1:CF:22:ARG:NH2	1:CF:55:LYS:O	2.34	0.55
1:CF:70:ILE:O	1:CF:70:ILE:HG13	2.07	0.55
1:CN:55:LYS:NZ	1:CN:75:ASN:OD1	2.28	0.55
1:CV:69:VAL:HG13	1:HL:64:CYS:SG	2.47	0.55
1:DO:57:PRO:HA	1:DO:73:ASN:HA	1.89	0.55
1:EH:34:GLN:NE2	1:EH:35:ARG:O	2.40	0.55
1:EN:51:VAL:HG22	1:EN:79:ARG:HG2	1.88	0.55
1:ET:63:GLY:HA2	1:EV:67:ALA:O	2.07	0.55
1:EZ:14:LYS:HZ1	1:EZ:28:SER:HB2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FM:33:ARG:HH12	1:FN:8:ILE:HG23	1.71	0.55
1:FQ:87:GLU:OE1	1:FQ:87:GLU:N	2.38	0.55
1:GG:98:THR:HG21	1:GG:126:SER:HA	1.88	0.55
1:GM:22:ARG:NH1	1:GM:24:SER:OG	2.39	0.55
1:GU:5:MET:SD	1:GV:125:SER:HB2	2.47	0.55
1:GU:37:LYS:NZ	1:GU:39:GLY:O	2.39	0.55
1:HQ:85:SER:OG	1:HQ:88:ASN:ND2	2.30	0.55
1:IG:35:ARG:HH12	1:IG:42:GLU:HB3	1.72	0.55
1:IL:5:MET:HG2	1:II:17:TRP:HB3	1.88	0.55
1:IJ:35:ARG:NH1	1:IJ:43:LEU:O	2.37	0.55
1:JE:95:GLU:OE2	1:JF:56:ARG:NH2	2.39	0.55
1:BA:107:PHE:HA	1:BA:112:ALA:HB3	1.89	0.55
1:BT:37:LYS:HA	1:BT:42:GLU:HA	1.87	0.55
1:BW:51:VAL:HG22	1:BW:79:ARG:HG2	1.88	0.55
1:CA:33:ARG:NH1	1:CB:115:GLY:O	2.39	0.55
1:CG:128:THR:OG1	1:CH:1:ALA:O	2.23	0.55
1:DC:33:ARG:NH1	1:DE:115:GLY:O	2.40	0.55
1:DK:37:LYS:NZ	1:DK:40:ILE:O	2.40	0.55
1:DZ:115:GLY:O	1:EA:33:ARG:NH1	2.39	0.55
1:EA:37:LYS:NZ	1:EA:40:ILE:O	2.40	0.55
1:EB:128:THR:HA	1:EC:2:ASN:HA	1.87	0.55
1:EL:115:GLY:O	1:EM:33:ARG:NH1	2.39	0.55
1:FB:37:LYS:NZ	1:FB:39:GLY:O	2.40	0.55
1:FW:19:ASP:HB3	1:FW:22:ARG:O	2.07	0.55
1:HJ:63:GLY:HA2	1:HL:67:ALA:O	2.07	0.55
1:HR:34:GLN:NE2	1:HR:35:ARG:O	2.39	0.55
1:IU:37:LYS:NZ	1:IU:38:VAL:O	2.32	0.55
1:IV:14:LYS:NZ	1:IV:15:ILE:O	2.39	0.55
1:BB:6:GLN:HE22	1:GL:111:ASN:HB2	1.71	0.55
1:BV:67:ALA:C	1:GH:62:GLU:HA	2.27	0.55
1:BZ:60:LYS:NZ	1:BZ:65:ALA:H	2.05	0.55
1:CJ:60:LYS:NZ	1:CJ:65:ALA:H	2.05	0.55
1:CZ:67:ALA:N	1:ID:65:ALA:H	2.05	0.55
1:DE:37:LYS:HA	1:DE:42:GLU:HA	1.88	0.55
1:DX:125:SER:O	1:DY:2:ASN:ND2	2.37	0.55
1:EQ:8:ILE:HA	1:IU:116:PHE:HB2	1.87	0.55
1:EQ:37:LYS:HA	1:EQ:42:GLU:HA	1.87	0.55
1:FP:14:LYS:HZ1	1:FP:28:SER:HB2	1.71	0.55
1:FZ:128:THR:HA	1:GA:2:ASN:HA	1.88	0.55
1:GS:117:LEU:HD21	1:GT:31:LEU:HD13	1.89	0.55
1:HB:5:MET:CG	1:HB:17:TRP:HB3	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HT:3:LYS:NZ	1:HU:129:THR:HG23	2.21	0.55
1:HV:24:SER:HB2	1:HV:55:LYS:HG3	1.88	0.55
1:IN:3:LYS:NZ	1:IO:129:THR:HG23	2.22	0.55
1:IN:57:PRO:HA	1:IN:73:ASN:HA	1.89	0.55
1:AA:115:GLY:O	1:AB:33:ARG:NH1	2.39	0.55
1:AJ:98:THR:HG21	1:AJ:126:SER:HA	1.89	0.55
1:AM:88:ASN:ND2	1:AN:74:GLU:OE2	2.31	0.55
1:BN:8:ILE:HA	1:FY:116:PHE:HB2	1.89	0.55
1:BV:67:ALA:HA	1:GH:63:GLY:N	2.19	0.55
1:CI:1:ALA:HB1	1:CJ:128:THR:HG23	1.88	0.55
1:CN:8:ILE:HA	1:EU:116:PHE:HB2	1.88	0.55
1:DW:55:LYS:NZ	1:DW:75:ASN:OD1	2.27	0.55
1:DZ:60:LYS:HG2	1:DZ:71:MET:HE1	1.88	0.55
1:EG:69:VAL:HG13	1:HX:64:CYS:SG	2.46	0.55
1:FI:71:MET:N	1:FI:71:MET:SD	2.79	0.55
1:FW:66:ASP:OD1	1:FW:68:CYS:N	2.39	0.55
1:HU:87:GLU:OE1	1:HU:87:GLU:N	2.39	0.55
1:HX:93:LYS:NZ	1:HY:108:ALA:O	2.38	0.55
1:AA:5:MET:SD	1:AB:125:SER:HB2	2.46	0.55
1:BF:37:LYS:NZ	1:BF:40:ILE:O	2.40	0.55
1:BX:67:ALA:N	1:JI:65:ALA:H	2.04	0.55
1:CQ:35:ARG:NH1	1:CQ:44:ASN:OD1	2.40	0.55
1:DB:56:ARG:O	1:DB:74:GLU:N	2.33	0.55
1:DH:57:PRO:HA	1:DH:73:ASN:HA	1.88	0.55
1:DX:5:MET:SD	1:DY:125:SER:HB2	2.46	0.55
1:EE:67:ALA:C	1:GU:62:GLU:HA	2.27	0.55
1:ET:39:GLY:HA3	1:EU:72:PRO:HG2	1.88	0.55
1:EV:56:ARG:O	1:EV:74:GLU:N	2.32	0.55
1:FF:65:ALA:N	1:FH:68:CYS:SG	2.79	0.55
1:FL:36:VAL:N	1:FL:43:LEU:O	2.32	0.55
1:HC:59:PRO:HG2	1:HD:87:GLU:HG3	1.88	0.55
1:AZ:37:LYS:NZ	1:AZ:40:ILE:O	2.39	0.55
1:BA:115:GLY:O	1:BB:33:ARG:NH1	2.40	0.55
1:BU:72:PRO:HG2	1:BV:38:VAL:HG22	1.88	0.55
1:BX:67:ALA:CA	1:JI:63:GLY:H	2.16	0.55
1:CF:56:ARG:O	1:CF:74:GLU:N	2.32	0.55
1:DG:56:ARG:O	1:DG:74:GLU:N	2.36	0.55
1:DI:67:ALA:C	1:FH:62:GLU:HA	2.27	0.55
1:DI:98:THR:HG21	1:DI:126:SER:HA	1.89	0.55
1:DV:5:MET:SD	1:DW:125:SER:HB2	2.46	0.55
1:EH:5:MET:SD	1:EI:125:SER:HB2	2.47	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EK:69:VAL:H	1:EV:64:CYS:H	1.53	0.55
1:EP:125:SER:O	1:EQ:2:ASN:ND2	2.36	0.55
1:EX:74:GLU:OE2	1:EY:88:ASN:ND2	2.40	0.55
1:FJ:20:PRO:HB3	1:FO:116:PHE:HE2	1.72	0.55
1:FL:125:SER:O	1:FM:2:ASN:ND2	2.36	0.55
1:GK:59:PRO:HG2	1:GL:87:GLU:HG3	1.87	0.55
1:HI:66:ASP:OD1	1:HI:68:CYS:N	2.38	0.55
1:IF:72:PRO:HG2	1:IG:38:VAL:HG12	1.89	0.55
1:IM:87:GLU:OE1	1:IM:87:GLU:N	2.39	0.55
1:IT:3:LYS:NZ	1:IU:129:THR:OG1	2.40	0.55
1:JF:56:ARG:O	1:JF:74:GLU:N	2.28	0.55
1:AI:12:ALA:HB2	1:GT:10:SER:H	1.71	0.55
1:AI:72:PRO:HG2	1:AJ:38:VAL:HG22	1.88	0.55
1:AT:37:LYS:HA	1:AT:42:GLU:HA	1.89	0.55
1:BD:8:ILE:HA	1:GE:116:PHE:HB2	1.88	0.55
1:BD:49:GLN:OE1	1:BD:79:ARG:NH2	2.33	0.55
1:BD:55:LYS:NZ	1:BD:75:ASN:OD1	2.27	0.55
1:BY:115:GLY:O	1:BZ:33:ARG:NH1	2.39	0.55
1:DJ:3:LYS:HZ2	1:DK:129:THR:HG23	1.72	0.55
1:DP:88:ASN:ND2	1:DQ:74:GLU:OE2	2.31	0.55
1:DV:128:THR:O	1:DW:3:LYS:NZ	2.33	0.55
1:EC:70:ILE:O	1:EC:70:ILE:HG13	2.05	0.55
1:FJ:22:ARG:NH1	1:FJ:24:SER:OG	2.40	0.55
1:FT:3:LYS:HZ1	1:FU:129:THR:HG23	1.69	0.55
1:GS:128:THR:HA	1:GT:2:ASN:HA	1.88	0.55
1:GW:57:PRO:HA	1:GW:73:ASN:HA	1.89	0.55
1:IG:106:LEU:HD11	1:IG:123:ILE:HD11	1.88	0.55
1:IS:106:LEU:HD11	1:IS:123:ILE:HD11	1.89	0.55
1:AF:23:LEU:HD22	1:GT:44:ASN:HD21	1.71	0.55
1:AF:56:ARG:O	1:AF:74:GLU:N	2.36	0.55
1:AN:67:ALA:HB1	1:JC:62:GLU:HG3	1.89	0.55
1:BG:88:ASN:ND2	1:BH:74:GLU:OE2	2.27	0.55
1:BR:69:VAL:H	1:FZ:64:CYS:N	2.04	0.55
1:CG:5:MET:SD	1:CH:125:SER:HB2	2.46	0.55
1:CM:60:LYS:NZ	1:CM:66:ASP:O	2.33	0.55
1:CV:5:MET:N	1:CV:5:MET:SD	2.80	0.55
1:CW:33:ARG:NH1	1:CX:115:GLY:O	2.40	0.55
1:CY:125:SER:O	1:CZ:2:ASN:ND2	2.37	0.55
1:DB:67:ALA:HB1	1:IF:64:CYS:HA	1.88	0.55
1:EI:57:PRO:HA	1:EI:73:ASN:HA	1.88	0.55
1:EZ:3:LYS:NZ	1:FA:129:THR:HG23	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FD:93:LYS:NZ	1:FE:108:ALA:O	2.39	0.55
1:FK:87:GLU:OE1	1:FK:87:GLU:N	2.37	0.55
1:FU:5:MET:HB3	1:FU:17:TRP:HB3	1.89	0.55
1:GW:96:TRP:NE1	1:GX:104:ASP:OD1	2.34	0.55
1:IK:98:THR:HG21	1:IK:126:SER:HA	1.87	0.55
1:AH:56:ARG:O	1:AH:74:GLU:N	2.31	0.55
1:BT:37:LYS:NZ	1:BT:40:ILE:O	2.39	0.55
1:DN:3:LYS:HZ1	1:DO:129:THR:HG23	1.71	0.55
1:EE:67:ALA:CA	1:GU:63:GLY:H	2.18	0.55
1:GB:88:ASN:ND2	1:GC:74:GLU:OE2	2.30	0.55
1:GH:22:ARG:NH1	1:GH:24:SER:OG	2.40	0.55
1:HJ:37:LYS:NZ	1:HJ:39:GLY:O	2.40	0.55
1:HL:76:GLN:HE21	1:HM:92:LEU:HD22	1.71	0.55
1:HR:60:LYS:HA	1:HR:71:MET:HE1	1.89	0.55
1:IS:116:PHE:HE1	1:IU:8:ILE:HB	1.72	0.55
1:AJ:67:ALA:C	1:GM:65:ALA:HB2	2.27	0.54
1:AL:37:LYS:NZ	1:AL:40:ILE:O	2.40	0.54
1:BD:60:LYS:NZ	1:BD:64:CYS:SG	2.66	0.54
1:BI:128:THR:OG1	1:BJ:1:ALA:O	2.25	0.54
1:BW:72:PRO:HG2	1:BX:38:VAL:HG22	1.89	0.54
1:CO:60:LYS:NZ	1:CO:66:ASP:H	2.05	0.54
1:DL:60:LYS:NZ	1:DL:66:ASP:H	2.04	0.54
1:DM:57:PRO:HA	1:DM:73:ASN:HA	1.88	0.54
1:DU:61:PRO:HB2	1:DU:64:CYS:HB3	1.88	0.54
1:FV:35:ARG:NH2	1:FV:36:VAL:O	2.28	0.54
1:GR:57:PRO:HA	1:GR:73:ASN:HA	1.88	0.54
1:HZ:22:ARG:NH1	1:HZ:24:SER:OG	2.40	0.54
1:AE:72:PRO:HG2	1:AF:38:VAL:HG22	1.88	0.54
1:AI:128:THR:OG1	1:AJ:1:ALA:O	2.23	0.54
1:AN:68:CYS:HB3	1:JC:65:ALA:CB	2.32	0.54
1:CI:5:MET:SD	1:CJ:125:SER:HB2	2.47	0.54
1:DE:106:LEU:HD21	1:DE:123:ILE:HD11	1.89	0.54
1:FR:57:PRO:HA	1:FR:73:ASN:HA	1.88	0.54
1:FW:71:MET:N	1:FW:71:MET:SD	2.80	0.54
1:HT:31:LEU:HD12	1:HU:117:LEU:HD22	1.90	0.54
1:IF:14:LYS:HZ1	1:IF:28:SER:HB2	1.73	0.54
1:IR:2:ASN:ND2	1:IS:125:SER:O	2.41	0.54
1:IR:93:LYS:NZ	1:IS:108:ALA:O	2.40	0.54
1:IV:22:ARG:NH1	1:IV:24:SER:OG	2.40	0.54
1:IV:93:LYS:NZ	1:IW:108:ALA:O	2.38	0.54
1:AC:101:ARG:HH22	1:AD:2:ASN:HD22	1.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:56:ARG:O	1:AJ:74:GLU:N	2.35	0.54
1:AO:57:PRO:HA	1:AO:73:ASN:HA	1.88	0.54
1:BJ:67:ALA:C	1:HZ:62:GLU:HA	2.28	0.54
1:BL:5:MET:SD	1:BL:5:MET:N	2.80	0.54
1:BX:55:LYS:NZ	1:BX:75:ASN:OD1	2.28	0.54
1:CH:98:THR:HG21	1:CH:126:SER:HA	1.88	0.54
1:CJ:106:LEU:HD21	1:CJ:123:ILE:HD11	1.89	0.54
1:CN:49:GLN:OE1	1:CN:79:ARG:NH2	2.33	0.54
1:DE:61:PRO:HB2	1:DE:64:CYS:HB3	1.90	0.54
1:DS:61:PRO:HB2	1:DS:64:CYS:HB3	1.88	0.54
1:FT:125:SER:HB2	1:FU:5:MET:HE1	1.88	0.54
1:FX:64:CYS:N	1:FZ:68:CYS:SG	2.80	0.54
1:GG:71:MET:N	1:GG:71:MET:SD	2.80	0.54
1:GK:34:GLN:NE2	1:GK:35:ARG:O	2.40	0.54
1:GU:14:LYS:HZ1	1:GU:28:SER:HB2	1.73	0.54
1:HU:35:ARG:HH21	1:HU:42:GLU:HG2	1.73	0.54
1:HU:105:THR:HG23	1:HU:106:LEU:HD12	1.87	0.54
1:IE:87:GLU:OE1	1:IE:87:GLU:N	2.38	0.54
1:JE:117:LEU:HD21	1:JF:31:LEU:HD13	1.89	0.54
1:AH:67:ALA:CA	1:JE:63:GLY:H	2.19	0.54
1:BI:88:ASN:ND2	1:BJ:74:GLU:OE2	2.35	0.54
1:BT:56:ARG:O	1:BT:74:GLU:N	2.34	0.54
1:CC:88:ASN:ND2	1:CD:74:GLU:OE2	2.35	0.54
1:CY:57:PRO:HA	1:CY:73:ASN:HA	1.88	0.54
1:CY:72:PRO:HG2	1:CZ:38:VAL:HG22	1.88	0.54
1:DG:8:ILE:HA	1:IO:116:PHE:HB2	1.89	0.54
1:DZ:3:LYS:HZ2	1:EA:129:THR:HG23	1.73	0.54
1:EB:128:THR:O	1:EC:3:LYS:NZ	2.36	0.54
1:EO:8:ILE:HA	1:FA:116:PHE:HB2	1.90	0.54
1:FP:14:LYS:NZ	1:FP:15:ILE:O	2.40	0.54
1:GN:19:ASP:HB3	1:GN:22:ARG:O	2.07	0.54
1:GS:14:LYS:NZ	1:GS:15:ILE:O	2.40	0.54
1:GV:87:GLU:OE1	1:GV:87:GLU:N	2.41	0.54
1:HZ:101:ARG:HH12	1:HZ:124:VAL:H	1.53	0.54
1:IR:14:LYS:NZ	1:IR:15:ILE:O	2.40	0.54
1:JI:117:LEU:HD21	1:JJ:31:LEU:HD13	1.89	0.54
1:AO:88:ASN:ND2	1:AP:74:GLU:OE2	2.30	0.54
1:AX:5:MET:N	1:AX:5:MET:SD	2.80	0.54
1:DJ:115:GLY:O	1:DK:33:ARG:NH1	2.41	0.54
1:EC:60:LYS:HZ1	1:EC:65:ALA:H	1.54	0.54
1:EU:56:ARG:O	1:EU:74:GLU:N	2.26	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:117:LEU:HD21	1:FC:31:LEU:HD13	1.89	0.54
1:FL:34:GLN:NE2	1:FL:35:ARG:O	2.40	0.54
1:GD:45:ASN:HA	1:GD:85:SER:HA	1.88	0.54
1:GO:72:PRO:HG2	1:GP:38:VAL:HG12	1.90	0.54
1:GU:117:LEU:HD21	1:GV:31:LEU:HD13	1.89	0.54
1:HR:61:PRO:HG2	1:HR:64:CYS:SG	2.48	0.54
1:HV:59:PRO:O	1:HV:61:PRO:HD3	2.06	0.54
1:IB:61:PRO:HG2	1:IB:64:CYS:SG	2.46	0.54
1:IG:87:GLU:OE1	1:IG:87:GLU:N	2.41	0.54
1:AL:37:LYS:HA	1:AL:42:GLU:HA	1.88	0.54
1:AY:124:VAL:HA	1:AZ:4:PRO:HA	1.90	0.54
1:CC:5:MET:SD	1:CD:125:SER:HB2	2.48	0.54
1:CQ:125:SER:O	1:CR:2:ASN:ND2	2.38	0.54
1:FL:84:GLY:HA3	1:FL:92:LEU:HD11	1.89	0.54
1:FP:22:ARG:NH1	1:FP:24:SER:OG	2.40	0.54
1:FR:92:LEU:HD22	1:FS:76:GLN:HE21	1.73	0.54
1:FS:98:THR:HG21	1:FS:126:SER:HA	1.89	0.54
1:HT:2:ASN:ND2	1:HU:125:SER:O	2.40	0.54
1:HW:37:LYS:NZ	1:HW:38:VAL:O	2.33	0.54
1:IP:117:LEU:HD21	1:IQ:31:LEU:HD13	1.88	0.54
1:JB:49:GLN:OE1	1:JB:79:ARG:NH2	2.40	0.54
1:AF:69:VAL:H	1:GS:64:CYS:H	1.54	0.54
1:AZ:60:LYS:HZ1	1:AZ:65:ALA:H	1.55	0.54
1:BK:35:ARG:NH1	1:BK:44:ASN:OD1	2.41	0.54
1:BK:57:PRO:HA	1:BK:73:ASN:HA	1.89	0.54
1:BR:5:MET:SD	1:BR:5:MET:N	2.80	0.54
1:CI:3:LYS:HZ2	1:CJ:129:THR:HG23	1.73	0.54
1:DA:72:PRO:HG2	1:DB:38:VAL:HG22	1.89	0.54
1:DQ:57:PRO:HA	1:DQ:73:ASN:HA	1.90	0.54
1:DX:107:PHE:HA	1:DX:112:ALA:HB3	1.90	0.54
1:EL:35:ARG:NH1	1:EL:44:ASN:OD1	2.41	0.54
1:FC:56:ARG:O	1:FC:74:GLU:N	2.29	0.54
1:GT:106:LEU:HD11	1:GT:123:ILE:HD11	1.89	0.54
1:GY:88:ASN:ND2	1:GZ:74:GLU:OE2	2.29	0.54
1:HR:117:LEU:HD21	1:HS:31:LEU:HD13	1.90	0.54
1:JC:117:LEU:HD21	1:JD:31:LEU:HD13	1.89	0.54
1:JG:11:THR:HB	1:JG:14:LYS:H	1.73	0.54
1:CA:88:ASN:ND2	1:CB:74:GLU:OE2	2.30	0.54
1:CC:51:VAL:HG22	1:CC:79:ARG:HG2	1.89	0.54
1:DC:125:SER:O	1:DE:2:ASN:ND2	2.35	0.54
1:DO:56:ARG:O	1:DO:74:GLU:N	2.31	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DZ:60:LYS:NZ	1:DZ:66:ASP:H	2.06	0.54
1:EJ:115:GLY:O	1:EK:33:ARG:NH1	2.41	0.54
1:FH:117:LEU:HD21	1:FI:31:LEU:HD13	1.90	0.54
1:FR:61:PRO:HG2	1:FR:64:CYS:SG	2.48	0.54
1:FV:5:MET:HE1	1:FW:123:ILE:HG22	1.89	0.54
1:FV:128:THR:HA	1:FW:2:ASN:HA	1.90	0.54
1:FX:85:SER:N	1:FY:74:GLU:OE2	2.36	0.54
1:GC:87:GLU:OE1	1:GC:87:GLU:N	2.38	0.54
1:HS:22:ARG:NH2	1:HS:55:LYS:O	2.40	0.54
1:HS:98:THR:HG21	1:HS:126:SER:HA	1.90	0.54
1:HW:60:LYS:HG2	1:HW:71:MET:HE1	1.89	0.54
1:ID:22:ARG:NH1	1:ID:24:SER:OG	2.41	0.54
1:ID:93:LYS:NZ	1:IE:108:ALA:O	2.40	0.54
1:IR:14:LYS:HZ1	1:IR:28:SER:HB2	1.72	0.54
1:IX:35:ARG:HH22	1:IX:44:ASN:HA	1.73	0.54
1:AL:5:MET:HG3	1:AL:17:TRP:HB3	1.90	0.54
1:CB:69:VAL:HG13	1:FJ:64:CYS:HB2	1.89	0.54
1:CJ:37:LYS:NZ	1:CJ:39:GLY:O	2.41	0.54
1:DX:13:ASN:ND2	1:DX:31:LEU:O	2.41	0.54
1:DX:115:GLY:O	1:DY:33:ARG:NH1	2.41	0.54
1:ED:88:ASN:ND2	1:EE:74:GLU:OE2	2.33	0.54
1:FC:37:LYS:HD3	1:FC:42:GLU:OE2	2.07	0.54
1:FG:56:ARG:O	1:FG:74:GLU:N	2.23	0.54
1:FJ:93:LYS:NZ	1:FK:108:ALA:O	2.38	0.54
1:FO:5:MET:HB3	1:FO:17:TRP:HB3	1.90	0.54
1:FT:93:LYS:NZ	1:FU:108:ALA:O	2.39	0.54
1:FU:87:GLU:OE1	1:FU:87:GLU:N	2.38	0.54
1:GR:49:GLN:OE1	1:GR:79:ARG:NH2	2.40	0.54
1:HF:101:ARG:NH1	1:HF:124:VAL:HG21	2.23	0.54
1:HR:60:LYS:HD2	1:HR:71:MET:HE1	1.89	0.54
1:IR:22:ARG:NH1	1:IR:24:SER:OG	2.40	0.54
1:JA:11:THR:HB	1:JA:14:LYS:H	1.73	0.54
1:AG:60:LYS:NZ	1:AG:66:ASP:H	2.06	0.54
1:AZ:5:MET:HG3	1:AZ:17:TRP:HB3	1.90	0.54
1:CH:67:ALA:HA	1:HA:63:GLY:N	2.22	0.54
1:CL:69:VAL:HG13	1:FN:64:CYS:SG	2.47	0.54
1:CV:67:ALA:C	1:HL:65:ALA:HB2	2.28	0.54
1:DA:5:MET:HE2	1:DB:123:ILE:HG22	1.90	0.54
1:DJ:128:THR:O	1:DK:3:LYS:NZ	2.34	0.54
1:DT:128:THR:OG1	1:DU:1:ALA:O	2.25	0.54
1:EJ:88:ASN:ND2	1:EK:74:GLU:OE2	2.29	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FH:123:ILE:HG22	1:FI:5:MET:HE1	1.89	0.54
1:FL:57:PRO:HA	1:FL:73:ASN:HA	1.88	0.54
1:FO:34:GLN:O	1:FO:45:ASN:N	2.41	0.54
1:FV:60:LYS:HA	1:FV:71:MET:HE1	1.90	0.54
1:GA:37:LYS:HD3	1:GA:42:GLU:OE2	2.08	0.54
1:AY:3:LYS:NZ	1:AZ:129:THR:HG23	2.23	0.53
1:BX:68:CYS:N	1:JI:64:CYS:H	2.05	0.53
1:DH:115:GLY:O	1:DI:33:ARG:NH1	2.41	0.53
1:DS:57:PRO:HA	1:DS:73:ASN:HA	1.90	0.53
1:DZ:5:MET:SD	1:EA:125:SER:HB2	2.48	0.53
1:EA:67:ALA:HB3	1:HK:64:CYS:HA	1.90	0.53
1:EF:34:GLN:O	1:EF:45:ASN:N	2.40	0.53
1:EV:74:GLU:OE2	1:EW:85:SER:OG	2.25	0.53
1:EY:60:LYS:HG2	1:EY:71:MET:HE1	1.91	0.53
1:FB:55:LYS:NZ	1:FB:73:ASN:HB2	2.23	0.53
1:FM:71:MET:N	1:FM:71:MET:SD	2.80	0.53
1:GM:14:LYS:HZ1	1:GM:28:SER:HB2	1.72	0.53
1:GV:60:LYS:HD3	1:GV:64:CYS:HB3	1.89	0.53
1:HO:87:GLU:OE1	1:HO:87:GLU:N	2.39	0.53
1:IQ:37:LYS:HD3	1:IQ:42:GLU:OE2	2.07	0.53
1:IT:87:GLU:OE1	1:IT:87:GLU:N	2.40	0.53
1:JF:37:LYS:HD3	1:JF:42:GLU:OE2	2.08	0.53
1:AB:37:LYS:NZ	1:AB:40:ILE:O	2.41	0.53
1:AG:34:GLN:O	1:AG:45:ASN:N	2.41	0.53
1:BJ:68:CYS:N	1:HZ:64:CYS:H	2.06	0.53
1:BN:98:THR:HG21	1:BN:126:SER:HA	1.89	0.53
1:BQ:35:ARG:NH1	1:BQ:44:ASN:OD1	2.41	0.53
1:CE:60:LYS:NZ	1:CE:66:ASP:O	2.32	0.53
1:CI:56:ARG:O	1:CI:74:GLU:N	2.27	0.53
1:CO:3:LYS:HZ2	1:CP:129:THR:HG23	1.73	0.53
1:CQ:107:PHE:HA	1:CQ:112:ALA:HB3	1.91	0.53
1:CS:1:ALA:HB1	1:CT:128:THR:HG23	1.89	0.53
1:CW:128:THR:OG1	1:CX:1:ALA:O	2.27	0.53
1:DH:107:PHE:HA	1:DH:112:ALA:HB3	1.89	0.53
1:DJ:5:MET:HE1	1:DK:123:ILE:HG22	1.89	0.53
1:DM:56:ARG:O	1:DM:74:GLU:N	2.34	0.53
1:EG:5:MET:HG3	1:EG:17:TRP:HB3	1.89	0.53
1:ER:5:MET:SD	1:ES:125:SER:HB2	2.47	0.53
1:ER:76:GLN:NE2	1:ES:91:THR:OG1	2.41	0.53
1:GB:35:ARG:NH1	1:GB:43:LEU:O	2.41	0.53
1:GU:123:ILE:HG22	1:GV:5:MET:HE1	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GY:5:MET:SD	1:GZ:125:SER:HB2	2.48	0.53
1:AJ:68:CYS:HB2	1:GM:64:CYS:SG	2.49	0.53
1:AL:61:PRO:HB2	1:AL:64:CYS:HB3	1.91	0.53
1:AO:12:ALA:HB2	1:JD:10:SER:N	2.22	0.53
1:BZ:37:LYS:NZ	1:BZ:40:ILE:O	2.42	0.53
1:CJ:57:PRO:HA	1:CJ:73:ASN:HA	1.90	0.53
1:CL:68:CYS:SG	1:FN:65:ALA:HA	2.47	0.53
1:CY:115:GLY:O	1:CZ:33:ARG:NH1	2.42	0.53
1:DL:14:LYS:NZ	1:DL:28:SER:HB2	2.24	0.53
1:DT:33:ARG:NH1	1:DU:115:GLY:O	2.40	0.53
1:DU:67:ALA:HA	1:FP:63:GLY:N	2.19	0.53
1:ED:35:ARG:NH1	1:ED:44:ASN:OD1	2.42	0.53
1:EP:33:ARG:NH1	1:EQ:115:GLY:O	2.42	0.53
1:FP:125:SER:HB2	1:FQ:5:MET:HE1	1.90	0.53
1:HE:93:LYS:NZ	1:HF:108:ALA:O	2.39	0.53
1:HS:36:VAL:N	1:HS:43:LEU:O	2.41	0.53
1:HT:22:ARG:NH1	1:HT:24:SER:OG	2.41	0.53
1:IO:101:ARG:HH12	1:IO:124:VAL:HG21	1.74	0.53
1:IW:87:GLU:OE1	1:IW:87:GLU:N	2.38	0.53
1:AO:128:THR:OG1	1:AP:1:ALA:O	2.24	0.53
1:BQ:71:MET:N	1:BQ:71:MET:SD	2.82	0.53
1:CK:124:VAL:HA	1:CL:4:PRO:HA	1.91	0.53
1:CK:125:SER:O	1:CL:2:ASN:ND2	2.39	0.53
1:DS:8:ILE:HA	1:II:116:PHE:HB2	1.91	0.53
1:DV:79:ARG:NH1	1:DV:79:ARG:HB2	2.24	0.53
1:EC:57:PRO:HA	1:EC:73:ASN:HA	1.90	0.53
1:EN:71:MET:N	1:EN:71:MET:SD	2.82	0.53
1:FJ:85:SER:OG	1:FK:74:GLU:OE1	2.19	0.53
1:FU:19:ASP:HB3	1:FU:22:ARG:O	2.08	0.53
1:GK:57:PRO:HA	1:GK:73:ASN:HA	1.90	0.53
1:GL:5:MET:HG2	1:GL:17:TRP:HB3	1.90	0.53
1:HC:37:LYS:NZ	1:HC:39:GLY:O	2.42	0.53
1:HE:123:ILE:HG22	1:HF:5:MET:HE2	1.90	0.53
1:HV:63:GLY:HA2	1:HX:67:ALA:O	2.08	0.53
1:IH:72:PRO:HG2	1:II:38:VAL:HG22	1.90	0.53
1:IL:5:MET:SD	1:IM:125:SER:HB2	2.47	0.53
1:JF:71:MET:SD	1:JF:71:MET:N	2.79	0.53
1:JH:49:GLN:OE1	1:JH:79:ARG:NH2	2.41	0.53
1:JJ:87:GLU:OE1	1:JJ:87:GLU:N	2.40	0.53
1:AK:128:THR:OG1	1:AL:1:ALA:O	2.26	0.53
1:AO:125:SER:O	1:AP:2:ASN:ND2	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:5:MET:SD	1:AR:125:SER:HB2	2.49	0.53
1:AV:5:MET:HB2	1:AV:18:SER:O	2.08	0.53
1:BR:68:CYS:HB2	1:FZ:64:CYS:SG	2.49	0.53
1:CI:125:SER:O	1:CJ:2:ASN:ND2	2.39	0.53
1:CN:5:MET:HB2	1:CN:18:SER:O	2.09	0.53
1:CT:106:LEU:HD11	1:CT:123:ILE:HD11	1.90	0.53
1:CY:128:THR:OG1	1:CZ:1:ALA:O	2.22	0.53
1:ED:60:LYS:NZ	1:ED:66:ASP:O	2.32	0.53
1:FF:65:ALA:HB1	1:FF:69:VAL:HB	1.91	0.53
1:FG:35:ARG:NH2	1:FG:42:GLU:HB3	2.23	0.53
1:FM:60:LYS:HA	1:FM:71:MET:HE2	1.90	0.53
1:GA:19:ASP:HB3	1:GA:22:ARG:O	2.09	0.53
1:GD:5:MET:HB3	1:GD:17:TRP:HB3	1.91	0.53
1:IF:117:LEU:HD21	1:IG:31:LEU:HD13	1.91	0.53
1:IF:125:SER:HB2	1:IG:5:MET:HE1	1.90	0.53
1:IR:20:PRO:HB3	1:IW:116:PHE:HE2	1.73	0.53
1:AF:5:MET:HB2	1:AF:18:SER:O	2.09	0.53
1:AF:68:CYS:SG	1:AF:69:VAL:HG13	2.49	0.53
1:AH:37:LYS:HA	1:AH:42:GLU:HA	1.90	0.53
1:AX:69:VAL:H	1:GY:64:CYS:N	2.06	0.53
1:BE:128:THR:OG1	1:BF:1:ALA:O	2.25	0.53
1:BN:5:MET:HB2	1:BN:18:SER:O	2.09	0.53
1:BX:56:ARG:O	1:BX:74:GLU:N	2.36	0.53
1:BY:125:SER:O	1:BZ:2:ASN:ND2	2.38	0.53
1:CH:67:ALA:C	1:HA:62:GLU:HA	2.29	0.53
1:CK:5:MET:HE1	1:CL:123:ILE:HG22	1.90	0.53
1:CM:72:PRO:HG2	1:CN:38:VAL:HG22	1.89	0.53
1:CV:68:CYS:SG	1:HL:65:ALA:HA	2.49	0.53
1:DJ:71:MET:N	1:DJ:71:MET:SD	2.82	0.53
1:ED:51:VAL:HG22	1:ED:79:ARG:HG2	1.90	0.53
1:EE:69:VAL:HG13	1:GU:64:CYS:HB2	1.91	0.53
1:EV:2:ASN:ND2	1:EW:125:SER:O	2.41	0.53
1:EV:66:ASP:OD2	1:EV:69:VAL:HG23	2.08	0.53
1:HM:19:ASP:HB3	1:HM:22:ARG:O	2.08	0.53
1:HT:14:LYS:NZ	1:HT:15:ILE:O	2.41	0.53
1:IG:56:ARG:O	1:IG:74:GLU:N	2.28	0.53
1:IP:55:LYS:NZ	1:IP:73:ASN:HB2	2.23	0.53
1:JC:123:ILE:HG22	1:JD:5:MET:HE1	1.90	0.53
1:AD:69:VAL:H	1:IV:64:CYS:N	2.06	0.53
1:AE:71:MET:N	1:AE:71:MET:SD	2.82	0.53
1:AL:98:THR:HG21	1:AL:126:SER:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:5:MET:HG3	1:BT:17:TRP:HB3	1.91	0.53
1:BY:128:THR:OG1	1:BZ:1:ALA:O	2.26	0.53
1:CO:60:LYS:HZ1	1:CO:66:ASP:H	1.56	0.53
1:CO:101:ARG:NH2	1:CP:2:ASN:HD22	2.07	0.53
1:EP:115:GLY:O	1:EQ:33:ARG:NH1	2.42	0.53
1:EW:74:GLU:HG2	1:EW:75:ASN:H	1.74	0.53
1:FT:22:ARG:NH1	1:FT:24:SER:OG	2.41	0.53
1:FX:57:PRO:HA	1:FX:73:ASN:HA	1.91	0.53
1:GN:87:GLU:OE1	1:GN:87:GLU:N	2.39	0.53
1:HL:128:THR:HA	1:HM:2:ASN:HA	1.89	0.53
1:HN:60:LYS:NZ	1:HN:69:VAL:O	2.35	0.53
1:IA:38:VAL:HG21	1:IA:43:LEU:HD22	1.90	0.53
1:IX:117:LEU:HD21	1:IZ:31:LEU:HD13	1.89	0.53
1:AL:57:PRO:HA	1:AL:73:ASN:HA	1.90	0.53
1:AR:55:LYS:NZ	1:AR:75:ASN:OD1	2.28	0.53
1:AW:57:PRO:HA	1:AW:73:ASN:HA	1.89	0.53
1:CA:34:GLN:O	1:CA:45:ASN:N	2.40	0.53
1:CJ:23:LEU:HD22	1:IK:44:ASN:ND2	2.23	0.53
1:DV:125:SER:O	1:DW:2:ASN:ND2	2.38	0.53
1:EJ:14:LYS:NZ	1:EJ:28:SER:HB2	2.24	0.53
1:ES:87:GLU:OE1	1:ES:87:GLU:N	2.40	0.53
1:EU:5:MET:N	1:EU:5:MET:SD	2.82	0.53
1:EX:44:ASN:N	1:EX:87:GLU:OE2	2.34	0.53
1:FB:56:ARG:O	1:FB:74:GLU:N	2.34	0.53
1:FB:66:ASP:OD2	1:FB:69:VAL:HG23	2.07	0.53
1:FR:93:LYS:O	1:FR:97:GLU:HG2	2.09	0.53
1:GH:14:LYS:HZ1	1:GH:28:SER:HB2	1.73	0.53
1:IC:35:ARG:NH2	1:IC:42:GLU:HB3	2.23	0.53
1:IP:74:GLU:OE2	1:IQ:85:SER:OG	2.22	0.53
1:AD:67:ALA:C	1:IV:65:ALA:HB2	2.29	0.53
1:AO:17:TRP:CD2	1:AP:123:ILE:HG13	2.44	0.53
1:BI:37:LYS:HA	1:BI:37:LYS:HE3	1.90	0.53
1:CL:67:ALA:C	1:FN:65:ALA:HB2	2.28	0.53
1:DE:57:PRO:HA	1:DE:73:ASN:HA	1.91	0.53
1:DM:67:ALA:HA	1:FB:63:GLY:N	2.19	0.53
1:DU:55:LYS:NZ	1:DU:75:ASN:OD1	2.27	0.53
1:EE:56:ARG:O	1:EE:74:GLU:N	2.37	0.53
1:EF:115:GLY:O	1:EG:33:ARG:NH1	2.42	0.53
1:EG:67:ALA:C	1:HX:65:ALA:HB2	2.29	0.53
1:EO:56:ARG:O	1:EO:74:GLU:N	2.35	0.53
1:EY:38:VAL:HG21	1:EY:43:LEU:HD22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FA:5:MET:N	1:FA:5:MET:SD	2.82	0.53
1:FU:60:LYS:HE2	1:FU:64:CYS:HB3	1.90	0.53
1:FZ:85:SER:OG	1:GA:74:GLU:OE1	2.19	0.53
1:GO:117:LEU:HD21	1:GP:31:LEU:HD13	1.90	0.53
1:HE:22:ARG:NH1	1:HE:24:SER:OG	2.42	0.53
1:HF:38:VAL:HG21	1:HF:43:LEU:HD22	1.91	0.53
1:HQ:32:LEU:HB3	1:HQ:47:SER:HB3	1.91	0.53
1:IP:93:LYS:NZ	1:IQ:108:ALA:O	2.39	0.53
1:JE:45:ASN:HA	1:JE:85:SER:HA	1.91	0.53
1:AO:5:MET:HE1	1:AP:123:ILE:HG22	1.91	0.53
1:AQ:5:MET:HE1	1:AR:123:ILE:HG22	1.91	0.53
1:AU:101:ARG:NH2	1:AV:2:ASN:HD22	2.07	0.53
1:BK:5:MET:SD	1:BL:125:SER:HB2	2.49	0.53
1:BN:37:LYS:HA	1:BN:42:GLU:HA	1.90	0.53
1:BN:37:LYS:NZ	1:BN:40:ILE:O	2.42	0.53
1:BX:5:MET:HB2	1:BX:18:SER:O	2.09	0.53
1:BX:67:ALA:C	1:JI:62:GLU:HA	2.29	0.53
1:BY:107:PHE:HA	1:BY:112:ALA:HB3	1.91	0.53
1:CI:35:ARG:NH1	1:CI:44:ASN:OD1	2.42	0.53
1:CT:5:MET:HB2	1:CT:18:SER:O	2.09	0.53
1:CV:101:ARG:CZ	1:CV:124:VAL:HG21	2.39	0.53
1:CX:6:GLN:HE22	1:FM:111:ASN:HB2	1.74	0.53
1:DF:71:MET:N	1:DF:71:MET:SD	2.83	0.53
1:DH:72:PRO:HG2	1:DI:38:VAL:HG22	1.91	0.53
1:DP:72:PRO:HG2	1:DQ:38:VAL:HG22	1.90	0.53
1:DX:105:THR:O	1:DX:109:SER:OG	2.27	0.53
1:EJ:3:LYS:NZ	1:EK:129:THR:HG23	2.24	0.53
1:EL:1:ALA:HB1	1:EM:128:THR:HG23	1.91	0.53
1:EM:61:PRO:HB2	1:EM:64:CYS:HB3	1.91	0.53
1:ER:93:LYS:NZ	1:ES:108:ALA:O	2.39	0.53
1:FO:60:LYS:HE2	1:FO:64:CYS:HB3	1.90	0.53
1:FQ:19:ASP:HB3	1:FQ:22:ARG:O	2.09	0.53
1:IB:22:ARG:NH1	1:IB:24:SER:OG	2.41	0.53
1:IT:71:MET:N	1:IT:71:MET:SD	2.82	0.53
1:AK:124:VAL:HA	1:AL:4:PRO:HA	1.91	0.52
1:AN:5:MET:HB2	1:AN:18:SER:O	2.09	0.52
1:AT:61:PRO:HB2	1:AT:64:CYS:HB3	1.90	0.52
1:AW:5:MET:SD	1:AX:125:SER:HB2	2.49	0.52
1:BD:5:MET:HB2	1:BD:18:SER:O	2.09	0.52
1:BD:6:GLN:HE22	1:GE:111:ASN:HB2	1.73	0.52
1:BK:3:LYS:HZ2	1:BL:129:THR:HG23	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:61:PRO:HB2	1:BN:64:CYS:HB3	1.91	0.52
1:BQ:79:ARG:HB2	1:BQ:79:ARG:NH1	2.24	0.52
1:BY:79:ARG:NH1	1:BY:79:ARG:HB2	2.24	0.52
1:CH:101:ARG:CZ	1:CH:124:VAL:HG21	2.40	0.52
1:CK:128:THR:OG1	1:CL:1:ALA:O	2.26	0.52
1:CY:5:MET:SD	1:CY:5:MET:N	2.83	0.52
1:DF:51:VAL:HG22	1:DF:79:ARG:HG2	1.91	0.52
1:EF:125:SER:O	1:EG:2:ASN:ND2	2.41	0.52
1:EO:5:MET:HB2	1:EO:18:SER:O	2.09	0.52
1:EO:61:PRO:HB2	1:EO:64:CYS:HB3	1.91	0.52
1:EQ:5:MET:HG3	1:EQ:17:TRP:HB3	1.91	0.52
1:EU:60:LYS:HA	1:EU:71:MET:SD	2.49	0.52
1:FB:125:SER:HB2	1:FC:5:MET:HE1	1.90	0.52
1:FF:60:LYS:HE3	1:FF:65:ALA:O	2.09	0.52
1:FQ:60:LYS:NZ	1:FQ:65:ALA:O	2.30	0.52
1:FV:31:LEU:HD12	1:FW:117:LEU:HD22	1.90	0.52
1:GB:60:LYS:NZ	1:GB:69:VAL:O	2.34	0.52
1:GT:38:VAL:HB	1:GT:41:ALA:HB3	1.91	0.52
1:HA:5:MET:HG2	1:HA:17:TRP:HB3	1.91	0.52
1:HT:93:LYS:NZ	1:HU:108:ALA:O	2.40	0.52
1:HX:56:ARG:O	1:HX:74:GLU:N	2.37	0.52
1:IE:98:THR:HG21	1:IE:126:SER:HA	1.90	0.52
1:IF:5:MET:SD	1:IG:125:SER:HB2	2.49	0.52
1:IR:36:VAL:HG23	1:IR:43:LEU:HB2	1.91	0.52
1:AH:57:PRO:HA	1:AH:73:ASN:HA	1.90	0.52
1:AO:105:THR:O	1:AO:109:SER:OG	2.28	0.52
1:BO:3:LYS:HZ2	1:BP:129:THR:HG23	1.75	0.52
1:BW:71:MET:N	1:BW:71:MET:SD	2.82	0.52
1:CB:61:PRO:HB2	1:CB:64:CYS:HB3	1.90	0.52
1:CE:5:MET:HE1	1:CF:123:ILE:HG22	1.92	0.52
1:CK:34:GLN:O	1:CK:45:ASN:N	2.42	0.52
1:CU:71:MET:N	1:CU:71:MET:SD	2.82	0.52
1:DB:5:MET:HB2	1:DB:18:SER:O	2.09	0.52
1:DC:115:GLY:O	1:DE:33:ARG:NH1	2.42	0.52
1:DG:5:MET:HB2	1:DG:18:SER:O	2.09	0.52
1:DH:128:THR:OG1	1:DI:1:ALA:O	2.23	0.52
1:DL:3:LYS:NZ	1:DM:129:THR:HG23	2.24	0.52
1:EA:5:MET:HB2	1:EA:18:SER:O	2.09	0.52
1:EB:5:MET:SD	1:EC:125:SER:HB2	2.49	0.52
1:EF:88:ASN:ND2	1:EG:74:GLU:OE2	2.28	0.52
1:FD:14:LYS:HZ1	1:FD:28:SER:HB2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FF:33:ARG:HD2	1:FG:115:GLY:HA3	1.91	0.52
1:FH:43:LEU:HD12	1:FH:85:SER:HB3	1.91	0.52
1:FJ:2:ASN:ND2	1:FK:125:SER:O	2.42	0.52
1:GS:123:ILE:HG22	1:GT:5:MET:HE1	1.91	0.52
1:GZ:19:ASP:HB3	1:GZ:22:ARG:O	2.09	0.52
1:HA:22:ARG:NH1	1:HA:24:SER:OG	2.42	0.52
1:HJ:125:SER:O	1:HK:2:ASN:ND2	2.30	0.52
1:HN:35:ARG:NH1	1:HN:43:LEU:O	2.41	0.52
1:HX:115:GLY:O	1:HY:33:ARG:NH1	2.43	0.52
1:IA:19:ASP:HB3	1:IA:22:ARG:O	2.09	0.52
1:IV:115:GLY:O	1:IW:33:ARG:NH1	2.42	0.52
1:IX:2:ASN:ND2	1:IZ:125:SER:O	2.41	0.52
1:AG:101:ARG:NH2	1:AH:2:ASN:HD22	2.07	0.52
1:AN:49:GLN:OE1	1:AN:79:ARG:NH2	2.33	0.52
1:AO:5:MET:SD	1:AP:125:SER:HB2	2.49	0.52
1:BC:101:ARG:NH2	1:BD:2:ASN:HD22	2.07	0.52
1:BH:60:LYS:HZ1	1:BH:65:ALA:H	1.55	0.52
1:BT:55:LYS:NZ	1:BT:75:ASN:OD1	2.28	0.52
1:BU:128:THR:OG1	1:BV:1:ALA:O	2.26	0.52
1:CG:35:ARG:NH1	1:CG:44:ASN:OD1	2.43	0.52
1:CW:125:SER:O	1:CX:2:ASN:ND2	2.40	0.52
1:DC:128:THR:OG1	1:DE:1:ALA:O	2.26	0.52
1:DI:69:VAL:HG13	1:FH:64:CYS:SG	2.49	0.52
1:DZ:5:MET:SD	1:DZ:5:MET:N	2.82	0.52
1:EL:71:MET:N	1:EL:71:MET:SD	2.83	0.52
1:ET:124:VAL:HA	1:EU:4:PRO:HA	1.91	0.52
1:FB:93:LYS:NZ	1:FC:108:ALA:O	2.40	0.52
1:FD:5:MET:HB2	1:FD:18:SER:O	2.08	0.52
1:FH:74:GLU:OE2	1:FI:88:ASN:ND2	2.42	0.52
1:FN:22:ARG:NH1	1:FN:24:SER:OG	2.42	0.52
1:FP:2:ASN:ND2	1:FQ:125:SER:O	2.42	0.52
1:FS:33:ARG:HH12	1:FT:8:ILE:HG23	1.75	0.52
1:FS:71:MET:N	1:FS:71:MET:SD	2.80	0.52
1:GO:34:GLN:NE2	1:GO:45:ASN:OD1	2.41	0.52
1:HT:101:ARG:HH21	1:HT:124:VAL:HG21	1.74	0.52
1:IB:116:PHE:CE1	1:ID:6:GLN:HB2	2.44	0.52
1:IP:125:SER:HB2	1:IQ:5:MET:HE1	1.91	0.52
1:AC:101:ARG:NH2	1:AD:2:ASN:HD22	2.07	0.52
1:AH:66:ASP:OD1	1:JE:64:CYS:HA	2.10	0.52
1:AW:128:THR:O	1:AX:3:LYS:NZ	2.37	0.52
1:BE:115:GLY:O	1:BF:33:ARG:NH1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:14:LYS:NZ	1:BM:28:SER:HB2	2.25	0.52
1:BM:60:LYS:NZ	1:BM:66:ASP:H	2.07	0.52
1:CA:30:SER:HB3	1:CA:49:GLN:HB3	1.91	0.52
1:CP:67:ALA:C	1:IP:65:ALA:HB2	2.30	0.52
1:CR:98:THR:HG21	1:CR:126:SER:HA	1.90	0.52
1:DE:101:ARG:CZ	1:DE:124:VAL:HG21	2.39	0.52
1:DN:115:GLY:O	1:DO:33:ARG:NH1	2.42	0.52
1:DP:115:GLY:O	1:DQ:33:ARG:NH1	2.43	0.52
1:DV:71:MET:SD	1:DV:71:MET:N	2.82	0.52
1:EA:37:LYS:HA	1:EA:42:GLU:HA	1.91	0.52
1:FR:5:MET:HE1	1:FS:123:ILE:HG22	1.92	0.52
1:GP:60:LYS:NZ	1:GP:65:ALA:O	2.32	0.52
1:HK:58:ALA:HB3	1:HK:71:MET:HG3	1.92	0.52
1:HX:22:ARG:NH1	1:HX:24:SER:OG	2.42	0.52
1:IR:61:PRO:HG2	1:IR:64:CYS:SG	2.50	0.52
1:AD:69:VAL:HG13	1:IV:64:CYS:SG	2.49	0.52
1:AS:101:ARG:NH2	1:AT:2:ASN:HD22	2.07	0.52
1:AT:37:LYS:NZ	1:AT:40:ILE:O	2.42	0.52
1:BI:107:PHE:HA	1:BI:112:ALA:HB3	1.91	0.52
1:BL:55:LYS:NZ	1:BL:75:ASN:OD1	2.28	0.52
1:BY:60:LYS:NZ	1:BY:66:ASP:O	2.24	0.52
1:CC:101:ARG:NH2	1:CD:2:ASN:HD22	2.07	0.52
1:CO:3:LYS:NZ	1:CP:129:THR:HG23	2.24	0.52
1:CY:13:ASN:ND2	1:CY:31:LEU:O	2.42	0.52
1:DR:3:LYS:HZ2	1:DS:129:THR:HG23	1.75	0.52
1:EE:5:MET:HB2	1:EE:18:SER:O	2.09	0.52
1:EM:60:LYS:HZ1	1:EM:65:ALA:H	1.56	0.52
1:FF:61:PRO:HG2	1:FF:64:CYS:SG	2.48	0.52
1:GE:32:LEU:HB3	1:GE:47:SER:HB3	1.90	0.52
1:GM:93:LYS:NZ	1:GN:108:ALA:O	2.39	0.52
1:HC:5:MET:HB2	1:HC:18:SER:O	2.09	0.52
1:HU:5:MET:HB3	1:HU:17:TRP:HB3	1.92	0.52
1:HU:19:ASP:HB3	1:HU:22:ARG:O	2.10	0.52
1:IG:60:LYS:HD3	1:IG:64:CYS:HB3	1.90	0.52
1:JI:1:ALA:O	1:JJ:129:THR:N	2.35	0.52
1:AQ:79:ARG:NH1	1:AQ:79:ARG:HB2	2.24	0.52
1:AW:71:MET:N	1:AW:71:MET:SD	2.83	0.52
1:BE:34:GLN:O	1:BE:45:ASN:N	2.42	0.52
1:BH:49:GLN:OE1	1:BH:79:ARG:NH2	2.33	0.52
1:BO:117:LEU:HD21	1:BP:31:LEU:HD13	1.91	0.52
1:BV:66:ASP:OD1	1:GH:64:CYS:HA	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:5:MET:SD	1:CL:125:SER:HB2	2.49	0.52
1:CM:71:MET:N	1:CM:71:MET:SD	2.82	0.52
1:CO:14:LYS:NZ	1:CO:28:SER:HB2	2.25	0.52
1:CP:60:LYS:HZ1	1:CP:65:ALA:HB3	1.74	0.52
1:CP:68:CYS:SG	1:IP:65:ALA:HA	2.50	0.52
1:DZ:88:ASN:ND2	1:EA:74:GLU:OE2	2.29	0.52
1:FH:14:LYS:HZ1	1:FH:28:SER:HB2	1.74	0.52
1:FI:56:ARG:O	1:FI:74:GLU:N	2.27	0.52
1:FZ:14:LYS:NZ	1:FZ:15:ILE:O	2.43	0.52
1:GO:3:LYS:NZ	1:GO:21:THR:OG1	2.29	0.52
1:HN:85:SER:OG	1:HO:74:GLU:OE1	2.19	0.52
1:IJ:15:ILE:HD13	1:IK:117:LEU:HD11	1.90	0.52
1:JE:35:ARG:HH22	1:JE:44:ASN:HA	1.74	0.52
1:AL:106:LEU:HD21	1:AL:123:ILE:HD11	1.91	0.52
1:AY:34:GLN:O	1:AY:45:ASN:N	2.42	0.52
1:AY:125:SER:O	1:AZ:2:ASN:ND2	2.37	0.52
1:BK:71:MET:N	1:BK:71:MET:SD	2.82	0.52
1:BR:101:ARG:CZ	1:BR:124:VAL:HG21	2.40	0.52
1:BS:125:SER:O	1:BT:2:ASN:ND2	2.40	0.52
1:DM:23:LEU:HD22	1:FC:44:ASN:ND2	2.25	0.52
1:DO:5:MET:HB2	1:DO:18:SER:O	2.09	0.52
1:DO:49:GLN:OE1	1:DO:79:ARG:NH2	2.33	0.52
1:DX:72:PRO:HG2	1:DY:38:VAL:HG22	1.91	0.52
1:EB:107:PHE:HA	1:EB:112:ALA:HB3	1.92	0.52
1:ED:71:MET:SD	1:ED:71:MET:N	2.82	0.52
1:EF:124:VAL:HA	1:EG:4:PRO:HA	1.90	0.52
1:FI:19:ASP:HB3	1:FI:22:ARG:O	2.09	0.52
1:FM:51:VAL:HG22	1:FM:79:ARG:HG2	1.92	0.52
1:FP:20:PRO:HB3	1:FU:116:PHE:HE2	1.74	0.52
1:GK:111:ASN:HB2	1:GK:116:PHE:HB2	1.91	0.52
1:HS:71:MET:N	1:HS:71:MET:SD	2.80	0.52
1:IT:93:LYS:O	1:IT:97:GLU:HG2	2.10	0.52
1:AA:107:PHE:HA	1:AA:112:ALA:HB3	1.91	0.52
1:AD:68:CYS:SG	1:IV:65:ALA:HA	2.50	0.52
1:AG:72:PRO:HG2	1:AH:38:VAL:HG22	1.92	0.52
1:AN:69:VAL:H	1:JC:64:CYS:H	1.57	0.52
1:AT:57:PRO:HA	1:AT:73:ASN:HA	1.92	0.52
1:BF:68:CYS:HB3	1:HW:61:PRO:HB2	1.90	0.52
1:BJ:67:ALA:CA	1:HZ:63:GLY:H	2.22	0.52
1:BM:101:ARG:NH2	1:BN:2:ASN:HD22	2.08	0.52
1:BT:6:GLN:HE22	1:FS:111:ASN:HB2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:72:PRO:HG2	1:CD:38:VAL:HG22	1.92	0.52
1:CS:5:MET:HE1	1:CT:123:ILE:HG22	1.91	0.52
1:CV:67:ALA:H	1:HL:65:ALA:H	1.58	0.52
1:EF:5:MET:HE1	1:EG:123:ILE:HG22	1.90	0.52
1:EN:72:PRO:HG2	1:EO:38:VAL:HG22	1.92	0.52
1:ER:74:GLU:OE2	1:ES:88:ASN:ND2	2.43	0.52
1:FL:63:GLY:HA2	1:FN:67:ALA:O	2.10	0.52
1:FN:5:MET:SD	1:FO:125:SER:HB2	2.50	0.52
1:FR:88:ASN:ND2	1:FS:56:ARG:HD2	2.25	0.52
1:FW:87:GLU:OE1	1:FW:87:GLU:N	2.42	0.52
1:GK:87:GLU:OE1	1:GK:87:GLU:N	2.41	0.52
1:GO:7:PRO:HA	1:GO:17:TRP:HA	1.92	0.52
1:HX:5:MET:SD	1:HY:125:SER:HB2	2.50	0.52
1:IB:36:VAL:N	1:IB:43:LEU:O	2.33	0.52
1:IC:71:MET:SD	1:IC:71:MET:N	2.78	0.52
1:IQ:71:MET:SD	1:IQ:71:MET:N	2.80	0.52
1:AF:68:CYS:H	1:GS:65:ALA:H	1.56	0.52
1:AO:107:PHE:HA	1:AO:112:ALA:HB3	1.91	0.52
1:AX:5:MET:HB2	1:AX:18:SER:O	2.10	0.52
1:BC:107:PHE:HA	1:BC:112:ALA:HB3	1.92	0.52
1:CP:67:ALA:H	1:IP:65:ALA:H	1.57	0.52
1:CU:79:ARG:NH1	1:CU:79:ARG:HB2	2.24	0.52
1:DQ:5:MET:HB2	1:DQ:18:SER:O	2.10	0.52
1:EA:8:ILE:HA	1:HK:116:PHE:HB2	1.90	0.52
1:EB:71:MET:N	1:EB:71:MET:SD	2.82	0.52
1:EH:35:ARG:NH1	1:EH:44:ASN:OD1	2.43	0.52
1:EI:5:MET:HB2	1:EI:18:SER:O	2.10	0.52
1:EN:88:ASN:ND2	1:EO:74:GLU:OE2	2.28	0.52
1:ET:33:ARG:NH1	1:EU:115:GLY:O	2.43	0.52
1:EX:35:ARG:HH22	1:EX:43:LEU:N	2.08	0.52
1:EZ:5:MET:HB3	1:EZ:17:TRP:HB3	1.91	0.52
1:FR:111:ASN:HB2	1:FR:116:PHE:HB2	1.92	0.52
1:GA:105:THR:HG23	1:GA:106:LEU:HD12	1.92	0.52
1:GF:60:LYS:HB3	1:GF:65:ALA:HB2	1.91	0.52
1:GS:22:ARG:NH1	1:GS:24:SER:OG	2.43	0.52
1:HD:71:MET:SD	1:HD:71:MET:N	2.83	0.52
1:HE:5:MET:SD	1:HF:125:SER:HB2	2.50	0.52
1:HG:5:MET:HE1	1:HI:123:ILE:HG22	1.90	0.52
1:HQ:74:GLU:HG2	1:HQ:75:ASN:H	1.75	0.52
1:HR:115:GLY:HA2	1:HS:31:LEU:HD23	1.92	0.52
1:HV:85:SER:OG	1:HW:74:GLU:OE1	2.19	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HX:85:SER:OG	1:HY:74:GLU:OE1	2.19	0.52
1:IQ:22:ARG:NH2	1:IQ:55:LYS:O	2.40	0.52
1:JD:19:ASP:HB3	1:JD:22:ARG:O	2.10	0.52
1:JD:87:GLU:OE1	1:JD:87:GLU:N	2.41	0.52
1:AN:68:CYS:N	1:JC:65:ALA:H	2.08	0.52
1:AS:14:LYS:NZ	1:AS:28:SER:HB2	2.25	0.52
1:AT:34:GLN:NE2	1:AT:35:ARG:O	2.43	0.52
1:BD:68:CYS:HB2	1:GE:64:CYS:HA	1.91	0.52
1:BN:57:PRO:HA	1:BN:73:ASN:HA	1.92	0.52
1:BO:14:LYS:NZ	1:BO:28:SER:HB2	2.25	0.52
1:BR:5:MET:HB2	1:BR:18:SER:O	2.10	0.52
1:BV:57:PRO:HA	1:BV:73:ASN:HA	1.93	0.52
1:CD:5:MET:HB2	1:CD:18:SER:O	2.09	0.52
1:CE:5:MET:SD	1:CF:125:SER:HB2	2.49	0.52
1:CG:88:ASN:ND2	1:CH:74:GLU:OE2	2.36	0.52
1:CX:37:LYS:NZ	1:CX:40:ILE:O	2.43	0.52
1:DC:107:PHE:HA	1:DC:112:ALA:HB3	1.92	0.52
1:DI:56:ARG:O	1:DI:74:GLU:N	2.40	0.52
1:DL:101:ARG:CZ	1:DL:124:VAL:HG21	2.40	0.52
1:EE:67:ALA:HA	1:GU:63:GLY:N	2.22	0.52
1:EG:68:CYS:SG	1:HX:65:ALA:HA	2.50	0.52
1:EZ:57:PRO:HA	1:EZ:73:ASN:HA	1.92	0.52
1:FT:74:GLU:OE1	1:FU:88:ASN:ND2	2.43	0.52
1:GZ:60:LYS:HG2	1:GZ:71:MET:HE1	1.92	0.52
1:ID:66:ASP:OD1	1:ID:69:VAL:HG23	2.10	0.52
1:IR:101:ARG:HH21	1:IR:124:VAL:HG21	1.75	0.52
1:AQ:71:MET:N	1:AQ:71:MET:SD	2.83	0.51
1:BC:115:GLY:O	1:BD:33:ARG:NH1	2.43	0.51
1:BM:88:ASN:ND2	1:BN:74:GLU:OE2	2.29	0.51
1:CP:5:MET:HB2	1:CP:18:SER:O	2.10	0.51
1:CT:67:ALA:HB1	1:HR:64:CYS:HA	1.91	0.51
1:CX:5:MET:HG3	1:CX:17:TRP:HB3	1.91	0.51
1:DF:101:ARG:NH2	1:DG:2:ASN:HD22	2.08	0.51
1:EJ:107:PHE:HA	1:EJ:112:ALA:HB3	1.92	0.51
1:ER:117:LEU:HD21	1:ES:31:LEU:HD13	1.92	0.51
1:GW:22:ARG:NH1	1:GW:24:SER:OG	2.43	0.51
1:HF:60:LYS:NZ	1:HF:66:ASP:O	2.42	0.51
1:HG:60:LYS:HA	1:HG:71:MET:HE1	1.92	0.51
1:HM:37:LYS:HD3	1:HM:42:GLU:OE2	2.09	0.51
1:IF:60:LYS:NZ	1:IF:69:VAL:O	2.40	0.51
1:IL:86:ALA:HB1	1:IM:114:LEU:HD23	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IP:22:ARG:NH1	1:IP:24:SER:OG	2.43	0.51
1:JJ:19:ASP:HB3	1:JJ:22:ARG:O	2.10	0.51
1:AG:60:LYS:NZ	1:AG:66:ASP:O	2.42	0.51
1:BC:72:PRO:HG2	1:BD:38:VAL:HG22	1.92	0.51
1:BH:6:GLN:HE22	1:HQ:111:ASN:HB2	1.75	0.51
1:CJ:5:MET:HB2	1:CJ:18:SER:O	2.10	0.51
1:CS:72:PRO:HG2	1:CT:38:VAL:HG22	1.93	0.51
1:CZ:67:ALA:HA	1:ID:63:GLY:N	2.18	0.51
1:DL:3:LYS:HZ2	1:DM:129:THR:HG23	1.75	0.51
1:DP:105:THR:O	1:DP:109:SER:OG	2.29	0.51
1:DU:57:PRO:HA	1:DU:73:ASN:HA	1.92	0.51
1:DZ:101:ARG:NH2	1:EA:2:ASN:HD22	2.08	0.51
1:EL:5:MET:HE1	1:EM:123:ILE:HG22	1.92	0.51
1:FB:22:ARG:NH1	1:FB:24:SER:OG	2.43	0.51
1:FC:19:ASP:HB3	1:FC:22:ARG:O	2.11	0.51
1:FH:98:THR:HG23	1:FH:101:ARG:HH21	1.75	0.51
1:GF:117:LEU:HD21	1:GG:31:LEU:HD13	1.91	0.51
1:HN:117:LEU:HD21	1:HO:31:LEU:HD13	1.93	0.51
1:HV:55:LYS:NZ	1:HV:75:ASN:OD1	2.30	0.51
1:IF:3:LYS:HZ3	1:IG:127:ASP:HB3	1.74	0.51
1:IH:35:ARG:HD2	1:IH:44:ASN:HB3	1.91	0.51
1:IZ:56:ARG:O	1:IZ:74:GLU:N	2.30	0.51
1:JC:128:THR:HA	1:JD:2:ASN:HA	1.93	0.51
1:JI:22:ARG:NH1	1:JI:24:SER:OG	2.43	0.51
1:AA:35:ARG:NH1	1:AA:44:ASN:OD1	2.44	0.51
1:AB:5:MET:HB2	1:AB:18:SER:O	2.10	0.51
1:AC:125:SER:O	1:AD:2:ASN:ND2	2.43	0.51
1:AH:5:MET:HB2	1:AH:18:SER:O	2.10	0.51
1:AP:74:GLU:OE2	1:AP:76:GLN:NE2	2.33	0.51
1:AY:115:GLY:O	1:AZ:33:ARG:NH1	2.43	0.51
1:AZ:60:LYS:NZ	1:AZ:65:ALA:H	2.07	0.51
1:BA:101:ARG:CZ	1:BA:124:VAL:HG21	2.40	0.51
1:CL:57:PRO:HA	1:CL:73:ASN:HA	1.91	0.51
1:CP:69:VAL:H	1:IP:64:CYS:N	2.07	0.51
1:DF:35:ARG:NH1	1:DF:44:ASN:OD1	2.43	0.51
1:DK:37:LYS:HA	1:DK:42:GLU:HA	1.92	0.51
1:EK:67:ALA:HA	1:EV:63:GLY:N	2.19	0.51
1:FD:117:LEU:HD21	1:FE:31:LEU:HD13	1.91	0.51
1:FI:87:GLU:OE1	1:FI:87:GLU:N	2.40	0.51
1:FL:5:MET:HG3	1:FL:19:ASP:HA	1.93	0.51
1:GP:105:THR:HG23	1:GP:106:LEU:HD12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HF:19:ASP:HB3	1:HF:22:ARG:O	2.11	0.51
1:JE:22:ARG:NH1	1:JE:24:SER:OG	2.43	0.51
1:JE:36:VAL:HG23	1:JE:43:LEU:HB2	1.93	0.51
1:AJ:5:MET:HB2	1:AJ:18:SER:O	2.10	0.51
1:AO:72:PRO:HG2	1:AP:38:VAL:HG22	1.92	0.51
1:AP:5:MET:HB2	1:AP:18:SER:O	2.11	0.51
1:BF:5:MET:HG3	1:BF:17:TRP:HB3	1.90	0.51
1:BZ:5:MET:HB2	1:BZ:18:SER:O	2.10	0.51
1:CC:107:PHE:HA	1:CC:112:ALA:HB3	1.92	0.51
1:CN:93:LYS:O	1:CN:96:TRP:HB3	2.10	0.51
1:CP:23:LEU:HD22	1:IQ:44:ASN:ND2	2.25	0.51
1:CS:101:ARG:NH2	1:CT:2:ASN:HD22	2.08	0.51
1:DB:60:LYS:NZ	1:DB:64:CYS:SG	2.70	0.51
1:DC:34:GLN:O	1:DC:45:ASN:N	2.41	0.51
1:DJ:1:ALA:HB1	1:DK:128:THR:HG23	1.93	0.51
1:DJ:87:GLU:HG3	1:DK:59:PRO:HG3	1.91	0.51
1:EU:101:ARG:HH12	1:EU:124:VAL:HG21	1.76	0.51
1:EW:22:ARG:NH2	1:EW:55:LYS:O	2.40	0.51
1:EY:87:GLU:OE1	1:EY:87:GLU:N	2.40	0.51
1:FC:22:ARG:NH2	1:FC:55:LYS:O	2.39	0.51
1:FI:57:PRO:HA	1:FI:73:ASN:HA	1.92	0.51
1:GP:22:ARG:NH2	1:GP:55:LYS:O	2.40	0.51
1:HG:128:THR:HA	1:HI:2:ASN:HA	1.92	0.51
1:HS:19:ASP:HB3	1:HS:22:ARG:O	2.11	0.51
1:HT:3:LYS:HZ1	1:HU:129:THR:HG23	1.74	0.51
1:HY:87:GLU:OE1	1:HY:87:GLU:N	2.39	0.51
1:IQ:35:ARG:NH2	1:IQ:43:LEU:O	2.43	0.51
1:IR:31:LEU:HD12	1:IS:117:LEU:HD22	1.91	0.51
1:JC:22:ARG:NH1	1:JC:24:SER:OG	2.44	0.51
1:AK:5:MET:SD	1:AK:5:MET:N	2.83	0.51
1:AP:8:ILE:HA	1:HD:116:PHE:HB2	1.92	0.51
1:AR:5:MET:HB2	1:AR:18:SER:O	2.10	0.51
1:BA:105:THR:O	1:BA:109:SER:OG	2.28	0.51
1:BO:72:PRO:HG2	1:BP:38:VAL:HG22	1.93	0.51
1:BP:5:MET:HB2	1:BP:18:SER:O	2.11	0.51
1:BR:106:LEU:HD21	1:BR:123:ILE:HD11	1.92	0.51
1:CI:107:PHE:HA	1:CI:112:ALA:HB3	1.91	0.51
1:CV:5:MET:HB2	1:CV:18:SER:O	2.10	0.51
1:DL:71:MET:N	1:DL:71:MET:SD	2.84	0.51
1:DM:5:MET:HB2	1:DM:18:SER:O	2.11	0.51
1:DY:60:LYS:HZ1	1:DY:65:ALA:H	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EN:101:ARG:NH2	1:EO:2:ASN:HD22	2.08	0.51
1:EW:19:ASP:HB3	1:EW:22:ARG:O	2.10	0.51
1:EX:86:ALA:HB1	1:EY:114:LEU:HD23	1.90	0.51
1:GL:56:ARG:O	1:GL:74:GLU:N	2.25	0.51
1:HE:92:LEU:HD13	1:HE:95:GLU:OE2	2.11	0.51
1:HG:123:ILE:HG22	1:HI:5:MET:HE2	1.92	0.51
1:HZ:93:LYS:NZ	1:IA:108:ALA:O	2.40	0.51
1:ID:98:THR:HG23	1:ID:101:ARG:HH21	1.76	0.51
1:IM:37:LYS:HD3	1:IM:42:GLU:OE2	2.10	0.51
1:IQ:19:ASP:HB3	1:IQ:22:ARG:O	2.11	0.51
1:AA:128:THR:OG1	1:AB:1:ALA:O	2.26	0.51
1:AM:107:PHE:HA	1:AM:112:ALA:HB3	1.92	0.51
1:AS:60:LYS:NZ	1:AS:66:ASP:H	2.09	0.51
1:BA:5:MET:SD	1:BB:125:SER:HB2	2.51	0.51
1:BG:72:PRO:HG2	1:BH:38:VAL:HG22	1.93	0.51
1:BH:5:MET:HB2	1:BH:18:SER:O	2.10	0.51
1:BV:5:MET:HB2	1:BV:18:SER:O	2.11	0.51
1:CA:5:MET:HE1	1:CB:123:ILE:HG22	1.92	0.51
1:CM:101:ARG:NH2	1:CN:2:ASN:HD22	2.09	0.51
1:CO:71:MET:N	1:CO:71:MET:SD	2.84	0.51
1:DH:105:THR:O	1:DH:109:SER:OG	2.28	0.51
1:DI:67:ALA:C	1:FH:65:ALA:HB2	2.30	0.51
1:EB:72:PRO:HG2	1:EC:38:VAL:HG22	1.93	0.51
1:ED:101:ARG:NH2	1:EE:2:ASN:HD22	2.08	0.51
1:EM:5:MET:HB2	1:EM:18:SER:O	2.11	0.51
1:EW:35:ARG:NH2	1:EW:43:LEU:O	2.44	0.51
1:FC:35:ARG:NH2	1:FC:43:LEU:O	2.44	0.51
1:GB:5:MET:HG2	1:GB:18:SER:C	2.31	0.51
1:GG:105:THR:HG23	1:GG:106:LEU:HD12	1.91	0.51
1:GS:35:ARG:NH2	1:GS:44:ASN:OD1	2.44	0.51
1:HB:57:PRO:HA	1:HB:73:ASN:HA	1.93	0.51
1:HK:43:LEU:HD12	1:HK:85:SER:HB2	1.92	0.51
1:HW:33:ARG:HH12	1:HX:8:ILE:HG23	1.75	0.51
1:IF:22:ARG:NH1	1:IF:24:SER:OG	2.44	0.51
1:IZ:8:ILE:N	1:IZ:16:VAL:O	2.39	0.51
1:JA:22:ARG:NH1	1:JA:24:SER:OG	2.44	0.51
1:JB:36:VAL:HG23	1:JB:43:LEU:HB2	1.93	0.51
1:AD:67:ALA:H	1:IV:65:ALA:H	1.57	0.51
1:BC:31:LEU:HD13	1:BD:117:LEU:HD21	1.92	0.51
1:CS:101:ARG:CZ	1:CS:124:VAL:HG21	2.40	0.51
1:DN:88:ASN:ND2	1:DO:74:GLU:OE2	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DZ:14:LYS:NZ	1:DZ:28:SER:HB2	2.25	0.51
1:ED:5:MET:SD	1:EE:125:SER:HB2	2.51	0.51
1:EI:56:ARG:O	1:EI:74:GLU:N	2.37	0.51
1:EM:37:LYS:NZ	1:EM:40:ILE:O	2.44	0.51
1:EO:116:PHE:CE1	1:IT:8:ILE:HD11	2.46	0.51
1:FA:56:ARG:O	1:FA:74:GLU:N	2.27	0.51
1:FA:71:MET:SD	1:FA:71:MET:N	2.83	0.51
1:GK:36:VAL:N	1:GK:43:LEU:O	2.38	0.51
1:GQ:65:ALA:HB1	1:GQ:69:VAL:HB	1.92	0.51
1:GZ:38:VAL:HG21	1:GZ:43:LEU:HD22	1.92	0.51
1:HZ:92:LEU:HD13	1:HZ:95:GLU:OE2	2.10	0.51
1:IF:60:LYS:HD2	1:IF:71:MET:HE1	1.91	0.51
1:IJ:61:PRO:HG2	1:IJ:64:CYS:SG	2.50	0.51
1:JA:57:PRO:HA	1:JA:73:ASN:HA	1.92	0.51
1:JF:8:ILE:N	1:JF:16:VAL:O	2.38	0.51
1:AA:79:ARG:HB2	1:AA:79:ARG:NH1	2.26	0.51
1:AW:5:MET:HE1	1:AX:123:ILE:HG22	1.93	0.51
1:AW:128:THR:HA	1:AX:2:ASN:HA	1.93	0.51
1:BB:5:MET:HB2	1:BB:18:SER:O	2.11	0.51
1:BG:101:ARG:NH2	1:BH:2:ASN:HD22	2.08	0.51
1:DJ:107:PHE:HA	1:DJ:112:ALA:HB3	1.92	0.51
1:DL:107:PHE:HA	1:DL:112:ALA:HB3	1.93	0.51
1:DU:69:VAL:N	1:FP:64:CYS:H	2.08	0.51
1:ED:72:PRO:HG2	1:EE:38:VAL:HG22	1.92	0.51
1:HA:93:LYS:NZ	1:HB:108:ALA:O	2.41	0.51
1:HP:87:GLU:OE1	1:HP:87:GLU:N	2.44	0.51
1:IB:14:LYS:NZ	1:IB:28:SER:HB2	2.25	0.51
1:JC:115:GLY:HA3	1:JD:33:ARG:HD3	1.92	0.51
1:AH:23:LEU:HD22	1:JF:44:ASN:ND2	2.25	0.51
1:AS:1:ALA:HB1	1:AT:128:THR:HG23	1.93	0.51
1:BI:105:THR:O	1:BI:109:SER:OG	2.29	0.51
1:BL:57:PRO:HA	1:BL:73:ASN:HA	1.92	0.51
1:BS:128:THR:OG1	1:BT:1:ALA:O	2.27	0.51
1:CF:5:MET:HB2	1:CF:18:SER:O	2.10	0.51
1:CI:5:MET:HE1	1:CJ:123:ILE:HG22	1.93	0.51
1:CU:3:LYS:NZ	1:CV:129:THR:HG23	2.26	0.51
1:CU:128:THR:O	1:CV:3:LYS:NZ	2.36	0.51
1:DE:55:LYS:NZ	1:DE:75:ASN:OD1	2.29	0.51
1:DQ:56:ARG:HD2	1:DQ:76:GLN:HE22	1.74	0.51
1:EC:8:ILE:HA	1:HN:116:PHE:HB2	1.93	0.51
1:EE:67:ALA:N	1:GU:65:ALA:H	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EG:67:ALA:H	1:HX:65:ALA:H	1.58	0.51
1:EJ:71:MET:N	1:EJ:71:MET:SD	2.84	0.51
1:EQ:60:LYS:HZ1	1:EQ:65:ALA:H	1.58	0.51
1:EV:55:LYS:HZ2	1:EV:73:ASN:HB2	1.75	0.51
1:GM:117:LEU:HD21	1:GN:31:LEU:HD13	1.93	0.51
1:GU:128:THR:HA	1:GV:2:ASN:HA	1.92	0.51
1:HD:37:LYS:HD2	1:HD:41:ALA:O	2.11	0.51
1:HP:128:THR:HA	1:HQ:2:ASN:HA	1.92	0.51
1:HW:94:ALA:O	1:HW:97:GLU:HG3	2.11	0.51
1:IC:32:LEU:HB3	1:IC:34:GLN:NE2	2.26	0.51
1:IS:87:GLU:OE1	1:IS:87:GLU:N	2.38	0.51
1:IT:63:GLY:HA2	1:IV:67:ALA:O	2.11	0.51
1:JD:56:ARG:O	1:JD:74:GLU:N	2.30	0.51
1:AT:8:ILE:HA	1:GX:116:PHE:HB2	1.92	0.51
1:AV:19:ASP:HB3	1:AV:22:ARG:O	2.11	0.51
1:AX:68:CYS:HB2	1:GY:64:CYS:SG	2.50	0.51
1:BO:101:ARG:CZ	1:BO:124:VAL:HG21	2.41	0.51
1:BX:61:PRO:HB2	1:BX:64:CYS:HB3	1.92	0.51
1:CG:71:MET:N	1:CG:71:MET:SD	2.84	0.51
1:CI:3:LYS:NZ	1:CJ:129:THR:HG23	2.26	0.51
1:CI:115:GLY:O	1:CJ:33:ARG:NH1	2.43	0.51
1:CU:88:ASN:ND2	1:CV:74:GLU:OE2	2.33	0.51
1:CV:106:LEU:HD21	1:CV:123:ILE:HD11	1.92	0.51
1:DA:71:MET:N	1:DA:71:MET:SD	2.84	0.51
1:DA:101:ARG:NH2	1:DB:2:ASN:HD22	2.09	0.51
1:DI:69:VAL:H	1:FH:64:CYS:N	2.09	0.51
1:DP:5:MET:SD	1:DQ:125:SER:HB2	2.51	0.51
1:DQ:98:THR:HG21	1:DQ:126:SER:HA	1.91	0.51
1:DS:98:THR:HG21	1:DS:126:SER:HA	1.91	0.51
1:DV:56:ARG:O	1:DV:74:GLU:N	2.43	0.51
1:EH:71:MET:N	1:EH:71:MET:SD	2.84	0.51
1:EK:5:MET:HB2	1:EK:18:SER:O	2.11	0.51
1:EM:5:MET:N	1:EM:5:MET:SD	2.84	0.51
1:FC:101:ARG:NH2	1:FC:124:VAL:HG21	2.25	0.51
1:GG:38:VAL:HG21	1:GG:43:LEU:HD22	1.93	0.51
1:GQ:2:ASN:HA	1:GR:128:THR:HA	1.92	0.51
1:HW:71:MET:SD	1:HW:71:MET:N	2.84	0.51
1:HY:105:THR:HG23	1:HY:106:LEU:HD12	1.93	0.51
1:HZ:117:LEU:HD21	1:IA:31:LEU:HD13	1.93	0.51
1:IF:3:LYS:NZ	1:IG:129:THR:HG23	2.26	0.51
1:IL:56:ARG:NH2	1:IM:95:GLU:OE2	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JH:94:ALA:O	1:JH:97:GLU:HG3	2.11	0.51
1:AS:34:GLN:O	1:AS:45:ASN:N	2.42	0.50
1:BI:72:PRO:HG2	1:BJ:38:VAL:HG22	1.93	0.50
1:CH:57:PRO:HA	1:CH:73:ASN:HA	1.92	0.50
1:CI:37:LYS:HZ3	1:CI:42:GLU:HB2	1.76	0.50
1:CY:71:MET:N	1:CY:71:MET:SD	2.84	0.50
1:DP:107:PHE:HA	1:DP:112:ALA:HB3	1.92	0.50
1:DY:56:ARG:HD2	1:DY:76:GLN:HE22	1.77	0.50
1:DZ:3:LYS:NZ	1:EA:129:THR:HG23	2.25	0.50
1:FK:37:LYS:HD3	1:FK:42:GLU:OE2	2.11	0.50
1:GM:66:ASP:OD1	1:GM:69:VAL:HG23	2.10	0.50
1:GO:22:ARG:NH1	1:GO:24:SER:OG	2.44	0.50
1:HI:19:ASP:HB3	1:HI:22:ARG:O	2.11	0.50
1:HR:22:ARG:NH1	1:HR:24:SER:OG	2.45	0.50
1:IF:5:MET:HE1	1:IG:123:ILE:HG22	1.93	0.50
1:IG:35:ARG:NH1	1:IG:42:GLU:HB3	2.25	0.50
1:IS:5:MET:HB3	1:IS:17:TRP:HB3	1.91	0.50
1:JB:94:ALA:O	1:JB:97:GLU:HG3	2.11	0.50
1:AD:37:LYS:NZ	1:AD:40:ILE:O	2.44	0.50
1:AU:14:LYS:NZ	1:AU:28:SER:HB2	2.26	0.50
1:AU:88:ASN:ND2	1:AV:74:GLU:OE2	2.30	0.50
1:BO:107:PHE:HA	1:BO:112:ALA:HB3	1.94	0.50
1:BZ:34:GLN:NE2	1:BZ:35:ARG:O	2.44	0.50
1:CO:107:PHE:HA	1:CO:112:ALA:HB3	1.92	0.50
1:CW:107:PHE:HA	1:CW:112:ALA:HB3	1.93	0.50
1:CY:3:LYS:NZ	1:CZ:129:THR:HG23	2.27	0.50
1:DF:31:LEU:HD13	1:DG:117:LEU:HD21	1.92	0.50
1:DK:5:MET:HB2	1:DK:18:SER:O	2.11	0.50
1:DO:116:PHE:CE1	1:FQ:8:ILE:HD11	2.45	0.50
1:DR:107:PHE:HA	1:DR:112:ALA:HB3	1.92	0.50
1:DT:5:MET:HE1	1:DU:123:ILE:HG22	1.93	0.50
1:ES:56:ARG:O	1:ES:74:GLU:N	2.28	0.50
1:GF:35:ARG:NH2	1:GF:44:ASN:OD1	2.44	0.50
1:GV:19:ASP:HB3	1:GV:22:ARG:O	2.10	0.50
1:IL:5:MET:HE1	1:IM:123:ILE:HG22	1.92	0.50
1:IL:44:ASN:N	1:IL:87:GLU:OE2	2.39	0.50
1:IM:19:ASP:HB3	1:IM:22:ARG:O	2.11	0.50
1:AO:71:MET:N	1:AO:71:MET:SD	2.84	0.50
1:BI:71:MET:N	1:BI:71:MET:SD	2.84	0.50
1:BK:128:THR:O	1:BL:3:LYS:NZ	2.36	0.50
1:BO:101:ARG:NH2	1:BP:2:ASN:HD22	2.08	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:128:THR:HA	1:CD:2:ASN:HA	1.94	0.50
1:CE:107:PHE:HA	1:CE:112:ALA:HB3	1.93	0.50
1:CS:14:LYS:NZ	1:CS:28:SER:HB2	2.26	0.50
1:CZ:5:MET:HB2	1:CZ:18:SER:O	2.11	0.50
1:DY:5:MET:HB2	1:DY:18:SER:O	2.11	0.50
1:ED:37:LYS:HZ3	1:ED:42:GLU:HB2	1.76	0.50
1:EQ:98:THR:HG21	1:EQ:126:SER:HA	1.93	0.50
1:EX:5:MET:HG2	1:EX:18:SER:C	2.31	0.50
1:HG:74:GLU:OE2	1:HI:85:SER:OG	2.25	0.50
1:IQ:101:ARG:NH2	1:IQ:124:VAL:HG21	2.25	0.50
1:AD:5:MET:HG3	1:AD:17:TRP:HB3	1.92	0.50
1:AN:69:VAL:H	1:JC:64:CYS:N	2.09	0.50
1:AQ:3:LYS:NZ	1:AR:129:THR:HG23	2.27	0.50
1:BO:1:ALA:HB1	1:BP:128:THR:HG23	1.93	0.50
1:CG:101:ARG:NH2	1:CH:2:ASN:HD22	2.10	0.50
1:CM:107:PHE:HA	1:CM:112:ALA:HB3	1.93	0.50
1:CQ:105:THR:O	1:CQ:109:SER:OG	2.28	0.50
1:CR:57:PRO:HA	1:CR:73:ASN:HA	1.92	0.50
1:CV:55:LYS:NZ	1:CV:75:ASN:OD1	2.29	0.50
1:DB:60:LYS:NZ	1:DB:65:ALA:H	2.09	0.50
1:DG:55:LYS:NZ	1:DG:75:ASN:OD1	2.28	0.50
1:DH:71:MET:SD	1:DH:71:MET:N	2.84	0.50
1:DN:107:PHE:HA	1:DN:112:ALA:HB3	1.93	0.50
1:DP:71:MET:N	1:DP:71:MET:SD	2.84	0.50
1:DS:5:MET:HB2	1:DS:18:SER:O	2.11	0.50
1:DZ:1:ALA:HB1	1:EA:128:THR:HG23	1.92	0.50
1:EB:3:LYS:NZ	1:EC:129:THR:HG23	2.27	0.50
1:EC:5:MET:HB2	1:EC:18:SER:O	2.12	0.50
1:EK:67:ALA:C	1:EV:62:GLU:HA	2.32	0.50
1:EP:107:PHE:HA	1:EP:112:ALA:HB3	1.92	0.50
1:EV:55:LYS:NZ	1:EV:73:ASN:HB2	2.26	0.50
1:EX:87:GLU:H	1:EX:87:GLU:CD	2.13	0.50
1:FX:65:ALA:HB1	1:FX:69:VAL:HB	1.94	0.50
1:GR:94:ALA:O	1:GR:97:GLU:HG3	2.11	0.50
1:HR:72:PRO:HG2	1:HS:38:VAL:HG12	1.92	0.50
1:IB:93:LYS:NZ	1:IC:108:ALA:O	2.40	0.50
1:IF:61:PRO:HG2	1:IF:64:CYS:SG	2.52	0.50
1:IU:71:MET:SD	1:IU:71:MET:N	2.76	0.50
1:IX:22:ARG:NH1	1:IX:24:SER:OG	2.45	0.50
1:JA:125:SER:O	1:JB:2:ASN:ND2	2.44	0.50
1:JH:60:LYS:HA	1:JH:71:MET:HE1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JI:66:ASP:OD1	1:JI:69:VAL:HG23	2.11	0.50
1:AI:71:MET:N	1:AI:71:MET:SD	2.85	0.50
1:AK:107:PHE:HA	1:AK:112:ALA:HB3	1.94	0.50
1:AW:3:LYS:HZ2	1:AX:129:THR:HG23	1.76	0.50
1:AW:31:LEU:HD23	1:AX:115:GLY:HA2	1.94	0.50
1:BA:71:MET:N	1:BA:71:MET:SD	2.85	0.50
1:BU:71:MET:SD	1:BU:71:MET:N	2.84	0.50
1:CI:71:MET:SD	1:CI:71:MET:N	2.85	0.50
1:DJ:3:LYS:NZ	1:DK:129:THR:HG23	2.26	0.50
1:DX:71:MET:N	1:DX:71:MET:SD	2.85	0.50
1:EG:56:ARG:HD2	1:EG:76:GLN:HE22	1.76	0.50
1:FF:113:GLY:O	1:FG:46:VAL:HG11	2.12	0.50
1:GP:71:MET:SD	1:GP:71:MET:N	2.80	0.50
1:GQ:22:ARG:NH1	1:GQ:24:SER:OG	2.44	0.50
1:GY:117:LEU:HD21	1:GZ:31:LEU:HD13	1.92	0.50
1:HC:5:MET:HG2	1:HC:17:TRP:HB3	1.94	0.50
1:HV:88:ASN:ND2	1:HW:56:ARG:HD2	2.22	0.50
1:HZ:43:LEU:HD12	1:HZ:85:SER:HB3	1.94	0.50
1:II:44:ASN:ND2	1:II:87:GLU:OE2	2.44	0.50
1:IX:92:LEU:HA	1:IX:95:GLU:OE2	2.12	0.50
1:AB:34:GLN:NE2	1:AB:35:ARG:O	2.44	0.50
1:AG:107:PHE:HA	1:AG:112:ALA:HB3	1.93	0.50
1:BE:107:PHE:HA	1:BE:112:ALA:HB3	1.94	0.50
1:BK:72:PRO:HG2	1:BL:38:VAL:HG22	1.92	0.50
1:BL:5:MET:HB2	1:BL:18:SER:O	2.10	0.50
1:BQ:3:LYS:NZ	1:BR:129:THR:HG23	2.26	0.50
1:BR:8:ILE:HA	1:FZ:116:PHE:HB2	1.94	0.50
1:BR:60:LYS:HZ1	1:BR:65:ALA:HB3	1.76	0.50
1:CW:5:MET:SD	1:CX:125:SER:HB2	2.51	0.50
1:CZ:60:LYS:HZ1	1:CZ:65:ALA:HB3	1.76	0.50
1:DI:74:GLU:OE2	1:DI:76:GLN:NE2	2.35	0.50
1:DT:34:GLN:O	1:DT:45:ASN:N	2.41	0.50
1:DX:3:LYS:HZ2	1:DY:129:THR:HG23	1.77	0.50
1:EB:105:THR:O	1:EB:109:SER:OG	2.30	0.50
1:EK:23:LEU:HD22	1:EW:44:ASN:ND2	2.27	0.50
1:EP:128:THR:OG1	1:EQ:1:ALA:O	2.26	0.50
1:ES:19:ASP:HB3	1:ES:22:ARG:O	2.12	0.50
1:EV:32:LEU:HD23	1:EV:34:GLN:HE22	1.77	0.50
1:FT:58:ALA:HB3	1:FT:71:MET:HG3	1.93	0.50
1:GK:14:LYS:NZ	1:GK:28:SER:HB2	2.25	0.50
1:GU:22:ARG:NH1	1:GU:24:SER:OG	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HG:22:ARG:NH1	1:HG:24:SER:OG	2.45	0.50
1:HG:55:LYS:NZ	1:HG:73:ASN:HB2	2.27	0.50
1:HX:14:LYS:NZ	1:HX:15:ILE:O	2.44	0.50
1:IV:66:ASP:OD1	1:IV:69:VAL:HG23	2.12	0.50
1:JE:34:GLN:NE2	1:JE:45:ASN:OD1	2.44	0.50
1:AB:8:ILE:HA	1:EX:116:PHE:HB2	1.93	0.50
1:BD:60:LYS:HZ1	1:BD:65:ALA:H	1.59	0.50
1:BW:5:MET:SD	1:BX:125:SER:HB2	2.52	0.50
1:BZ:55:LYS:NZ	1:BZ:75:ASN:OD1	2.27	0.50
1:CH:8:ILE:HA	1:HA:116:PHE:HB2	1.94	0.50
1:CJ:55:LYS:NZ	1:CJ:75:ASN:OD1	2.28	0.50
1:CQ:71:MET:N	1:CQ:71:MET:SD	2.84	0.50
1:DF:5:MET:N	1:DF:5:MET:SD	2.85	0.50
1:DR:105:THR:O	1:DR:109:SER:OG	2.30	0.50
1:DX:3:LYS:NZ	1:DY:129:THR:HG23	2.27	0.50
1:EY:19:ASP:HB3	1:EY:22:ARG:O	2.11	0.50
1:FL:5:MET:SD	1:FM:125:SER:HB2	2.51	0.50
1:FO:105:THR:HG23	1:FO:106:LEU:HD12	1.94	0.50
1:FV:14:LYS:NZ	1:FV:15:ILE:O	2.44	0.50
1:GE:101:ARG:HH12	1:GE:124:VAL:HG21	1.77	0.50
1:GO:37:LYS:NZ	1:GO:39:GLY:O	2.45	0.50
1:GO:60:LYS:HA	1:GO:71:MET:HE1	1.93	0.50
1:GT:19:ASP:HB3	1:GT:22:ARG:O	2.12	0.50
1:GW:64:CYS:N	1:GY:68:CYS:SG	2.85	0.50
1:HA:92:LEU:HD13	1:HA:95:GLU:OE2	2.11	0.50
1:HE:117:LEU:HD21	1:HF:31:LEU:HD13	1.93	0.50
1:HR:60:LYS:HB3	1:HR:65:ALA:HB2	1.94	0.50
1:IQ:74:GLU:HG2	1:IQ:75:ASN:H	1.77	0.50
1:IR:3:LYS:HZ1	1:IS:129:THR:HG23	1.76	0.50
1:JE:2:ASN:ND2	1:JF:125:SER:O	2.45	0.50
1:AC:5:MET:HE1	1:AD:123:ILE:HG22	1.93	0.50
1:AL:5:MET:HB2	1:AL:18:SER:O	2.12	0.50
1:AT:5:MET:HB2	1:AT:18:SER:O	2.12	0.50
1:BA:128:THR:OG1	1:BB:1:ALA:O	2.25	0.50
1:BM:3:LYS:NZ	1:BN:129:THR:HG23	2.26	0.50
1:BP:101:ARG:CZ	1:BP:124:VAL:HG21	2.42	0.50
1:BT:5:MET:HB2	1:BT:18:SER:O	2.12	0.50
1:BW:101:ARG:NH2	1:BX:2:ASN:HD22	2.09	0.50
1:CB:55:LYS:NZ	1:CB:75:ASN:OD1	2.29	0.50
1:CK:107:PHE:HA	1:CK:112:ALA:HB3	1.93	0.50
1:CL:5:MET:HB2	1:CL:18:SER:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:69:VAL:HG13	1:IP:64:CYS:SG	2.52	0.50
1:CV:8:ILE:HA	1:HL:116:PHE:HB2	1.94	0.50
1:CZ:67:ALA:H	1:ID:65:ALA:CB	2.24	0.50
1:DF:72:PRO:HG2	1:DG:38:VAL:HG22	1.93	0.50
1:DN:37:LYS:HZ3	1:DN:42:GLU:HB2	1.76	0.50
1:DN:72:PRO:HG2	1:DO:38:VAL:HG22	1.92	0.50
1:EH:128:THR:OG1	1:EI:1:ALA:O	2.26	0.50
1:EM:57:PRO:HA	1:EM:73:ASN:HA	1.94	0.50
1:EO:98:THR:HG21	1:EO:126:SER:HA	1.94	0.50
1:FS:34:GLN:NE2	1:FS:35:ARG:O	2.45	0.50
1:FS:106:LEU:HD11	1:FS:123:ILE:HD11	1.94	0.50
1:FV:22:ARG:NH1	1:FV:24:SER:OG	2.45	0.50
1:GB:61:PRO:HG2	1:GB:64:CYS:SG	2.52	0.50
1:GF:3:LYS:NZ	1:GF:21:THR:OG1	2.30	0.50
1:GF:123:ILE:HG22	1:GG:5:MET:HE1	1.92	0.50
1:GP:56:ARG:O	1:GP:74:GLU:N	2.28	0.50
1:HN:76:GLN:NE2	1:HO:91:THR:OG1	2.43	0.50
1:II:37:LYS:HD2	1:II:41:ALA:O	2.12	0.50
1:IK:19:ASP:HB3	1:IK:22:ARG:O	2.12	0.50
1:IL:87:GLU:H	1:IL:87:GLU:CD	2.13	0.50
1:IX:20:PRO:HB3	1:JD:116:PHE:HE2	1.76	0.50
1:IX:45:ASN:HA	1:IX:85:SER:HA	1.94	0.50
1:IX:115:GLY:HA3	1:IZ:33:ARG:HD3	1.93	0.50
1:AI:12:ALA:HB2	1:GT:10:SER:N	2.27	0.50
1:AJ:101:ARG:CZ	1:AJ:124:VAL:HG21	2.42	0.50
1:AL:8:ILE:HA	1:IR:116:PHE:HB2	1.93	0.50
1:AS:3:LYS:NZ	1:AT:129:THR:HG23	2.27	0.50
1:BD:61:PRO:HB2	1:BD:64:CYS:HB3	1.94	0.50
1:BM:34:GLN:O	1:BM:45:ASN:N	2.41	0.50
1:CB:5:MET:HB2	1:CB:18:SER:O	2.12	0.50
1:CG:101:ARG:HH22	1:CH:2:ASN:HD22	1.57	0.50
1:CG:107:PHE:HA	1:CG:112:ALA:HB3	1.93	0.50
1:CL:5:MET:HG3	1:CL:17:TRP:HB3	1.94	0.50
1:CL:37:LYS:NZ	1:CL:40:ILE:O	2.45	0.50
1:CQ:115:GLY:O	1:CR:33:ARG:NH1	2.45	0.50
1:DM:67:ALA:C	1:FB:62:GLU:HA	2.31	0.50
1:DR:71:MET:N	1:DR:71:MET:SD	2.85	0.50
1:DR:72:PRO:HG2	1:DS:38:VAL:HG22	1.93	0.50
1:DX:35:ARG:NH1	1:DX:44:ASN:OD1	2.44	0.50
1:EG:56:ARG:HD2	1:EG:76:GLN:NE2	2.27	0.50
1:EL:88:ASN:ND2	1:EM:74:GLU:OE2	2.32	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EV:22:ARG:NH1	1:EV:24:SER:OG	2.44	0.50
1:FH:66:ASP:OD1	1:FH:69:VAL:HG23	2.11	0.50
1:FO:87:GLU:OE1	1:FO:87:GLU:N	2.38	0.50
1:GO:35:ARG:HH22	1:GO:44:ASN:HA	1.77	0.50
1:HJ:96:TRP:NE1	1:HK:104:ASP:OD1	2.35	0.50
1:HO:19:ASP:HB3	1:HO:22:ARG:O	2.11	0.50
1:HY:35:ARG:HH21	1:HY:42:GLU:HG2	1.76	0.50
1:IA:57:PRO:HA	1:IA:73:ASN:HA	1.94	0.50
1:IP:71:MET:SD	1:IP:72:PRO:HD2	2.52	0.50
1:AE:14:LYS:NZ	1:AE:15:ILE:O	2.45	0.49
1:AF:68:CYS:SG	1:AF:69:VAL:N	2.85	0.49
1:AM:101:ARG:NH2	1:AN:2:ASN:HD22	2.09	0.49
1:AS:71:MET:N	1:AS:71:MET:SD	2.85	0.49
1:BL:60:LYS:HZ1	1:BL:65:ALA:H	1.59	0.49
1:CW:60:LYS:NZ	1:CW:66:ASP:O	2.24	0.49
1:CX:5:MET:HB2	1:CX:18:SER:O	2.12	0.49
1:DE:60:LYS:HZ1	1:DE:65:ALA:H	1.59	0.49
1:DR:14:LYS:NZ	1:DR:28:SER:HB2	2.26	0.49
1:DT:71:MET:N	1:DT:71:MET:SD	2.84	0.49
1:DZ:101:ARG:CZ	1:DZ:124:VAL:HG21	2.42	0.49
1:EA:57:PRO:HA	1:EA:73:ASN:HA	1.92	0.49
1:EC:34:GLN:NE2	1:EC:35:ARG:O	2.45	0.49
1:EE:93:LYS:O	1:EE:96:TRP:HB3	2.12	0.49
1:ER:37:LYS:NZ	1:ER:40:ILE:O	2.36	0.49
1:FC:74:GLU:HG2	1:FC:75:ASN:H	1.77	0.49
1:FD:43:LEU:HD12	1:FD:85:SER:HB3	1.94	0.49
1:FK:105:THR:HG23	1:FK:106:LEU:HD12	1.94	0.49
1:FX:61:PRO:HG2	1:FX:64:CYS:HB3	1.94	0.49
1:GD:128:THR:HA	1:GE:2:ASN:HA	1.92	0.49
1:GS:43:LEU:HD12	1:GS:85:SER:HB2	1.94	0.49
1:HZ:123:ILE:HG22	1:IA:5:MET:HE1	1.94	0.49
1:IB:113:GLY:O	1:IC:46:VAL:HG11	2.12	0.49
1:ID:117:LEU:HD21	1:IE:31:LEU:HD13	1.94	0.49
1:IX:61:PRO:HG2	1:IX:64:CYS:SG	2.52	0.49
1:IZ:22:ARG:NH2	1:IZ:55:LYS:O	2.43	0.49
1:AG:117:LEU:HD23	1:AH:15:ILE:HG13	1.93	0.49
1:AH:19:ASP:HB3	1:AH:22:ARG:O	2.12	0.49
1:AW:1:ALA:HB1	1:AX:128:THR:HG23	1.94	0.49
1:BA:5:MET:SD	1:BA:5:MET:N	2.84	0.49
1:BM:71:MET:SD	1:BM:71:MET:N	2.85	0.49
1:CU:1:ALA:HB1	1:CV:128:THR:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DW:5:MET:HB2	1:DW:18:SER:O	2.12	0.49
1:DZ:34:GLN:O	1:DZ:45:ASN:N	2.45	0.49
1:EB:88:ASN:ND2	1:EC:74:GLU:OE2	2.33	0.49
1:EH:115:GLY:O	1:EI:33:ARG:NH1	2.45	0.49
1:EL:5:MET:SD	1:EL:5:MET:N	2.86	0.49
1:EL:107:PHE:HA	1:EL:112:ALA:HB3	1.93	0.49
1:EQ:5:MET:HB2	1:EQ:18:SER:O	2.13	0.49
1:FB:5:MET:SD	1:FC:125:SER:HB2	2.52	0.49
1:FF:14:LYS:NZ	1:FF:28:SER:HB2	2.25	0.49
1:FL:88:ASN:ND2	1:FM:56:ARG:HD2	2.27	0.49
1:FW:60:LYS:HG2	1:FW:71:MET:HE1	1.93	0.49
1:FW:65:ALA:HB2	1:FY:68:CYS:SG	2.52	0.49
1:GF:22:ARG:NH1	1:GF:24:SER:OG	2.44	0.49
1:HB:92:LEU:HA	1:HB:95:GLU:OE2	2.12	0.49
1:HE:60:LYS:HB3	1:HE:65:ALA:HB2	1.94	0.49
1:HF:87:GLU:OE1	1:HF:87:GLU:N	2.40	0.49
1:HS:87:GLU:OE1	1:HS:87:GLU:N	2.40	0.49
1:IP:45:ASN:HA	1:IP:85:SER:HA	1.93	0.49
1:IT:113:GLY:O	1:IU:46:VAL:HG11	2.12	0.49
1:AE:107:PHE:HA	1:AE:112:ALA:HB3	1.93	0.49
1:AF:98:THR:HG21	1:AF:126:SER:HA	1.94	0.49
1:AJ:69:VAL:H	1:GM:64:CYS:N	2.10	0.49
1:AL:68:CYS:HA	1:IR:64:CYS:SG	2.52	0.49
1:AO:35:ARG:NH1	1:AO:44:ASN:OD1	2.45	0.49
1:AT:5:MET:HG3	1:AT:17:TRP:HB3	1.94	0.49
1:BA:72:PRO:HG2	1:BB:38:VAL:HG22	1.93	0.49
1:BK:128:THR:HA	1:BL:2:ASN:HA	1.94	0.49
1:BS:14:LYS:HE3	1:BS:28:SER:HB2	1.94	0.49
1:BU:107:PHE:HA	1:BU:112:ALA:HB3	1.94	0.49
1:CH:68:CYS:N	1:HA:63:GLY:H	2.09	0.49
1:CR:5:MET:HB2	1:CR:18:SER:O	2.12	0.49
1:DC:71:MET:N	1:DC:71:MET:SD	2.85	0.49
1:DR:34:GLN:O	1:DR:45:ASN:N	2.43	0.49
1:DU:5:MET:HB2	1:DU:18:SER:O	2.13	0.49
1:DX:37:LYS:HD3	1:DX:42:GLU:OE2	2.12	0.49
1:EY:57:PRO:HA	1:EY:73:ASN:HA	1.94	0.49
1:FB:71:MET:SD	1:FB:72:PRO:HD2	2.52	0.49
1:FR:113:GLY:O	1:FS:46:VAL:HG11	2.12	0.49
1:FW:64:CYS:HA	1:FY:67:ALA:HB3	1.93	0.49
1:GB:117:LEU:HD21	1:GC:31:LEU:HD13	1.94	0.49
1:GO:93:LYS:NZ	1:GP:108:ALA:O	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GR:56:ARG:O	1:GR:74:GLU:N	2.26	0.49
1:GR:105:THR:HG23	1:GR:106:LEU:HD12	1.94	0.49
1:HB:87:GLU:OE1	1:HB:87:GLU:N	2.39	0.49
1:HE:43:LEU:HD12	1:HE:85:SER:HB3	1.94	0.49
1:HL:85:SER:OG	1:HM:74:GLU:OE1	2.20	0.49
1:HT:61:PRO:HG2	1:HT:64:CYS:SG	2.52	0.49
1:IG:65:ALA:HB2	1:II:68:CYS:SG	2.52	0.49
1:IJ:117:LEU:HD21	1:IK:31:LEU:HD13	1.93	0.49
1:IV:35:ARG:NH2	1:IV:44:ASN:OD1	2.44	0.49
1:AJ:57:PRO:HA	1:AJ:73:ASN:HA	1.93	0.49
1:AK:71:MET:SD	1:AK:71:MET:N	2.85	0.49
1:AU:14:LYS:HZ1	1:AU:28:SER:HB2	1.77	0.49
1:AW:3:LYS:NZ	1:AX:129:THR:HG23	2.26	0.49
1:AY:14:LYS:HE3	1:AY:28:SER:HB2	1.94	0.49
1:AZ:5:MET:HB2	1:AZ:18:SER:O	2.13	0.49
1:BJ:56:ARG:HD2	1:BJ:76:GLN:HE22	1.76	0.49
1:BL:37:LYS:NZ	1:BL:40:ILE:O	2.45	0.49
1:BV:69:VAL:O	1:GH:63:GLY:HA3	2.11	0.49
1:CF:19:ASP:HB3	1:CF:22:ARG:O	2.13	0.49
1:DE:5:MET:HB2	1:DE:18:SER:O	2.12	0.49
1:DI:56:ARG:HD2	1:DI:76:GLN:HE22	1.77	0.49
1:DJ:105:THR:O	1:DJ:109:SER:OG	2.30	0.49
1:DP:35:ARG:NH1	1:DP:44:ASN:OD1	2.46	0.49
1:EH:1:ALA:HB1	1:EI:128:THR:HG23	1.95	0.49
1:FM:37:LYS:NZ	1:FM:38:VAL:O	2.45	0.49
1:GK:65:ALA:N	1:GM:68:CYS:SG	2.85	0.49
1:GU:70:ILE:HD11	1:GY:40:ILE:HD12	1.94	0.49
1:GW:93:LYS:O	1:GW:97:GLU:HG2	2.13	0.49
1:IF:55:LYS:NZ	1:IF:73:ASN:HB2	2.28	0.49
1:IZ:117:LEU:H	1:IZ:117:LEU:HD23	1.77	0.49
1:JC:115:GLY:O	1:JD:33:ARG:NH1	2.46	0.49
1:AH:67:ALA:C	1:JE:62:GLU:HA	2.31	0.49
1:BA:3:LYS:NZ	1:BB:129:THR:HG23	2.28	0.49
1:BR:35:ARG:HB3	1:BR:42:GLU:OE2	2.12	0.49
1:BZ:32:LEU:HB3	1:BZ:47:SER:HB3	1.95	0.49
1:CB:69:VAL:N	1:FJ:64:CYS:H	2.08	0.49
1:CD:67:ALA:HB1	1:HG:64:CYS:HA	1.94	0.49
1:CE:71:MET:N	1:CE:71:MET:SD	2.85	0.49
1:CT:98:THR:HG21	1:CT:126:SER:HA	1.94	0.49
1:CV:34:GLN:NE2	1:CV:35:ARG:O	2.45	0.49
1:DI:5:MET:HB2	1:DI:18:SER:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DL:101:ARG:NH2	1:DM:2:ASN:HD22	2.11	0.49
1:DR:101:ARG:NH2	1:DS:2:ASN:HD22	2.11	0.49
1:DV:107:PHE:HA	1:DV:112:ALA:HB3	1.93	0.49
1:EA:5:MET:HG3	1:EA:17:TRP:HB3	1.94	0.49
1:EH:72:PRO:HG2	1:EI:38:VAL:HG22	1.93	0.49
1:EP:71:MET:N	1:EP:71:MET:SD	2.86	0.49
1:FT:61:PRO:HG2	1:FT:64:CYS:SG	2.52	0.49
1:GD:87:GLU:N	1:GD:87:GLU:OE1	2.44	0.49
1:GH:117:LEU:HD21	1:GI:31:LEU:HD13	1.93	0.49
1:HP:22:ARG:NH1	1:HP:24:SER:OG	2.46	0.49
1:HR:5:MET:HG2	1:HS:123:ILE:HG22	1.94	0.49
1:HY:106:LEU:HD11	1:HY:123:ILE:HD11	1.94	0.49
1:IB:91:THR:O	1:IB:94:ALA:N	2.45	0.49
1:IC:32:LEU:HB2	1:IC:47:SER:HB3	1.94	0.49
1:JF:22:ARG:NH2	1:JF:55:LYS:O	2.43	0.49
1:AC:3:LYS:NZ	1:AD:129:THR:HG23	2.27	0.49
1:BF:101:ARG:CZ	1:BF:124:VAL:HG21	2.43	0.49
1:BG:71:MET:SD	1:BG:71:MET:N	2.86	0.49
1:BJ:101:ARG:CZ	1:BJ:124:VAL:HG21	2.43	0.49
1:BL:8:ILE:HA	1:GB:116:PHE:HB2	1.94	0.49
1:BM:72:PRO:HG2	1:BN:38:VAL:HG22	1.95	0.49
1:BU:3:LYS:NZ	1:BV:129:THR:HG23	2.28	0.49
1:CB:67:ALA:C	1:FJ:62:GLU:HA	2.32	0.49
1:CC:14:LYS:NZ	1:CC:15:ILE:O	2.46	0.49
1:CC:71:MET:N	1:CC:71:MET:SD	2.86	0.49
1:CE:34:GLN:O	1:CE:45:ASN:N	2.42	0.49
1:CH:5:MET:HB2	1:CH:18:SER:O	2.12	0.49
1:CH:19:ASP:HB3	1:CH:22:ARG:O	2.12	0.49
1:CL:67:ALA:H	1:FN:65:ALA:H	1.59	0.49
1:DA:117:LEU:HD21	1:DB:31:LEU:HD13	1.94	0.49
1:DG:93:LYS:O	1:DG:96:TRP:HB3	2.12	0.49
1:DM:69:VAL:N	1:FB:64:CYS:H	2.10	0.49
1:ED:5:MET:HE1	1:EE:123:ILE:HG22	1.94	0.49
1:EK:67:ALA:C	1:EV:65:ALA:HB2	2.33	0.49
1:FB:115:GLY:HA3	1:FC:33:ARG:HD3	1.95	0.49
1:FG:5:MET:HG2	1:FG:17:TRP:HB3	1.94	0.49
1:FI:36:VAL:N	1:FI:43:LEU:O	2.46	0.49
1:FJ:3:LYS:HZ1	1:FK:129:THR:HG23	1.77	0.49
1:FX:115:GLY:HA2	1:FY:31:LEU:HD23	1.94	0.49
1:FY:71:MET:SD	1:FY:71:MET:N	2.79	0.49
1:FZ:35:ARG:NH2	1:FZ:42:GLU:HA	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GG:22:ARG:NH2	1:GG:55:LYS:O	2.41	0.49
1:GI:19:ASP:HB3	1:GI:22:ARG:O	2.12	0.49
1:GM:92:LEU:HD13	1:GM:95:GLU:OE2	2.11	0.49
1:GP:19:ASP:HB3	1:GP:22:ARG:O	2.12	0.49
1:HB:19:ASP:HB3	1:HB:22:ARG:O	2.12	0.49
1:HZ:70:ILE:HD11	1:ID:40:ILE:HG23	1.94	0.49
1:IP:5:MET:SD	1:IQ:125:SER:HB2	2.53	0.49
1:IZ:35:ARG:HG3	1:IZ:42:GLU:OE2	2.12	0.49
1:AA:105:THR:O	1:AA:109:SER:OG	2.31	0.49
1:AC:5:MET:N	1:AC:5:MET:SD	2.86	0.49
1:AM:71:MET:N	1:AM:71:MET:SD	2.86	0.49
1:AM:72:PRO:HG2	1:AN:38:VAL:HG22	1.93	0.49
1:AX:34:GLN:NE2	1:AX:35:ARG:O	2.46	0.49
1:BS:107:PHE:HA	1:BS:112:ALA:HB3	1.93	0.49
1:CA:5:MET:N	1:CA:5:MET:SD	2.86	0.49
1:CI:105:THR:O	1:CI:109:SER:OG	2.31	0.49
1:CL:8:ILE:HA	1:FN:116:PHE:HB2	1.95	0.49
1:CS:107:PHE:HA	1:CS:112:ALA:HB3	1.93	0.49
1:CU:5:MET:HE2	1:CV:125:SER:HB2	1.94	0.49
1:DN:71:MET:N	1:DN:71:MET:SD	2.85	0.49
1:DO:19:ASP:HB3	1:DO:22:ARG:O	2.13	0.49
1:DR:101:ARG:CZ	1:DR:124:VAL:HG21	2.42	0.49
1:DV:128:THR:OG1	1:DW:1:ALA:O	2.27	0.49
1:EK:19:ASP:HB3	1:EK:22:ARG:O	2.12	0.49
1:EN:5:MET:N	1:EN:5:MET:SD	2.86	0.49
1:ES:45:ASN:HA	1:ES:85:SER:HA	1.93	0.49
1:EU:37:LYS:HD3	1:EU:42:GLU:OE2	2.12	0.49
1:FF:116:PHE:CE1	1:FH:6:GLN:HB2	2.48	0.49
1:FY:58:ALA:HB3	1:FY:71:MET:HG3	1.93	0.49
1:GI:92:LEU:HA	1:GI:95:GLU:OE2	2.12	0.49
1:GV:23:LEU:O	1:GV:24:SER:OG	2.30	0.49
1:GW:14:LYS:NZ	1:GW:28:SER:HB2	2.28	0.49
1:HA:37:LYS:NZ	1:HA:39:GLY:O	2.46	0.49
1:IP:66:ASP:OD1	1:IP:69:VAL:HG23	2.11	0.49
1:IV:3:LYS:HZ1	1:IW:129:THR:HG23	1.77	0.49
1:JC:37:LYS:NZ	1:JC:39:GLY:O	2.46	0.49
1:JG:22:ARG:NH1	1:JG:24:SER:OG	2.45	0.49
1:AY:71:MET:SD	1:AY:71:MET:N	2.86	0.49
1:BD:93:LYS:O	1:BD:96:TRP:HB3	2.12	0.49
1:BJ:5:MET:HB2	1:BJ:18:SER:O	2.13	0.49
1:BK:3:LYS:NZ	1:BL:129:THR:HG23	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:5:MET:HG2	1:BL:17:TRP:HB3	1.95	0.49
1:CD:19:ASP:HB3	1:CD:22:ARG:O	2.13	0.49
1:CV:19:ASP:HB3	1:CV:22:ARG:O	2.13	0.49
1:DB:111:ASN:HB3	1:DB:116:PHE:HD2	1.77	0.49
1:EF:107:PHE:HA	1:EF:112:ALA:HB3	1.95	0.49
1:EJ:101:ARG:NH2	1:EK:2:ASN:HD22	2.10	0.49
1:ER:85:SER:OG	1:ES:74:GLU:OE1	2.18	0.49
1:EV:115:GLY:HA3	1:EW:33:ARG:HD3	1.94	0.49
1:FM:106:LEU:HD11	1:FM:123:ILE:HD11	1.95	0.49
1:GG:19:ASP:HB3	1:GG:22:ARG:O	2.12	0.49
1:GP:35:ARG:NH1	1:GP:42:GLU:OE2	2.45	0.49
1:GT:37:LYS:HE2	1:GT:42:GLU:OE2	2.12	0.49
1:HK:55:LYS:NZ	1:HK:73:ASN:HB2	2.28	0.49
1:HS:117:LEU:HD23	1:HS:117:LEU:H	1.77	0.49
1:II:34:GLN:NE2	1:II:35:ARG:O	2.46	0.49
1:IU:19:ASP:HB3	1:IU:22:ARG:O	2.13	0.49
1:JD:35:ARG:NE	1:JD:42:GLU:OE1	2.45	0.49
1:JE:20:PRO:HB3	1:JJ:116:PHE:HE2	1.78	0.49
1:JH:105:THR:HG23	1:JH:106:LEU:HD12	1.95	0.49
1:AY:5:MET:SD	1:AZ:125:SER:HB2	2.52	0.49
1:AZ:56:ARG:O	1:AZ:74:GLU:N	2.37	0.49
1:BF:5:MET:HB2	1:BF:18:SER:O	2.12	0.49
1:BR:34:GLN:NE2	1:BR:35:ARG:O	2.45	0.49
1:BR:56:ARG:HD2	1:BR:76:GLN:NE2	2.28	0.49
1:CZ:8:ILE:HA	1:ID:116:PHE:HB2	1.94	0.49
1:DF:107:PHE:HA	1:DF:112:ALA:HB3	1.94	0.49
1:DI:57:PRO:HA	1:DI:73:ASN:HA	1.94	0.49
1:DY:8:ILE:HA	1:HE:116:PHE:HB2	1.95	0.49
1:EF:5:MET:N	1:EF:5:MET:SD	2.86	0.49
1:EJ:3:LYS:HZ2	1:EK:129:THR:HG23	1.78	0.49
1:FE:19:ASP:HB3	1:FE:22:ARG:O	2.12	0.49
1:FL:93:LYS:O	1:FL:97:GLU:HG2	2.12	0.49
1:GN:56:ARG:O	1:GN:74:GLU:N	2.29	0.49
1:GU:115:GLY:HA2	1:GV:31:LEU:HD23	1.95	0.49
1:GX:60:LYS:NZ	1:GX:69:VAL:O	2.42	0.49
1:HJ:93:LYS:O	1:HJ:97:GLU:HG2	2.13	0.49
1:HL:115:GLY:HA2	1:HM:31:LEU:HD23	1.95	0.49
1:HQ:101:ARG:HH12	1:HQ:124:VAL:HG21	1.77	0.49
1:HW:98:THR:HG21	1:HW:126:SER:HA	1.94	0.49
1:IV:123:ILE:HG22	1:IW:5:MET:HE2	1.94	0.49
1:JF:117:LEU:HD23	1:JF:117:LEU:H	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JG:60:LYS:HE3	1:JG:65:ALA:O	2.13	0.49
1:JI:87:GLU:N	1:JI:87:GLU:OE1	2.45	0.49
1:AL:66:ASP:OD2	1:AL:68:CYS:N	2.46	0.49
1:AR:35:ARG:HB3	1:AR:42:GLU:OE2	2.12	0.49
1:AZ:67:ALA:HB1	1:HT:64:CYS:HA	1.95	0.49
1:BY:3:LYS:HZ1	1:BZ:129:THR:HG23	1.78	0.49
1:BY:105:THR:O	1:BY:109:SER:OG	2.31	0.49
1:CH:56:ARG:HD2	1:CH:76:GLN:HE22	1.78	0.49
1:CJ:8:ILE:HA	1:IJ:116:PHE:HB2	1.93	0.49
1:CL:98:THR:HG21	1:CL:126:SER:HA	1.95	0.49
1:DR:115:GLY:HA2	1:DS:31:LEU:HD23	1.94	0.49
1:EE:68:CYS:N	1:GU:64:CYS:H	2.04	0.49
1:EK:25:THR:O	1:EK:25:THR:OG1	2.31	0.49
1:EL:128:THR:HA	1:EM:2:ASN:HA	1.94	0.49
1:EW:117:LEU:HD23	1:EW:117:LEU:H	1.78	0.49
1:FE:92:LEU:HA	1:FE:95:GLU:OE2	2.13	0.49
1:FK:106:LEU:HD11	1:FK:123:ILE:HD11	1.94	0.49
1:FL:59:PRO:O	1:FL:61:PRO:HD3	2.13	0.49
1:FS:19:ASP:HB3	1:FS:22:ARG:O	2.13	0.49
1:GC:56:ARG:O	1:GC:74:GLU:N	2.29	0.49
1:GH:101:ARG:HH21	1:GH:124:VAL:HG21	1.77	0.49
1:GP:117:LEU:HD23	1:GP:117:LEU:H	1.78	0.49
1:HX:66:ASP:OD1	1:HX:69:VAL:HG23	2.13	0.49
1:IE:57:PRO:HA	1:IE:73:ASN:HA	1.95	0.49
1:IU:51:VAL:HG22	1:IU:79:ARG:HG2	1.94	0.49
1:JC:3:LYS:NZ	1:JD:129:THR:HG23	2.27	0.49
1:AG:71:MET:N	1:AG:71:MET:SD	2.86	0.48
1:AQ:56:ARG:O	1:AQ:74:GLU:N	2.45	0.48
1:AX:8:ILE:HA	1:GY:116:PHE:HB2	1.93	0.48
1:BE:71:MET:N	1:BE:71:MET:SD	2.85	0.48
1:BK:5:MET:HE1	1:BL:123:ILE:HG22	1.93	0.48
1:BQ:37:LYS:HZ3	1:BQ:42:GLU:HB2	1.78	0.48
1:BQ:56:ARG:O	1:BQ:74:GLU:N	2.45	0.48
1:CR:8:ILE:HA	1:FG:116:PHE:HB2	1.95	0.48
1:CV:67:ALA:C	1:HL:63:GLY:H	2.16	0.48
1:DW:35:ARG:HB3	1:DW:42:GLU:OE2	2.12	0.48
1:ED:31:LEU:HD13	1:EE:117:LEU:HD21	1.95	0.48
1:EG:5:MET:HB2	1:EG:18:SER:O	2.13	0.48
1:EK:67:ALA:H	1:EV:65:ALA:CB	2.26	0.48
1:EM:34:GLN:NE2	1:EM:35:ARG:O	2.46	0.48
1:EX:60:LYS:NZ	1:EX:69:VAL:O	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FZ:115:GLY:HA2	1:GA:31:LEU:HD23	1.95	0.48
1:GH:37:LYS:NZ	1:GH:39:GLY:O	2.46	0.48
1:GW:61:PRO:HG2	1:GW:64:CYS:HB3	1.95	0.48
1:IZ:19:ASP:HB3	1:IZ:22:ARG:O	2.13	0.48
1:JL:85:SER:HB3	1:JJ:74:GLU:OE2	2.13	0.48
1:AA:71:MET:N	1:AA:71:MET:SD	2.86	0.48
1:AX:19:ASP:HB3	1:AX:22:ARG:O	2.13	0.48
1:BG:5:MET:SD	1:BH:125:SER:HB2	2.53	0.48
1:BJ:67:ALA:HA	1:HZ:63:GLY:N	2.26	0.48
1:BK:1:ALA:HB1	1:BL:128:THR:HG23	1.94	0.48
1:CA:71:MET:N	1:CA:71:MET:SD	2.85	0.48
1:DN:14:LYS:NZ	1:DN:15:ILE:O	2.46	0.48
1:DN:116:PHE:HE2	1:DP:20:PRO:HB3	1.79	0.48
1:EE:68:CYS:N	1:GU:63:GLY:H	2.10	0.48
1:EF:3:LYS:NZ	1:EG:129:THR:HG23	2.28	0.48
1:EG:56:ARG:O	1:EG:74:GLU:N	2.37	0.48
1:EH:128:THR:O	1:EI:3:LYS:NZ	2.43	0.48
1:EU:101:ARG:NH1	1:EU:124:VAL:HG21	2.28	0.48
1:GA:35:ARG:NH2	1:GA:43:LEU:O	2.45	0.48
1:GP:35:ARG:HH12	1:GP:42:GLU:HB3	1.77	0.48
1:GT:117:LEU:H	1:GT:117:LEU:HD23	1.79	0.48
1:GY:5:MET:HE1	1:GZ:123:ILE:HG22	1.95	0.48
1:HA:85:SER:OG	1:HB:74:GLU:OE1	2.17	0.48
1:HF:57:PRO:HA	1:HF:73:ASN:HA	1.95	0.48
1:HI:92:LEU:HA	1:HI:95:GLU:OE1	2.13	0.48
1:HV:113:GLY:O	1:HW:46:VAL:HG11	2.13	0.48
1:IM:92:LEU:HA	1:IM:95:GLU:OE1	2.13	0.48
1:AK:34:GLN:O	1:AK:45:ASN:N	2.42	0.48
1:AM:31:LEU:HD13	1:AN:117:LEU:HD21	1.95	0.48
1:AQ:1:ALA:HB1	1:AR:128:THR:HG23	1.94	0.48
1:AQ:107:PHE:HA	1:AQ:112:ALA:HB3	1.95	0.48
1:BB:57:PRO:HA	1:BB:73:ASN:HA	1.94	0.48
1:BJ:66:ASP:OD1	1:HZ:65:ALA:N	2.46	0.48
1:BJ:67:ALA:H	1:HZ:65:ALA:CB	2.27	0.48
1:BK:107:PHE:HA	1:BK:112:ALA:HB3	1.95	0.48
1:BR:19:ASP:HB3	1:BR:22:ARG:O	2.12	0.48
1:CG:5:MET:SD	1:CG:5:MET:N	2.87	0.48
1:CS:71:MET:N	1:CS:71:MET:SD	2.86	0.48
1:DJ:5:MET:SD	1:DJ:5:MET:N	2.86	0.48
1:DR:60:LYS:NZ	1:DR:66:ASP:H	2.11	0.48
1:DU:37:LYS:NZ	1:DU:40:ILE:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ER:115:GLY:HA2	1:ES:31:LEU:HD23	1.95	0.48
1:EZ:14:LYS:NZ	1:EZ:28:SER:HB2	2.28	0.48
1:FP:17:TRP:CD2	1:FQ:123:ILE:HG13	2.48	0.48
1:FW:92:LEU:HA	1:FW:95:GLU:OE1	2.13	0.48
1:HJ:111:ASN:HB2	1:HJ:116:PHE:HB2	1.95	0.48
1:HL:35:ARG:NH2	1:HL:42:GLU:HB3	2.28	0.48
1:HX:11:THR:HB	1:HX:14:LYS:H	1.78	0.48
1:IB:92:LEU:HA	1:IB:95:GLU:OE2	2.14	0.48
1:IE:92:LEU:HA	1:IE:95:GLU:OE2	2.13	0.48
1:IL:87:GLU:OE1	1:IL:87:GLU:N	2.34	0.48
1:IP:56:ARG:O	1:IP:74:GLU:N	2.34	0.48
1:IU:56:ARG:O	1:IU:74:GLU:N	2.26	0.48
1:JF:19:ASP:HB3	1:JF:22:ARG:O	2.13	0.48
1:AI:107:PHE:HA	1:AI:112:ALA:HB3	1.95	0.48
1:AU:107:PHE:HA	1:AU:112:ALA:HB3	1.95	0.48
1:BB:106:LEU:HD21	1:BB:123:ILE:HD11	1.96	0.48
1:BC:5:MET:SD	1:BD:125:SER:HB2	2.54	0.48
1:BE:101:ARG:CZ	1:BE:124:VAL:HG21	2.44	0.48
1:BG:35:ARG:NH1	1:BG:44:ASN:OD1	2.46	0.48
1:BI:3:LYS:NZ	1:BJ:129:THR:HG23	2.28	0.48
1:BL:32:LEU:HB3	1:BL:47:SER:HB3	1.96	0.48
1:BQ:1:ALA:HB1	1:BR:128:THR:HG23	1.94	0.48
1:BX:69:VAL:HG13	1:JI:64:CYS:HB2	1.95	0.48
1:CA:11:THR:HB	1:CA:14:LYS:H	1.77	0.48
1:CM:5:MET:N	1:CM:5:MET:SD	2.86	0.48
1:CU:5:MET:HG2	1:CU:19:ASP:N	2.29	0.48
1:CY:107:PHE:HA	1:CY:112:ALA:HB3	1.96	0.48
1:DO:37:LYS:NZ	1:DO:40:ILE:O	2.45	0.48
1:DT:5:MET:N	1:DT:5:MET:SD	2.86	0.48
1:EN:107:PHE:HA	1:EN:112:ALA:HB3	1.94	0.48
1:EX:117:LEU:HD21	1:EY:31:LEU:HD13	1.94	0.48
1:FD:61:PRO:HG2	1:FD:64:CYS:SG	2.54	0.48
1:FD:101:ARG:NH2	1:FD:124:VAL:HG21	2.22	0.48
1:FL:74:GLU:OE2	1:FM:85:SER:OG	2.28	0.48
1:GL:87:GLU:OE1	1:GL:87:GLU:N	2.39	0.48
1:GQ:39:GLY:HA3	1:GR:72:PRO:HG2	1.95	0.48
1:GZ:22:ARG:NH2	1:GZ:55:LYS:O	2.43	0.48
1:HC:14:LYS:NZ	1:HC:28:SER:HB2	2.28	0.48
1:HL:57:PRO:HA	1:HL:73:ASN:HA	1.94	0.48
1:IA:87:GLU:OE1	1:IA:87:GLU:N	2.40	0.48
1:IL:115:GLY:HA2	1:IM:31:LEU:HD23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IS:19:ASP:HB3	1:IS:22:ARG:O	2.14	0.48
1:JB:98:THR:HG21	1:JB:126:SER:HA	1.94	0.48
1:JG:113:GLY:O	1:JH:46:VAL:HG11	2.13	0.48
1:JH:19:ASP:HB3	1:JH:22:ARG:O	2.13	0.48
1:AQ:88:ASN:ND2	1:AR:74:GLU:OE2	2.32	0.48
1:AX:37:LYS:NZ	1:AX:40:ILE:O	2.46	0.48
1:BA:1:ALA:HB1	1:BB:128:THR:HG23	1.94	0.48
1:BC:71:MET:N	1:BC:71:MET:SD	2.86	0.48
1:BN:23:LEU:HD13	1:FX:44:ASN:HD21	1.78	0.48
1:BO:3:LYS:NZ	1:BP:129:THR:HG23	2.27	0.48
1:BQ:5:MET:HE3	1:BR:123:ILE:HG22	1.94	0.48
1:BR:5:MET:HG2	1:BR:17:TRP:HB3	1.95	0.48
1:CB:5:MET:HG3	1:CB:17:TRP:HB3	1.94	0.48
1:CY:5:MET:SD	1:CZ:125:SER:HB2	2.54	0.48
1:CZ:67:ALA:C	1:ID:62:GLU:HA	2.33	0.48
1:DK:32:LEU:HB3	1:DK:47:SER:HB3	1.95	0.48
1:DX:49:GLN:OE1	1:DX:79:ARG:NH1	2.37	0.48
1:EI:56:ARG:HD2	1:EI:76:GLN:HE22	1.76	0.48
1:EO:6:GLN:HE22	1:FA:111:ASN:HB2	1.79	0.48
1:FB:74:GLU:OE2	1:FC:85:SER:OG	2.22	0.48
1:FJ:35:ARG:NH2	1:FJ:44:ASN:OD1	2.46	0.48
1:FM:60:LYS:HG2	1:FM:71:MET:HE1	1.96	0.48
1:FR:11:THR:HB	1:FR:14:LYS:H	1.79	0.48
1:FW:37:LYS:HD3	1:FW:42:GLU:OE2	2.13	0.48
1:FZ:57:PRO:HA	1:FZ:73:ASN:HA	1.95	0.48
1:GE:35:ARG:NH2	1:GE:42:GLU:HB3	2.28	0.48
1:GK:37:LYS:HD3	1:GK:42:GLU:HG2	1.95	0.48
1:GR:62:GLU:HG2	1:GR:62:GLU:O	2.14	0.48
1:HV:87:GLU:N	1:HV:87:GLU:OE1	2.46	0.48
1:HZ:98:THR:HG23	1:HZ:101:ARG:HH21	1.77	0.48
1:IF:60:LYS:HA	1:IF:71:MET:HE1	1.96	0.48
1:JF:65:ALA:HB2	1:JH:68:CYS:SG	2.53	0.48
1:JG:2:ASN:HA	1:JH:128:THR:HA	1.94	0.48
1:AA:72:PRO:HG2	1:AB:38:VAL:HG22	1.96	0.48
1:AN:70:ILE:HG13	1:AN:70:ILE:O	2.14	0.48
1:BO:5:MET:SD	1:BP:125:SER:HB2	2.53	0.48
1:BQ:3:LYS:HZ2	1:BR:129:THR:HG23	1.79	0.48
1:CA:3:LYS:NZ	1:CB:129:THR:HG23	2.28	0.48
1:CA:101:ARG:NH2	1:CB:2:ASN:HD22	2.12	0.48
1:CG:72:PRO:HG2	1:CH:38:VAL:HG22	1.94	0.48
1:CU:56:ARG:O	1:CU:74:GLU:N	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:23:LEU:HD22	1:HM:44:ASN:ND2	2.29	0.48
1:DJ:72:PRO:HG2	1:DK:38:VAL:HG22	1.96	0.48
1:DL:14:LYS:HZ3	1:DL:28:SER:HB2	1.78	0.48
1:DW:34:GLN:NE2	1:DW:35:ARG:O	2.47	0.48
1:DY:56:ARG:O	1:DY:74:GLU:N	2.35	0.48
1:DZ:72:PRO:HG2	1:EA:38:VAL:HG22	1.94	0.48
1:EH:107:PHE:HA	1:EH:112:ALA:HB3	1.95	0.48
1:EN:37:LYS:HZ3	1:EN:42:GLU:HB2	1.78	0.48
1:EX:56:ARG:NH2	1:EY:95:GLU:OE2	2.37	0.48
1:FJ:17:TRP:CD2	1:FK:123:ILE:HG13	2.49	0.48
1:FO:19:ASP:HB3	1:FO:22:ARG:O	2.13	0.48
1:FO:106:LEU:HD11	1:FO:123:ILE:HD11	1.95	0.48
1:HF:92:LEU:HA	1:HF:95:GLU:OE2	2.13	0.48
1:HJ:5:MET:N	1:HJ:5:MET:SD	2.87	0.48
1:HJ:115:GLY:HA2	1:HK:31:LEU:HD23	1.95	0.48
1:HR:123:ILE:HB	1:HS:5:MET:HB2	1.96	0.48
1:HV:37:LYS:NZ	1:HV:40:ILE:O	2.44	0.48
1:IG:117:LEU:HD23	1:IG:117:LEU:H	1.79	0.48
1:IP:115:GLY:HA2	1:IQ:31:LEU:HD23	1.95	0.48
1:JF:85:SER:HG	1:JF:88:ASN:HD22	1.61	0.48
1:AG:5:MET:N	1:AG:5:MET:SD	2.87	0.48
1:AG:88:ASN:ND2	1:AH:74:GLU:OE2	2.36	0.48
1:AO:3:LYS:NZ	1:AP:129:THR:HG23	2.29	0.48
1:AO:37:LYS:HD3	1:AO:42:GLU:OE2	2.13	0.48
1:AX:67:ALA:C	1:GY:65:ALA:HB2	2.33	0.48
1:AY:107:PHE:HA	1:AY:112:ALA:HB3	1.95	0.48
1:BJ:69:VAL:N	1:HZ:64:CYS:H	2.10	0.48
1:BZ:8:ILE:HA	1:ER:116:PHE:HB2	1.94	0.48
1:CA:5:MET:SD	1:CB:125:SER:HB2	2.53	0.48
1:CD:98:THR:HG21	1:CD:126:SER:HA	1.95	0.48
1:CR:101:ARG:CZ	1:CR:124:VAL:HG21	2.44	0.48
1:CW:14:LYS:HE3	1:CW:28:SER:HB2	1.94	0.48
1:DK:57:PRO:HA	1:DK:73:ASN:HA	1.96	0.48
1:DU:8:ILE:HA	1:FP:116:PHE:HB2	1.95	0.48
1:DX:1:ALA:HB1	1:DY:128:THR:HG23	1.95	0.48
1:EB:1:ALA:HB1	1:EC:128:THR:HG23	1.96	0.48
1:EH:105:THR:O	1:EH:109:SER:OG	2.32	0.48
1:FD:115:GLY:HA2	1:FE:31:LEU:HD23	1.96	0.48
1:FH:115:GLY:HA2	1:FI:31:LEU:HD23	1.95	0.48
1:FI:117:LEU:HD23	1:FI:117:LEU:H	1.79	0.48
1:FJ:68:CYS:HB3	1:FO:64:CYS:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FX:14:LYS:NZ	1:FX:28:SER:HB2	2.27	0.48
1:GK:115:GLY:HA2	1:GL:31:LEU:HD23	1.95	0.48
1:GR:19:ASP:HB3	1:GR:22:ARG:O	2.14	0.48
1:GR:58:ALA:HB3	1:GR:71:MET:HB3	1.95	0.48
1:HJ:11:THR:HB	1:HJ:14:LYS:H	1.79	0.48
1:HK:60:LYS:HD2	1:HK:71:MET:HE1	1.95	0.48
1:IE:19:ASP:HB3	1:IE:22:ARG:O	2.14	0.48
1:IS:60:LYS:NZ	1:IS:65:ALA:O	2.33	0.48
1:IT:59:PRO:O	1:IT:61:PRO:HD3	2.13	0.48
1:JD:117:LEU:HD23	1:JD:117:LEU:H	1.79	0.48
1:AC:5:MET:SD	1:AD:125:SER:HB2	2.53	0.48
1:AJ:19:ASP:HB3	1:AJ:22:ARG:O	2.13	0.48
1:AN:19:ASP:HB3	1:AN:22:ARG:O	2.14	0.48
1:AN:55:LYS:NZ	1:AN:75:ASN:OD1	2.28	0.48
1:AT:101:ARG:CZ	1:AT:124:VAL:HG21	2.43	0.48
1:AU:71:MET:N	1:AU:71:MET:SD	2.86	0.48
1:CS:3:LYS:HZ2	1:CT:129:THR:HG23	1.79	0.48
1:CU:107:PHE:HA	1:CU:112:ALA:HB3	1.96	0.48
1:DE:8:ILE:HA	1:FT:116:PHE:HB2	1.95	0.48
1:DP:5:MET:SD	1:DP:5:MET:N	2.86	0.48
1:DT:5:MET:SD	1:DU:125:SER:HB2	2.53	0.48
1:ER:40:ILE:HD12	1:EU:70:ILE:HD11	1.95	0.48
1:EY:45:ASN:HA	1:EY:85:SER:HA	1.96	0.48
1:EZ:93:LYS:O	1:EZ:97:GLU:HG2	2.14	0.48
1:FA:19:ASP:HB3	1:FA:22:ARG:O	2.13	0.48
1:FB:35:ARG:HH22	1:FB:44:ASN:HA	1.77	0.48
1:FE:57:PRO:HA	1:FE:73:ASN:HA	1.94	0.48
1:FL:92:LEU:HD22	1:FM:76:GLN:NE2	2.29	0.48
1:GD:111:ASN:HB2	1:GD:116:PHE:HB2	1.96	0.48
1:GG:87:GLU:OE1	1:GG:87:GLU:N	2.40	0.48
1:GW:5:MET:HG3	1:GW:19:ASP:HA	1.96	0.48
1:II:105:THR:HA	1:II:109:SER:HB2	1.96	0.48
1:IS:105:THR:HG23	1:IS:106:LEU:HD12	1.95	0.48
1:JB:19:ASP:HB3	1:JB:22:ARG:O	2.14	0.48
1:AI:5:MET:SD	1:AI:5:MET:N	2.87	0.48
1:AP:56:ARG:O	1:AP:74:GLU:N	2.40	0.48
1:CI:88:ASN:ND2	1:CJ:74:GLU:OE2	2.33	0.48
1:CJ:32:LEU:HB3	1:CJ:47:SER:HB3	1.95	0.48
1:CN:61:PRO:HB2	1:CN:64:CYS:HB3	1.96	0.48
1:CV:5:MET:HG2	1:CV:17:TRP:HB3	1.95	0.48
1:CY:88:ASN:ND2	1:CZ:74:GLU:OE2	2.33	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:67:ALA:H	1:ID:65:ALA:H	1.61	0.48
1:DG:6:GLN:HE22	1:IO:111:ASN:HB2	1.79	0.48
1:DW:60:LYS:HZ1	1:DW:65:ALA:H	1.60	0.48
1:FF:93:LYS:O	1:FF:97:GLU:HG2	2.14	0.48
1:FM:55:LYS:HZ2	1:FM:73:ASN:HB2	1.78	0.48
1:FQ:106:LEU:HD11	1:FQ:123:ILE:HD11	1.96	0.48
1:FR:35:ARG:HD2	1:FR:44:ASN:HB3	1.94	0.48
1:FV:72:PRO:HG2	1:FW:38:VAL:HG12	1.96	0.48
1:GA:22:ARG:NH2	1:GA:55:LYS:O	2.44	0.48
1:GD:93:LYS:O	1:GD:97:GLU:HG2	2.14	0.48
1:GH:115:GLY:HA2	1:GI:31:LEU:HD23	1.96	0.48
1:GP:87:GLU:OE1	1:GP:87:GLU:N	2.40	0.48
1:GQ:60:LYS:HZ3	1:GQ:63:GLY:H	1.61	0.48
1:GV:117:LEU:HD23	1:GV:117:LEU:H	1.79	0.48
1:GW:5:MET:N	1:GW:5:MET:SD	2.87	0.48
1:HJ:61:PRO:HG2	1:HJ:64:CYS:SG	2.53	0.48
1:HR:36:VAL:HG23	1:HR:43:LEU:HB2	1.96	0.48
1:HR:125:SER:HB2	1:HS:5:MET:HE1	1.96	0.48
1:IM:8:ILE:N	1:IM:16:VAL:O	2.39	0.48
1:IN:124:VAL:HA	1:IO:4:PRO:HA	1.96	0.48
1:IP:115:GLY:HA3	1:IQ:33:ARG:HD3	1.95	0.48
1:AD:5:MET:HB2	1:AD:18:SER:O	2.12	0.48
1:AD:101:ARG:CZ	1:AD:124:VAL:HG21	2.44	0.48
1:AG:101:ARG:CZ	1:AG:124:VAL:HG21	2.44	0.48
1:AH:69:VAL:HG22	1:JE:64:CYS:SG	2.54	0.48
1:AW:107:PHE:HA	1:AW:112:ALA:HB3	1.95	0.48
1:BN:101:ARG:CZ	1:BN:124:VAL:HG21	2.44	0.48
1:BR:67:ALA:C	1:FZ:65:ALA:HB2	2.34	0.48
1:BU:101:ARG:NH2	1:BV:2:ASN:HD22	2.12	0.48
1:BV:19:ASP:HB3	1:BV:22:ARG:O	2.14	0.48
1:CH:5:MET:HG2	1:CH:17:TRP:HB3	1.96	0.48
1:CM:31:LEU:HD13	1:CN:117:LEU:HD21	1.96	0.48
1:DC:17:TRP:CD2	1:DE:123:ILE:HG13	2.49	0.48
1:DC:72:PRO:HG2	1:DE:38:VAL:HG22	1.96	0.48
1:DI:101:ARG:CZ	1:DI:124:VAL:HG21	2.44	0.48
1:DO:55:LYS:NZ	1:DO:75:ASN:OD1	2.28	0.48
1:DT:101:ARG:CZ	1:DT:124:VAL:HG21	2.44	0.48
1:ET:93:LYS:O	1:ET:97:GLU:HG2	2.14	0.48
1:FA:89:LEU:HG	1:FA:93:LYS:HE3	1.95	0.48
1:FF:72:PRO:HG2	1:FG:38:VAL:HG22	1.95	0.48
1:GG:93:LYS:O	1:GG:97:GLU:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GZ:117:LEU:HD23	1:GZ:117:LEU:H	1.79	0.48
1:HL:76:GLN:NE2	1:HM:91:THR:OG1	2.46	0.48
1:HO:56:ARG:O	1:HO:74:GLU:N	2.28	0.48
1:HS:56:ARG:O	1:HS:74:GLU:N	2.34	0.48
1:IN:22:ARG:NH1	1:IN:24:SER:OG	2.47	0.48
1:IU:56:ARG:NE	1:IU:76:GLN:OE1	2.40	0.48
1:JD:92:LEU:HA	1:JD:95:GLU:OE1	2.14	0.48
1:JJ:92:LEU:HA	1:JJ:95:GLU:OE1	2.14	0.48
1:AX:5:MET:HG2	1:AX:17:TRP:HB3	1.95	0.47
1:AY:3:LYS:HZ1	1:AZ:127:ASP:C	2.17	0.47
1:BF:56:ARG:HD2	1:BF:76:GLN:NE2	2.28	0.47
1:BP:25:THR:O	1:BP:25:THR:OG1	2.32	0.47
1:BY:71:MET:N	1:BY:71:MET:SD	2.86	0.47
1:CA:128:THR:OG1	1:CB:1:ALA:O	2.28	0.47
1:CU:34:GLN:O	1:CU:45:ASN:N	2.47	0.47
1:CY:1:ALA:HB1	1:CZ:128:THR:HG23	1.95	0.47
1:DR:5:MET:N	1:DR:5:MET:SD	2.87	0.47
1:DT:14:LYS:NZ	1:DT:30:SER:HB2	2.29	0.47
1:FN:85:SER:OG	1:FO:74:GLU:OE1	2.19	0.47
1:FU:117:LEU:H	1:FU:117:LEU:HD23	1.79	0.47
1:FX:5:MET:N	1:FX:5:MET:SD	2.87	0.47
1:GC:19:ASP:HB3	1:GC:22:ARG:O	2.14	0.47
1:GL:37:LYS:HD3	1:GL:42:GLU:OE2	2.14	0.47
1:GN:117:LEU:HD23	1:GN:117:LEU:H	1.79	0.47
1:GP:5:MET:N	1:GP:5:MET:SD	2.87	0.47
1:HA:117:LEU:HD21	1:HB:31:LEU:HD13	1.96	0.47
1:HQ:35:ARG:NH2	1:HQ:42:GLU:HB3	2.28	0.47
1:HV:128:THR:HA	1:HW:2:ASN:HA	1.95	0.47
1:IH:93:LYS:O	1:IH:97:GLU:HG2	2.14	0.47
1:IM:57:PRO:HA	1:IM:73:ASN:HA	1.96	0.47
1:IN:14:LYS:NZ	1:IN:28:SER:HB2	2.28	0.47
1:IU:58:ALA:HB3	1:IU:71:MET:HG3	1.95	0.47
1:IW:117:LEU:HD23	1:IW:117:LEU:H	1.79	0.47
1:AH:69:VAL:N	1:JE:64:CYS:H	2.10	0.47
1:AI:101:ARG:NH2	1:AI:124:VAL:HG21	2.29	0.47
1:AN:67:ALA:CA	1:JC:63:GLY:H	2.17	0.47
1:AX:57:PRO:HA	1:AX:73:ASN:HA	1.95	0.47
1:BM:107:PHE:HA	1:BM:112:ALA:HB3	1.96	0.47
1:BT:60:LYS:HZ1	1:BT:65:ALA:H	1.61	0.47
1:CO:34:GLN:O	1:CO:45:ASN:N	2.46	0.47
1:CS:3:LYS:NZ	1:CT:129:THR:HG23	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:37:LYS:NZ	1:CV:40:ILE:O	2.47	0.47
1:DL:34:GLN:O	1:DL:45:ASN:N	2.47	0.47
1:DM:67:ALA:C	1:FB:65:ALA:HB2	2.33	0.47
1:DV:58:ALA:HB3	1:DV:71:MET:HG3	1.96	0.47
1:DW:56:ARG:O	1:DW:74:GLU:N	2.42	0.47
1:EK:69:VAL:N	1:EV:64:CYS:H	2.11	0.47
1:EV:125:SER:HB2	1:EW:5:MET:CE	2.45	0.47
1:FF:11:THR:HB	1:FF:14:LYS:H	1.79	0.47
1:FO:22:ARG:NH2	1:FO:55:LYS:O	2.42	0.47
1:FP:72:PRO:HG2	1:FQ:38:VAL:HG12	1.96	0.47
1:FS:51:VAL:HG22	1:FS:79:ARG:HG2	1.95	0.47
1:FT:115:GLY:HA2	1:FU:31:LEU:HD23	1.96	0.47
1:FV:43:LEU:HD12	1:FV:85:SER:HB2	1.95	0.47
1:GC:117:LEU:H	1:GC:117:LEU:HD23	1.79	0.47
1:HD:106:LEU:CD1	1:HD:123:ILE:HD11	2.44	0.47
1:HI:23:LEU:O	1:HI:24:SER:OG	2.29	0.47
1:HX:31:LEU:HD12	1:HY:117:LEU:HD22	1.95	0.47
1:IR:55:LYS:NZ	1:IR:73:ASN:HB2	2.29	0.47
1:IZ:65:ALA:HB2	1:JB:68:CYS:SG	2.55	0.47
1:JE:115:GLY:HA3	1:JF:33:ARG:HD3	1.97	0.47
1:BO:60:LYS:HG3	1:BO:61:PRO:HD2	1.95	0.47
1:BQ:5:MET:HG2	1:BQ:19:ASP:N	2.28	0.47
1:BV:69:VAL:H	1:GH:64:CYS:N	2.12	0.47
1:DM:37:LYS:NZ	1:DM:40:ILE:O	2.47	0.47
1:DM:67:ALA:C	1:FB:63:GLY:H	2.18	0.47
1:DN:34:GLN:O	1:DN:45:ASN:N	2.46	0.47
1:DS:116:PHE:CE2	1:IB:20:PRO:HA	2.50	0.47
1:DZ:107:PHE:HA	1:DZ:112:ALA:HB3	1.95	0.47
1:EB:125:SER:O	1:EC:2:ASN:ND2	2.40	0.47
1:EC:55:LYS:NZ	1:EC:75:ASN:OD1	2.28	0.47
1:EV:115:GLY:HA2	1:EW:31:LEU:HD23	1.96	0.47
1:FA:101:ARG:HH12	1:FA:124:VAL:HG21	1.78	0.47
1:FE:56:ARG:O	1:FE:74:GLU:N	2.26	0.47
1:FX:11:THR:HB	1:FX:14:LYS:H	1.79	0.47
1:GD:14:LYS:NZ	1:GD:28:SER:HB2	2.29	0.47
1:GQ:14:LYS:NZ	1:GQ:28:SER:HB2	2.28	0.47
1:HA:96:TRP:NE1	1:HA:100:LYS:HE2	2.29	0.47
1:HG:115:GLY:HA2	1:HI:31:LEU:HD23	1.95	0.47
1:HK:60:LYS:NZ	1:HK:69:VAL:HG23	2.30	0.47
1:HP:111:ASN:HB2	1:HP:116:PHE:HB2	1.96	0.47
1:IF:115:GLY:HA2	1:IG:31:LEU:HD23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:II:55:LYS:NZ	1:II:73:ASN:HB2	2.29	0.47
1:IJ:22:ARG:NH1	1:IJ:24:SER:OG	2.47	0.47
1:IR:115:GLY:HA2	1:IS:31:LEU:HD23	1.97	0.47
1:IX:36:VAL:HG23	1:IX:43:LEU:HB2	1.96	0.47
1:JA:115:GLY:O	1:JB:33:ARG:NH1	2.48	0.47
1:JH:98:THR:HG21	1:JH:126:SER:HA	1.96	0.47
1:AF:70:ILE:HG13	1:AF:70:ILE:O	2.14	0.47
1:AI:1:ALA:HB1	1:AJ:128:THR:HG23	1.95	0.47
1:AI:105:THR:O	1:AI:109:SER:OG	2.32	0.47
1:AT:106:LEU:HD11	1:AT:123:ILE:HD11	1.97	0.47
1:BP:106:LEU:HD11	1:BP:123:ILE:HD11	1.96	0.47
1:BU:12:ALA:HB2	1:JJ:10:SER:H	1.79	0.47
1:CJ:19:ASP:HB3	1:CJ:22:ARG:O	2.14	0.47
1:DA:14:LYS:NZ	1:DA:28:SER:HB2	2.28	0.47
1:DG:60:LYS:NZ	1:DG:64:CYS:SG	2.67	0.47
1:DV:105:THR:O	1:DV:109:SER:OG	2.32	0.47
1:DY:19:ASP:HB3	1:DY:22:ARG:O	2.14	0.47
1:DY:101:ARG:CZ	1:DY:124:VAL:HG21	2.44	0.47
1:EA:98:THR:HG21	1:EA:126:SER:HA	1.96	0.47
1:EL:105:THR:O	1:EL:109:SER:OG	2.32	0.47
1:EY:117:LEU:HD23	1:EY:117:LEU:H	1.79	0.47
1:FJ:115:GLY:HA2	1:FK:31:LEU:HD23	1.97	0.47
1:FR:22:ARG:NH1	1:FR:24:SER:OG	2.47	0.47
1:FR:92:LEU:HD22	1:FS:76:GLN:NE2	2.29	0.47
1:FZ:2:ASN:ND2	1:GA:125:SER:O	2.46	0.47
1:GF:61:PRO:HG2	1:GF:64:CYS:SG	2.54	0.47
1:GN:98:THR:HG21	1:GN:126:SER:HA	1.95	0.47
1:GY:115:GLY:HA2	1:GZ:31:LEU:HD23	1.96	0.47
1:HL:14:LYS:HD3	1:HL:30:SER:HB2	1.97	0.47
1:HP:93:LYS:O	1:HP:97:GLU:HG2	2.14	0.47
1:HZ:37:LYS:NZ	1:HZ:39:GLY:O	2.47	0.47
1:HZ:128:THR:HA	1:IA:2:ASN:HA	1.97	0.47
1:AB:19:ASP:HB3	1:AB:22:ARG:O	2.15	0.47
1:AE:3:LYS:HZ1	1:AF:129:THR:HG23	1.79	0.47
1:AN:67:ALA:C	1:JC:62:GLU:HA	2.35	0.47
1:AS:5:MET:SD	1:AT:125:SER:HB2	2.54	0.47
1:AS:72:PRO:HG2	1:AT:38:VAL:HG22	1.96	0.47
1:AS:107:PHE:HA	1:AS:112:ALA:HB3	1.95	0.47
1:BI:101:ARG:CZ	1:BI:124:VAL:HG21	2.44	0.47
1:BV:8:ILE:HA	1:GH:116:PHE:HB2	1.95	0.47
1:BV:37:LYS:HE3	1:BV:37:LYS:HB3	1.73	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:101:ARG:CZ	1:CB:124:VAL:HG21	2.44	0.47
1:CF:5:MET:HG2	1:CF:17:TRP:HB3	1.96	0.47
1:CO:17:TRP:CD2	1:CP:123:ILE:HG13	2.50	0.47
1:CO:101:ARG:CZ	1:CO:124:VAL:HG21	2.44	0.47
1:CT:116:PHE:CE1	1:IE:8:ILE:HD11	2.50	0.47
1:CY:105:THR:O	1:CY:109:SER:OG	2.32	0.47
1:DR:3:LYS:NZ	1:DS:129:THR:HG23	2.30	0.47
1:DR:5:MET:SD	1:DS:125:SER:HB2	2.54	0.47
1:EE:69:VAL:N	1:GU:64:CYS:H	2.11	0.47
1:EF:128:THR:OG1	1:EG:1:ALA:O	2.28	0.47
1:EL:37:LYS:HZ3	1:EL:42:GLU:HB2	1.79	0.47
1:EM:19:ASP:HB3	1:EM:22:ARG:O	2.14	0.47
1:EQ:57:PRO:HA	1:EQ:73:ASN:HA	1.96	0.47
1:FH:37:LYS:NZ	1:FH:39:GLY:O	2.47	0.47
1:FL:111:ASN:HB2	1:FL:116:PHE:HB2	1.97	0.47
1:FN:55:LYS:HZ3	1:FN:73:ASN:HB2	1.79	0.47
1:FS:94:ALA:O	1:FS:97:GLU:HG3	2.14	0.47
1:FV:125:SER:HB2	1:FW:5:MET:HE1	1.96	0.47
1:HI:37:LYS:HD3	1:HI:42:GLU:OE2	2.14	0.47
1:HT:125:SER:HB2	1:HU:5:MET:CE	2.43	0.47
1:HW:34:GLN:NE2	1:HW:35:ARG:O	2.47	0.47
1:IU:37:LYS:HD2	1:IU:41:ALA:O	2.14	0.47
1:AD:8:ILE:HA	1:IV:116:PHE:HB2	1.96	0.47
1:AJ:67:ALA:C	1:GM:63:GLY:H	2.18	0.47
1:AR:34:GLN:NE2	1:AR:35:ARG:O	2.48	0.47
1:AU:3:LYS:NZ	1:AV:129:THR:HG23	2.30	0.47
1:AU:101:ARG:CZ	1:AU:124:VAL:HG21	2.44	0.47
1:AV:5:MET:HG2	1:AV:17:TRP:HB3	1.96	0.47
1:AZ:8:ILE:HA	1:HT:116:PHE:HB2	1.97	0.47
1:CB:56:ARG:HD2	1:CB:76:GLN:NE2	2.29	0.47
1:CC:31:LEU:HD13	1:CD:117:LEU:HD21	1.96	0.47
1:CO:5:MET:SD	1:CP:125:SER:HB2	2.55	0.47
1:DM:67:ALA:H	1:FB:65:ALA:CB	2.27	0.47
1:EF:5:MET:SD	1:EG:125:SER:HB2	2.54	0.47
1:EL:56:ARG:O	1:EL:74:GLU:N	2.47	0.47
1:FH:1:ALA:O	1:FI:129:THR:N	2.34	0.47
1:FL:5:MET:HB3	1:FL:17:TRP:HB3	1.95	0.47
1:FO:117:LEU:HD23	1:FO:117:LEU:H	1.79	0.47
1:GF:7:PRO:HA	1:GF:17:TRP:HA	1.95	0.47
1:GK:22:ARG:NH1	1:GK:24:SER:OG	2.47	0.47
1:GM:85:SER:OG	1:GN:74:GLU:OE1	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GO:5:MET:HG2	1:GP:123:ILE:HG22	1.96	0.47
1:GT:35:ARG:NH2	1:GT:42:GLU:HB3	2.26	0.47
1:GV:101:ARG:HH21	1:GV:124:VAL:HG21	1.79	0.47
1:HC:87:GLU:N	1:HC:87:GLU:OE1	2.46	0.47
1:HE:96:TRP:NE1	1:HE:100:LYS:HE2	2.30	0.47
1:HN:115:GLY:HA2	1:HO:31:LEU:HD23	1.97	0.47
1:HQ:57:PRO:HA	1:HQ:73:ASN:HA	1.97	0.47
1:HZ:5:MET:HB2	1:HZ:18:SER:O	2.14	0.47
1:IB:46:VAL:HG11	1:IC:113:GLY:O	2.15	0.47
1:ID:115:GLY:HA2	1:IE:31:LEU:HD23	1.97	0.47
1:IF:5:MET:HB3	1:IF:17:TRP:HB3	1.97	0.47
1:IH:11:THR:HB	1:IH:14:LYS:H	1.79	0.47
1:JA:88:ASN:ND2	1:JB:56:ARG:HD2	2.27	0.47
1:JA:113:GLY:O	1:JB:46:VAL:HG11	2.14	0.47
1:JB:35:ARG:NH1	1:JB:42:GLU:HG2	2.30	0.47
1:AO:1:ALA:HB1	1:AP:128:THR:HG23	1.97	0.47
1:BJ:68:CYS:N	1:HZ:63:GLY:H	2.12	0.47
1:BL:19:ASP:HB3	1:BL:22:ARG:O	2.13	0.47
1:BM:1:ALA:HB1	1:BN:128:THR:HG23	1.95	0.47
1:BP:105:THR:HG23	1:BP:106:LEU:HD12	1.97	0.47
1:BQ:58:ALA:HB3	1:BQ:71:MET:HG3	1.97	0.47
1:BR:23:LEU:HD22	1:GA:44:ASN:ND2	2.29	0.47
1:BU:1:ALA:HB1	1:BV:128:THR:HG23	1.95	0.47
1:BU:117:LEU:HD11	1:BV:31:LEU:HD13	1.97	0.47
1:BZ:60:LYS:HZ1	1:BZ:65:ALA:H	1.63	0.47
1:CG:101:ARG:CZ	1:CG:124:VAL:HG21	2.45	0.47
1:CR:56:ARG:HD2	1:CR:76:GLN:HE22	1.79	0.47
1:CS:34:GLN:O	1:CS:45:ASN:N	2.48	0.47
1:DF:5:MET:SD	1:DG:125:SER:HB2	2.54	0.47
1:DG:98:THR:HG21	1:DG:126:SER:HA	1.97	0.47
1:DH:1:ALA:HB1	1:DI:128:THR:HG23	1.96	0.47
1:DI:60:LYS:NZ	1:DI:65:ALA:HB3	2.29	0.47
1:DW:23:LEU:HD13	1:IM:44:ASN:HD21	1.79	0.47
1:DZ:71:MET:N	1:DZ:71:MET:SD	2.87	0.47
1:EA:61:PRO:HB2	1:EA:64:CYS:HB3	1.95	0.47
1:EE:8:ILE:HA	1:GU:116:PHE:HB2	1.97	0.47
1:EG:8:ILE:HA	1:HX:116:PHE:HB2	1.96	0.47
1:EK:37:LYS:NZ	1:EK:40:ILE:O	2.48	0.47
1:EN:60:LYS:NZ	1:EN:66:ASP:H	2.13	0.47
1:EP:101:ARG:CZ	1:EP:124:VAL:HG21	2.44	0.47
1:ER:5:MET:HE1	1:ES:123:ILE:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ET:37:LYS:HD3	1:ET:42:GLU:HG2	1.95	0.47
1:EU:62:GLU:HG2	1:EU:62:GLU:O	2.14	0.47
1:EU:89:LEU:HG	1:EU:93:LYS:HE3	1.96	0.47
1:FD:2:ASN:ND2	1:FE:125:SER:O	2.47	0.47
1:FF:96:TRP:NE1	1:FG:104:ASP:OD1	2.41	0.47
1:FT:71:MET:SD	1:FT:71:MET:N	2.87	0.47
1:FV:61:PRO:HG2	1:FV:64:CYS:SG	2.54	0.47
1:FW:118:ASP:OD2	1:FW:120:THR:OG1	2.20	0.47
1:GB:72:PRO:HG2	1:GC:38:VAL:HG12	1.96	0.47
1:GG:8:ILE:N	1:GG:16:VAL:O	2.40	0.47
1:GK:36:VAL:HG23	1:GK:43:LEU:HB2	1.96	0.47
1:GN:57:PRO:HA	1:GN:73:ASN:HA	1.96	0.47
1:GZ:57:PRO:HA	1:GZ:73:ASN:HA	1.96	0.47
1:HG:5:MET:SD	1:HI:125:SER:HB2	2.55	0.47
1:HP:14:LYS:NZ	1:HP:28:SER:HB2	2.29	0.47
1:HR:125:SER:HB2	1:HS:5:MET:CE	2.45	0.47
1:HS:8:ILE:N	1:HS:16:VAL:O	2.38	0.47
1:HZ:58:ALA:HB3	1:HZ:71:MET:HG2	1.96	0.47
1:ID:43:LEU:HD12	1:ID:85:SER:HB2	1.97	0.47
1:IG:57:PRO:HA	1:IG:73:ASN:HA	1.97	0.47
1:IN:93:LYS:O	1:IN:97:GLU:HG2	2.15	0.47
1:IN:101:ARG:HH21	1:IN:124:VAL:HG21	1.80	0.47
1:IR:125:SER:HB2	1:IS:5:MET:CE	2.44	0.47
1:IU:98:THR:HG21	1:IU:126:SER:HA	1.95	0.47
1:JA:5:MET:SD	1:JA:5:MET:N	2.88	0.47
1:JD:23:LEU:O	1:JD:24:SER:OG	2.29	0.47
1:JE:74:GLU:OE2	1:JF:85:SER:OG	2.23	0.47
1:BH:19:ASP:HB3	1:BH:22:ARG:O	2.15	0.47
1:BQ:107:PHE:HA	1:BQ:112:ALA:HB3	1.97	0.47
1:BU:105:THR:O	1:BU:109:SER:OG	2.33	0.47
1:CB:56:ARG:HD2	1:CB:76:GLN:HE22	1.79	0.47
1:CI:128:THR:HA	1:CJ:2:ASN:HA	1.97	0.47
1:CK:1:ALA:HB1	1:CL:128:THR:HG23	1.97	0.47
1:DB:19:ASP:HB3	1:DB:22:ARG:O	2.14	0.47
1:DP:37:LYS:HA	1:DP:37:LYS:HD2	1.69	0.47
1:EL:125:SER:O	1:EM:2:ASN:ND2	2.41	0.47
1:EP:72:PRO:HG2	1:EQ:38:VAL:HG22	1.97	0.47
1:EV:36:VAL:HG23	1:EV:43:LEU:HB2	1.96	0.47
1:GB:115:GLY:HA2	1:GC:31:LEU:HD23	1.97	0.47
1:GK:11:THR:HB	1:GK:14:LYS:H	1.80	0.47
1:HC:115:GLY:HA2	1:HD:31:LEU:HD23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HE:95:GLU:OE2	1:HF:76:GLN:HB3	2.15	0.47
1:HL:66:ASP:OD1	1:HL:69:VAL:HG23	2.14	0.47
1:HN:14:LYS:HD3	1:HN:30:SER:HB2	1.97	0.47
1:HR:115:GLY:HA3	1:HS:33:ARG:HD3	1.95	0.47
1:ID:124:VAL:HG12	1:IE:4:PRO:HB3	1.97	0.47
1:II:19:ASP:HB3	1:II:22:ARG:O	2.14	0.47
1:IT:60:LYS:HE2	1:IT:65:ALA:HB3	1.96	0.47
1:IV:115:GLY:HA2	1:IW:31:LEU:HD23	1.96	0.47
1:JA:2:ASN:HA	1:JB:128:THR:HA	1.97	0.47
1:JE:115:GLY:HA2	1:JF:31:LEU:HD23	1.95	0.47
1:AJ:8:ILE:HA	1:GM:116:PHE:HB2	1.95	0.47
1:AT:105:THR:HG23	1:AT:106:LEU:HD12	1.97	0.47
1:AV:23:LEU:HD22	1:GP:44:ASN:ND2	2.30	0.47
1:AZ:56:ARG:HD2	1:AZ:76:GLN:NE2	2.30	0.47
1:BC:5:MET:HE1	1:BD:123:ILE:HG22	1.97	0.47
1:BD:19:ASP:HB3	1:BD:22:ARG:O	2.15	0.47
1:BM:5:MET:HB3	1:BM:17:TRP:HB3	1.97	0.47
1:BP:60:LYS:HZ1	1:BP:65:ALA:H	1.63	0.47
1:BR:67:ALA:HA	1:FZ:63:GLY:N	2.18	0.47
1:CA:17:TRP:CD2	1:CB:123:ILE:HG13	2.50	0.47
1:CC:34:GLN:O	1:CC:45:ASN:N	2.48	0.47
1:CR:61:PRO:HB2	1:CR:64:CYS:HB3	1.97	0.47
1:DQ:56:ARG:HD2	1:DQ:76:GLN:NE2	2.30	0.47
1:DS:5:MET:HG3	1:DS:17:TRP:HB3	1.97	0.47
1:DX:101:ARG:CZ	1:DX:124:VAL:HG21	2.45	0.47
1:EA:19:ASP:HB3	1:EA:22:ARG:O	2.15	0.47
1:ED:3:LYS:NZ	1:EE:129:THR:HG23	2.30	0.47
1:EG:5:MET:CG	1:EG:17:TRP:HB3	2.45	0.47
1:EJ:101:ARG:CZ	1:EJ:124:VAL:HG21	2.44	0.47
1:ES:57:PRO:HA	1:ES:73:ASN:HA	1.97	0.47
1:EV:35:ARG:NH2	1:EV:44:ASN:HA	2.30	0.47
1:EZ:60:LYS:HA	1:EZ:71:MET:HE1	1.97	0.47
1:FG:55:LYS:HB3	1:FG:73:ASN:HD22	1.80	0.47
1:FJ:31:LEU:HD12	1:FK:117:LEU:HD22	1.96	0.47
1:GD:22:ARG:NH1	1:GD:24:SER:OG	2.48	0.47
1:HD:19:ASP:HB3	1:HD:22:ARG:O	2.14	0.47
1:HN:61:PRO:HG2	1:HN:64:CYS:SG	2.55	0.47
1:HZ:95:GLU:OE2	1:IA:76:GLN:HB3	2.15	0.47
1:IC:62:GLU:O	1:IC:62:GLU:HG2	2.15	0.47
1:IH:5:MET:SD	1:IH:5:MET:N	2.88	0.47
1:IH:96:TRP:NE1	1:II:104:ASP:OD1	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IN:46:VAL:HG11	1:IO:113:GLY:O	2.14	0.47
1:IR:11:THR:HB	1:IR:14:LYS:H	1.79	0.47
1:JB:117:LEU:HD23	1:JB:117:LEU:H	1.80	0.47
1:JC:115:GLY:HA2	1:JD:31:LEU:HD23	1.96	0.47
1:AI:128:THR:HA	1:AJ:2:ASN:HA	1.97	0.47
1:AM:3:LYS:NZ	1:AN:129:THR:HG23	2.30	0.47
1:AQ:37:LYS:HD3	1:AQ:42:GLU:OE2	2.15	0.47
1:BB:70:ILE:HD11	1:GK:40:ILE:HB	1.96	0.47
1:DE:19:ASP:HB3	1:DE:22:ARG:O	2.15	0.47
1:DU:67:ALA:C	1:FP:62:GLU:HA	2.35	0.47
1:DY:74:GLU:OE2	1:DY:76:GLN:NE2	2.39	0.47
1:EB:5:MET:HE1	1:EC:123:ILE:HG22	1.96	0.47
1:EC:37:LYS:NZ	1:EC:40:ILE:O	2.48	0.47
1:ET:11:THR:HB	1:ET:14:LYS:H	1.80	0.47
1:ET:63:GLY:C	1:EV:68:CYS:HA	2.35	0.47
1:FF:22:ARG:NH1	1:FF:24:SER:OG	2.48	0.47
1:FF:46:VAL:HG11	1:FG:113:GLY:O	2.15	0.47
1:FK:117:LEU:HD23	1:FK:117:LEU:H	1.79	0.47
1:FP:31:LEU:HD12	1:FQ:117:LEU:HD22	1.96	0.47
1:FP:115:GLY:HA2	1:FQ:31:LEU:HD23	1.97	0.47
1:FV:74:GLU:OE2	1:FW:85:SER:OG	2.27	0.47
1:FV:115:GLY:HA2	1:FW:31:LEU:HD23	1.96	0.47
1:FZ:11:THR:HB	1:FZ:14:LYS:H	1.80	0.47
1:GM:96:TRP:NE1	1:GM:100:LYS:HE2	2.29	0.47
1:GT:92:LEU:HA	1:GT:95:GLU:OE2	2.14	0.47
1:HD:117:LEU:HD23	1:HD:117:LEU:H	1.80	0.47
1:HE:115:GLY:HA2	1:HF:31:LEU:HD23	1.97	0.47
1:HL:17:TRP:CD2	1:HM:123:ILE:HG13	2.49	0.47
1:HR:7:PRO:HA	1:HR:17:TRP:HA	1.96	0.47
1:HU:60:LYS:NZ	1:HU:65:ALA:O	2.33	0.47
1:HV:93:LYS:O	1:HV:97:GLU:HG2	2.14	0.47
1:IH:14:LYS:NZ	1:IH:28:SER:HB2	2.26	0.47
1:IL:74:GLU:OE2	1:IM:85:SER:OG	2.32	0.47
1:IR:70:ILE:HD11	1:IV:40:ILE:HD12	1.96	0.47
1:AD:67:ALA:C	1:IV:63:GLY:H	2.18	0.46
1:AF:69:VAL:H	1:GS:64:CYS:N	2.13	0.46
1:AZ:56:ARG:HD2	1:AZ:76:GLN:HE22	1.80	0.46
1:BL:60:LYS:NZ	1:BL:65:ALA:H	2.13	0.46
1:BO:115:GLY:HA2	1:BP:31:LEU:HD23	1.97	0.46
1:BU:101:ARG:HH22	1:BV:2:ASN:HD22	1.63	0.46
1:BZ:19:ASP:HB3	1:BZ:22:ARG:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:117:LEU:HD23	1:CP:15:ILE:HG13	1.97	0.46
1:CS:17:TRP:CD2	1:CT:123:ILE:HG13	2.50	0.46
1:CV:70:ILE:HG23	1:HL:61:PRO:HB2	1.97	0.46
1:CX:19:ASP:HB3	1:CX:22:ARG:O	2.15	0.46
1:CZ:19:ASP:HB3	1:CZ:22:ARG:O	2.15	0.46
1:DO:98:THR:HG21	1:DO:126:SER:HA	1.96	0.46
1:DR:60:LYS:NZ	1:DR:66:ASP:O	2.32	0.46
1:EG:67:ALA:C	1:HX:63:GLY:H	2.19	0.46
1:EX:22:ARG:NH1	1:EX:24:SER:OG	2.48	0.46
1:EX:115:GLY:HA2	1:EY:31:LEU:HD23	1.96	0.46
1:FF:87:GLU:OE1	1:FF:87:GLU:N	2.45	0.46
1:FT:35:ARG:NH2	1:FT:44:ASN:OD1	2.47	0.46
1:FX:93:LYS:O	1:FX:97:GLU:HG2	2.14	0.46
1:GE:74:GLU:HG2	1:GE:75:ASN:H	1.80	0.46
1:GK:74:GLU:OE2	1:GL:88:ASN:ND2	2.47	0.46
1:GW:71:MET:N	1:GW:71:MET:SD	2.88	0.46
1:GX:60:LYS:NZ	1:GX:69:VAL:HG23	2.30	0.46
1:HB:117:LEU:H	1:HB:117:LEU:HD23	1.80	0.46
1:HC:96:TRP:NE1	1:HD:104:ASP:OD1	2.40	0.46
1:HN:72:PRO:HG2	1:HO:38:VAL:HG12	1.97	0.46
1:HT:20:PRO:HB3	1:HY:116:PHE:HE2	1.80	0.46
1:HT:115:GLY:HA2	1:HU:31:LEU:HD23	1.97	0.46
1:HW:37:LYS:HD2	1:HW:41:ALA:O	2.15	0.46
1:IC:117:LEU:HD23	1:IC:117:LEU:H	1.80	0.46
1:IF:1:ALA:O	1:IG:129:THR:N	2.39	0.46
1:IH:22:ARG:NH1	1:IH:24:SER:OG	2.48	0.46
1:IP:125:SER:HB2	1:IQ:5:MET:CE	2.44	0.46
1:IT:22:ARG:NH1	1:IT:24:SER:OG	2.48	0.46
1:IV:17:TRP:CD2	1:IW:123:ILE:HG13	2.50	0.46
1:AF:8:ILE:HA	1:GS:116:PHE:HB2	1.97	0.46
1:AG:5:MET:HE1	1:AH:123:ILE:HG22	1.97	0.46
1:AK:14:LYS:NZ	1:AK:28:SER:HB2	2.31	0.46
1:AZ:5:MET:CG	1:AZ:17:TRP:HB3	2.45	0.46
1:BW:34:GLN:O	1:BW:45:ASN:N	2.47	0.46
1:CC:105:THR:O	1:CC:109:SER:OG	2.33	0.46
1:CE:101:ARG:CZ	1:CE:124:VAL:HG21	2.45	0.46
1:CH:69:VAL:N	1:HA:64:CYS:H	2.13	0.46
1:CJ:25:THR:O	1:CJ:25:THR:OG1	2.32	0.46
1:DP:14:LYS:NZ	1:DP:28:SER:HB2	2.27	0.46
1:DQ:19:ASP:HB3	1:DQ:22:ARG:O	2.16	0.46
1:DX:51:VAL:HG22	1:DX:79:ARG:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:101:ARG:CZ	1:EA:124:VAL:HG21	2.45	0.46
1:EC:19:ASP:HB3	1:EC:22:ARG:O	2.15	0.46
1:EK:67:ALA:C	1:EV:63:GLY:H	2.18	0.46
1:EX:14:LYS:HD3	1:EX:30:SER:HB2	1.97	0.46
1:EX:61:PRO:HG2	1:EX:64:CYS:SG	2.55	0.46
1:EZ:46:VAL:HG11	1:FA:113:GLY:O	2.14	0.46
1:FL:61:PRO:HG2	1:FL:64:CYS:SG	2.55	0.46
1:FN:115:GLY:HA2	1:FO:31:LEU:HD23	1.97	0.46
1:FR:5:MET:SD	1:FS:125:SER:HB2	2.55	0.46
1:GF:5:MET:HG2	1:GG:123:ILE:HG22	1.96	0.46
1:GL:62:GLU:O	1:GL:62:GLU:HG2	2.15	0.46
1:GU:5:MET:HE1	1:GV:123:ILE:HG22	1.96	0.46
1:GX:44:ASN:ND2	1:GY:23:LEU:HB2	2.30	0.46
1:HM:87:GLU:OE1	1:HM:87:GLU:N	2.42	0.46
1:HZ:115:GLY:HA2	1:IA:31:LEU:HD23	1.97	0.46
1:IL:14:LYS:HD3	1:IL:30:SER:HB2	1.97	0.46
1:IQ:8:ILE:N	1:IQ:16:VAL:O	2.39	0.46
1:JJ:117:LEU:HD23	1:JJ:117:LEU:H	1.79	0.46
1:AC:14:LYS:NZ	1:AC:30:SER:HB2	2.29	0.46
1:AG:5:MET:SD	1:AH:125:SER:HB2	2.55	0.46
1:AJ:56:ARG:HD2	1:AJ:76:GLN:NE2	2.31	0.46
1:AM:19:ASP:HB3	1:AM:22:ARG:O	2.15	0.46
1:AY:5:MET:SD	1:AY:5:MET:N	2.88	0.46
1:BL:34:GLN:NE2	1:BL:35:ARG:O	2.48	0.46
1:BU:101:ARG:CZ	1:BU:124:VAL:HG21	2.46	0.46
1:CH:67:ALA:N	1:HA:65:ALA:H	2.14	0.46
1:CM:14:LYS:NZ	1:CM:15:ILE:O	2.49	0.46
1:CS:105:THR:O	1:CS:109:SER:OG	2.33	0.46
1:CU:5:MET:HG2	1:CU:18:SER:C	2.35	0.46
1:CU:37:LYS:HD3	1:CU:42:GLU:OE2	2.15	0.46
1:CZ:68:CYS:HB2	1:ID:64:CYS:SG	2.55	0.46
1:DE:68:CYS:HA	1:FT:64:CYS:SG	2.55	0.46
1:DI:56:ARG:HD2	1:DI:76:GLN:NE2	2.30	0.46
1:DJ:31:LEU:HD23	1:DK:115:GLY:HA2	1.95	0.46
1:DR:60:LYS:HZ3	1:DR:66:ASP:H	1.63	0.46
1:EB:58:ALA:HB3	1:EB:71:MET:HG3	1.98	0.46
1:EJ:34:GLN:O	1:EJ:45:ASN:N	2.48	0.46
1:EL:58:ALA:HB3	1:EL:71:MET:HG3	1.98	0.46
1:FG:32:LEU:HB3	1:FG:47:SER:HB3	1.97	0.46
1:FI:60:LYS:HE2	1:FI:64:CYS:HB3	1.96	0.46
1:FQ:117:LEU:HD23	1:FQ:117:LEU:H	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FT:60:LYS:HB3	1:FT:65:ALA:HB2	1.97	0.46
1:GM:43:LEU:HD12	1:GM:85:SER:HB2	1.96	0.46
1:HC:93:LYS:O	1:HC:97:GLU:HG2	2.16	0.46
1:HD:62:GLU:HG2	1:HD:62:GLU:O	2.16	0.46
1:HF:117:LEU:HD23	1:HF:117:LEU:H	1.80	0.46
1:HI:87:GLU:OE1	1:HI:87:GLU:N	2.42	0.46
1:HL:2:ASN:ND2	1:HM:125:SER:O	2.46	0.46
1:IA:117:LEU:H	1:IA:117:LEU:HD23	1.80	0.46
1:JB:34:GLN:NE2	1:JB:35:ARG:O	2.48	0.46
1:JF:35:ARG:NH2	1:JF:43:LEU:O	2.48	0.46
1:JH:60:LYS:HE2	1:JH:71:MET:HE1	1.97	0.46
1:JI:115:GLY:HA2	1:JJ:31:LEU:HD23	1.96	0.46
1:AB:32:LEU:HB3	1:AB:47:SER:HB3	1.96	0.46
1:AD:19:ASP:HB3	1:AD:22:ARG:O	2.16	0.46
1:AR:19:ASP:HB3	1:AR:22:ARG:O	2.15	0.46
1:AS:105:THR:O	1:AS:109:SER:OG	2.34	0.46
1:BC:14:LYS:NZ	1:BC:15:ILE:O	2.49	0.46
1:BF:56:ARG:HD2	1:BF:76:GLN:HE22	1.79	0.46
1:BI:37:LYS:HD2	1:BI:42:GLU:OE1	2.15	0.46
1:BO:105:THR:O	1:BO:109:SER:OG	2.33	0.46
1:BR:68:CYS:SG	1:FZ:65:ALA:HA	2.56	0.46
1:BW:3:LYS:NZ	1:BX:129:THR:HG23	2.30	0.46
1:CG:1:ALA:HB1	1:CH:128:THR:HG23	1.97	0.46
1:CJ:68:CYS:HA	1:IJ:64:CYS:SG	2.56	0.46
1:CL:67:ALA:C	1:FN:63:GLY:H	2.19	0.46
1:CZ:57:PRO:HA	1:CZ:73:ASN:HA	1.96	0.46
1:DU:67:ALA:C	1:FP:63:GLY:H	2.18	0.46
1:DY:56:ARG:HD2	1:DY:76:GLN:NE2	2.30	0.46
1:ER:31:LEU:HD11	1:ES:117:LEU:HB3	1.97	0.46
1:FF:37:LYS:NZ	1:FF:40:ILE:O	2.48	0.46
1:FN:125:SER:HB2	1:FO:5:MET:CE	2.44	0.46
1:FW:34:GLN:OE1	1:FW:36:VAL:HG13	2.15	0.46
1:HC:113:GLY:O	1:HD:46:VAL:HG11	2.15	0.46
1:HI:34:GLN:OE1	1:HI:36:VAL:HG13	2.15	0.46
1:HT:60:LYS:HB3	1:HT:65:ALA:HB2	1.97	0.46
1:IC:19:ASP:HB3	1:IC:22:ARG:O	2.15	0.46
1:II:35:ARG:NH2	1:II:44:ASN:HA	2.30	0.46
1:IK:38:VAL:HG21	1:IK:43:LEU:HD22	1.96	0.46
1:IQ:37:LYS:NZ	1:IQ:38:VAL:O	2.37	0.46
1:IZ:71:MET:SD	1:IZ:71:MET:N	2.79	0.46
1:JB:105:THR:HG23	1:JB:106:LEU:HD12	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JD:74:GLU:HG2	1:JD:75:ASN:H	1.79	0.46
1:AG:5:MET:HB2	1:AG:17:TRP:HB3	1.98	0.46
1:AJ:56:ARG:HD2	1:AJ:76:GLN:HE22	1.79	0.46
1:AN:8:ILE:HA	1:JC:116:PHE:HB2	1.97	0.46
1:AO:5:MET:SD	1:AO:5:MET:N	2.89	0.46
1:AY:128:THR:OG1	1:AZ:1:ALA:O	2.25	0.46
1:BH:37:LYS:NZ	1:BH:40:ILE:O	2.45	0.46
1:BI:3:LYS:HZ1	1:BJ:127:ASP:HB3	1.81	0.46
1:BI:8:ILE:HG13	1:BI:18:SER:HB3	1.96	0.46
1:BK:34:GLN:O	1:BK:45:ASN:N	2.48	0.46
1:BM:101:ARG:CZ	1:BM:124:VAL:HG21	2.46	0.46
1:CB:8:ILE:HA	1:FJ:116:PHE:HB2	1.97	0.46
1:CJ:67:ALA:HB1	1:IJ:64:CYS:HA	1.96	0.46
1:CO:105:THR:O	1:CO:109:SER:OG	2.33	0.46
1:DK:19:ASP:HB3	1:DK:22:ARG:O	2.16	0.46
1:DQ:106:LEU:HD21	1:DQ:123:ILE:HD11	1.98	0.46
1:DU:5:MET:HG3	1:DU:17:TRP:HB3	1.98	0.46
1:ED:14:LYS:NZ	1:ED:15:ILE:O	2.48	0.46
1:ET:22:ARG:NH1	1:ET:24:SER:OG	2.48	0.46
1:FB:115:GLY:HA2	1:FC:31:LEU:HD23	1.96	0.46
1:GF:72:PRO:HG2	1:GG:38:VAL:HG12	1.97	0.46
1:GH:96:TRP:NE1	1:GH:100:LYS:HE2	2.30	0.46
1:HN:5:MET:HG2	1:HN:19:ASP:N	2.30	0.46
1:HR:37:LYS:NZ	1:HR:39:GLY:O	2.48	0.46
1:IB:93:LYS:O	1:IB:97:GLU:HG2	2.16	0.46
1:IN:37:LYS:HD3	1:IN:42:GLU:HG2	1.97	0.46
1:IQ:117:LEU:HD23	1:IQ:117:LEU:H	1.81	0.46
1:IW:106:LEU:HD11	1:IW:123:ILE:HD11	1.96	0.46
1:IX:34:GLN:NE2	1:IX:45:ASN:OD1	2.48	0.46
1:IX:115:GLY:HA2	1:IZ:31:LEU:HD23	1.96	0.46
1:JF:64:CYS:HA	1:JH:67:ALA:HB3	1.97	0.46
1:AJ:5:MET:CG	1:AJ:17:TRP:HB3	2.46	0.46
1:AV:106:LEU:HD11	1:AV:123:ILE:HD11	1.97	0.46
1:BC:3:LYS:NZ	1:BD:129:THR:HG23	2.31	0.46
1:BI:1:ALA:HB1	1:BJ:128:THR:HG23	1.96	0.46
1:BY:56:ARG:O	1:BY:74:GLU:N	2.45	0.46
1:CE:60:LYS:NZ	1:CE:66:ASP:H	2.13	0.46
1:CM:37:LYS:HZ3	1:CM:42:GLU:HB2	1.80	0.46
1:CU:58:ALA:HB3	1:CU:71:MET:HG3	1.98	0.46
1:DL:17:TRP:CD2	1:DM:123:ILE:HG13	2.51	0.46
1:DL:105:THR:O	1:DL:109:SER:OG	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DO:8:ILE:HA	1:FV:116:PHE:HB2	1.97	0.46
1:DP:1:ALA:HB1	1:DQ:128:THR:HG23	1.97	0.46
1:DP:12:ALA:HB2	1:FW:10:SER:N	2.23	0.46
1:DW:19:ASP:HB3	1:DW:22:ARG:O	2.15	0.46
1:DX:8:ILE:HG13	1:DX:18:SER:HB3	1.98	0.46
1:EA:106:LEU:HD11	1:EA:123:ILE:HD11	1.98	0.46
1:EE:5:MET:CG	1:EE:17:TRP:HB3	2.45	0.46
1:EE:68:CYS:HB2	1:GU:64:CYS:C	2.36	0.46
1:ER:56:ARG:NH2	1:ES:95:GLU:OE2	2.36	0.46
1:ER:61:PRO:HG2	1:ER:64:CYS:SG	2.55	0.46
1:FB:125:SER:HB2	1:FC:5:MET:CE	2.45	0.46
1:FT:55:LYS:NZ	1:FT:73:ASN:HB2	2.31	0.46
1:FV:5:MET:SD	1:FW:125:SER:HB2	2.55	0.46
1:FW:60:LYS:HE3	1:FW:64:CYS:HB3	1.97	0.46
1:GP:65:ALA:HB2	1:GR:68:CYS:SG	2.56	0.46
1:GX:37:LYS:HD2	1:GX:41:ALA:O	2.16	0.46
1:HO:8:ILE:N	1:HO:16:VAL:O	2.39	0.46
1:IL:22:ARG:NH1	1:IL:24:SER:OG	2.49	0.46
1:IM:117:LEU:HD23	1:IM:117:LEU:H	1.80	0.46
1:IR:85:SER:OG	1:IS:74:GLU:OE1	2.19	0.46
1:IS:36:VAL:N	1:IS:43:LEU:O	2.48	0.46
1:AC:17:TRP:CD2	1:AD:123:ILE:HG13	2.51	0.46
1:AS:17:TRP:CD2	1:AT:123:ILE:HG13	2.50	0.46
1:AW:37:LYS:HB2	1:AW:42:GLU:OE2	2.15	0.46
1:BP:8:ILE:HA	1:GF:116:PHE:HB2	1.97	0.46
1:BT:98:THR:HG21	1:BT:126:SER:HA	1.98	0.46
1:CD:37:LYS:NZ	1:CD:40:ILE:O	2.45	0.46
1:CD:116:PHE:CE1	1:FK:8:ILE:HD11	2.51	0.46
1:CJ:101:ARG:CZ	1:CJ:124:VAL:HG21	2.46	0.46
1:CN:19:ASP:HB3	1:CN:22:ARG:O	2.16	0.46
1:CP:19:ASP:HB3	1:CP:22:ARG:O	2.16	0.46
1:CP:57:PRO:HA	1:CP:73:ASN:HA	1.97	0.46
1:CX:98:THR:HG21	1:CX:126:SER:HA	1.98	0.46
1:DF:105:THR:O	1:DF:109:SER:OG	2.33	0.46
1:DG:68:CYS:HB3	1:IO:64:CYS:HB2	1.51	0.46
1:DR:5:MET:HE1	1:DS:123:ILE:HG22	1.97	0.46
1:DU:19:ASP:HB3	1:DU:22:ARG:O	2.15	0.46
1:DZ:12:ALA:HB2	1:HF:10:SER:N	2.29	0.46
1:EI:66:ASP:OD2	1:EI:68:CYS:N	2.49	0.46
1:EJ:117:LEU:HD23	1:EK:15:ILE:HG13	1.98	0.46
1:EL:3:LYS:NZ	1:EM:129:THR:HG23	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EY:8:ILE:N	1:EY:16:VAL:O	2.39	0.46
1:FE:117:LEU:HD23	1:FE:117:LEU:H	1.80	0.46
1:FH:96:TRP:NE1	1:FH:100:LYS:HE2	2.31	0.46
1:FL:113:GLY:O	1:FM:46:VAL:HG11	2.15	0.46
1:FR:11:THR:HG22	1:FR:13:ASN:H	1.79	0.46
1:GI:117:LEU:HD23	1:GI:117:LEU:H	1.80	0.46
1:GV:92:LEU:HA	1:GV:95:GLU:OE2	2.16	0.46
1:HF:8:ILE:N	1:HF:16:VAL:O	2.39	0.46
1:HJ:22:ARG:NH1	1:HJ:24:SER:OG	2.49	0.46
1:HP:5:MET:N	1:HP:5:MET:SD	2.89	0.46
1:IE:5:MET:SD	1:IE:5:MET:N	2.89	0.46
1:IE:117:LEU:HD23	1:IE:117:LEU:H	1.80	0.46
1:II:38:VAL:HB	1:II:43:LEU:HD12	1.97	0.46
1:IJ:115:GLY:HA2	1:IK:31:LEU:HD23	1.96	0.46
1:IO:62:GLU:O	1:IO:62:GLU:HG2	2.16	0.46
1:IT:3:LYS:HE3	1:IT:21:THR:HG21	1.96	0.46
1:AF:23:LEU:HD22	1:GT:44:ASN:ND2	2.30	0.46
1:AM:5:MET:SD	1:AM:5:MET:N	2.89	0.46
1:AM:105:THR:O	1:AM:109:SER:OG	2.33	0.46
1:BO:17:TRP:CD2	1:BP:123:ILE:HG13	2.51	0.46
1:BR:57:PRO:HA	1:BR:73:ASN:HA	1.98	0.46
1:BY:101:ARG:CZ	1:BY:124:VAL:HG21	2.46	0.46
1:DR:17:TRP:CD2	1:DS:123:ILE:HG13	2.50	0.46
1:EC:35:ARG:HB3	1:EC:42:GLU:OE2	2.16	0.46
1:EJ:5:MET:SD	1:EK:125:SER:HB2	2.55	0.46
1:EN:5:MET:SD	1:EO:125:SER:HB2	2.56	0.46
1:EP:62:GLU:O	1:EP:62:GLU:HG2	2.16	0.46
1:EU:92:LEU:HA	1:EU:95:GLU:OE2	2.16	0.46
1:EU:117:LEU:HD23	1:EU:117:LEU:H	1.81	0.46
1:FD:96:TRP:NE1	1:FD:100:LYS:HE2	2.31	0.46
1:FY:19:ASP:HB3	1:FY:22:ARG:O	2.15	0.46
1:GE:89:LEU:HG	1:GE:93:LYS:HE3	1.97	0.46
1:GI:57:PRO:HA	1:GI:73:ASN:HA	1.97	0.46
1:GO:55:LYS:HZ3	1:GO:73:ASN:HB2	1.81	0.46
1:HO:117:LEU:HD23	1:HO:117:LEU:H	1.80	0.46
1:HX:115:GLY:HA2	1:HY:31:LEU:HD23	1.97	0.46
1:HY:22:ARG:NH2	1:HY:55:LYS:O	2.45	0.46
1:JE:35:ARG:NH2	1:JE:44:ASN:HA	2.31	0.46
1:AH:5:MET:HG2	1:AH:17:TRP:HB3	1.96	0.46
1:AK:72:PRO:HG2	1:AL:38:VAL:HG22	1.97	0.46
1:AU:105:THR:O	1:AU:109:SER:OG	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:35:ARG:HB3	1:AX:42:GLU:OE2	2.15	0.46
1:BP:19:ASP:HB3	1:BP:22:ARG:O	2.16	0.46
1:BU:12:ALA:HB2	1:JJ:10:SER:N	2.31	0.46
1:BX:19:ASP:HB3	1:BX:22:ARG:O	2.16	0.46
1:CQ:1:ALA:O	1:CQ:3:LYS:NZ	2.48	0.46
1:DA:5:MET:SD	1:DB:125:SER:HB2	2.56	0.46
1:DO:25:THR:O	1:DO:25:THR:OG1	2.33	0.46
1:EJ:105:THR:O	1:EJ:109:SER:OG	2.34	0.46
1:ER:11:THR:HB	1:ER:14:LYS:H	1.81	0.46
1:ER:22:ARG:NH1	1:ER:24:SER:OG	2.49	0.46
1:EX:5:MET:HG2	1:EX:19:ASP:N	2.30	0.46
1:GI:38:VAL:HG21	1:GI:43:LEU:HD12	1.98	0.46
1:GI:56:ARG:O	1:GI:74:GLU:N	2.27	0.46
1:GK:46:VAL:HG11	1:GL:113:GLY:O	2.16	0.46
1:GO:20:PRO:HB3	1:GT:116:PHE:HE2	1.81	0.46
1:GU:68:CYS:HB3	1:GZ:64:CYS:HA	1.97	0.46
1:HI:117:LEU:HD23	1:HI:117:LEU:H	1.79	0.46
1:HM:117:LEU:HD23	1:HM:117:LEU:H	1.80	0.46
1:HT:3:LYS:HZ2	1:HU:127:ASP:C	2.20	0.46
1:HT:46:VAL:HG11	1:HU:113:GLY:O	2.16	0.46
1:IE:62:GLU:HG2	1:IE:62:GLU:O	2.15	0.46
1:IH:39:GLY:HA3	1:II:72:PRO:HG2	1.96	0.46
1:IX:86:ALA:HB1	1:IZ:114:LEU:HD23	1.98	0.46
1:AB:58:ALA:HB3	1:AB:71:MET:HE1	1.98	0.46
1:AE:31:LEU:HD13	1:AF:117:LEU:HD21	1.98	0.46
1:AE:60:LYS:NZ	1:AE:66:ASP:H	2.14	0.46
1:AF:19:ASP:HB3	1:AF:22:ARG:O	2.16	0.46
1:AG:1:ALA:HB1	1:AH:128:THR:HG23	1.98	0.46
1:AX:67:ALA:C	1:GY:63:GLY:H	2.19	0.46
1:BF:19:ASP:HB3	1:BF:22:ARG:O	2.16	0.46
1:BN:105:THR:HG23	1:BN:106:LEU:HD12	1.97	0.46
1:BO:34:GLN:O	1:BO:45:ASN:N	2.48	0.46
1:BQ:5:MET:HG2	1:BQ:18:SER:C	2.35	0.46
1:CI:101:ARG:CZ	1:CI:124:VAL:HG21	2.46	0.46
1:CM:105:THR:O	1:CM:109:SER:OG	2.33	0.46
1:CV:35:ARG:HB3	1:CV:42:GLU:OE2	2.15	0.46
1:DI:8:ILE:HA	1:FH:116:PHE:HB2	1.97	0.46
1:DV:34:GLN:O	1:DV:45:ASN:N	2.46	0.46
1:EE:55:LYS:NZ	1:EE:75:ASN:OD1	2.30	0.46
1:EF:72:PRO:HG2	1:EG:38:VAL:HG22	1.98	0.46
1:EG:19:ASP:HB3	1:EG:22:ARG:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EL:116:PHE:HE2	1:EP:20:PRO:HB3	1.81	0.46
1:FC:8:ILE:N	1:FC:16:VAL:O	2.37	0.46
1:FD:70:ILE:HD11	1:FH:40:ILE:HD12	1.97	0.46
1:FR:95:GLU:OE2	1:FS:76:GLN:NE2	2.49	0.46
1:GQ:56:ARG:O	1:GQ:74:GLU:N	2.30	0.46
1:GQ:113:GLY:O	1:GR:46:VAL:HG11	2.15	0.46
1:HC:46:VAL:HG11	1:HD:113:GLY:O	2.16	0.46
1:JJ:37:LYS:NZ	1:JJ:38:VAL:O	2.41	0.46
1:AC:124:VAL:HA	1:AD:4:PRO:HA	1.99	0.45
1:AC:128:THR:OG1	1:AD:1:ALA:O	2.28	0.45
1:AE:14:LYS:NZ	1:AE:28:SER:HB2	2.29	0.45
1:AG:115:GLY:O	1:AH:33:ARG:NH1	2.49	0.45
1:AO:101:ARG:CZ	1:AO:124:VAL:HG21	2.46	0.45
1:AQ:58:ALA:HB3	1:AQ:71:MET:HG3	1.98	0.45
1:AU:14:LYS:HD2	1:AU:14:LYS:HA	1.84	0.45
1:BA:3:LYS:HZ2	1:BB:129:THR:HG23	1.80	0.45
1:BP:98:THR:HG21	1:BP:126:SER:HA	1.98	0.45
1:BX:69:VAL:HG22	1:JI:64:CYS:HB2	1.99	0.45
1:CA:101:ARG:CZ	1:CA:124:VAL:HG21	2.46	0.45
1:CL:70:ILE:HG23	1:FN:61:PRO:HB2	1.97	0.45
1:CM:5:MET:SD	1:CN:125:SER:HB2	2.56	0.45
1:CM:34:GLN:O	1:CM:45:ASN:N	2.49	0.45
1:CR:19:ASP:HB3	1:CR:22:ARG:O	2.15	0.45
1:DF:60:LYS:NZ	1:DF:66:ASP:H	2.15	0.45
1:DL:5:MET:SD	1:DM:125:SER:HB2	2.55	0.45
1:DU:67:ALA:H	1:FP:65:ALA:CB	2.29	0.45
1:EK:105:THR:HG23	1:EK:106:LEU:HD12	1.98	0.45
1:EU:19:ASP:HB3	1:EU:22:ARG:O	2.15	0.45
1:EW:71:MET:N	1:EW:71:MET:SD	2.79	0.45
1:EZ:22:ARG:NH1	1:EZ:24:SER:OG	2.50	0.45
1:FF:60:LYS:HZ3	1:FF:63:GLY:H	1.63	0.45
1:FL:5:MET:HE1	1:FM:123:ILE:HG22	1.98	0.45
1:FM:62:GLU:O	1:FM:62:GLU:HG2	2.16	0.45
1:FU:35:ARG:HH21	1:FU:43:LEU:C	2.19	0.45
1:GL:19:ASP:HB3	1:GL:22:ARG:O	2.16	0.45
1:GS:115:GLY:HA2	1:GT:31:LEU:HD23	1.98	0.45
1:GV:45:ASN:HA	1:GV:85:SER:HA	1.97	0.45
1:GY:76:GLN:NE2	1:GZ:91:THR:OG1	2.49	0.45
1:HG:61:PRO:HG2	1:HG:64:CYS:SG	2.55	0.45
1:HK:117:LEU:HD23	1:HK:117:LEU:H	1.81	0.45
1:HO:5:MET:N	1:HO:5:MET:SD	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IH:5:MET:HG3	1:IH:19:ASP:HA	1.99	0.45
1:JA:14:LYS:NZ	1:JA:28:SER:HB2	2.27	0.45
1:JG:14:LYS:NZ	1:JG:28:SER:HB2	2.28	0.45
1:JI:37:LYS:NZ	1:JI:39:GLY:O	2.50	0.45
1:AI:115:GLY:O	1:AJ:33:ARG:NH1	2.49	0.45
1:AS:101:ARG:CZ	1:AS:124:VAL:HG21	2.47	0.45
1:AY:72:PRO:HG2	1:AZ:38:VAL:HG22	1.96	0.45
1:BE:3:LYS:NZ	1:BF:129:THR:HG23	2.30	0.45
1:BG:3:LYS:NZ	1:BH:129:THR:HG23	2.30	0.45
1:BK:37:LYS:HZ3	1:BK:42:GLU:HB2	1.80	0.45
1:BT:19:ASP:HB3	1:BT:22:ARG:O	2.15	0.45
1:BX:8:ILE:HA	1:JI:116:PHE:HB2	1.98	0.45
1:FN:66:ASP:OD1	1:FN:69:VAL:HG23	2.15	0.45
1:FS:37:LYS:HD2	1:FS:41:ALA:O	2.17	0.45
1:FS:117:LEU:HD23	1:FS:117:LEU:H	1.81	0.45
1:FX:22:ARG:NH1	1:FX:24:SER:OG	2.49	0.45
1:GL:105:THR:HA	1:GL:109:SER:HB2	1.98	0.45
1:GR:35:ARG:NH2	1:GR:42:GLU:HG2	2.31	0.45
1:HJ:116:PHE:CE1	1:HL:6:GLN:HB2	2.52	0.45
1:HW:19:ASP:HB3	1:HW:22:ARG:O	2.17	0.45
1:IC:58:ALA:HB3	1:IC:71:MET:HG3	1.98	0.45
1:IJ:56:ARG:O	1:IJ:74:GLU:N	2.42	0.45
1:IO:19:ASP:HB3	1:IO:22:ARG:O	2.16	0.45
1:AA:125:SER:O	1:AB:2:ASN:ND2	2.38	0.45
1:AU:5:MET:SD	1:AV:125:SER:HB2	2.55	0.45
1:AV:62:GLU:HG2	1:AV:62:GLU:O	2.16	0.45
1:AZ:68:CYS:HA	1:HT:64:CYS:SG	2.56	0.45
1:BO:125:SER:O	1:BP:2:ASN:ND2	2.50	0.45
1:CB:56:ARG:O	1:CB:74:GLU:N	2.37	0.45
1:CI:17:TRP:CD2	1:CJ:123:ILE:HG13	2.52	0.45
1:CL:19:ASP:HB3	1:CL:22:ARG:O	2.17	0.45
1:DE:62:GLU:HG2	1:DE:62:GLU:O	2.16	0.45
1:DI:70:ILE:HG23	1:FH:61:PRO:HB2	1.98	0.45
1:EI:56:ARG:HD2	1:EI:76:GLN:NE2	2.31	0.45
1:EK:23:LEU:HD22	1:EW:44:ASN:HD21	1.81	0.45
1:EN:49:GLN:OE1	1:EN:79:ARG:NH2	2.35	0.45
1:FH:74:GLU:OE2	1:FI:85:SER:OG	2.32	0.45
1:FN:31:LEU:HD12	1:FO:117:LEU:HD22	1.99	0.45
1:FP:68:CYS:HB3	1:FU:64:CYS:HA	1.98	0.45
1:FZ:17:TRP:CD2	1:GA:123:ILE:HG13	2.51	0.45
1:GA:56:ARG:O	1:GA:74:GLU:N	2.28	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GK:113:GLY:O	1:GL:46:VAL:HG11	2.15	0.45
1:GO:115:GLY:HA2	1:GP:31:LEU:HD23	1.97	0.45
1:HK:19:ASP:HB3	1:HK:22:ARG:O	2.15	0.45
1:HL:43:LEU:HD22	1:HL:87:GLU:OE2	2.15	0.45
1:HU:93:LYS:O	1:HU:97:GLU:HG2	2.17	0.45
1:HW:35:ARG:NH2	1:HW:42:GLU:HG2	2.31	0.45
1:ID:66:ASP:OD2	1:ID:68:CYS:HB2	2.17	0.45
1:IR:46:VAL:HG11	1:IS:113:GLY:O	2.16	0.45
1:IU:94:ALA:O	1:IU:97:GLU:HG3	2.16	0.45
1:AA:116:PHE:HE2	1:AC:20:PRO:HB3	1.81	0.45
1:AE:34:GLN:O	1:AE:45:ASN:N	2.49	0.45
1:AH:60:LYS:HZ1	1:AH:65:ALA:HB3	1.81	0.45
1:AP:101:ARG:CZ	1:AP:124:VAL:HG21	2.46	0.45
1:AV:98:THR:HG21	1:AV:126:SER:HA	1.97	0.45
1:BK:58:ALA:HB3	1:BK:71:MET:HG3	1.98	0.45
1:BX:62:GLU:H	1:BX:62:GLU:CD	2.20	0.45
1:CP:37:LYS:NZ	1:CP:40:ILE:O	2.48	0.45
1:CV:67:ALA:O	1:HL:65:ALA:HB2	2.16	0.45
1:CY:128:THR:HA	1:CZ:2:ASN:HA	1.99	0.45
1:DM:105:THR:HG23	1:DM:106:LEU:HD12	1.98	0.45
1:DO:60:LYS:HZ1	1:DO:65:ALA:H	1.64	0.45
1:DQ:25:THR:O	1:DQ:25:THR:OG1	2.34	0.45
1:DX:88:ASN:ND2	1:DY:74:GLU:OE2	2.34	0.45
1:EO:19:ASP:HB3	1:EO:22:ARG:O	2.17	0.45
1:FK:19:ASP:HB3	1:FK:22:ARG:O	2.16	0.45
1:FS:37:LYS:NZ	1:FS:38:VAL:O	2.37	0.45
1:FT:32:LEU:HG	1:FT:34:GLN:OE1	2.16	0.45
1:GK:93:LYS:O	1:GK:97:GLU:HG2	2.16	0.45
1:HL:87:GLU:OE1	1:HL:87:GLU:N	2.37	0.45
1:HN:35:ARG:HH12	1:HN:43:LEU:C	2.20	0.45
1:HN:43:LEU:HD22	1:HN:87:GLU:OE2	2.17	0.45
1:IJ:87:GLU:OE1	1:IJ:87:GLU:N	2.40	0.45
1:IT:65:ALA:N	1:IV:68:CYS:HB3	2.31	0.45
1:IU:117:LEU:HD23	1:IU:117:LEU:H	1.81	0.45
1:AE:105:THR:O	1:AE:109:SER:OG	2.34	0.45
1:AH:68:CYS:N	1:JE:64:CYS:H	2.09	0.45
1:AI:17:TRP:CD2	1:AJ:123:ILE:HG13	2.51	0.45
1:AJ:68:CYS:HA	1:GM:61:PRO:O	2.17	0.45
1:BH:6:GLN:OE1	1:HQ:111:ASN:ND2	2.50	0.45
1:BV:68:CYS:N	1:GH:63:GLY:H	2.15	0.45
1:BY:34:GLN:O	1:BY:45:ASN:N	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:116:PHE:CE2	1:CA:20:PRO:HB3	2.52	0.45
1:BY:116:PHE:HE2	1:CA:20:PRO:HB3	1.81	0.45
1:CB:62:GLU:H	1:CB:62:GLU:CD	2.20	0.45
1:CM:116:PHE:CE1	1:CQ:6:GLN:HB2	2.51	0.45
1:CW:14:LYS:HD3	1:CW:30:SER:HB2	1.98	0.45
1:DR:88:ASN:ND2	1:DS:74:GLU:OE1	2.35	0.45
1:DS:19:ASP:HB3	1:DS:22:ARG:O	2.16	0.45
1:DX:5:MET:SD	1:DX:5:MET:N	2.90	0.45
1:EE:37:LYS:NZ	1:EE:40:ILE:O	2.47	0.45
1:EE:116:PHE:CE1	1:HY:8:ILE:HD11	2.51	0.45
1:EW:101:ARG:NH2	1:EW:124:VAL:HG21	2.31	0.45
1:FD:5:MET:N	1:FD:5:MET:SD	2.90	0.45
1:FO:93:LYS:O	1:FO:97:GLU:HG2	2.17	0.45
1:FZ:43:LEU:HD22	1:FZ:87:GLU:OE2	2.16	0.45
1:GE:101:ARG:NH1	1:GE:124:VAL:HG21	2.31	0.45
1:GQ:37:LYS:HD3	1:GQ:42:GLU:OE2	2.17	0.45
1:GR:98:THR:HG21	1:GR:126:SER:HA	1.97	0.45
1:GX:117:LEU:HD23	1:GX:117:LEU:H	1.81	0.45
1:HD:56:ARG:NE	1:HD:76:GLN:OE1	2.33	0.45
1:HK:71:MET:SD	1:HK:71:MET:N	2.85	0.45
1:HV:22:ARG:NH1	1:HV:24:SER:OG	2.49	0.45
1:HX:35:ARG:NH2	1:HX:44:ASN:OD1	2.50	0.45
1:IL:68:CYS:HB3	1:IQ:64:CYS:HA	1.98	0.45
1:IW:93:LYS:O	1:IW:97:GLU:HG2	2.17	0.45
1:JI:123:ILE:HG22	1:JJ:5:MET:HE2	1.98	0.45
1:JJ:45:ASN:HA	1:JJ:85:SER:HA	1.99	0.45
1:AF:116:PHE:CE1	1:IW:8:ILE:HD11	2.51	0.45
1:AT:98:THR:HG21	1:AT:126:SER:HA	1.98	0.45
1:AZ:19:ASP:HB3	1:AZ:22:ARG:O	2.16	0.45
1:BC:105:THR:O	1:BC:109:SER:OG	2.33	0.45
1:BE:72:PRO:HG2	1:BF:38:VAL:HG22	1.97	0.45
1:BK:31:LEU:HD23	1:BL:115:GLY:HA2	1.99	0.45
1:BR:55:LYS:NZ	1:BR:75:ASN:OD1	2.28	0.45
1:BU:17:TRP:CD2	1:BV:123:ILE:HG13	2.51	0.45
1:BY:72:PRO:HG2	1:BZ:38:VAL:HG22	1.99	0.45
1:CE:128:THR:OG1	1:CF:1:ALA:O	2.29	0.45
1:CS:60:LYS:NZ	1:CS:66:ASP:O	2.27	0.45
1:DF:116:PHE:CE1	1:DH:6:GLN:HB2	2.51	0.45
1:DJ:58:ALA:HB3	1:DJ:71:MET:HG3	1.99	0.45
1:DV:72:PRO:HG2	1:DW:38:VAL:HG22	1.98	0.45
1:DW:8:ILE:HA	1:IL:116:PHE:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EF:14:LYS:HE3	1:EF:28:SER:HB2	1.97	0.45
1:EI:101:ARG:CZ	1:EI:124:VAL:HG21	2.47	0.45
1:ES:22:ARG:NH2	1:ES:55:LYS:O	2.47	0.45
1:EU:34:GLN:NE2	1:EU:35:ARG:O	2.49	0.45
1:EZ:116:PHE:HE2	1:FB:20:PRO:HB3	1.82	0.45
1:FC:71:MET:SD	1:FC:71:MET:N	2.90	0.45
1:FC:117:LEU:HD23	1:FC:117:LEU:H	1.81	0.45
1:FG:117:LEU:H	1:FG:117:LEU:HD23	1.82	0.45
1:FM:117:LEU:HD23	1:FM:117:LEU:H	1.81	0.45
1:FY:35:ARG:NH1	1:FY:43:LEU:O	2.50	0.45
1:GB:5:MET:HG2	1:GB:19:ASP:N	2.31	0.45
1:GB:35:ARG:NH2	1:GB:42:GLU:HB3	2.32	0.45
1:GG:117:LEU:HD23	1:GG:117:LEU:H	1.81	0.45
1:GM:31:LEU:HD12	1:GN:117:LEU:HD22	1.99	0.45
1:GX:19:ASP:HB3	1:GX:22:ARG:O	2.16	0.45
1:HN:22:ARG:NH1	1:HN:24:SER:OG	2.50	0.45
1:HP:37:LYS:HA	1:HP:37:LYS:HD2	1.83	0.45
1:HT:37:LYS:NZ	1:HT:40:ILE:O	2.40	0.45
1:HW:117:LEU:HD23	1:HW:117:LEU:H	1.81	0.45
1:HZ:124:VAL:HG12	1:IA:4:PRO:HB3	1.99	0.45
1:II:64:CYS:SG	1:II:65:ALA:N	2.90	0.45
1:IJ:35:ARG:NH2	1:IJ:42:GLU:HB3	2.30	0.45
1:JE:68:CYS:HB3	1:JJ:64:CYS:HA	1.98	0.45
1:JI:3:LYS:HZ3	1:JJ:127:ASP:HB3	1.80	0.45
1:JI:3:LYS:NZ	1:JJ:129:THR:HG23	2.32	0.45
1:AA:56:ARG:O	1:AA:74:GLU:N	2.44	0.45
1:AF:37:LYS:NZ	1:AF:40:ILE:O	2.47	0.45
1:AJ:67:ALA:HA	1:GM:63:GLY:N	2.17	0.45
1:AN:116:PHE:CE1	1:IS:8:ILE:HD11	2.52	0.45
1:BF:12:ALA:HB2	1:BG:10:SER:H	1.81	0.45
1:BN:106:LEU:HD11	1:BN:123:ILE:HD11	1.97	0.45
1:BQ:17:TRP:CD2	1:BR:123:ILE:HG13	2.52	0.45
1:BV:25:THR:O	1:BV:25:THR:OG1	2.34	0.45
1:BX:69:VAL:N	1:JI:64:CYS:H	2.12	0.45
1:CA:72:PRO:HG2	1:CB:38:VAL:HG22	1.98	0.45
1:CB:19:ASP:HB3	1:CB:22:ARG:O	2.16	0.45
1:CE:1:ALA:HB1	1:CF:128:THR:HG23	1.99	0.45
1:CG:5:MET:HG3	1:CG:19:ASP:N	2.32	0.45
1:CG:17:TRP:CD2	1:CH:123:ILE:HG13	2.51	0.45
1:CH:60:LYS:NZ	1:CH:65:ALA:HB3	2.32	0.45
1:CS:125:SER:O	1:CT:2:ASN:ND2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:12:ALA:HB2	1:IG:10:SER:N	2.31	0.45
1:CZ:69:VAL:H	1:ID:64:CYS:H	1.64	0.45
1:DI:19:ASP:HB3	1:DI:22:ARG:O	2.17	0.45
1:DN:128:THR:HA	1:DO:2:ASN:HA	1.98	0.45
1:DP:116:PHE:CE1	1:DR:6:GLN:HB2	2.51	0.45
1:DQ:37:LYS:HE3	1:DQ:37:LYS:HB3	1.71	0.45
1:DT:3:LYS:NZ	1:DU:129:THR:HG23	2.32	0.45
1:DT:95:GLU:OE1	1:DU:76:GLN:NE2	2.49	0.45
1:EC:68:CYS:HA	1:HN:64:CYS:SG	2.57	0.45
1:EJ:17:TRP:CD2	1:EK:123:ILE:HG13	2.51	0.45
1:EL:34:GLN:O	1:EL:45:ASN:N	2.48	0.45
1:FG:62:GLU:O	1:FG:62:GLU:HG2	2.16	0.45
1:FP:46:VAL:HG11	1:FQ:113:GLY:O	2.17	0.45
1:GB:96:TRP:NE1	1:GB:100:LYS:HE2	2.32	0.45
1:GS:56:ARG:O	1:GS:74:GLU:N	2.40	0.45
1:GV:9:THR:O	1:GV:15:ILE:HA	2.17	0.45
1:GV:74:GLU:HG2	1:GV:75:ASN:H	1.82	0.45
1:HN:70:ILE:HD11	1:HR:40:ILE:HD12	1.99	0.45
1:HQ:89:LEU:HG	1:HQ:93:LYS:HE3	1.97	0.45
1:IG:45:ASN:HA	1:IG:85:SER:HA	1.98	0.45
1:IW:19:ASP:HB3	1:IW:22:ARG:O	2.16	0.45
1:JE:3:LYS:NZ	1:JE:21:THR:OG1	2.29	0.45
1:AA:101:ARG:CZ	1:AA:124:VAL:HG21	2.45	0.45
1:AL:5:MET:CG	1:AL:17:TRP:HB3	2.46	0.45
1:AM:5:MET:CE	1:AN:123:ILE:HG22	2.45	0.45
1:AW:58:ALA:HB3	1:AW:71:MET:HG3	1.98	0.45
1:BN:62:GLU:H	1:BN:62:GLU:CD	2.20	0.45
1:BT:65:ALA:HB1	1:BT:69:VAL:HG21	1.98	0.45
1:BZ:101:ARG:NH1	1:BZ:124:VAL:HG21	2.32	0.45
1:CA:3:LYS:HZ2	1:CB:129:THR:HG23	1.81	0.45
1:CL:5:MET:CG	1:CL:17:TRP:HB3	2.47	0.45
1:CO:37:LYS:HZ3	1:CO:42:GLU:HB2	1.82	0.45
1:DU:101:ARG:CZ	1:DU:124:VAL:HG21	2.46	0.45
1:DW:101:ARG:CZ	1:DW:124:VAL:HG21	2.47	0.45
1:EA:95:GLU:HA	1:EA:95:GLU:OE2	2.17	0.45
1:EA:105:THR:HG23	1:EA:106:LEU:HD12	1.99	0.45
1:EN:34:GLN:O	1:EN:45:ASN:N	2.49	0.45
1:FL:92:LEU:HD13	1:FL:95:GLU:OE2	2.17	0.45
1:FM:19:ASP:HB3	1:FM:22:ARG:O	2.17	0.45
1:FN:35:ARG:NH2	1:FN:44:ASN:OD1	2.49	0.45
1:FP:31:LEU:HD13	1:FQ:115:GLY:HA2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GD:115:GLY:HA2	1:GE:31:LEU:HD23	1.99	0.45
1:GI:5:MET:N	1:GI:5:MET:SD	2.89	0.45
1:GP:35:ARG:NH2	1:GP:42:GLU:HB3	2.30	0.45
1:GR:89:LEU:HG	1:GR:93:LYS:HE3	1.99	0.45
1:HJ:14:LYS:NZ	1:HJ:28:SER:HB2	2.27	0.45
1:HL:22:ARG:NH1	1:HL:24:SER:OG	2.50	0.45
1:HN:35:ARG:NH2	1:HN:42:GLU:HB3	2.32	0.45
1:HP:115:GLY:HA2	1:HQ:31:LEU:HD23	1.99	0.45
1:HV:45:ASN:HA	1:HV:85:SER:HA	1.98	0.45
1:HX:101:ARG:HH21	1:HX:124:VAL:HG21	1.81	0.45
1:II:117:LEU:HD23	1:II:117:LEU:H	1.81	0.45
1:JH:35:ARG:HG2	1:JH:44:ASN:ND2	2.32	0.45
1:JH:35:ARG:NH2	1:JH:42:GLU:HG2	2.32	0.45
1:AC:95:GLU:OE1	1:AD:76:GLN:NE2	2.50	0.45
1:AI:5:MET:HG3	1:AI:19:ASP:N	2.32	0.45
1:AP:19:ASP:HB3	1:AP:22:ARG:O	2.17	0.45
1:AR:68:CYS:HB2	1:GR:64:CYS:HA	1.98	0.45
1:AS:88:ASN:ND2	1:AT:74:GLU:OE1	2.35	0.45
1:AT:95:GLU:HA	1:AT:95:GLU:OE2	2.17	0.45
1:AV:60:LYS:HZ3	1:AV:65:ALA:H	1.65	0.45
1:AX:56:ARG:HD2	1:AX:76:GLN:NE2	2.32	0.45
1:CE:115:GLY:O	1:CF:33:ARG:NH1	2.49	0.45
1:CR:37:LYS:HE3	1:CR:37:LYS:HB3	1.73	0.45
1:CT:95:GLU:HA	1:CT:95:GLU:OE2	2.17	0.45
1:CU:17:TRP:CD2	1:CV:123:ILE:HG13	2.52	0.45
1:CW:34:GLN:O	1:CW:45:ASN:N	2.49	0.45
1:CZ:25:THR:O	1:CZ:25:THR:OG1	2.34	0.45
1:DC:37:LYS:HZ3	1:DC:42:GLU:HB2	1.82	0.45
1:DJ:19:ASP:HB3	1:DJ:22:ARG:O	2.16	0.45
1:DN:116:PHE:CE2	1:DP:20:PRO:HB3	2.52	0.45
1:DR:14:LYS:HZ1	1:DR:28:SER:HB2	1.82	0.45
1:DZ:31:LEU:HD13	1:EA:117:LEU:HD21	1.99	0.45
1:DZ:105:THR:O	1:DZ:109:SER:OG	2.34	0.45
1:EE:19:ASP:HB3	1:EE:22:ARG:O	2.16	0.45
1:FA:62:GLU:O	1:FA:62:GLU:HG2	2.16	0.45
1:FK:93:LYS:O	1:FK:97:GLU:HG2	2.17	0.45
1:FN:123:ILE:HB	1:FO:5:MET:HB2	1.99	0.45
1:FP:3:LYS:HZ3	1:FQ:127:ASP:HB3	1.81	0.45
1:FS:60:LYS:HA	1:FS:71:MET:HE2	1.98	0.45
1:FT:125:SER:HB2	1:FU:5:MET:CE	2.47	0.45
1:GM:95:GLU:OE2	1:GN:76:GLN:HB3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GT:37:LYS:HD3	1:GT:42:GLU:HG3	1.99	0.45
1:HA:95:GLU:OE2	1:HB:76:GLN:HB3	2.16	0.45
1:HA:101:ARG:NH2	1:HA:124:VAL:HG21	2.29	0.45
1:HE:37:LYS:NZ	1:HE:39:GLY:O	2.50	0.45
1:IJ:11:THR:HB	1:IJ:14:LYS:H	1.81	0.45
1:IN:116:PHE:HE2	1:IP:20:PRO:HB3	1.81	0.45
1:IO:92:LEU:HA	1:IO:95:GLU:OE2	2.17	0.45
1:IT:111:ASN:HB2	1:IT:116:PHE:HB2	1.98	0.45
1:AB:62:GLU:HG2	1:AB:62:GLU:O	2.17	0.45
1:AB:101:ARG:NH1	1:AB:124:VAL:HG21	2.32	0.45
1:AN:5:MET:CG	1:AN:17:TRP:HB3	2.46	0.45
1:BB:25:THR:O	1:BB:25:THR:OG1	2.33	0.45
1:BN:19:ASP:HB3	1:BN:22:ARG:O	2.17	0.45
1:BO:6:GLN:HG3	1:BU:116:PHE:CE2	2.51	0.45
1:BP:95:GLU:HA	1:BP:95:GLU:OE2	2.17	0.45
1:BW:60:LYS:NZ	1:BW:66:ASP:H	2.15	0.45
1:BZ:62:GLU:HG2	1:BZ:62:GLU:O	2.17	0.45
1:CA:111:ASN:OD1	1:CA:116:PHE:HE1	2.00	0.45
1:CG:105:THR:O	1:CG:109:SER:OG	2.34	0.45
1:CK:37:LYS:HZ3	1:CK:42:GLU:HB2	1.82	0.45
1:CV:5:MET:CG	1:CV:17:TRP:HB3	2.47	0.45
1:DS:95:GLU:HA	1:DS:95:GLU:OE2	2.18	0.45
1:EM:101:ARG:CZ	1:EM:124:VAL:HG21	2.46	0.45
1:FU:93:LYS:O	1:FU:97:GLU:HG2	2.17	0.45
1:FW:93:LYS:O	1:FW:97:GLU:HG2	2.17	0.45
1:FZ:74:GLU:OE2	1:GA:85:SER:OG	2.32	0.45
1:GF:96:TRP:NE1	1:GF:100:LYS:HE2	2.32	0.45
1:GO:115:GLY:HA3	1:GP:33:ARG:HD3	1.99	0.45
1:HA:115:GLY:HA2	1:HB:31:LEU:HD23	1.99	0.45
1:HG:43:LEU:HD13	1:HG:87:GLU:OE2	2.17	0.45
1:HR:96:TRP:NE1	1:HR:100:LYS:HE2	2.32	0.45
1:HZ:66:ASP:CG	1:HZ:68:CYS:H	2.20	0.45
1:IO:101:ARG:NH1	1:IO:124:VAL:HG21	2.31	0.45
1:AD:5:MET:CG	1:AD:17:TRP:HB3	2.46	0.44
1:AE:19:ASP:HB3	1:AE:22:ARG:O	2.17	0.44
1:AQ:17:TRP:CD2	1:AR:123:ILE:HG13	2.52	0.44
1:AW:34:GLN:O	1:AW:45:ASN:N	2.50	0.44
1:BJ:19:ASP:HB3	1:BJ:22:ARG:O	2.17	0.44
1:BP:68:CYS:HA	1:GF:64:CYS:SG	2.57	0.44
1:BR:5:MET:CG	1:BR:17:TRP:HB3	2.47	0.44
1:BS:34:GLN:O	1:BS:45:ASN:N	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BU:88:ASN:ND2	1:BV:74:GLU:OE2	2.36	0.44
1:CB:68:CYS:N	1:FJ:64:CYS:H	2.12	0.44
1:CM:3:LYS:HZ1	1:CN:129:THR:HG23	1.81	0.44
1:DA:31:LEU:HD13	1:DB:117:LEU:HD21	1.99	0.44
1:DC:20:PRO:HB3	1:DJ:116:PHE:HE2	1.82	0.44
1:DC:116:PHE:CE1	1:DF:6:GLN:HB2	2.52	0.44
1:DJ:101:ARG:CZ	1:DJ:124:VAL:HG21	2.47	0.44
1:EH:17:TRP:CD2	1:EI:123:ILE:HG13	2.53	0.44
1:FF:115:GLY:HA2	1:FG:31:LEU:HD23	1.99	0.44
1:FG:89:LEU:HG	1:FG:93:LYS:HE3	1.99	0.44
1:FP:59:PRO:O	1:FP:61:PRO:HD3	2.16	0.44
1:FS:56:ARG:NE	1:FS:76:GLN:OE1	2.36	0.44
1:FT:106:LEU:HD23	1:FT:106:LEU:HA	1.84	0.44
1:FY:117:LEU:HD23	1:FY:117:LEU:H	1.82	0.44
1:GF:115:GLY:HA2	1:GG:31:LEU:HD23	1.97	0.44
1:GO:5:MET:HG3	1:GO:17:TRP:HB3	1.98	0.44
1:GR:35:ARG:HG2	1:GR:44:ASN:ND2	2.32	0.44
1:GX:105:THR:HA	1:GX:109:SER:HB2	1.99	0.44
1:GY:124:VAL:HA	1:GZ:4:PRO:HA	1.99	0.44
1:HM:35:ARG:NH2	1:HM:43:LEU:O	2.50	0.44
1:HT:55:LYS:HZ3	1:HT:73:ASN:HB2	1.81	0.44
1:IN:2:ASN:HB2	1:IO:124:VAL:HB	1.99	0.44
1:IS:60:LYS:HE2	1:IS:64:CYS:HB3	1.99	0.44
1:IV:2:ASN:OD1	1:IW:128:THR:OG1	2.32	0.44
1:AF:5:MET:CG	1:AF:17:TRP:HB3	2.48	0.44
1:AF:67:ALA:C	1:GS:62:GLU:HA	2.37	0.44
1:AV:66:ASP:OD2	1:AV:68:CYS:N	2.50	0.44
1:AV:95:GLU:HA	1:AV:95:GLU:OE2	2.17	0.44
1:BB:19:ASP:HB3	1:BB:22:ARG:O	2.16	0.44
1:BM:31:LEU:HD13	1:BN:117:LEU:HD21	1.99	0.44
1:BX:25:THR:O	1:BX:25:THR:OG1	2.35	0.44
1:CF:60:LYS:HZ3	1:CF:65:ALA:H	1.63	0.44
1:CR:37:LYS:HD2	1:CR:42:GLU:HB3	1.99	0.44
1:CV:68:CYS:N	1:HL:63:GLY:N	2.66	0.44
1:CW:5:MET:SD	1:CW:5:MET:N	2.90	0.44
1:DG:19:ASP:HB3	1:DG:22:ARG:O	2.17	0.44
1:DN:19:ASP:HB3	1:DN:22:ARG:O	2.17	0.44
1:EI:5:MET:HG2	1:EI:17:TRP:HB3	2.00	0.44
1:EN:60:LYS:HZ3	1:EN:66:ASP:H	1.64	0.44
1:ER:23:LEU:HB2	1:EV:44:ASN:ND2	2.32	0.44
1:FP:125:SER:HB2	1:FQ:5:MET:CE	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GC:57:PRO:HA	1:GC:73:ASN:HA	1.99	0.44
1:GH:92:LEU:HD13	1:GH:95:GLU:OE2	2.17	0.44
1:GL:51:VAL:HG22	1:GL:79:ARG:HG2	1.99	0.44
1:GU:39:GLY:HA3	1:GV:72:PRO:HG2	1.99	0.44
1:GW:11:THR:HB	1:GW:14:LYS:H	1.82	0.44
1:HE:1:ALA:O	1:HF:129:THR:N	2.35	0.44
1:HG:68:CYS:HB3	1:HM:64:CYS:HA	1.99	0.44
1:HQ:19:ASP:HB3	1:HQ:22:ARG:O	2.17	0.44
1:IF:55:LYS:HG3	1:IF:73:ASN:HB2	1.98	0.44
1:IF:101:ARG:NH2	1:IF:124:VAL:HG21	2.33	0.44
1:IM:34:GLN:OE1	1:IM:36:VAL:HG13	2.17	0.44
1:AH:105:THR:HG23	1:AH:106:LEU:HD12	2.00	0.44
1:AL:12:ALA:HB2	1:AM:10:SER:H	1.82	0.44
1:AL:101:ARG:CZ	1:AL:124:VAL:HG21	2.47	0.44
1:AO:14:LYS:NZ	1:AO:28:SER:HB2	2.29	0.44
1:AS:5:MET:HB3	1:AS:17:TRP:HB3	1.99	0.44
1:AV:5:MET:CG	1:AV:17:TRP:HB3	2.46	0.44
1:BB:101:ARG:CZ	1:BB:124:VAL:HG21	2.48	0.44
1:BM:105:THR:O	1:BM:109:SER:OG	2.34	0.44
1:BO:71:MET:N	1:BO:71:MET:SD	2.91	0.44
1:CP:105:THR:HG23	1:CP:106:LEU:HD12	1.98	0.44
1:DK:32:LEU:HG	1:DK:34:GLN:HE22	1.83	0.44
1:DO:68:CYS:HA	1:FV:64:CYS:SG	2.57	0.44
1:EB:31:LEU:HD23	1:EC:115:GLY:HA2	2.00	0.44
1:EP:34:GLN:O	1:EP:45:ASN:N	2.46	0.44
1:ER:96:TRP:NE1	1:ER:100:LYS:HE2	2.33	0.44
1:EX:20:PRO:HB3	1:FC:116:PHE:HE2	1.83	0.44
1:EY:56:ARG:O	1:EY:74:GLU:N	2.27	0.44
1:EZ:37:LYS:HD3	1:EZ:42:GLU:HG2	2.00	0.44
1:FB:55:LYS:HZ3	1:FB:73:ASN:HB2	1.83	0.44
1:FG:37:LYS:HD2	1:FG:41:ALA:O	2.17	0.44
1:FH:31:LEU:HD12	1:FI:117:LEU:HD22	2.00	0.44
1:FT:123:ILE:HB	1:FU:5:MET:HB2	1.99	0.44
1:GG:23:LEU:O	1:GG:24:SER:OG	2.30	0.44
1:GM:1:ALA:O	1:GN:129:THR:N	2.35	0.44
1:HB:45:ASN:HA	1:HB:85:SER:HA	1.99	0.44
1:HE:19:ASP:HB3	1:HE:22:ARG:O	2.18	0.44
1:HJ:74:GLU:OE2	1:HK:85:SER:OG	2.31	0.44
1:HT:36:VAL:HG23	1:HT:43:LEU:HB2	1.99	0.44
1:IZ:60:LYS:HG2	1:IZ:71:MET:HE1	1.99	0.44
1:JA:56:ARG:O	1:JA:74:GLU:N	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JD:9:THR:O	1:JD:15:ILE:HA	2.18	0.44
1:JD:93:LYS:O	1:JD:97:GLU:HG2	2.18	0.44
1:AX:67:ALA:HA	1:GY:63:GLY:N	2.19	0.44
1:BI:3:LYS:HZ2	1:BJ:129:THR:HG23	1.82	0.44
1:BR:60:LYS:NZ	1:BR:65:ALA:HB3	2.32	0.44
1:CD:60:LYS:HZ3	1:CD:65:ALA:H	1.64	0.44
1:CK:8:ILE:N	1:CK:16:VAL:O	2.50	0.44
1:DH:116:PHE:CE1	1:DL:6:GLN:HB2	2.52	0.44
1:DS:105:THR:HG23	1:DS:106:LEU:HD12	1.98	0.44
1:DW:66:ASP:OD1	1:DW:69:VAL:HG13	2.17	0.44
1:EZ:2:ASN:HB2	1:FA:124:VAL:HB	1.99	0.44
1:FD:31:LEU:HD12	1:FE:117:LEU:HD22	2.00	0.44
1:FT:72:PRO:HG2	1:FU:38:VAL:HG12	2.00	0.44
1:FX:96:TRP:NE1	1:FY:104:ASP:OD1	2.39	0.44
1:GG:45:ASN:HA	1:GG:85:SER:HA	1.99	0.44
1:HV:11:THR:HB	1:HV:14:LYS:H	1.83	0.44
1:HV:111:ASN:HB2	1:HV:116:PHE:HB2	1.99	0.44
1:HY:93:LYS:O	1:HY:97:GLU:HG2	2.17	0.44
1:IG:9:THR:O	1:IG:15:ILE:HA	2.18	0.44
1:II:60:LYS:HZ3	1:II:71:MET:HB3	1.83	0.44
1:JC:3:LYS:HZ2	1:JD:129:THR:HG23	1.83	0.44
1:JG:59:PRO:O	1:JG:61:PRO:HD3	2.17	0.44
1:JI:106:LEU:HD23	1:JI:106:LEU:HA	1.83	0.44
1:AD:70:ILE:HG23	1:IV:61:PRO:HB2	1.99	0.44
1:AI:37:LYS:HA	1:AI:37:LYS:HD2	1.65	0.44
1:AW:17:TRP:CD2	1:AX:123:ILE:HG13	2.53	0.44
1:BM:17:TRP:CD2	1:BN:123:ILE:HG13	2.52	0.44
1:BQ:88:ASN:ND2	1:BR:74:GLU:OE2	2.36	0.44
1:BX:67:ALA:C	1:JI:63:GLY:H	2.21	0.44
1:CA:124:VAL:HA	1:CB:4:PRO:HA	2.00	0.44
1:CP:67:ALA:C	1:IP:63:GLY:H	2.21	0.44
1:DE:5:MET:HG3	1:DE:17:TRP:HB3	1.98	0.44
1:DT:3:LYS:HZ2	1:DU:129:THR:HG23	1.82	0.44
1:DU:106:LEU:HD21	1:DU:123:ILE:HD11	2.00	0.44
1:EI:37:LYS:HE3	1:EI:37:LYS:HB3	1.71	0.44
1:ET:3:LYS:HZ1	1:EU:129:THR:HG23	1.81	0.44
1:FB:45:ASN:HA	1:FB:85:SER:HA	2.00	0.44
1:FL:35:ARG:HD2	1:FL:44:ASN:HB3	1.99	0.44
1:FN:3:LYS:HZ3	1:FO:127:ASP:HB3	1.82	0.44
1:FP:88:ASN:ND2	1:FQ:74:GLU:OE2	2.42	0.44
1:FY:44:ASN:ND2	1:FZ:23:LEU:HB2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GE:57:PRO:HA	1:GE:73:ASN:HA	1.99	0.44
1:GV:111:ASN:HB2	1:GV:116:PHE:HB2	2.00	0.44
1:HC:5:MET:CG	1:HC:17:TRP:HB3	2.47	0.44
1:HD:43:LEU:HD12	1:HD:87:GLU:CD	2.38	0.44
1:HK:105:THR:HA	1:HK:109:SER:HB2	1.99	0.44
1:HR:5:MET:HG3	1:HR:17:TRP:HB3	1.99	0.44
1:IA:56:ARG:O	1:IA:74:GLU:N	2.27	0.44
1:IH:115:GLY:HA2	1:II:31:LEU:HD23	2.00	0.44
1:IX:74:GLU:OE2	1:IZ:85:SER:OG	2.30	0.44
1:IX:91:THR:O	1:IX:94:ALA:N	2.50	0.44
1:AG:105:THR:O	1:AG:109:SER:OG	2.35	0.44
1:AK:5:MET:HE1	1:AL:123:ILE:HG22	2.00	0.44
1:AL:62:GLU:O	1:AL:62:GLU:HG2	2.17	0.44
1:AO:101:ARG:NH2	1:AO:124:VAL:HG21	2.33	0.44
1:AP:37:LYS:HB3	1:AP:37:LYS:HE3	1.71	0.44
1:AR:57:PRO:HA	1:AR:73:ASN:HA	1.99	0.44
1:AV:8:ILE:HA	1:GO:116:PHE:HB2	1.99	0.44
1:BD:37:LYS:NZ	1:BD:40:ILE:O	2.47	0.44
1:BG:14:LYS:NZ	1:BG:15:ILE:O	2.50	0.44
1:BJ:56:ARG:HD2	1:BJ:76:GLN:NE2	2.32	0.44
1:BO:88:ASN:ND2	1:BP:74:GLU:OE1	2.36	0.44
1:BQ:34:GLN:O	1:BQ:45:ASN:N	2.49	0.44
1:BR:32:LEU:HB3	1:BR:47:SER:HB3	1.98	0.44
1:BY:5:MET:HE1	1:BZ:123:ILE:HG22	2.00	0.44
1:CD:5:MET:HG2	1:CD:17:TRP:HB3	2.00	0.44
1:CD:8:ILE:HA	1:HG:116:PHE:HB2	1.99	0.44
1:CL:23:LEU:HD13	1:FO:44:ASN:HD21	1.81	0.44
1:CO:117:LEU:HD11	1:CP:31:LEU:HD13	1.99	0.44
1:DB:62:GLU:H	1:DB:62:GLU:CD	2.21	0.44
1:DU:68:CYS:HB2	1:FP:64:CYS:C	2.38	0.44
1:EQ:68:CYS:HB3	1:IU:61:PRO:HB2	1.99	0.44
1:ET:65:ALA:N	1:EV:68:CYS:HB3	2.33	0.44
1:FL:95:GLU:OE2	1:FM:76:GLN:NE2	2.51	0.44
1:FZ:37:LYS:NZ	1:FZ:39:GLY:O	2.50	0.44
1:FZ:96:TRP:NE1	1:FZ:100:LYS:HE2	2.33	0.44
1:GB:43:LEU:HD22	1:GB:87:GLU:OE2	2.18	0.44
1:GF:37:LYS:NZ	1:GF:39:GLY:O	2.51	0.44
1:GU:115:GLY:O	1:GV:33:ARG:NH1	2.50	0.44
1:HE:31:LEU:HD12	1:HF:117:LEU:HD22	2.00	0.44
1:HG:72:PRO:HG2	1:HI:38:VAL:HG12	2.00	0.44
1:HI:45:ASN:HA	1:HI:85:SER:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HX:31:LEU:HD11	1:HY:117:LEU:HB3	1.98	0.44
1:ID:31:LEU:HD12	1:IE:117:LEU:HD22	2.00	0.44
1:IJ:31:LEU:HD12	1:IK:117:LEU:HD22	1.99	0.44
1:JA:65:ALA:N	1:JC:68:CYS:SG	2.90	0.44
1:AA:87:GLU:HB3	1:AB:59:PRO:HG3	2.00	0.44
1:AC:3:LYS:HZ1	1:AD:127:ASP:HB3	1.83	0.44
1:AQ:34:GLN:O	1:AQ:45:ASN:N	2.48	0.44
1:BK:17:TRP:CD2	1:BL:123:ILE:HG13	2.52	0.44
1:BV:37:LYS:NZ	1:BV:40:ILE:O	2.51	0.44
1:BW:31:LEU:HD23	1:BX:115:GLY:HA2	2.00	0.44
1:BW:128:THR:HA	1:BX:2:ASN:HA	1.99	0.44
1:CH:56:ARG:HD2	1:CH:76:GLN:NE2	2.33	0.44
1:CM:14:LYS:NZ	1:CM:28:SER:HB2	2.28	0.44
1:CO:6:GLN:HB2	1:CQ:116:PHE:CE1	2.52	0.44
1:CP:70:ILE:HG23	1:IP:61:PRO:HB2	2.00	0.44
1:CR:5:MET:HG2	1:CR:17:TRP:HB3	2.00	0.44
1:CS:80:THR:OG1	1:CT:99:HIS:NE2	2.46	0.44
1:DJ:5:MET:CE	1:DK:123:ILE:HG22	2.48	0.44
1:DN:101:ARG:CZ	1:DN:124:VAL:HG21	2.48	0.44
1:DR:37:LYS:HZ3	1:DR:42:GLU:HB2	1.81	0.44
1:DU:62:GLU:H	1:DU:62:GLU:CD	2.21	0.44
1:EI:8:ILE:HA	1:FD:116:PHE:HB2	1.98	0.44
1:GB:20:PRO:HB3	1:GG:116:PHE:HE2	1.82	0.44
1:GD:2:ASN:HB2	1:GE:124:VAL:HB	1.99	0.44
1:GY:43:LEU:HD22	1:GY:87:GLU:OE2	2.18	0.44
1:HA:31:LEU:HD12	1:HB:117:LEU:HD22	1.98	0.44
1:HX:5:MET:HG3	1:HX:19:ASP:HA	2.00	0.44
1:II:35:ARG:HH22	1:II:44:ASN:HA	1.83	0.44
1:IM:56:ARG:O	1:IM:74:GLU:N	2.28	0.44
1:IS:93:LYS:O	1:IS:97:GLU:HG2	2.16	0.44
1:JC:87:GLU:OE1	1:JC:87:GLU:N	2.49	0.44
1:JG:56:ARG:O	1:JG:74:GLU:N	2.30	0.44
1:AD:67:ALA:O	1:IV:65:ALA:HB2	2.18	0.44
1:AM:115:GLY:HA2	1:AN:31:LEU:HD23	2.00	0.44
1:AO:3:LYS:HZ1	1:AP:127:ASP:HB3	1.83	0.44
1:AS:37:LYS:HZ3	1:AS:42:GLU:HB2	1.82	0.44
1:AU:34:GLN:O	1:AU:45:ASN:N	2.50	0.44
1:BB:61:PRO:HB2	1:BB:64:CYS:HB3	2.00	0.44
1:BG:128:THR:OG1	1:BH:1:ALA:O	2.33	0.44
1:BR:67:ALA:C	1:FZ:63:GLY:H	2.20	0.44
1:BX:116:PHE:CE2	1:FR:20:PRO:HA	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:67:ALA:C	1:HA:63:GLY:H	2.21	0.44
1:CN:116:PHE:CE1	1:FO:8:ILE:HD11	2.53	0.44
1:CO:14:LYS:HZ1	1:CO:28:SER:HB2	1.83	0.44
1:CP:5:MET:HG2	1:CP:17:TRP:HB3	2.00	0.44
1:CT:23:LEU:HD22	1:HS:44:ASN:HD21	1.82	0.44
1:CT:105:THR:HG23	1:CT:106:LEU:HD12	2.00	0.44
1:DF:14:LYS:NZ	1:DF:15:ILE:O	2.51	0.44
1:DJ:34:GLN:O	1:DJ:45:ASN:N	2.47	0.44
1:DY:67:ALA:HB1	1:HE:64:CYS:HA	2.00	0.44
1:EB:34:GLN:O	1:EB:45:ASN:N	2.47	0.44
1:EG:70:ILE:HG23	1:HX:61:PRO:HB2	1.99	0.44
1:EH:35:ARG:HB3	1:EH:42:GLU:OE2	2.18	0.44
1:EH:101:ARG:CZ	1:EH:124:VAL:HG21	2.48	0.44
1:EJ:37:LYS:HZ3	1:EJ:42:GLU:HB2	1.83	0.44
1:EO:68:CYS:HB3	1:FA:64:CYS:HB2	1.32	0.44
1:EQ:19:ASP:HB3	1:EQ:22:ARG:O	2.16	0.44
1:FD:5:MET:HB2	1:FD:18:SER:C	2.38	0.44
1:FW:57:PRO:HA	1:FW:73:ASN:HA	1.99	0.44
1:GQ:101:ARG:HH21	1:GQ:124:VAL:HG21	1.82	0.44
1:GT:57:PRO:HA	1:GT:73:ASN:HA	1.99	0.44
1:GT:93:LYS:O	1:GT:97:GLU:HG2	2.18	0.44
1:GY:96:TRP:NE1	1:GY:100:LYS:HE2	2.33	0.44
1:HF:5:MET:SD	1:HF:5:MET:N	2.91	0.44
1:HG:87:GLU:OE1	1:HG:87:GLU:N	2.46	0.44
1:HN:96:TRP:NE1	1:HN:100:LYS:HE2	2.32	0.44
1:HY:19:ASP:HB3	1:HY:22:ARG:O	2.17	0.44
1:ID:1:ALA:O	1:IE:129:THR:N	2.35	0.44
1:IJ:17:TRP:CD2	1:IK:123:ILE:HG13	2.53	0.44
1:IR:33:ARG:HH11	1:IU:8:ILE:HD11	1.82	0.44
1:AE:62:GLU:HG2	1:AE:62:GLU:O	2.17	0.44
1:AG:127:ASP:OD1	1:AG:127:ASP:N	2.51	0.44
1:AJ:67:ALA:O	1:GM:65:ALA:HB2	2.18	0.44
1:AU:1:ALA:HB1	1:AV:128:THR:HG23	1.99	0.44
1:BD:3:LYS:HE2	1:BD:3:LYS:HB3	1.76	0.44
1:BI:17:TRP:CD2	1:BJ:123:ILE:HG13	2.53	0.44
1:BJ:69:VAL:O	1:HZ:63:GLY:HA3	2.18	0.44
1:CC:14:LYS:NZ	1:CC:28:SER:HB2	2.28	0.44
1:CI:116:PHE:HE2	1:CK:20:PRO:HB3	1.82	0.44
1:CL:62:GLU:H	1:CL:62:GLU:CD	2.21	0.44
1:CO:1:ALA:HB1	1:CP:128:THR:HG23	1.99	0.44
1:CY:34:GLN:O	1:CY:45:ASN:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DI:23:LEU:HD13	1:FI:44:ASN:HD21	1.81	0.44
1:DJ:17:TRP:CD2	1:DK:123:ILE:HG13	2.52	0.44
1:DR:1:ALA:HB1	1:DS:128:THR:HG23	1.99	0.44
1:DS:55:LYS:NZ	1:DS:75:ASN:OD1	2.30	0.44
1:DW:62:GLU:O	1:DW:62:GLU:HG2	2.17	0.44
1:ER:31:LEU:HD12	1:ES:117:LEU:HD22	2.00	0.44
1:FJ:31:LEU:HD13	1:FK:115:GLY:HA2	2.00	0.44
1:FN:55:LYS:HZ2	1:FN:73:ASN:HB2	1.83	0.44
1:GE:64:CYS:SG	1:GE:69:VAL:HG21	2.57	0.44
1:GF:56:ARG:O	1:GF:74:GLU:N	2.39	0.44
1:HC:11:THR:HB	1:HC:14:LYS:H	1.81	0.44
1:HG:5:MET:HB3	1:HG:17:TRP:HB3	2.00	0.44
1:HZ:68:CYS:HB2	1:IE:64:CYS:O	2.18	0.44
1:IA:60:LYS:NZ	1:IA:66:ASP:O	2.51	0.44
1:IB:101:ARG:NH2	1:IB:124:VAL:HG21	2.33	0.44
1:IC:5:MET:HG2	1:IC:19:ASP:N	2.33	0.44
1:IG:93:LYS:O	1:IG:97:GLU:HG2	2.18	0.44
1:IJ:96:TRP:NE1	1:IJ:100:LYS:HE2	2.33	0.44
1:IK:22:ARG:NH2	1:IK:55:LYS:O	2.47	0.44
1:IN:106:LEU:HD23	1:IN:106:LEU:HA	1.77	0.44
1:IR:31:LEU:HD11	1:IS:117:LEU:HB3	1.98	0.44
1:IT:35:ARG:HD2	1:IT:44:ASN:HB3	1.99	0.44
1:IV:106:LEU:HD23	1:IV:106:LEU:HA	1.85	0.44
1:IX:35:ARG:NH2	1:IX:44:ASN:HA	2.31	0.44
1:IZ:93:LYS:O	1:IZ:97:GLU:HG2	2.18	0.44
1:AA:116:PHE:CE2	1:AC:20:PRO:HB3	2.52	0.43
1:AF:62:GLU:H	1:AF:62:GLU:CD	2.20	0.43
1:AG:125:SER:O	1:AH:2:ASN:ND2	2.51	0.43
1:AN:67:ALA:N	1:JC:65:ALA:H	2.15	0.43
1:AP:56:ARG:HD2	1:AP:76:GLN:HE22	1.82	0.43
1:AX:5:MET:CG	1:AX:17:TRP:HB3	2.47	0.43
1:BJ:5:MET:CG	1:BJ:17:TRP:HB3	2.48	0.43
1:BY:127:ASP:OD1	1:BY:127:ASP:N	2.51	0.43
1:CA:15:ILE:HD12	1:CB:117:LEU:HD12	2.00	0.43
1:CD:62:GLU:O	1:CD:62:GLU:HG2	2.18	0.43
1:CM:60:LYS:NZ	1:CM:66:ASP:H	2.16	0.43
1:CO:60:LYS:NZ	1:CO:66:ASP:O	2.48	0.43
1:CP:62:GLU:H	1:CP:62:GLU:CD	2.21	0.43
1:CR:37:LYS:NZ	1:CR:40:ILE:O	2.51	0.43
1:CT:25:THR:O	1:CT:25:THR:OG1	2.33	0.43
1:CZ:37:LYS:NZ	1:CZ:40:ILE:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DQ:70:ILE:HD11	1:IB:40:ILE:HB	1.99	0.43
1:DY:37:LYS:HE3	1:DY:37:LYS:HB3	1.71	0.43
1:ET:35:ARG:HD2	1:ET:44:ASN:HB3	1.99	0.43
1:EU:35:ARG:CZ	1:EU:35:ARG:HA	2.47	0.43
1:EX:76:GLN:NE2	1:EY:91:THR:OG1	2.49	0.43
1:EZ:115:GLY:O	1:FA:33:ARG:NH1	2.52	0.43
1:FA:101:ARG:NH1	1:FA:124:VAL:HG21	2.33	0.43
1:FP:123:ILE:HB	1:FQ:5:MET:HB2	1.99	0.43
1:FV:5:MET:HB3	1:FV:17:TRP:HB3	2.00	0.43
1:FZ:66:ASP:OD1	1:FZ:69:VAL:HG23	2.17	0.43
1:GM:101:ARG:NH2	1:GM:124:VAL:HG21	2.29	0.43
1:GV:57:PRO:HA	1:GV:73:ASN:HA	2.01	0.43
1:GY:11:THR:HB	1:GY:14:LYS:H	1.83	0.43
1:GY:66:ASP:OD1	1:GY:69:VAL:HG23	2.18	0.43
1:HC:22:ARG:NH1	1:HC:24:SER:OG	2.51	0.43
1:HC:60:LYS:HA	1:HC:71:MET:HE1	1.99	0.43
1:IJ:35:ARG:HH12	1:IJ:43:LEU:C	2.19	0.43
1:IR:60:LYS:HD2	1:IR:71:MET:HE1	2.00	0.43
1:AB:60:LYS:HZ3	1:AB:65:ALA:H	1.65	0.43
1:AJ:37:LYS:HD2	1:AJ:42:GLU:HB3	1.99	0.43
1:AK:105:THR:O	1:AK:109:SER:OG	2.37	0.43
1:AL:19:ASP:HB3	1:AL:22:ARG:O	2.17	0.43
1:AR:32:LEU:HB3	1:AR:47:SER:HB3	2.00	0.43
1:AV:68:CYS:HA	1:GO:64:CYS:SG	2.58	0.43
1:AX:55:LYS:NZ	1:AX:75:ASN:OD1	2.29	0.43
1:BO:5:MET:HG3	1:BO:19:ASP:N	2.34	0.43
1:BO:5:MET:HB3	1:BO:17:TRP:HB3	1.99	0.43
1:BU:34:GLN:O	1:BU:45:ASN:N	2.51	0.43
1:BV:5:MET:HG2	1:BV:17:TRP:HB3	2.01	0.43
1:CK:5:MET:SD	1:CK:5:MET:N	2.91	0.43
1:CQ:17:TRP:CD2	1:CR:123:ILE:HG13	2.53	0.43
1:DH:17:TRP:CD2	1:DI:123:ILE:HG13	2.52	0.43
1:DH:123:ILE:HG13	1:DI:17:TRP:CD2	2.52	0.43
1:DZ:62:GLU:O	1:DZ:62:GLU:HG2	2.18	0.43
1:EB:17:TRP:CD2	1:EC:123:ILE:HG13	2.54	0.43
1:EM:32:LEU:HB3	1:EM:47:SER:HB3	2.00	0.43
1:EO:37:LYS:NZ	1:EO:40:ILE:O	2.48	0.43
1:EP:56:ARG:O	1:EP:74:GLU:N	2.50	0.43
1:ER:68:CYS:HB3	1:EW:64:CYS:HA	1.99	0.43
1:FQ:93:LYS:O	1:FQ:97:GLU:HG2	2.17	0.43
1:FZ:124:VAL:HA	1:GA:4:PRO:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GE:19:ASP:HB3	1:GE:22:ARG:O	2.17	0.43
1:GV:93:LYS:O	1:GV:97:GLU:HG2	2.17	0.43
1:HM:5:MET:N	1:HM:5:MET:SD	2.91	0.43
1:HW:62:GLU:HG2	1:HW:62:GLU:O	2.18	0.43
1:IL:61:PRO:HG2	1:IL:64:CYS:SG	2.59	0.43
1:IL:96:TRP:NE1	1:IL:100:LYS:HE2	2.33	0.43
1:IM:5:MET:N	1:IM:5:MET:SD	2.92	0.43
1:JF:60:LYS:HG2	1:JF:71:MET:HE1	2.00	0.43
1:JG:5:MET:HB3	1:JG:17:TRP:HB3	1.99	0.43
1:JG:88:ASN:ND2	1:JH:56:ARG:HD2	2.27	0.43
1:JH:117:LEU:HD23	1:JH:117:LEU:H	1.83	0.43
1:AI:115:GLY:HA2	1:AJ:31:LEU:HD23	1.99	0.43
1:AJ:55:LYS:HE3	1:AJ:73:ASN:OD1	2.18	0.43
1:AW:3:LYS:HB2	1:AW:3:LYS:HE2	1.87	0.43
1:BB:37:LYS:HE3	1:BB:37:LYS:HB3	1.72	0.43
1:BM:124:VAL:HA	1:BN:4:PRO:HA	2.00	0.43
1:BW:19:ASP:HB3	1:BW:22:ARG:O	2.18	0.43
1:BX:5:MET:HG2	1:BX:17:TRP:HB3	2.00	0.43
1:CB:106:LEU:HD21	1:CB:123:ILE:HD11	2.01	0.43
1:CC:115:GLY:HA2	1:CD:31:LEU:HD23	2.00	0.43
1:CI:72:PRO:HG2	1:CJ:38:VAL:HG22	1.99	0.43
1:CM:58:ALA:HB3	1:CM:71:MET:HG3	2.00	0.43
1:CZ:62:GLU:H	1:CZ:62:GLU:CD	2.22	0.43
1:CZ:66:ASP:OD2	1:ID:65:ALA:N	2.51	0.43
1:DS:101:ARG:CZ	1:DS:124:VAL:HG21	2.49	0.43
1:DX:12:ALA:HB2	1:GV:10:SER:N	2.33	0.43
1:EC:32:LEU:HB3	1:EC:47:SER:HB3	2.00	0.43
1:EI:19:ASP:HB3	1:EI:22:ARG:O	2.18	0.43
1:EK:106:LEU:HD11	1:EK:123:ILE:HD11	2.01	0.43
1:EP:105:THR:O	1:EP:109:SER:OG	2.35	0.43
1:ER:20:PRO:HB3	1:EW:116:PHE:HE2	1.81	0.43
1:ES:62:GLU:O	1:ES:62:GLU:HG2	2.18	0.43
1:EV:17:TRP:CD2	1:EW:123:ILE:HG13	2.53	0.43
1:FH:124:VAL:HG12	1:FI:4:PRO:HB3	2.00	0.43
1:FL:22:ARG:NH1	1:FL:24:SER:OG	2.51	0.43
1:FR:92:LEU:HD13	1:FR:95:GLU:OE2	2.17	0.43
1:FY:60:LYS:HD2	1:FY:64:CYS:HB3	2.00	0.43
1:GK:96:TRP:NE1	1:GL:104:ASP:OD1	2.43	0.43
1:GM:115:GLY:HA2	1:GN:31:LEU:HD23	1.99	0.43
1:GO:60:LYS:HD2	1:GO:71:MET:HE1	2.00	0.43
1:GO:123:ILE:HG22	1:GP:5:MET:HE2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GQ:46:VAL:HG11	1:GR:113:GLY:O	2.18	0.43
1:GW:115:GLY:HA2	1:GX:31:LEU:HD23	2.00	0.43
1:GY:22:ARG:NH1	1:GY:24:SER:OG	2.51	0.43
1:HI:93:LYS:O	1:HI:97:GLU:HG2	2.18	0.43
1:HS:23:LEU:O	1:HS:24:SER:OG	2.31	0.43
1:HV:115:GLY:O	1:HW:33:ARG:NH1	2.52	0.43
1:IH:33:ARG:HD2	1:II:115:GLY:HA3	2.00	0.43
1:IX:17:TRP:CD2	1:IZ:123:ILE:HG13	2.53	0.43
1:JJ:93:LYS:O	1:JJ:97:GLU:HG2	2.18	0.43
1:AH:5:MET:CG	1:AH:17:TRP:HB3	2.47	0.43
1:AT:62:GLU:H	1:AT:62:GLU:CD	2.21	0.43
1:AW:105:THR:O	1:AW:109:SER:OG	2.37	0.43
1:BA:3:LYS:HZ1	1:BB:127:ASP:HB3	1.83	0.43
1:BA:17:TRP:CD2	1:BB:123:ILE:HG13	2.53	0.43
1:BG:17:TRP:CD2	1:BH:123:ILE:HG13	2.53	0.43
1:BG:34:GLN:O	1:BG:45:ASN:N	2.51	0.43
1:BG:56:ARG:O	1:BG:74:GLU:N	2.46	0.43
1:BH:67:ALA:HB3	1:HQ:64:CYS:HA	1.99	0.43
1:BW:14:LYS:NZ	1:BW:28:SER:HB2	2.29	0.43
1:CE:105:THR:O	1:CE:109:SER:OG	2.35	0.43
1:CI:116:PHE:CE2	1:CK:20:PRO:HB3	2.53	0.43
1:CN:60:LYS:NZ	1:CN:65:ALA:H	2.16	0.43
1:CY:8:ILE:HG13	1:CY:18:SER:HB3	2.01	0.43
1:DB:5:MET:CG	1:DB:17:TRP:HB3	2.47	0.43
1:DL:123:ILE:HG13	1:DM:17:TRP:CD2	2.54	0.43
1:DQ:101:ARG:CZ	1:DQ:124:VAL:HG21	2.48	0.43
1:DS:62:GLU:H	1:DS:62:GLU:CD	2.21	0.43
1:EL:116:PHE:CE2	1:EP:20:PRO:HB3	2.53	0.43
1:ER:106:LEU:HD23	1:ER:106:LEU:HA	1.82	0.43
1:EW:57:PRO:HA	1:EW:73:ASN:HA	2.01	0.43
1:EZ:115:GLY:HA2	1:FA:31:LEU:HD23	2.00	0.43
1:FE:8:ILE:N	1:FE:16:VAL:O	2.39	0.43
1:FG:19:ASP:HB3	1:FG:22:ARG:O	2.18	0.43
1:FJ:123:ILE:HG22	1:FK:5:MET:HE2	1.99	0.43
1:FR:59:PRO:HG2	1:FS:87:GLU:HB3	1.99	0.43
1:FW:8:ILE:N	1:FW:16:VAL:O	2.39	0.43
1:GH:95:GLU:OE2	1:GI:76:GLN:HB3	2.17	0.43
1:GQ:72:PRO:HG2	1:GR:38:VAL:HG22	2.01	0.43
1:HA:106:LEU:HA	1:HA:106:LEU:HD23	1.82	0.43
1:HL:96:TRP:NE1	1:HL:100:LYS:HE2	2.33	0.43
1:HX:46:VAL:HG11	1:HY:113:GLY:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HZ:31:LEU:HD12	1:IA:117:LEU:HD22	1.99	0.43
1:IF:14:LYS:NZ	1:IF:28:SER:HB2	2.33	0.43
1:IZ:101:ARG:NH2	1:IZ:124:VAL:HG21	2.33	0.43
1:JC:43:LEU:HA	1:JC:87:GLU:OE2	2.18	0.43
1:AA:62:GLU:O	1:AA:62:GLU:HG2	2.17	0.43
1:AE:115:GLY:HA2	1:AF:31:LEU:HD23	2.00	0.43
1:AJ:37:LYS:NZ	1:AJ:40:ILE:O	2.51	0.43
1:AM:14:LYS:NZ	1:AM:28:SER:HB2	2.28	0.43
1:AS:5:MET:HG3	1:AS:19:ASP:N	2.34	0.43
1:AZ:25:THR:O	1:AZ:25:THR:OG1	2.34	0.43
1:BL:68:CYS:HA	1:GB:64:CYS:SG	2.59	0.43
1:BW:17:TRP:CD2	1:BX:123:ILE:HG13	2.53	0.43
1:CA:12:ALA:HB2	1:ES:10:SER:N	2.25	0.43
1:CA:127:ASP:OD1	1:CA:127:ASP:N	2.51	0.43
1:CD:5:MET:CG	1:CD:17:TRP:HB3	2.48	0.43
1:CF:8:ILE:HA	1:IX:116:PHE:HB2	1.99	0.43
1:CK:5:MET:CE	1:CL:123:ILE:HG22	2.49	0.43
1:CK:56:ARG:O	1:CK:74:GLU:N	2.49	0.43
1:CK:116:PHE:CE1	1:CM:6:GLN:HB2	2.52	0.43
1:CL:68:CYS:N	1:FN:63:GLY:N	2.67	0.43
1:CQ:14:LYS:NZ	1:CQ:28:SER:HB2	2.29	0.43
1:CV:68:CYS:CA	1:HL:64:CYS:H	2.32	0.43
1:DH:101:ARG:CZ	1:DH:124:VAL:HG21	2.49	0.43
1:DJ:128:THR:HA	1:DK:2:ASN:HA	1.98	0.43
1:DM:19:ASP:HB3	1:DM:22:ARG:O	2.19	0.43
1:DN:105:THR:O	1:DN:109:SER:OG	2.36	0.43
1:DW:67:ALA:HB1	1:IL:64:CYS:HA	1.99	0.43
1:DX:14:LYS:NZ	1:DX:15:ILE:O	2.52	0.43
1:ED:128:THR:HA	1:EE:2:ASN:HA	2.01	0.43
1:EG:67:ALA:HA	1:HX:63:GLY:N	2.23	0.43
1:EN:14:LYS:NZ	1:EN:15:ILE:O	2.52	0.43
1:EN:14:LYS:NZ	1:EN:28:SER:HB2	2.29	0.43
1:EQ:5:MET:CG	1:EQ:17:TRP:HB3	2.49	0.43
1:EQ:55:LYS:NZ	1:EQ:75:ASN:OD1	2.30	0.43
1:ET:5:MET:HG3	1:ET:19:ASP:HA	1.99	0.43
1:ET:115:GLY:HA2	1:EU:31:LEU:HD23	2.01	0.43
1:EX:8:ILE:HB	1:FC:116:PHE:HE1	1.83	0.43
1:EX:96:TRP:NE1	1:EX:100:LYS:HE2	2.33	0.43
1:FK:60:LYS:NZ	1:FK:65:ALA:O	2.31	0.43
1:GH:101:ARG:NH2	1:GH:124:VAL:HG21	2.33	0.43
1:GO:35:ARG:NH2	1:GO:44:ASN:HA	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GS:14:LYS:NZ	1:GS:28:SER:HB2	2.34	0.43
1:GW:116:PHE:CE1	1:GY:6:GLN:HB2	2.53	0.43
1:GY:35:ARG:NH2	1:GY:42:GLU:HB3	2.33	0.43
1:GZ:5:MET:N	1:GZ:5:MET:SD	2.91	0.43
1:HB:56:ARG:O	1:HB:74:GLU:N	2.27	0.43
1:HJ:45:ASN:HA	1:HJ:85:SER:HA	2.01	0.43
1:HT:72:PRO:HG2	1:HU:38:VAL:HG12	2.00	0.43
1:HV:124:VAL:HA	1:HW:4:PRO:HA	1.98	0.43
1:IC:105:THR:HA	1:IC:109:SER:HB2	2.00	0.43
1:II:45:ASN:HA	1:II:85:SER:HA	1.99	0.43
1:IK:57:PRO:HA	1:IK:73:ASN:HA	1.99	0.43
1:IR:3:LYS:HZ3	1:IS:127:ASP:HB3	1.84	0.43
1:IX:68:CYS:HB3	1:JD:64:CYS:HA	1.98	0.43
1:AE:58:ALA:HB3	1:AE:71:MET:HG3	2.00	0.43
1:AG:31:LEU:HD13	1:AH:117:LEU:HD21	2.01	0.43
1:AM:128:THR:HA	1:AN:2:ASN:HA	2.00	0.43
1:AN:68:CYS:N	1:JC:65:ALA:N	2.66	0.43
1:AO:3:LYS:HZ2	1:AP:129:THR:HG23	1.83	0.43
1:AP:61:PRO:HB2	1:AP:64:CYS:HB3	2.00	0.43
1:AR:62:GLU:O	1:AR:62:GLU:HG2	2.19	0.43
1:AU:128:THR:OG1	1:AV:1:ALA:O	2.33	0.43
1:BA:128:THR:O	1:BB:3:LYS:NZ	2.48	0.43
1:BI:5:MET:SD	1:BI:5:MET:N	2.91	0.43
1:BI:14:LYS:HD2	1:BI:14:LYS:HA	1.78	0.43
1:BK:105:THR:O	1:BK:109:SER:OG	2.37	0.43
1:BL:5:MET:CG	1:BL:17:TRP:HB3	2.48	0.43
1:BS:1:ALA:HB1	1:BT:128:THR:HG23	2.01	0.43
1:BX:67:ALA:H	1:JI:65:ALA:CB	2.31	0.43
1:CE:5:MET:SD	1:CE:5:MET:N	2.91	0.43
1:CI:5:MET:SD	1:CI:5:MET:N	2.91	0.43
1:CJ:37:LYS:HZ2	1:CJ:37:LYS:HG3	1.51	0.43
1:CQ:1:ALA:HB1	1:CR:128:THR:HG23	2.01	0.43
1:CV:68:CYS:HA	1:HL:61:PRO:O	2.19	0.43
1:CZ:37:LYS:HE3	1:CZ:37:LYS:HB3	1.73	0.43
1:CZ:67:ALA:C	1:ID:63:GLY:H	2.22	0.43
1:DO:5:MET:CG	1:DO:17:TRP:HB3	2.48	0.43
1:EA:25:THR:O	1:EA:25:THR:OG1	2.34	0.43
1:EG:68:CYS:HA	1:HX:61:PRO:O	2.19	0.43
1:ER:55:LYS:NZ	1:ER:75:ASN:OD1	2.37	0.43
1:EX:68:CYS:HB3	1:FC:64:CYS:HA	1.99	0.43
1:FD:60:LYS:NZ	1:FD:69:VAL:O	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FT:56:ARG:O	1:FT:74:GLU:N	2.32	0.43
1:GB:68:CYS:HB3	1:GG:64:CYS:HA	2.00	0.43
1:GH:106:LEU:HD23	1:GH:106:LEU:HA	1.82	0.43
1:GO:31:LEU:HD11	1:GP:117:LEU:HB3	2.01	0.43
1:GO:61:PRO:HG2	1:GO:64:CYS:SG	2.57	0.43
1:GQ:61:PRO:HG2	1:GQ:64:CYS:SG	2.59	0.43
1:GR:117:LEU:HD23	1:GR:117:LEU:H	1.83	0.43
1:GU:56:ARG:O	1:GU:74:GLU:N	2.44	0.43
1:GY:35:ARG:HH12	1:GY:43:LEU:C	2.19	0.43
1:HC:5:MET:SD	1:HD:123:ILE:HG22	2.59	0.43
1:HN:35:ARG:NH2	1:HN:42:GLU:OE1	2.49	0.43
1:HR:55:LYS:NZ	1:HR:73:ASN:HB2	2.33	0.43
1:IB:106:LEU:HD23	1:IB:106:LEU:HA	1.84	0.43
1:II:36:VAL:HG23	1:II:43:LEU:HB2	2.01	0.43
1:IP:5:MET:SD	1:IP:5:MET:N	2.91	0.43
1:IS:22:ARG:NH2	1:IS:55:LYS:O	2.44	0.43
1:JF:101:ARG:NH2	1:JF:124:VAL:HG21	2.34	0.43
1:AE:101:ARG:CZ	1:AE:124:VAL:HG21	2.48	0.43
1:AM:1:ALA:HB1	1:AN:128:THR:HG23	2.01	0.43
1:AM:101:ARG:CZ	1:AM:124:VAL:HG21	2.49	0.43
1:AO:19:ASP:HB3	1:AO:22:ARG:O	2.19	0.43
1:AU:5:MET:HE1	1:AV:123:ILE:HG22	2.01	0.43
1:BH:101:ARG:HE	1:BH:101:ARG:HB3	1.71	0.43
1:BJ:8:ILE:HA	1:HZ:116:PHE:HB2	2.00	0.43
1:BJ:67:ALA:H	1:HZ:65:ALA:HB2	1.84	0.43
1:BL:37:LYS:HA	1:BL:42:GLU:HA	2.01	0.43
1:CB:5:MET:CG	1:CB:17:TRP:HB3	2.48	0.43
1:CN:66:ASP:OD1	1:CN:66:ASP:N	2.49	0.43
1:CP:66:ASP:OD1	1:CP:66:ASP:N	2.47	0.43
1:CZ:60:LYS:NZ	1:CZ:65:ALA:HB3	2.34	0.43
1:DB:57:PRO:HA	1:DB:73:ASN:HA	2.00	0.43
1:DG:37:LYS:NZ	1:DG:40:ILE:O	2.48	0.43
1:EK:5:MET:HG2	1:EK:17:TRP:HB3	2.00	0.43
1:EN:19:ASP:HB3	1:EN:22:ARG:O	2.19	0.43
1:FC:93:LYS:O	1:FC:97:GLU:HG2	2.19	0.43
1:FD:5:MET:CG	1:FD:17:TRP:HB3	2.48	0.43
1:FV:101:ARG:NH2	1:FV:124:VAL:HG21	2.34	0.43
1:FY:74:GLU:HG2	1:FY:75:ASN:H	1.84	0.43
1:GK:63:GLY:CA	1:GM:68:CYS:HA	2.43	0.43
1:GW:46:VAL:HG11	1:GX:113:GLY:O	2.18	0.43
1:HA:43:LEU:HD12	1:HA:85:SER:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HR:6:GLN:HG2	1:HR:20:PRO:HD3	2.01	0.43
1:HZ:106:LEU:HD23	1:HZ:106:LEU:HA	1.82	0.43
1:IU:38:VAL:HB	1:IU:43:LEU:HD12	2.01	0.43
1:JA:35:ARG:HD2	1:JA:44:ASN:HB3	2.01	0.43
1:JA:127:ASP:OD1	1:JA:127:ASP:N	2.49	0.43
1:JG:37:LYS:HD3	1:JG:42:GLU:OE2	2.18	0.43
1:AH:62:GLU:H	1:AH:62:GLU:CD	2.21	0.43
1:AN:5:MET:HG2	1:AN:17:TRP:HB3	2.00	0.43
1:BF:12:ALA:HB1	1:BG:9:THR:HA	2.01	0.43
1:BK:88:ASN:ND2	1:BL:74:GLU:OE2	2.34	0.43
1:BU:14:LYS:NZ	1:BU:28:SER:HB2	2.29	0.43
1:CE:31:LEU:HD13	1:CF:117:LEU:HD21	2.00	0.43
1:CG:92:LEU:HA	1:CG:95:GLU:OE1	2.19	0.43
1:CJ:60:LYS:HZ1	1:CJ:65:ALA:H	1.65	0.43
1:CZ:5:MET:CG	1:CZ:17:TRP:HB3	2.49	0.43
1:CZ:37:LYS:HD2	1:CZ:42:GLU:HB3	2.01	0.43
1:DA:49:GLN:OE1	1:DA:79:ARG:NH2	2.38	0.43
1:DC:101:ARG:CZ	1:DC:124:VAL:HG21	2.49	0.43
1:DI:25:THR:O	1:DI:25:THR:OG1	2.32	0.43
1:DO:62:GLU:O	1:DO:62:GLU:HG2	2.17	0.43
1:DU:5:MET:CG	1:DU:17:TRP:HB3	2.48	0.43
1:DX:17:TRP:CD2	1:DY:123:ILE:HG13	2.53	0.43
1:EE:62:GLU:H	1:EE:62:GLU:CD	2.21	0.43
1:EF:14:LYS:HD3	1:EF:30:SER:HB2	2.01	0.43
1:EM:35:ARG:HB3	1:EM:42:GLU:OE2	2.18	0.43
1:EU:36:VAL:HG13	1:EU:43:LEU:HB2	2.01	0.43
1:EX:55:LYS:HZ2	1:EX:73:ASN:HB2	1.84	0.43
1:FK:38:VAL:HG21	1:FK:43:LEU:HD22	2.01	0.43
1:FM:32:LEU:HG	1:FM:34:GLN:NE2	2.33	0.43
1:FX:46:VAL:HG11	1:FY:113:GLY:O	2.19	0.43
1:FX:60:LYS:HA	1:FX:71:MET:HE3	2.01	0.43
1:FY:37:LYS:HD2	1:FY:41:ALA:O	2.18	0.43
1:GA:57:PRO:HA	1:GA:73:ASN:HA	2.00	0.43
1:GD:3:LYS:HZ3	1:GE:127:ASP:C	2.22	0.43
1:HK:35:ARG:HH22	1:HK:42:GLU:HB3	1.84	0.43
1:IA:8:ILE:N	1:IA:16:VAL:O	2.40	0.43
1:IB:5:MET:SD	1:IB:5:MET:N	2.92	0.43
1:IJ:1:ALA:O	1:IK:129:THR:N	2.34	0.43
1:IM:62:GLU:HG2	1:IM:62:GLU:O	2.19	0.43
1:IW:60:LYS:HB3	1:IW:71:MET:HE3	2.00	0.43
1:JA:37:LYS:HD3	1:JA:42:GLU:OE2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JB:89:LEU:HG	1:JB:93:LYS:HE3	2.01	0.43
1:AA:17:TRP:CD2	1:AB:123:ILE:HG13	2.54	0.43
1:AT:6:GLN:NE2	1:GX:114:LEU:HD22	2.34	0.43
1:AZ:62:GLU:O	1:AZ:62:GLU:HG2	2.19	0.43
1:BA:35:ARG:NH2	1:BA:42:GLU:HG2	2.33	0.43
1:BA:56:ARG:O	1:BA:74:GLU:N	2.46	0.43
1:BE:1:ALA:HB1	1:BF:128:THR:HG23	2.01	0.43
1:BE:5:MET:SD	1:BE:5:MET:N	2.92	0.43
1:BM:125:SER:O	1:BN:2:ASN:ND2	2.51	0.43
1:BU:58:ALA:HB3	1:BU:71:MET:HG3	2.01	0.43
1:BW:58:ALA:HB3	1:BW:71:MET:HG3	2.00	0.43
1:CC:19:ASP:HB3	1:CC:22:ARG:O	2.18	0.43
1:CF:105:THR:HG23	1:CF:106:LEU:HD12	1.99	0.43
1:CK:31:LEU:HD22	1:CL:115:GLY:HA2	2.01	0.43
1:CR:116:PHE:CE1	1:ET:8:ILE:HD11	2.54	0.43
1:CT:19:ASP:HB3	1:CT:22:ARG:O	2.19	0.43
1:CU:105:THR:O	1:CU:109:SER:OG	2.37	0.43
1:DI:5:MET:CG	1:DI:17:TRP:HB3	2.49	0.43
1:DI:37:LYS:HB3	1:DI:37:LYS:HE3	1.72	0.43
1:DI:67:ALA:C	1:FH:63:GLY:H	2.22	0.43
1:DN:14:LYS:NZ	1:DN:28:SER:HB2	2.27	0.43
1:DP:37:LYS:HD3	1:DP:42:GLU:OE2	2.19	0.43
1:DS:106:LEU:HD11	1:DS:123:ILE:HD11	2.01	0.43
1:DT:5:MET:HB2	1:DT:17:TRP:HB3	2.00	0.43
1:EI:62:GLU:HG2	1:EI:62:GLU:O	2.18	0.43
1:EI:68:CYS:HA	1:FD:64:CYS:SG	2.59	0.43
1:ES:9:THR:O	1:ES:15:ILE:HA	2.19	0.43
1:EY:62:GLU:O	1:EY:62:GLU:HG2	2.19	0.43
1:FB:106:LEU:HD23	1:FB:106:LEU:HA	1.82	0.43
1:FC:87:GLU:OE1	1:FC:87:GLU:N	2.45	0.43
1:FH:95:GLU:OE2	1:FI:76:GLN:HB3	2.18	0.43
1:FH:128:THR:HA	1:FI:2:ASN:HA	2.01	0.43
1:FJ:46:VAL:HG11	1:FK:113:GLY:O	2.19	0.43
1:FM:37:LYS:HD2	1:FM:41:ALA:O	2.19	0.43
1:FN:66:ASP:OD2	1:FN:68:CYS:HB2	2.19	0.43
1:FP:35:ARG:NH2	1:FP:44:ASN:OD1	2.51	0.43
1:GK:5:MET:N	1:GK:5:MET:SD	2.92	0.43
1:GL:117:LEU:HD23	1:GL:117:LEU:H	1.83	0.43
1:GO:74:GLU:OE2	1:GP:85:SER:OG	2.28	0.43
1:GP:8:ILE:N	1:GP:16:VAL:O	2.39	0.43
1:GT:9:THR:O	1:GT:15:ILE:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GY:57:PRO:HA	1:GY:73:ASN:HA	2.01	0.43
1:HT:11:THR:HB	1:HT:14:LYS:H	1.83	0.43
1:HT:35:ARG:NH2	1:HT:44:ASN:OD1	2.50	0.43
1:IO:89:LEU:HG	1:IO:93:LYS:HE3	2.01	0.43
1:IV:31:LEU:HD12	1:IW:117:LEU:HD22	2.00	0.43
1:JB:43:LEU:HD22	1:JB:87:GLU:OE2	2.19	0.43
1:JF:23:LEU:O	1:JF:24:SER:OG	2.30	0.43
1:AQ:127:ASP:OD1	1:AQ:127:ASP:N	2.52	0.43
1:AV:55:LYS:NZ	1:AV:75:ASN:OD1	2.30	0.43
1:BC:14:LYS:NZ	1:BC:28:SER:HB2	2.28	0.43
1:BF:106:LEU:HD21	1:BF:123:ILE:HD11	2.01	0.43
1:BG:31:LEU:HD13	1:BH:117:LEU:HD21	2.01	0.43
1:BI:13:ASN:OD1	1:BI:14:LYS:N	2.52	0.43
1:BU:8:ILE:HG13	1:BU:18:SER:HB3	2.01	0.43
1:CY:14:LYS:NZ	1:CY:15:ILE:O	2.52	0.43
1:DA:19:ASP:HB3	1:DA:22:ARG:O	2.19	0.43
1:DC:56:ARG:O	1:DC:74:GLU:N	2.46	0.43
1:DL:117:LEU:HD23	1:DM:15:ILE:HG13	2.00	0.43
1:DX:117:LEU:HD11	1:DY:31:LEU:HD13	2.01	0.43
1:EF:60:LYS:NZ	1:EF:66:ASP:O	2.26	0.43
1:EI:5:MET:CG	1:EI:17:TRP:HB3	2.49	0.43
1:EL:129:THR:N	1:EM:1:ALA:O	2.48	0.43
1:EN:105:THR:O	1:EN:109:SER:OG	2.36	0.43
1:ET:2:ASN:HB2	1:EU:124:VAL:HB	2.00	0.43
1:EY:5:MET:N	1:EY:5:MET:SD	2.92	0.43
1:FF:63:GLY:CA	1:FH:68:CYS:HA	2.45	0.43
1:FV:125:SER:HB2	1:FW:5:MET:CE	2.48	0.43
1:FW:9:THR:O	1:FW:15:ILE:HA	2.19	0.43
1:GB:106:LEU:HD23	1:GB:106:LEU:HA	1.82	0.43
1:GN:36:VAL:N	1:GN:43:LEU:O	2.49	0.43
1:GP:85:SER:HG	1:GP:88:ASN:HD22	1.67	0.43
1:GS:91:THR:OG1	1:GT:76:GLN:NE2	2.34	0.43
1:HB:60:LYS:NZ	1:HB:66:ASP:O	2.52	0.43
1:HF:36:VAL:N	1:HF:43:LEU:O	2.49	0.43
1:HK:55:LYS:HZ2	1:HK:73:ASN:HB2	1.82	0.43
1:HL:124:VAL:HA	1:HM:4:PRO:HA	2.01	0.43
1:HM:57:PRO:HA	1:HM:73:ASN:HA	2.01	0.43
1:IH:72:PRO:HG3	1:II:39:GLY:HA3	2.01	0.43
1:IJ:31:LEU:HD11	1:IK:117:LEU:HB3	2.00	0.43
1:IR:31:LEU:HD13	1:IS:115:GLY:HA2	2.00	0.43
1:IS:102:ASN:O	1:IS:105:THR:HG22	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JA:59:PRO:O	1:JA:61:PRO:HD3	2.18	0.43
1:JF:93:LYS:O	1:JF:97:GLU:HG2	2.19	0.43
1:AI:58:ALA:HB3	1:AI:71:MET:HG3	2.01	0.42
1:AO:58:ALA:HB3	1:AO:71:MET:HG3	2.01	0.42
1:AR:5:MET:HG3	1:AR:17:TRP:HB3	2.01	0.42
1:AT:19:ASP:HB3	1:AT:22:ARG:O	2.19	0.42
1:BE:17:TRP:CD2	1:BF:123:ILE:HG13	2.54	0.42
1:BV:5:MET:CG	1:BV:17:TRP:HB3	2.49	0.42
1:CM:14:LYS:HZ1	1:CM:28:SER:CB	2.27	0.42
1:CM:19:ASP:HB3	1:CM:22:ARG:O	2.19	0.42
1:CV:32:LEU:HB3	1:CV:47:SER:HB3	2.01	0.42
1:DE:5:MET:CG	1:DE:17:TRP:HB3	2.49	0.42
1:DP:19:ASP:HB3	1:DP:22:ARG:O	2.19	0.42
1:DV:5:MET:HE1	1:DW:123:ILE:HG22	2.01	0.42
1:DX:101:ARG:NH2	1:DX:124:VAL:HG21	2.34	0.42
1:DZ:104:ASP:OD2	1:EA:100:LYS:NZ	2.52	0.42
1:EG:68:CYS:N	1:HX:63:GLY:N	2.67	0.42
1:EQ:61:PRO:HB2	1:EQ:64:CYS:HB3	2.01	0.42
1:EZ:106:LEU:HD23	1:EZ:106:LEU:HA	1.77	0.42
1:FY:55:LYS:NZ	1:FY:73:ASN:HB2	2.33	0.42
1:FY:62:GLU:HG2	1:FY:62:GLU:O	2.19	0.42
1:GB:35:ARG:HH12	1:GB:43:LEU:C	2.21	0.42
1:GF:79:ARG:HB2	1:GF:79:ARG:NH1	2.34	0.42
1:GU:115:GLY:HA3	1:GV:33:ARG:HD3	2.00	0.42
1:HX:14:LYS:NZ	1:HX:28:SER:HB2	2.33	0.42
1:IH:46:VAL:HG11	1:II:113:GLY:O	2.19	0.42
1:IJ:43:LEU:HD22	1:IJ:87:GLU:OE2	2.18	0.42
1:IK:5:MET:N	1:IK:5:MET:SD	2.92	0.42
1:IL:20:PRO:HB3	1:IQ:116:PHE:HE2	1.83	0.42
1:IQ:93:LYS:O	1:IQ:97:GLU:HG2	2.19	0.42
1:JF:62:GLU:O	1:JF:62:GLU:HG2	2.19	0.42
1:JI:66:ASP:CG	1:JI:68:CYS:H	2.22	0.42
1:JI:115:GLY:O	1:JJ:33:ARG:NH1	2.52	0.42
1:AA:3:LYS:HZ1	1:AB:129:THR:HG23	1.84	0.42
1:AQ:128:THR:OG1	1:AR:1:ALA:O	2.29	0.42
1:AV:105:THR:HG23	1:AV:106:LEU:HD12	1.99	0.42
1:BD:5:MET:CG	1:BD:17:TRP:HB3	2.50	0.42
1:BS:31:LEU:HD13	1:BT:117:LEU:HD21	2.01	0.42
1:BX:5:MET:CG	1:BX:17:TRP:HB3	2.48	0.42
1:CA:14:LYS:NZ	1:CA:30:SER:OG	2.52	0.42
1:CF:5:MET:CG	1:CF:17:TRP:HB3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:62:GLU:O	1:CI:62:GLU:HG2	2.20	0.42
1:CO:125:SER:O	1:CP:2:ASN:ND2	2.52	0.42
1:CV:60:LYS:NZ	1:CV:65:ALA:HB3	2.34	0.42
1:CW:115:GLY:O	1:CX:33:ARG:NH1	2.52	0.42
1:CX:57:PRO:HA	1:CX:73:ASN:HA	2.01	0.42
1:CY:58:ALA:HB3	1:CY:71:MET:HG3	2.01	0.42
1:DL:127:ASP:N	1:DL:127:ASP:OD1	2.51	0.42
1:DP:56:ARG:O	1:DP:74:GLU:N	2.47	0.42
1:DQ:61:PRO:HB2	1:DQ:64:CYS:HB3	2.01	0.42
1:DY:5:MET:HG2	1:DY:17:TRP:HB3	2.01	0.42
1:EB:14:LYS:NZ	1:EB:15:ILE:O	2.52	0.42
1:ED:58:ALA:HB3	1:ED:71:MET:HG3	2.00	0.42
1:EG:67:ALA:O	1:HX:65:ALA:HB2	2.19	0.42
1:EN:128:THR:OG1	1:EO:1:ALA:O	2.30	0.42
1:ES:5:MET:N	1:ES:5:MET:SD	2.92	0.42
1:FC:37:LYS:NZ	1:FC:38:VAL:O	2.38	0.42
1:FH:92:LEU:HD13	1:FH:95:GLU:OE2	2.18	0.42
1:FK:62:GLU:HG2	1:FK:62:GLU:O	2.19	0.42
1:FL:87:GLU:OE1	1:FL:87:GLU:N	2.47	0.42
1:FM:32:LEU:HG	1:FM:34:GLN:HE22	1.84	0.42
1:FP:59:PRO:O	1:FP:71:MET:HE3	2.18	0.42
1:FQ:62:GLU:HG2	1:FQ:62:GLU:O	2.20	0.42
1:FX:116:PHE:CE1	1:FZ:6:GLN:HB2	2.54	0.42
1:GE:12:ALA:HB1	1:GF:9:THR:HG23	2.01	0.42
1:GE:117:LEU:HD23	1:GE:117:LEU:H	1.84	0.42
1:GK:65:ALA:HB1	1:GK:69:VAL:HB	2.01	0.42
1:GU:14:LYS:NZ	1:GU:28:SER:HB2	2.34	0.42
1:GY:85:SER:OG	1:GZ:74:GLU:OE1	2.18	0.42
1:HQ:117:LEU:HD23	1:HQ:117:LEU:H	1.84	0.42
1:HR:3:LYS:NZ	1:HR:21:THR:OG1	2.33	0.42
1:HV:65:ALA:N	1:HX:68:CYS:HB3	2.34	0.42
1:IT:115:GLY:HA2	1:IU:31:LEU:HD23	2.01	0.42
1:IW:22:ARG:NH2	1:IW:55:LYS:O	2.44	0.42
1:AC:34:GLN:O	1:AC:45:ASN:N	2.50	0.42
1:AE:101:ARG:NH2	1:AF:2:ASN:HD22	2.17	0.42
1:AE:116:PHE:CE1	1:AI:6:GLN:HB2	2.54	0.42
1:AL:66:ASP:OD2	1:AL:69:VAL:HG13	2.19	0.42
1:AQ:72:PRO:HG2	1:AR:38:VAL:HG22	2.01	0.42
1:AR:116:PHE:CE2	1:GW:20:PRO:HA	2.54	0.42
1:AS:58:ALA:HB3	1:AS:71:MET:HG3	2.01	0.42
1:AU:125:SER:O	1:AV:2:ASN:ND2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:56:ARG:O	1:AY:74:GLU:N	2.50	0.42
1:BC:19:ASP:HB3	1:BC:22:ARG:O	2.19	0.42
1:BQ:101:ARG:CZ	1:BQ:124:VAL:HG21	2.49	0.42
1:BW:60:LYS:HZ3	1:BW:66:ASP:H	1.67	0.42
1:BY:17:TRP:CD2	1:BZ:123:ILE:HG13	2.54	0.42
1:CE:127:ASP:OD1	1:CE:127:ASP:N	2.51	0.42
1:CR:6:GLN:HE22	1:FG:111:ASN:HB3	1.84	0.42
1:CT:66:ASP:OD2	1:CT:68:CYS:N	2.52	0.42
1:DJ:6:GLN:HB2	1:DL:116:PHE:HE2	1.84	0.42
1:DL:1:ALA:HB1	1:DM:128:THR:HG23	2.00	0.42
1:DR:62:GLU:O	1:DR:62:GLU:HG2	2.18	0.42
1:EB:62:GLU:O	1:EB:62:GLU:HG2	2.19	0.42
1:ED:60:LYS:NZ	1:ED:66:ASP:H	2.17	0.42
1:EJ:1:ALA:HB1	1:EK:128:THR:HG23	2.00	0.42
1:ET:31:LEU:HD21	1:EU:112:ALA:HB1	2.00	0.42
1:EV:87:GLU:OE1	1:EV:87:GLU:N	2.36	0.42
1:FH:106:LEU:HD23	1:FH:106:LEU:HA	1.82	0.42
1:FY:105:THR:HA	1:FY:109:SER:HB2	2.01	0.42
1:GA:5:MET:N	1:GA:5:MET:SD	2.92	0.42
1:GB:35:ARG:NH2	1:GB:42:GLU:OE1	2.51	0.42
1:GF:6:GLN:HG2	1:GF:20:PRO:HD3	2.01	0.42
1:GL:56:ARG:NE	1:GL:76:GLN:OE1	2.34	0.42
1:GO:14:LYS:HZ3	1:GO:30:SER:HB2	1.85	0.42
1:GU:35:ARG:NH1	1:GU:42:GLU:OE1	2.51	0.42
1:HC:56:ARG:O	1:HC:74:GLU:HG2	2.19	0.42
1:HE:124:VAL:HA	1:HF:4:PRO:HA	2.01	0.42
1:HM:43:LEU:HD12	1:HM:85:SER:HB2	2.01	0.42
1:HP:106:LEU:HD23	1:HP:106:LEU:HA	1.76	0.42
1:HR:14:LYS:HZ3	1:HR:30:SER:HB2	1.84	0.42
1:IQ:87:GLU:OE1	1:IQ:87:GLU:N	2.45	0.42
1:JD:45:ASN:HA	1:JD:85:SER:HA	2.00	0.42
1:JH:89:LEU:HG	1:JH:93:LYS:HE3	2.01	0.42
1:AE:128:THR:HA	1:AF:2:ASN:HA	2.00	0.42
1:AH:8:ILE:HA	1:JE:116:PHE:HB2	2.00	0.42
1:AN:37:LYS:NZ	1:AN:40:ILE:O	2.51	0.42
1:AS:128:THR:HA	1:AT:2:ASN:HA	2.01	0.42
1:AY:37:LYS:HZ3	1:AY:42:GLU:HB2	1.84	0.42
1:BC:127:ASP:OD1	1:BC:127:ASP:N	2.50	0.42
1:BC:128:THR:OG1	1:BD:1:ALA:O	2.31	0.42
1:BL:101:ARG:CZ	1:BL:124:VAL:HG21	2.50	0.42
1:BP:55:LYS:NZ	1:BP:75:ASN:OD1	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:72:PRO:HG2	1:BT:38:VAL:HG22	2.01	0.42
1:BX:70:ILE:O	1:BX:70:ILE:HG13	2.19	0.42
1:CU:19:ASP:HB3	1:CU:22:ARG:O	2.19	0.42
1:DA:128:THR:HA	1:DB:2:ASN:HA	2.01	0.42
1:DJ:35:ARG:NH1	1:DJ:44:ASN:OD1	2.53	0.42
1:DU:67:ALA:N	1:FP:65:ALA:H	2.18	0.42
1:ED:19:ASP:HB3	1:ED:22:ARG:O	2.18	0.42
1:EE:67:ALA:H	1:GU:65:ALA:H	1.65	0.42
1:EI:60:LYS:HZ1	1:EI:65:ALA:H	1.64	0.42
1:ER:60:LYS:HB3	1:ER:65:ALA:HB2	2.02	0.42
1:EZ:35:ARG:HD2	1:EZ:44:ASN:HB3	2.01	0.42
1:FB:5:MET:SD	1:FB:5:MET:N	2.92	0.42
1:FE:5:MET:HG3	1:FE:19:ASP:HA	2.01	0.42
1:FM:32:LEU:HB3	1:FM:47:SER:HB3	2.00	0.42
1:FP:31:LEU:HD11	1:FQ:117:LEU:HB3	2.02	0.42
1:FP:85:SER:OG	1:FQ:74:GLU:OE1	2.20	0.42
1:FQ:116:PHE:HE1	1:FS:8:ILE:HB	1.84	0.42
1:FW:71:MET:HE3	1:FW:71:MET:HB3	1.91	0.42
1:GC:64:CYS:HA	1:GE:67:ALA:HB3	2.02	0.42
1:GO:44:ASN:H	1:GO:87:GLU:CD	2.23	0.42
1:HR:35:ARG:HH21	1:HR:43:LEU:C	2.23	0.42
1:IB:87:GLU:OE1	1:IB:87:GLU:N	2.47	0.42
1:JA:5:MET:HG3	1:JA:19:ASP:HA	2.01	0.42
1:JE:17:TRP:CD2	1:JF:123:ILE:HG13	2.54	0.42
1:JG:118:ASP:OD1	1:JG:120:THR:OG1	2.36	0.42
1:JJ:5:MET:N	1:JJ:5:MET:SD	2.93	0.42
1:AD:62:GLU:H	1:AD:62:GLU:CD	2.21	0.42
1:AX:60:LYS:NZ	1:AX:65:ALA:HB3	2.34	0.42
1:AX:101:ARG:CZ	1:AX:124:VAL:HG21	2.50	0.42
1:BH:61:PRO:HB2	1:BH:64:CYS:HB3	2.02	0.42
1:BQ:19:ASP:HB3	1:BQ:22:ARG:O	2.19	0.42
1:BQ:80:THR:OG1	1:BR:99:HIS:NE2	2.41	0.42
1:CH:67:ALA:H	1:HA:65:ALA:CB	2.32	0.42
1:CL:68:CYS:CA	1:FN:64:CYS:H	2.33	0.42
1:CU:101:ARG:CZ	1:CU:124:VAL:HG21	2.50	0.42
1:DF:58:ALA:HB3	1:DF:71:MET:HG3	2.01	0.42
1:EB:37:LYS:HZ3	1:EB:42:GLU:HB2	1.85	0.42
1:EF:37:LYS:HZ3	1:EF:42:GLU:HB2	1.83	0.42
1:EG:62:GLU:H	1:EG:62:GLU:CD	2.21	0.42
1:EN:58:ALA:HB3	1:EN:71:MET:HG3	2.01	0.42
1:ER:14:LYS:HA	1:ER:14:LYS:HD2	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ER:43:LEU:HD12	1:ER:85:SER:HB2	2.02	0.42
1:FN:14:LYS:NZ	1:FN:28:SER:HB2	2.33	0.42
1:FV:31:LEU:HD13	1:FW:115:GLY:HA2	2.02	0.42
1:GA:8:ILE:N	1:GA:16:VAL:O	2.38	0.42
1:GQ:124:VAL:HA	1:GR:4:PRO:HA	2.01	0.42
1:HA:11:THR:N	1:HA:14:LYS:O	2.52	0.42
1:HU:62:GLU:O	1:HU:62:GLU:HG2	2.20	0.42
1:HV:72:PRO:HG2	1:HW:38:VAL:HG22	2.01	0.42
1:IA:5:MET:N	1:IA:5:MET:SD	2.92	0.42
1:IC:36:VAL:HG23	1:IC:43:LEU:HB2	2.02	0.42
1:IL:14:LYS:HZ2	1:IL:29:ALA:N	2.17	0.42
1:IN:35:ARG:HD2	1:IN:44:ASN:HB3	2.01	0.42
1:IN:60:LYS:HA	1:IN:71:MET:HE1	2.01	0.42
1:AC:56:ARG:O	1:AC:74:GLU:N	2.50	0.42
1:AL:12:ALA:HB1	1:AM:9:THR:HA	2.02	0.42
1:AR:101:ARG:CZ	1:AR:124:VAL:HG21	2.50	0.42
1:AW:101:ARG:CZ	1:AW:124:VAL:HG21	2.50	0.42
1:AW:127:ASP:OD1	1:AW:127:ASP:N	2.51	0.42
1:BG:46:VAL:HG11	1:BH:113:GLY:O	2.19	0.42
1:BO:127:ASP:OD1	1:BO:127:ASP:N	2.51	0.42
1:BQ:105:THR:O	1:BQ:109:SER:OG	2.37	0.42
1:CI:123:ILE:HG13	1:CJ:17:TRP:CD2	2.54	0.42
1:CZ:101:ARG:CZ	1:CZ:124:VAL:HG21	2.49	0.42
1:DA:58:ALA:HB3	1:DA:71:MET:HG3	2.01	0.42
1:DB:68:CYS:HA	1:IF:64:CYS:SG	2.60	0.42
1:DB:116:PHE:CE1	1:FL:8:ILE:HD11	2.55	0.42
1:DH:58:ALA:HB3	1:DH:71:MET:HG3	2.02	0.42
1:DJ:6:GLN:HB2	1:DL:116:PHE:CE2	2.55	0.42
1:DV:128:THR:HA	1:DW:2:ASN:HA	2.01	0.42
1:EH:116:PHE:CE1	1:EJ:6:GLN:HB2	2.55	0.42
1:EL:19:ASP:HB3	1:EL:22:ARG:O	2.19	0.42
1:EP:2:ASN:CG	1:EQ:101:ARG:HH22	2.22	0.42
1:EV:44:ASN:HB2	1:EV:87:GLU:OE1	2.20	0.42
1:FB:44:ASN:H	1:FB:87:GLU:CD	2.23	0.42
1:FD:106:LEU:HD23	1:FD:106:LEU:HA	1.82	0.42
1:FF:60:LYS:HE2	1:FF:64:CYS:H	1.84	0.42
1:FF:111:ASN:HB3	1:FF:114:LEU:HD12	2.02	0.42
1:FM:101:ARG:HE	1:FM:101:ARG:HB2	1.63	0.42
1:GL:43:LEU:HD12	1:GL:87:GLU:CD	2.40	0.42
1:GP:89:LEU:HD12	1:GP:92:LEU:HD23	2.01	0.42
1:GU:5:MET:HB3	1:GU:17:TRP:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GW:88:ASN:ND2	1:GX:56:ARG:HD2	2.26	0.42
1:HG:14:LYS:NZ	1:HG:28:SER:HB2	2.34	0.42
1:HJ:8:ILE:HD13	1:HJ:8:ILE:HA	1.90	0.42
1:HN:68:CYS:HB3	1:HS:64:CYS:HA	2.01	0.42
1:HO:57:PRO:HA	1:HO:73:ASN:HA	2.01	0.42
1:HR:106:LEU:HD23	1:HR:106:LEU:HA	1.82	0.42
1:HT:37:LYS:HD2	1:HT:41:ALA:O	2.19	0.42
1:IF:86:ALA:HB1	1:IG:114:LEU:HD23	2.00	0.42
1:IF:106:LEU:HA	1:IF:106:LEU:HD23	1.82	0.42
1:IG:74:GLU:HG2	1:IG:75:ASN:H	1.83	0.42
1:IN:113:GLY:O	1:IO:46:VAL:HG11	2.19	0.42
1:IS:62:GLU:HG2	1:IS:62:GLU:O	2.20	0.42
1:IV:46:VAL:HG11	1:IW:113:GLY:O	2.20	0.42
1:JE:106:LEU:HD23	1:JE:106:LEU:HA	1.82	0.42
1:JI:35:ARG:NH2	1:JI:42:GLU:OE1	2.52	0.42
1:JJ:23:LEU:O	1:JJ:24:SER:OG	2.29	0.42
1:AC:3:LYS:HZ2	1:AD:129:THR:HG23	1.83	0.42
1:AD:69:VAL:HG22	1:IV:64:CYS:CB	2.48	0.42
1:AH:101:ARG:CZ	1:AH:124:VAL:HG21	2.49	0.42
1:AY:14:LYS:HD3	1:AY:30:SER:HB2	2.01	0.42
1:BC:34:GLN:O	1:BC:45:ASN:N	2.52	0.42
1:CI:14:LYS:NZ	1:CI:15:ILE:O	2.52	0.42
1:CI:71:MET:HB3	1:CI:71:MET:HE3	1.92	0.42
1:CK:105:THR:O	1:CK:109:SER:OG	2.37	0.42
1:CO:3:LYS:HZ1	1:CP:127:ASP:HB3	1.85	0.42
1:CP:106:LEU:HD11	1:CP:123:ILE:HD11	2.01	0.42
1:DB:5:MET:HG2	1:DB:17:TRP:HB3	2.00	0.42
1:DF:19:ASP:HB3	1:DF:22:ARG:O	2.20	0.42
1:DI:66:ASP:OD2	1:FH:64:CYS:HA	2.19	0.42
1:DN:49:GLN:OE1	1:DN:79:ARG:NH2	2.38	0.42
1:DP:58:ALA:HB3	1:DP:71:MET:HG3	2.02	0.42
1:DP:101:ARG:CZ	1:DP:124:VAL:HG21	2.50	0.42
1:DW:32:LEU:HB3	1:DW:47:SER:HB3	2.01	0.42
1:DZ:17:TRP:CD2	1:EA:123:ILE:HG13	2.54	0.42
1:ED:124:VAL:HA	1:EE:4:PRO:HA	2.00	0.42
1:EJ:127:ASP:OD1	1:EJ:127:ASP:N	2.51	0.42
1:EK:5:MET:CG	1:EK:17:TRP:HB3	2.49	0.42
1:FA:38:VAL:HG22	1:FA:39:GLY:H	1.84	0.42
1:FD:11:THR:N	1:FD:14:LYS:O	2.52	0.42
1:FI:60:LYS:HG2	1:FI:71:MET:HE1	2.02	0.42
1:FM:56:ARG:NE	1:FM:76:GLN:OE1	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FN:5:MET:HG3	1:FN:19:ASP:HA	2.01	0.42
1:FV:96:TRP:NE1	1:FV:100:LYS:HE2	2.35	0.42
1:HQ:37:LYS:HD2	1:HQ:41:ALA:O	2.19	0.42
1:HT:31:LEU:HD11	1:HU:117:LEU:HB3	2.01	0.42
1:HZ:96:TRP:NE1	1:HZ:100:LYS:HE2	2.35	0.42
1:IF:37:LYS:NZ	1:IF:39:GLY:O	2.53	0.42
1:IR:88:ASN:ND2	1:IS:74:GLU:OE2	2.44	0.42
1:IS:35:ARG:NE	1:IS:42:GLU:OE2	2.53	0.42
1:IZ:60:LYS:HG2	1:IZ:71:MET:CE	2.50	0.42
1:AB:25:THR:O	1:AB:25:THR:OG1	2.35	0.42
1:BM:127:ASP:OD1	1:BM:127:ASP:N	2.52	0.42
1:BO:123:ILE:HG13	1:BP:17:TRP:CD2	2.54	0.42
1:BR:68:CYS:N	1:FZ:64:CYS:N	2.46	0.42
1:CD:25:THR:O	1:CD:25:THR:OG1	2.34	0.42
1:CD:101:ARG:HE	1:CD:101:ARG:HB3	1.73	0.42
1:CQ:58:ALA:HB3	1:CQ:71:MET:HG3	2.00	0.42
1:CQ:101:ARG:NH2	1:CQ:124:VAL:HG21	2.35	0.42
1:DB:66:ASP:OD1	1:DB:69:VAL:HG13	2.19	0.42
1:DC:20:PRO:HB3	1:DJ:116:PHE:CE2	2.53	0.42
1:DL:58:ALA:HB3	1:DL:71:MET:HG3	2.02	0.42
1:DM:106:LEU:HD11	1:DM:123:ILE:HD11	2.00	0.42
1:DN:101:ARG:NH2	1:DO:2:ASN:HD22	2.18	0.42
1:ED:56:ARG:O	1:ED:74:GLU:N	2.46	0.42
1:EP:71:MET:HB3	1:EP:71:MET:HE3	1.92	0.42
1:FT:115:GLY:HA3	1:FU:33:ARG:HD3	2.01	0.42
1:FX:88:ASN:ND2	1:FY:56:ARG:HD2	2.28	0.42
1:GM:106:LEU:HD23	1:GM:106:LEU:HA	1.82	0.42
1:GP:62:GLU:O	1:GP:62:GLU:HG2	2.20	0.42
1:GS:33:ARG:NH1	1:GT:115:GLY:O	2.53	0.42
1:GX:35:ARG:CZ	1:GX:42:GLU:HG3	2.49	0.42
1:GY:37:LYS:NZ	1:GY:40:ILE:O	2.47	0.42
1:HL:35:ARG:HH12	1:HL:43:LEU:C	2.22	0.42
1:HS:93:LYS:O	1:HS:97:GLU:HG2	2.19	0.42
1:HT:58:ALA:HB3	1:HT:71:MET:CE	2.48	0.42
1:HV:63:GLY:C	1:HX:68:CYS:HA	2.39	0.42
1:IP:96:TRP:NE1	1:IP:100:LYS:HE2	2.35	0.42
1:IR:37:LYS:NZ	1:IR:40:ILE:O	2.44	0.42
1:IR:72:PRO:HG2	1:IS:38:VAL:HG12	2.01	0.42
1:JC:96:TRP:NE1	1:JC:100:LYS:HE2	2.35	0.42
1:JI:96:TRP:NE1	1:JI:100:LYS:HE2	2.35	0.42
1:AA:71:MET:HE3	1:AA:71:MET:HB3	1.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:36:VAL:O	1:AB:43:LEU:N	2.45	0.42
1:AC:101:ARG:CZ	1:AC:124:VAL:HG21	2.49	0.42
1:AX:68:CYS:SG	1:GY:65:ALA:HA	2.60	0.42
1:BI:58:ALA:HB3	1:BI:71:MET:HG3	2.02	0.42
1:CE:19:ASP:HB3	1:CE:22:ARG:O	2.20	0.42
1:CG:19:ASP:HB3	1:CG:22:ARG:O	2.20	0.42
1:CG:34:GLN:O	1:CG:45:ASN:N	2.52	0.42
1:CM:115:GLY:HA2	1:CN:31:LEU:HD23	2.02	0.42
1:CP:60:LYS:NZ	1:CP:65:ALA:HB3	2.34	0.42
1:DC:19:ASP:HB3	1:DC:22:ARG:O	2.20	0.42
1:DT:17:TRP:CD2	1:DU:123:ILE:HG13	2.55	0.42
1:DT:115:GLY:O	1:DU:33:ARG:HD3	2.20	0.42
1:EB:104:ASP:OD2	1:EC:100:LYS:NZ	2.52	0.42
1:EJ:14:LYS:HZ3	1:EJ:28:SER:HB2	1.85	0.42
1:EK:68:CYS:HA	1:EV:61:PRO:O	2.19	0.42
1:EK:101:ARG:CZ	1:EK:124:VAL:HG21	2.50	0.42
1:ER:8:ILE:HB	1:EW:116:PHE:HE1	1.84	0.42
1:ES:23:LEU:O	1:ES:24:SER:OG	2.30	0.42
1:EW:37:LYS:HD3	1:EW:42:GLU:OE1	2.20	0.42
1:FP:37:LYS:HD2	1:FP:41:ALA:O	2.20	0.42
1:FT:46:VAL:HG11	1:FU:113:GLY:O	2.20	0.42
1:GO:96:TRP:NE1	1:GO:100:LYS:HE2	2.35	0.42
1:GX:74:GLU:HG2	1:GX:75:ASN:H	1.84	0.42
1:HC:106:LEU:HA	1:HC:106:LEU:HD23	1.85	0.42
1:HV:117:LEU:HD11	1:HW:31:LEU:HD22	2.02	0.42
1:HY:5:MET:N	1:HY:5:MET:SD	2.93	0.42
1:IC:5:MET:HG2	1:IC:18:SER:C	2.40	0.42
1:IJ:1:ALA:HB1	1:IK:128:THR:HG23	2.01	0.42
1:IN:115:GLY:HA2	1:IO:31:LEU:HD23	2.01	0.42
1:IO:117:LEU:H	1:IO:117:LEU:HD23	1.85	0.42
1:IZ:62:GLU:O	1:IZ:62:GLU:HG2	2.20	0.42
1:JF:11:THR:HG22	1:JF:13:ASN:H	1.85	0.42
1:AB:101:ARG:CZ	1:AB:124:VAL:HG21	2.50	0.42
1:AF:3:LYS:HE2	1:AF:3:LYS:HB3	1.77	0.42
1:AJ:70:ILE:HG23	1:GM:61:PRO:HB2	2.02	0.42
1:AO:14:LYS:NZ	1:AO:15:ILE:O	2.53	0.42
1:AQ:105:THR:O	1:AQ:109:SER:OG	2.37	0.42
1:BF:5:MET:SD	1:BF:5:MET:N	2.93	0.42
1:BM:19:ASP:HB3	1:BM:22:ARG:O	2.20	0.42
1:BP:18:SER:HB2	1:BP:26:THR:HG22	2.02	0.42
1:BT:61:PRO:HB2	1:BT:64:CYS:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:101:ARG:CZ	1:BZ:124:VAL:HG21	2.50	0.42
1:CG:117:LEU:HD11	1:CH:31:LEU:HD13	2.02	0.42
1:DX:19:ASP:HB3	1:DX:22:ARG:O	2.20	0.42
1:EA:62:GLU:H	1:EA:62:GLU:CD	2.20	0.42
1:EH:19:ASP:HB3	1:EH:22:ARG:O	2.20	0.42
1:EH:58:ALA:HB3	1:EH:71:MET:HG3	2.02	0.42
1:EL:104:ASP:OD2	1:EM:100:LYS:NZ	2.53	0.42
1:EO:25:THR:O	1:EO:25:THR:OG1	2.34	0.42
1:EU:35:ARG:NH2	1:EU:43:LEU:O	2.52	0.42
1:GE:37:LYS:HD2	1:GE:41:ALA:O	2.20	0.42
1:GN:23:LEU:O	1:GN:24:SER:OG	2.30	0.42
1:GY:19:ASP:HB3	1:GY:22:ARG:O	2.20	0.42
1:HS:101:ARG:NH2	1:HS:124:VAL:HG21	2.35	0.42
1:HY:123:ILE:HD12	1:HY:123:ILE:HG23	1.85	0.42
1:IE:38:VAL:HG21	1:IE:43:LEU:HD12	2.02	0.42
1:IJ:14:LYS:HZ1	1:IJ:29:ALA:N	2.18	0.42
1:JF:74:GLU:HG2	1:JF:75:ASN:H	1.85	0.42
1:JG:106:LEU:HD23	1:JG:106:LEU:HA	1.87	0.42
1:JI:43:LEU:HA	1:JI:87:GLU:OE2	2.20	0.42
1:JI:115:GLY:HA3	1:JJ:33:ARG:HD3	2.02	0.42
1:AA:2:ASN:HB2	1:AB:124:VAL:HB	2.02	0.41
1:AC:115:GLY:O	1:AD:33:ARG:HD3	2.20	0.41
1:AE:37:LYS:HZ3	1:AE:42:GLU:N	2.18	0.41
1:AW:71:MET:HB3	1:AW:71:MET:HE3	1.92	0.41
1:BC:101:ARG:CZ	1:BC:124:VAL:HG21	2.50	0.41
1:BV:67:ALA:C	1:GH:63:GLY:H	2.23	0.41
1:BW:37:LYS:HE2	1:BW:42:GLU:OE2	2.20	0.41
1:BW:101:ARG:CZ	1:BW:124:VAL:HG21	2.50	0.41
1:CE:37:LYS:HZ3	1:CE:42:GLU:HB2	1.85	0.41
1:CI:6:GLN:HB2	1:CO:116:PHE:CE2	2.54	0.41
1:CP:5:MET:CG	1:CP:17:TRP:HB3	2.49	0.41
1:CT:8:ILE:HA	1:HR:116:PHE:HB2	2.03	0.41
1:DB:37:LYS:NZ	1:DB:40:ILE:O	2.51	0.41
1:DF:37:LYS:HE2	1:DF:42:GLU:OE2	2.20	0.41
1:DH:37:LYS:CD	1:DH:42:GLU:HG2	2.50	0.41
1:DM:101:ARG:CZ	1:DM:124:VAL:HG21	2.50	0.41
1:DT:3:LYS:HZ1	1:DU:127:ASP:C	2.23	0.41
1:DT:104:ASP:OD2	1:DU:100:LYS:NZ	2.52	0.41
1:DY:62:GLU:O	1:DY:62:GLU:HG2	2.19	0.41
1:EN:3:LYS:HZ1	1:EO:129:THR:HG23	1.85	0.41
1:ER:128:THR:HA	1:ES:2:ASN:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EV:91:THR:OG1	1:EW:76:GLN:NE2	2.33	0.41
1:EV:106:LEU:HA	1:EV:106:LEU:HD23	1.82	0.41
1:FA:117:LEU:HD23	1:FA:117:LEU:H	1.85	0.41
1:FB:35:ARG:NH2	1:FB:44:ASN:HA	2.35	0.41
1:FM:5:MET:HG2	1:FM:19:ASP:N	2.35	0.41
1:FT:3:LYS:NZ	1:FU:127:ASP:HB3	2.34	0.41
1:FW:45:ASN:HA	1:FW:85:SER:HA	2.01	0.41
1:GO:8:ILE:HB	1:GT:116:PHE:HE1	1.84	0.41
1:GU:35:ARG:NH1	1:GU:42:GLU:HB3	2.31	0.41
1:GU:96:TRP:NE1	1:GU:100:LYS:HE2	2.34	0.41
1:GV:37:LYS:NZ	1:GV:38:VAL:O	2.50	0.41
1:GY:14:LYS:NZ	1:GY:28:SER:HB2	2.34	0.41
1:HB:62:GLU:O	1:HB:62:GLU:HG2	2.20	0.41
1:HQ:38:VAL:HG22	1:HQ:39:GLY:H	1.85	0.41
1:HT:68:CYS:HB3	1:HY:64:CYS:HA	2.01	0.41
1:ID:106:LEU:HD23	1:ID:106:LEU:HA	1.82	0.41
1:IE:101:ARG:HH21	1:IE:124:VAL:CG2	2.33	0.41
1:IF:87:GLU:OE1	1:IF:87:GLU:N	2.50	0.41
1:IP:5:MET:HG3	1:IP:19:ASP:HA	2.02	0.41
1:IS:101:ARG:CZ	1:IS:124:VAL:HG21	2.50	0.41
1:AA:104:ASP:OD2	1:AB:100:LYS:NZ	2.53	0.41
1:AF:5:MET:HG2	1:AF:17:TRP:HB3	2.02	0.41
1:AL:60:LYS:HZ1	1:AL:65:ALA:H	1.68	0.41
1:AQ:101:ARG:NH2	1:AQ:124:VAL:HG21	2.35	0.41
1:BG:19:ASP:HB3	1:BG:22:ARG:O	2.19	0.41
1:BM:37:LYS:HZ3	1:BM:42:GLU:HB2	1.85	0.41
1:BM:115:GLY:O	1:BN:33:ARG:NH1	2.53	0.41
1:BX:37:LYS:NZ	1:BX:40:ILE:O	2.51	0.41
1:BY:5:MET:HB3	1:BY:17:TRP:HB3	2.02	0.41
1:CC:3:LYS:HZ1	1:CD:129:THR:HG23	1.85	0.41
1:CG:58:ALA:HB3	1:CG:71:MET:HG3	2.02	0.41
1:CL:67:ALA:O	1:FN:65:ALA:HB2	2.19	0.41
1:CL:68:CYS:HA	1:FN:61:PRO:O	2.19	0.41
1:CN:5:MET:CG	1:CN:17:TRP:HB3	2.50	0.41
1:CY:19:ASP:HB3	1:CY:22:ARG:O	2.20	0.41
1:DT:71:MET:HB3	1:DT:71:MET:HE3	1.90	0.41
1:EH:14:LYS:NZ	1:EH:28:SER:HB2	2.29	0.41
1:EH:117:LEU:HD11	1:EI:31:LEU:HD13	2.02	0.41
1:EL:3:LYS:HZ2	1:EM:129:THR:HG23	1.85	0.41
1:EN:6:GLN:HB2	1:EP:116:PHE:CE1	2.55	0.41
1:ER:14:LYS:HD3	1:ER:30:SER:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ET:116:PHE:HE2	1:EV:20:PRO:HB3	1.85	0.41
1:EV:37:LYS:NZ	1:EV:39:GLY:O	2.53	0.41
1:FF:5:MET:N	1:FF:5:MET:SD	2.92	0.41
1:FM:36:VAL:HG23	1:FM:43:LEU:HB2	2.02	0.41
1:FR:60:LYS:HE2	1:FR:65:ALA:HB3	2.02	0.41
1:FX:35:ARG:HD2	1:FX:44:ASN:HB3	2.02	0.41
1:GB:11:THR:HB	1:GB:14:LYS:H	1.85	0.41
1:GB:22:ARG:NH1	1:GB:24:SER:OG	2.53	0.41
1:GO:31:LEU:HD12	1:GP:117:LEU:HD22	2.02	0.41
1:GS:96:TRP:NE1	1:GS:100:LYS:HE2	2.35	0.41
1:GV:62:GLU:O	1:GV:62:GLU:HG2	2.20	0.41
1:GX:38:VAL:HG22	1:GX:39:GLY:H	1.85	0.41
1:HA:72:PRO:HG2	1:HB:38:VAL:HG12	2.03	0.41
1:HG:106:LEU:HD23	1:HG:106:LEU:HA	1.83	0.41
1:HP:5:MET:HE1	1:HQ:123:ILE:HG22	2.02	0.41
1:HQ:12:ALA:HB1	1:HR:9:THR:HG23	2.01	0.41
1:HU:101:ARG:CZ	1:HU:124:VAL:HG21	2.49	0.41
1:HW:36:VAL:HG23	1:HW:43:LEU:HB2	2.02	0.41
1:IO:38:VAL:HG22	1:IO:39:GLY:H	1.84	0.41
1:IV:72:PRO:HG2	1:IW:38:VAL:HG12	2.02	0.41
1:AA:123:ILE:HG13	1:AB:17:TRP:CD2	2.56	0.41
1:AC:19:ASP:HB3	1:AC:22:ARG:O	2.20	0.41
1:AD:60:LYS:NZ	1:AD:65:ALA:HB3	2.35	0.41
1:AH:98:THR:HG21	1:AH:126:SER:HA	2.02	0.41
1:AQ:3:LYS:HZ2	1:AR:129:THR:HG23	1.85	0.41
1:AV:60:LYS:HE2	1:AV:65:ALA:HB3	2.02	0.41
1:AW:104:ASP:OD2	1:AX:100:LYS:NZ	2.51	0.41
1:BA:19:ASP:HB3	1:BA:22:ARG:O	2.19	0.41
1:BD:62:GLU:HG2	1:BD:62:GLU:O	2.20	0.41
1:BD:101:ARG:HE	1:BD:101:ARG:HB3	1.70	0.41
1:BJ:37:LYS:HB3	1:BJ:37:LYS:HE3	1.71	0.41
1:BJ:67:ALA:N	1:HZ:65:ALA:H	2.18	0.41
1:BS:105:THR:O	1:BS:109:SER:OG	2.37	0.41
1:CC:5:MET:HG3	1:CC:19:ASP:HA	2.02	0.41
1:CE:17:TRP:CD2	1:CF:123:ILE:HG13	2.54	0.41
1:CF:101:ARG:CZ	1:CF:124:VAL:HG21	2.50	0.41
1:CI:34:GLN:O	1:CI:45:ASN:N	2.52	0.41
1:CS:31:LEU:HD23	1:CT:115:GLY:HA2	2.02	0.41
1:CT:32:LEU:HB3	1:CT:34:GLN:NE2	2.23	0.41
1:DB:25:THR:O	1:DB:25:THR:OG1	2.35	0.41
1:DF:115:GLY:HA2	1:DG:31:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DG:3:LYS:HE2	1:DG:3:LYS:HB3	1.77	0.41
1:DO:13:ASN:N	1:DO:13:ASN:OD1	2.52	0.41
1:DP:101:ARG:NH2	1:DP:124:VAL:HG21	2.35	0.41
1:EL:14:LYS:NZ	1:EL:15:ILE:O	2.53	0.41
1:FV:106:LEU:HD23	1:FV:106:LEU:HA	1.82	0.41
1:GP:37:LYS:HD3	1:GP:42:GLU:HG2	2.03	0.41
1:GQ:72:PRO:HG3	1:GR:39:GLY:HA3	2.02	0.41
1:GW:113:GLY:O	1:GX:46:VAL:HG11	2.20	0.41
1:HJ:4:PRO:HA	1:HK:124:VAL:HA	2.02	0.41
1:HK:44:ASN:ND2	1:HL:23:LEU:HB2	2.34	0.41
1:HU:3:LYS:HE3	1:HU:19:ASP:OD2	2.20	0.41
1:IJ:85:SER:OG	1:IK:74:GLU:OE1	2.19	0.41
1:IN:5:MET:N	1:IN:5:MET:SD	2.94	0.41
1:IQ:123:ILE:HD12	1:IQ:123:ILE:HG23	1.88	0.41
1:IR:37:LYS:HD2	1:IR:41:ALA:O	2.20	0.41
1:IX:8:ILE:HB	1:JD:116:PHE:HE1	1.85	0.41
1:JC:86:ALA:HB1	1:JD:114:LEU:HD23	2.02	0.41
1:AD:68:CYS:N	1:IV:63:GLY:N	2.67	0.41
1:AK:71:MET:HB3	1:AK:71:MET:HE3	1.90	0.41
1:BF:5:MET:CG	1:BF:17:TRP:HB3	2.49	0.41
1:BG:128:THR:HA	1:BH:2:ASN:HA	2.02	0.41
1:BH:68:CYS:SG	1:HQ:61:PRO:HD2	2.60	0.41
1:BU:128:THR:HA	1:BV:2:ASN:HA	2.02	0.41
1:BW:115:GLY:O	1:BX:33:ARG:HD3	2.19	0.41
1:CC:116:PHE:CE1	1:CG:6:GLN:HB2	2.55	0.41
1:CP:67:ALA:O	1:IP:65:ALA:HB2	2.21	0.41
1:CP:68:CYS:N	1:IP:63:GLY:N	2.69	0.41
1:CY:17:TRP:CD2	1:CZ:123:ILE:HG13	2.55	0.41
1:CZ:5:MET:HG2	1:CZ:17:TRP:HB3	2.01	0.41
1:DQ:55:LYS:HB2	1:DQ:55:LYS:HE3	1.81	0.41
1:DT:37:LYS:HZ3	1:DT:42:GLU:HB2	1.85	0.41
1:EB:14:LYS:NZ	1:EB:28:SER:HB2	2.29	0.41
1:EB:35:ARG:NH1	1:EB:44:ASN:OD1	2.54	0.41
1:EI:101:ARG:HE	1:EI:101:ARG:HB3	1.75	0.41
1:EJ:104:ASP:OD2	1:EK:100:LYS:NZ	2.54	0.41
1:EQ:5:MET:SD	1:EQ:5:MET:N	2.93	0.41
1:EV:86:ALA:HB1	1:EW:114:LEU:HD23	2.03	0.41
1:EV:96:TRP:NE1	1:EV:100:LYS:HE2	2.36	0.41
1:EZ:3:LYS:HZ3	1:FA:129:THR:HG23	1.85	0.41
1:FH:35:ARG:NH2	1:FH:42:GLU:HB3	2.35	0.41
1:FK:102:ASN:O	1:FK:105:THR:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FN:1:ALA:O	1:FO:129:THR:N	2.44	0.41
1:GA:62:GLU:O	1:GA:62:GLU:HG2	2.21	0.41
1:GP:102:ASN:O	1:GP:105:THR:HG22	2.21	0.41
1:HE:37:LYS:HD2	1:HE:41:ALA:O	2.21	0.41
1:HN:87:GLU:OE1	1:HN:87:GLU:N	2.38	0.41
1:HT:17:TRP:CE2	1:HU:123:ILE:HG13	2.55	0.41
1:IN:115:GLY:O	1:IO:33:ARG:NH1	2.54	0.41
1:IQ:35:ARG:NH2	1:IQ:42:GLU:OE1	2.53	0.41
1:JE:96:TRP:NE1	1:JE:100:LYS:HE2	2.35	0.41
1:JG:24:SER:HB2	1:JG:55:LYS:HG2	2.02	0.41
1:AN:62:GLU:H	1:AN:62:GLU:CD	2.20	0.41
1:AS:127:ASP:OD1	1:AS:127:ASP:N	2.51	0.41
1:AT:60:LYS:NZ	1:AT:65:ALA:H	2.16	0.41
1:AU:17:TRP:CD2	1:AV:123:ILE:HG13	2.56	0.41
1:BG:37:LYS:HE2	1:BG:42:GLU:OE2	2.19	0.41
1:BJ:5:MET:HB2	1:BJ:18:SER:C	2.40	0.41
1:BJ:5:MET:N	1:BJ:5:MET:SD	2.93	0.41
1:BK:3:LYS:HB2	1:BK:3:LYS:HE2	1.87	0.41
1:BL:62:GLU:H	1:BL:62:GLU:CD	2.23	0.41
1:BM:58:ALA:HB3	1:BM:71:MET:HG3	2.02	0.41
1:BN:36:VAL:O	1:BN:43:LEU:N	2.40	0.41
1:CC:12:ALA:HB1	1:FK:8:ILE:O	2.21	0.41
1:CI:3:LYS:HB2	1:CI:3:LYS:HE2	1.85	0.41
1:CQ:101:ARG:CZ	1:CQ:124:VAL:HG21	2.51	0.41
1:CR:70:ILE:HD11	1:FF:40:ILE:HB	2.02	0.41
1:DH:5:MET:SD	1:DH:5:MET:N	2.94	0.41
1:DH:19:ASP:HB3	1:DH:22:ARG:O	2.20	0.41
1:DI:67:ALA:HA	1:FH:63:GLY:N	2.20	0.41
1:DJ:89:LEU:HG	1:DJ:93:LYS:HE3	2.03	0.41
1:DK:101:ARG:NH1	1:DK:124:VAL:HG21	2.34	0.41
1:DM:68:CYS:HA	1:FB:61:PRO:O	2.20	0.41
1:EK:8:ILE:HA	1:EV:116:PHE:HB2	2.02	0.41
1:EK:69:VAL:HG22	1:EV:64:CYS:SG	2.60	0.41
1:EL:127:ASP:OD1	1:EL:127:ASP:N	2.52	0.41
1:EO:5:MET:CG	1:EO:17:TRP:HB3	2.51	0.41
1:ET:46:VAL:HG11	1:EU:113:GLY:O	2.21	0.41
1:FF:88:ASN:ND2	1:FG:74:GLU:OE2	2.47	0.41
1:FR:14:LYS:NZ	1:FR:28:SER:HB2	2.29	0.41
1:GB:8:ILE:HB	1:GG:116:PHE:HE1	1.85	0.41
1:GC:64:CYS:SG	1:GE:68:CYS:HA	2.60	0.41
1:GG:57:PRO:HA	1:GG:73:ASN:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GO:6:GLN:HG2	1:GO:20:PRO:HD3	2.01	0.41
1:GU:106:LEU:HA	1:GU:106:LEU:HD23	1.83	0.41
1:HK:60:LYS:HZ1	1:HK:69:VAL:HG23	1.85	0.41
1:HL:115:GLY:HA3	1:HM:33:ARG:HD3	2.02	0.41
1:HM:9:THR:O	1:HM:15:ILE:HA	2.20	0.41
1:HM:56:ARG:O	1:HM:74:GLU:N	2.28	0.41
1:HO:38:VAL:N	1:HO:41:ALA:O	2.53	0.41
1:HU:60:LYS:HE2	1:HU:64:CYS:HB3	2.01	0.41
1:HX:66:ASP:OD2	1:HX:68:CYS:HB2	2.21	0.41
1:IA:35:ARG:NE	1:IA:44:ASN:OD1	2.54	0.41
1:IF:125:SER:HB2	1:IG:5:MET:CE	2.50	0.41
1:IK:85:SER:HG	1:IK:88:ASN:HD22	1.66	0.41
1:IL:115:GLY:HA3	1:IM:33:ARG:HD3	2.02	0.41
1:IV:17:TRP:CE2	1:IW:123:ILE:HG13	2.55	0.41
1:IZ:57:PRO:HA	1:IZ:73:ASN:HA	2.02	0.41
1:JH:56:ARG:O	1:JH:74:GLU:N	2.28	0.41
1:AI:92:LEU:HA	1:AI:95:GLU:OE1	2.20	0.41
1:AJ:60:LYS:NZ	1:AJ:65:ALA:HB3	2.34	0.41
1:AJ:62:GLU:H	1:AJ:62:GLU:CD	2.21	0.41
1:AV:25:THR:O	1:AV:25:THR:OG1	2.32	0.41
1:BE:14:LYS:HA	1:BE:14:LYS:HD2	1.85	0.41
1:BG:101:ARG:CZ	1:BG:124:VAL:HG21	2.50	0.41
1:BK:101:ARG:CZ	1:BK:124:VAL:HG21	2.50	0.41
1:BT:5:MET:CG	1:BT:17:TRP:HB3	2.51	0.41
1:CA:56:ARG:O	1:CA:74:GLU:N	2.50	0.41
1:CL:55:LYS:NZ	1:CL:75:ASN:OD1	2.31	0.41
1:CM:124:VAL:HA	1:CN:4:PRO:HA	2.03	0.41
1:CN:3:LYS:HB3	1:CN:3:LYS:HE2	1.77	0.41
1:CO:104:ASP:OD2	1:CP:100:LYS:NZ	2.53	0.41
1:CT:101:ARG:CZ	1:CT:124:VAL:HG21	2.51	0.41
1:DH:101:ARG:NH2	1:DH:124:VAL:HG21	2.36	0.41
1:DL:37:LYS:HZ3	1:DL:42:GLU:HB2	1.84	0.41
1:DO:5:MET:HG2	1:DO:17:TRP:HB3	2.01	0.41
1:DU:68:CYS:O	1:FP:61:PRO:HG2	2.20	0.41
1:DV:5:MET:HB3	1:DV:17:TRP:HB3	2.03	0.41
1:DX:58:ALA:HB3	1:DX:71:MET:HG3	2.02	0.41
1:DY:5:MET:CG	1:DY:17:TRP:HB3	2.50	0.41
1:EC:67:ALA:HB1	1:HN:64:CYS:HA	2.02	0.41
1:EE:67:ALA:C	1:GU:63:GLY:H	2.24	0.41
1:EN:5:MET:HB2	1:EN:17:TRP:HB3	2.02	0.41
1:EP:19:ASP:HB3	1:EP:22:ARG:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FE:60:LYS:NZ	1:FE:66:ASP:O	2.54	0.41
1:FE:71:MET:HE3	1:FE:71:MET:HB3	1.99	0.41
1:FM:35:ARG:HH21	1:FM:42:GLU:HG3	1.85	0.41
1:FR:5:MET:CE	1:FS:123:ILE:HG22	2.50	0.41
1:FS:101:ARG:HE	1:FS:101:ARG:HB2	1.64	0.41
1:FZ:22:ARG:NH1	1:FZ:24:SER:OG	2.53	0.41
1:GA:87:GLU:OE1	1:GA:87:GLU:N	2.43	0.41
1:GF:14:LYS:HZ3	1:GF:30:SER:HB2	1.86	0.41
1:GO:31:LEU:HD13	1:GP:115:GLY:HA2	2.02	0.41
1:GO:56:ARG:O	1:GO:74:GLU:N	2.34	0.41
1:GP:93:LYS:O	1:GP:97:GLU:HG2	2.19	0.41
1:HS:57:PRO:HA	1:HS:73:ASN:HA	2.03	0.41
1:IJ:14:LYS:HA	1:IJ:14:LYS:HD2	1.88	0.41
1:IR:14:LYS:NZ	1:IR:28:SER:HB2	2.35	0.41
1:IV:37:LYS:HD2	1:IV:41:ALA:O	2.21	0.41
1:IW:49:GLN:NE2	1:IW:79:ARG:HH21	2.18	0.41
1:JB:13:ASN:N	1:JB:13:ASN:OD1	2.54	0.41
1:AH:25:THR:O	1:AH:25:THR:OG1	2.31	0.41
1:AK:19:ASP:HB3	1:AK:22:ARG:O	2.20	0.41
1:AK:37:LYS:HZ3	1:AK:42:GLU:HB2	1.85	0.41
1:BC:56:ARG:O	1:BC:74:GLU:N	2.45	0.41
1:BU:14:LYS:HZ1	1:BU:28:SER:CB	2.29	0.41
1:BW:1:ALA:HB1	1:BX:128:THR:HG23	2.02	0.41
1:BX:3:LYS:HB3	1:BX:3:LYS:HE2	1.77	0.41
1:BX:67:ALA:H	1:JI:65:ALA:HB3	1.85	0.41
1:BY:14:LYS:HZ1	1:BY:28:SER:CB	2.29	0.41
1:BY:58:ALA:HB3	1:BY:71:MET:HG3	2.03	0.41
1:CA:37:LYS:HZ3	1:CA:42:GLU:HB2	1.85	0.41
1:CA:112:ALA:HA	1:CA:116:PHE:O	2.21	0.41
1:CH:68:CYS:HB2	1:HA:64:CYS:C	2.41	0.41
1:CK:72:PRO:HG2	1:CL:38:VAL:HG22	2.03	0.41
1:CQ:35:ARG:HB3	1:CQ:42:GLU:OE1	2.21	0.41
1:CU:62:GLU:O	1:CU:62:GLU:HG2	2.21	0.41
1:DA:101:ARG:CZ	1:DA:124:VAL:HG21	2.50	0.41
1:DB:116:PHE:CE2	1:FL:20:PRO:HA	2.56	0.41
1:DC:60:LYS:NZ	1:DC:66:ASP:O	2.26	0.41
1:DN:31:LEU:HD23	1:DO:115:GLY:HA2	2.02	0.41
1:DP:17:TRP:CD2	1:DQ:123:ILE:HG13	2.55	0.41
1:DR:31:LEU:HD23	1:DS:115:GLY:HA2	2.01	0.41
1:DW:5:MET:CG	1:DW:17:TRP:HB3	2.51	0.41
1:DZ:115:GLY:HA2	1:EA:31:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DZ:128:THR:HA	1:EA:2:ASN:HA	2.02	0.41
1:EN:101:ARG:NH2	1:EN:124:VAL:HG21	2.36	0.41
1:EV:87:GLU:H	1:EV:87:GLU:CD	2.21	0.41
1:EX:40:ILE:HD12	1:FA:70:ILE:HD11	2.02	0.41
1:FA:58:ALA:HB3	1:FA:71:MET:HG3	2.03	0.41
1:FM:35:ARG:HA	1:FM:35:ARG:CZ	2.51	0.41
1:FO:102:ASN:O	1:FO:105:THR:HG22	2.21	0.41
1:FQ:3:LYS:HD2	1:FQ:21:THR:HG21	2.03	0.41
1:FT:14:LYS:NZ	1:FT:28:SER:HB2	2.32	0.41
1:FW:62:GLU:O	1:FW:62:GLU:HG2	2.20	0.41
1:GO:101:ARG:NH2	1:GO:124:VAL:HG21	2.36	0.41
1:GQ:106:LEU:HD23	1:GQ:106:LEU:HA	1.87	0.41
1:GX:62:GLU:O	1:GX:62:GLU:HG2	2.20	0.41
1:HJ:71:MET:SD	1:HJ:71:MET:N	2.88	0.41
1:HN:60:LYS:HB3	1:HN:65:ALA:HB2	2.01	0.41
1:HX:19:ASP:HB3	1:HX:22:ARG:O	2.21	0.41
1:II:60:LYS:HA	1:II:71:MET:SD	2.61	0.41
1:IL:8:ILE:HB	1:IQ:116:PHE:HE1	1.85	0.41
1:IR:32:LEU:HB3	1:IR:47:SER:OG	2.20	0.41
1:JA:24:SER:HB2	1:JA:55:LYS:HG2	2.03	0.41
1:JA:59:PRO:HG2	1:JB:87:GLU:HG3	2.03	0.41
1:JB:60:LYS:HE2	1:JB:71:MET:HE1	2.02	0.41
1:JF:34:GLN:OE1	1:JF:36:VAL:HG13	2.20	0.41
1:JF:102:ASN:O	1:JF:105:THR:HG22	2.21	0.41
1:JI:124:VAL:HG12	1:JJ:4:PRO:HB3	2.03	0.41
1:AE:28:SER:OG	1:AE:51:VAL:HB	2.21	0.41
1:AM:5:MET:HG3	1:AM:19:ASP:HA	2.02	0.41
1:AM:37:LYS:HE2	1:AM:42:GLU:OE2	2.20	0.41
1:AN:69:VAL:HG22	1:JC:64:CYS:HB3	2.03	0.41
1:BF:62:GLU:O	1:BF:62:GLU:HG2	2.21	0.41
1:CB:69:VAL:HG22	1:FJ:64:CYS:HB2	2.03	0.41
1:CD:116:PHE:CE2	1:FK:20:PRO:HA	2.56	0.41
1:CJ:62:GLU:H	1:CJ:62:GLU:CD	2.21	0.41
1:CN:60:LYS:NZ	1:CN:64:CYS:SG	2.68	0.41
1:CN:101:ARG:HE	1:CN:101:ARG:HB3	1.72	0.41
1:CZ:64:CYS:SG	1:CZ:65:ALA:N	2.94	0.41
1:DM:18:SER:HB2	1:DM:26:THR:HG22	2.03	0.41
1:DR:115:GLY:O	1:DS:33:ARG:NH1	2.53	0.41
1:DY:70:ILE:HG23	1:DY:70:ILE:O	2.20	0.41
1:EJ:58:ALA:HB3	1:EJ:71:MET:HG3	2.02	0.41
1:EU:43:LEU:HD22	1:EU:87:GLU:OE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FI:23:LEU:O	1:FI:24:SER:OG	2.30	0.41
1:FJ:14:LYS:NZ	1:FJ:28:SER:HB2	2.35	0.41
1:FN:101:ARG:NH2	1:FN:124:VAL:HG21	2.36	0.41
1:FP:33:ARG:HH11	1:FS:8:ILE:HD11	1.86	0.41
1:FT:11:THR:HB	1:FT:14:LYS:H	1.86	0.41
1:FZ:115:GLY:HA3	1:GA:33:ARG:HD3	2.02	0.41
1:GB:60:LYS:HB3	1:GB:65:ALA:HB2	2.02	0.41
1:GC:38:VAL:N	1:GC:41:ALA:O	2.53	0.41
1:HI:57:PRO:HA	1:HI:73:ASN:HA	2.03	0.41
1:HJ:113:GLY:O	1:HK:46:VAL:HG11	2.21	0.41
1:HP:113:GLY:O	1:HQ:46:VAL:HG11	2.20	0.41
1:ID:128:THR:HA	1:IE:2:ASN:HA	2.03	0.41
1:IQ:9:THR:O	1:IQ:15:ILE:HA	2.21	0.41
1:IU:38:VAL:HG22	1:IU:39:GLY:H	1.86	0.41
1:IU:60:LYS:HA	1:IU:71:MET:HE1	2.03	0.41
1:IV:85:SER:OG	1:IW:74:GLU:OE1	2.19	0.41
1:AA:5:MET:HB3	1:AA:17:TRP:HB3	2.01	0.41
1:AC:5:MET:HB2	1:AC:17:TRP:HB3	2.01	0.41
1:AD:25:THR:O	1:AD:25:THR:OG1	2.36	0.41
1:AD:102:ASN:HA	1:AD:105:THR:HG22	2.03	0.41
1:AD:106:LEU:HD21	1:AD:123:ILE:HD11	2.03	0.41
1:AH:67:ALA:C	1:JE:63:GLY:H	2.24	0.41
1:AI:14:LYS:NZ	1:AI:15:ILE:O	2.53	0.41
1:BB:101:ARG:HE	1:BB:101:ARG:HB3	1.75	0.41
1:BC:115:GLY:HA2	1:BD:31:LEU:HD23	2.03	0.41
1:BD:116:PHE:CE2	1:HU:20:PRO:HA	2.55	0.41
1:BG:14:LYS:HZ1	1:BG:28:SER:CB	2.28	0.41
1:BI:56:ARG:O	1:BI:74:GLU:N	2.46	0.41
1:BI:101:ARG:NH2	1:BI:124:VAL:HG21	2.36	0.41
1:BJ:67:ALA:C	1:HZ:63:GLY:H	2.23	0.41
1:BU:14:LYS:NZ	1:BU:15:ILE:O	2.53	0.41
1:BV:68:CYS:N	1:GH:63:GLY:N	2.69	0.41
1:BW:5:MET:HE1	1:BX:123:ILE:HG22	2.03	0.41
1:BY:123:ILE:HG13	1:BZ:17:TRP:CD2	2.55	0.41
1:CB:67:ALA:HA	1:FJ:63:GLY:N	2.26	0.41
1:CC:101:ARG:CZ	1:CC:124:VAL:HG21	2.51	0.41
1:CE:128:THR:HA	1:CF:2:ASN:HA	2.03	0.41
1:CG:56:ARG:O	1:CG:74:GLU:N	2.46	0.41
1:CI:19:ASP:HB3	1:CI:22:ARG:O	2.20	0.41
1:CK:19:ASP:HB3	1:CK:22:ARG:O	2.21	0.41
1:CK:127:ASP:OD1	1:CK:127:ASP:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:56:ARG:O	1:CM:74:GLU:N	2.45	0.41
1:CZ:56:ARG:HD2	1:CZ:76:GLN:HE22	1.86	0.41
1:DA:37:LYS:HE2	1:DA:42:GLU:OE2	2.21	0.41
1:DC:8:ILE:N	1:DC:16:VAL:O	2.53	0.41
1:DF:5:MET:HB2	1:DF:17:TRP:HB3	2.02	0.41
1:DF:34:GLN:O	1:DF:45:ASN:N	2.52	0.41
1:DH:35:ARG:HB3	1:DH:42:GLU:OE1	2.21	0.41
1:DJ:3:LYS:HE2	1:DJ:3:LYS:HB2	1.85	0.41
1:DM:69:VAL:HG22	1:FB:64:CYS:SG	2.60	0.41
1:DR:19:ASP:HB3	1:DR:22:ARG:O	2.21	0.41
1:DR:124:VAL:HA	1:DS:4:PRO:HA	2.03	0.41
1:DR:128:THR:HA	1:DS:2:ASN:HA	2.03	0.41
1:DT:8:ILE:N	1:DT:16:VAL:O	2.52	0.41
1:DZ:14:LYS:HZ1	1:DZ:28:SER:HB2	1.85	0.41
1:EC:62:GLU:H	1:EC:62:GLU:CD	2.22	0.41
1:ED:1:ALA:HB1	1:EE:128:THR:HG23	2.01	0.41
1:EF:89:LEU:HG	1:EF:93:LYS:HE3	2.03	0.41
1:EP:58:ALA:HB3	1:EP:71:MET:HG3	2.03	0.41
1:EV:31:LEU:HD12	1:EW:117:LEU:HD22	2.02	0.41
1:EY:38:VAL:N	1:EY:41:ALA:O	2.54	0.41
1:EZ:34:GLN:O	1:EZ:45:ASN:N	2.54	0.41
1:FC:35:ARG:NH2	1:FC:42:GLU:OE1	2.54	0.41
1:FD:60:LYS:HB3	1:FD:65:ALA:HB2	2.03	0.41
1:FN:3:LYS:HZ1	1:FO:129:THR:HG23	1.86	0.41
1:FN:37:LYS:HD2	1:FN:41:ALA:O	2.20	0.41
1:FT:17:TRP:CE2	1:FU:123:ILE:HG13	2.56	0.41
1:FT:37:LYS:HD2	1:FT:41:ALA:O	2.20	0.41
1:FU:49:GLN:NE2	1:FU:79:ARG:HH21	2.19	0.41
1:FX:113:GLY:O	1:FY:46:VAL:HG11	2.20	0.41
1:FZ:87:GLU:OE1	1:FZ:87:GLU:N	2.39	0.41
1:GB:14:LYS:NZ	1:GB:28:SER:HB2	2.34	0.41
1:GC:23:LEU:O	1:GC:24:SER:OG	2.31	0.41
1:GD:46:VAL:HG11	1:GE:113:GLY:O	2.20	0.41
1:GI:8:ILE:N	1:GI:16:VAL:O	2.42	0.41
1:GO:2:ASN:HB3	1:GP:124:VAL:HB	2.02	0.41
1:GP:9:THR:O	1:GP:15:ILE:HA	2.21	0.41
1:GP:35:ARG:HH12	1:GP:42:GLU:C	2.24	0.41
1:GQ:59:PRO:O	1:GQ:61:PRO:HD3	2.20	0.41
1:HG:55:LYS:HG3	1:HG:73:ASN:HB2	2.03	0.41
1:HG:124:VAL:HA	1:HI:4:PRO:HA	2.02	0.41
1:HJ:60:LYS:HE2	1:HJ:65:ALA:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HL:66:ASP:OD2	1:HL:68:CYS:HB2	2.21	0.41
1:HP:24:SER:HB2	1:HP:55:LYS:HG3	2.03	0.41
1:HT:55:LYS:HZ2	1:HT:73:ASN:HB2	1.82	0.41
1:HT:127:ASP:HB2	1:HU:3:LYS:HE2	2.02	0.41
1:HU:49:GLN:NE2	1:HU:79:ARG:HH21	2.18	0.41
1:HV:19:ASP:OD1	1:HV:21:THR:N	2.52	0.41
1:HV:116:PHE:CD1	1:HX:6:GLN:HB2	2.56	0.41
1:IB:101:ARG:CZ	1:IB:124:VAL:HG21	2.51	0.41
1:IF:96:TRP:NE1	1:IF:100:LYS:HE2	2.35	0.41
1:IK:9:THR:O	1:IK:15:ILE:HA	2.21	0.41
1:IP:1:ALA:O	1:IQ:129:THR:N	2.38	0.41
1:IU:101:ARG:HE	1:IU:101:ARG:HB2	1.65	0.41
1:IV:14:LYS:NZ	1:IV:28:SER:HB2	2.33	0.41
1:IZ:43:LEU:HD23	1:IZ:85:SER:HB3	2.02	0.41
1:JB:62:GLU:H	1:JB:62:GLU:CD	2.24	0.41
1:JJ:9:THR:O	1:JJ:15:ILE:HA	2.20	0.41
1:AB:68:CYS:HA	1:EX:64:CYS:SG	2.60	0.41
1:AE:12:ALA:HB1	1:IW:8:ILE:O	2.21	0.41
1:AN:102:ASN:HA	1:AN:105:THR:HG22	2.03	0.41
1:AU:115:GLY:HA2	1:AV:31:LEU:HD23	2.02	0.41
1:AX:32:LEU:HB3	1:AX:47:SER:HB3	2.01	0.41
1:BA:58:ALA:HB3	1:BA:71:MET:HG3	2.02	0.41
1:BE:105:THR:O	1:BE:109:SER:OG	2.38	0.41
1:BF:57:PRO:HA	1:BF:73:ASN:HA	2.03	0.41
1:BI:19:ASP:HB3	1:BI:22:ARG:O	2.20	0.41
1:CH:68:CYS:O	1:HA:61:PRO:HG2	2.21	0.41
1:CI:127:ASP:OD1	1:CI:127:ASP:N	2.52	0.41
1:CQ:19:ASP:HB3	1:CQ:22:ARG:O	2.20	0.41
1:CS:19:ASP:HB3	1:CS:22:ARG:O	2.21	0.41
1:CV:68:CYS:N	1:HL:63:GLY:H	2.19	0.41
1:CZ:68:CYS:N	1:ID:63:GLY:N	2.69	0.41
1:DB:102:ASN:HA	1:DB:105:THR:HG22	2.03	0.41
1:DF:124:VAL:HA	1:DG:4:PRO:HA	2.03	0.41
1:DG:93:LYS:O	1:DG:97:GLU:OE1	2.39	0.41
1:DS:37:LYS:HA	1:DS:42:GLU:HA	2.03	0.41
1:DS:60:LYS:NZ	1:DS:65:ALA:H	2.17	0.41
1:DW:106:LEU:HD21	1:DW:123:ILE:HD11	2.02	0.41
1:DZ:125:SER:O	1:EA:2:ASN:ND2	2.54	0.41
1:EC:101:ARG:CZ	1:EC:124:VAL:HG21	2.51	0.41
1:ET:14:LYS:NZ	1:ET:28:SER:HB2	2.35	0.41
1:EW:93:LYS:O	1:EW:97:GLU:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EZ:113:GLY:O	1:FA:46:VAL:HG11	2.20	0.41
1:FK:49:GLN:NE2	1:FK:79:ARG:HH21	2.19	0.41
1:FO:49:GLN:NE2	1:FO:79:ARG:HH21	2.19	0.41
1:FT:5:MET:HG3	1:FT:18:SER:C	2.41	0.41
1:GD:71:MET:SD	1:GD:71:MET:N	2.92	0.41
1:GD:72:PRO:HG3	1:GE:39:GLY:HA3	2.03	0.41
1:GF:31:LEU:HD11	1:GG:117:LEU:HB3	2.02	0.41
1:GF:46:VAL:HG11	1:GG:113:GLY:O	2.21	0.41
1:GU:55:LYS:NZ	1:GU:73:ASN:HB2	2.36	0.41
1:HN:14:LYS:CE	1:HN:28:SER:HB2	2.51	0.41
1:HS:9:THR:O	1:HS:15:ILE:HA	2.20	0.41
1:HV:14:LYS:HE3	1:HV:28:SER:HB2	2.03	0.41
1:IJ:14:LYS:HD3	1:IJ:30:SER:HB2	2.02	0.41
1:IN:5:MET:HG3	1:IN:19:ASP:HA	2.03	0.41
1:IR:35:ARG:NH2	1:IR:44:ASN:OD1	2.52	0.41
1:IS:49:GLN:NE2	1:IS:79:ARG:HH21	2.19	0.41
1:IT:17:TRP:CE2	1:IU:123:ILE:HG13	2.55	0.41
1:IU:33:ARG:HH12	1:IV:8:ILE:HG23	1.85	0.41
1:IX:74:GLU:CD	1:IZ:85:SER:HG	2.23	0.41
1:AH:32:LEU:HB2	1:AH:47:SER:HB3	2.03	0.40
1:AH:55:LYS:NZ	1:AH:75:ASN:OD1	2.31	0.40
1:AI:19:ASP:HB3	1:AI:22:ARG:O	2.20	0.40
1:AJ:68:CYS:N	1:GM:63:GLY:N	2.69	0.40
1:AQ:96:TRP:NE1	1:AR:104:ASP:OD1	2.45	0.40
1:AU:104:ASP:OD2	1:AV:100:LYS:NZ	2.54	0.40
1:AY:89:LEU:HG	1:AY:93:LYS:HE3	2.03	0.40
1:AY:127:ASP:OD1	1:AY:127:ASP:N	2.53	0.40
1:BO:14:LYS:HZ3	1:BO:28:SER:HB2	1.85	0.40
1:BP:32:LEU:HB2	1:BP:47:SER:HB3	2.03	0.40
1:BU:5:MET:SD	1:BV:125:SER:HB2	2.61	0.40
1:BV:70:ILE:HG13	1:BV:70:ILE:O	2.21	0.40
1:CO:58:ALA:HB3	1:CO:71:MET:HG3	2.02	0.40
1:CQ:123:ILE:HG13	1:CR:17:TRP:CD2	2.56	0.40
1:CR:5:MET:CG	1:CR:17:TRP:HB3	2.51	0.40
1:CT:60:LYS:HZ3	1:CT:65:ALA:H	1.68	0.40
1:CU:104:ASP:OD2	1:CV:100:LYS:NZ	2.54	0.40
1:CW:105:THR:O	1:CW:109:SER:OG	2.38	0.40
1:DA:1:ALA:HB1	1:DB:128:THR:HG23	2.02	0.40
1:DE:102:ASN:HA	1:DE:105:THR:HG22	2.03	0.40
1:DX:56:ARG:O	1:DX:74:GLU:N	2.47	0.40
1:DY:66:ASP:OD1	1:DY:69:VAL:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ED:60:LYS:HZ3	1:ED:66:ASP:H	1.68	0.40
1:EG:60:LYS:NZ	1:EG:65:ALA:HB3	2.35	0.40
1:EH:117:LEU:HD23	1:EI:15:ILE:HG13	2.03	0.40
1:EX:14:LYS:HA	1:EX:14:LYS:HD2	1.90	0.40
1:FA:55:LYS:NZ	1:FA:73:ASN:HB2	2.36	0.40
1:FB:96:TRP:NE1	1:FB:100:LYS:HE2	2.36	0.40
1:FF:76:GLN:HB3	1:FG:95:GLU:OE2	2.21	0.40
1:FP:37:LYS:NZ	1:FP:40:ILE:O	2.51	0.40
1:FQ:49:GLN:NE2	1:FQ:79:ARG:HH21	2.19	0.40
1:FS:38:VAL:HG22	1:FS:39:GLY:H	1.86	0.40
1:FT:85:SER:OG	1:FU:74:GLU:OE1	2.20	0.40
1:FY:64:CYS:SG	1:FY:69:VAL:HG21	2.61	0.40
1:GD:113:GLY:O	1:GE:46:VAL:HG11	2.21	0.40
1:GE:38:VAL:HG22	1:GE:39:GLY:H	1.85	0.40
1:GL:32:LEU:HG	1:GL:34:GLN:NE2	2.36	0.40
1:GQ:24:SER:HB2	1:GQ:55:LYS:HG2	2.01	0.40
1:GU:124:VAL:HA	1:GV:4:PRO:HA	2.03	0.40
1:HG:96:TRP:NE1	1:HG:100:LYS:HE2	2.35	0.40
1:HI:9:THR:O	1:HI:15:ILE:HA	2.21	0.40
1:HV:3:LYS:NZ	1:HW:129:THR:OG1	2.54	0.40
1:IF:68:CYS:HB3	1:IK:64:CYS:HA	2.02	0.40
1:IF:74:GLU:OE2	1:IG:88:ASN:OD1	2.40	0.40
1:IM:45:ASN:OD1	1:IM:46:VAL:N	2.54	0.40
1:IT:14:LYS:HE3	1:IT:28:SER:HB2	2.04	0.40
1:IW:57:PRO:HA	1:IW:73:ASN:HA	2.03	0.40
1:IX:14:LYS:HZ3	1:IX:30:SER:HB2	1.86	0.40
1:JD:8:ILE:N	1:JD:16:VAL:O	2.40	0.40
1:JD:37:LYS:HD3	1:JD:42:GLU:OE2	2.21	0.40
1:JG:5:MET:SD	1:JH:125:SER:HB2	2.61	0.40
1:AE:8:ILE:HG13	1:AE:18:SER:HB3	2.03	0.40
1:AM:34:GLN:O	1:AM:45:ASN:N	2.52	0.40
1:AV:37:LYS:NZ	1:AV:40:ILE:O	2.54	0.40
1:AY:3:LYS:HB2	1:AY:3:LYS:HE2	1.79	0.40
1:BE:37:LYS:HZ3	1:BE:42:GLU:HB2	1.86	0.40
1:BV:37:LYS:HD2	1:BV:42:GLU:HB3	2.02	0.40
1:BV:68:CYS:O	1:GH:61:PRO:HG2	2.21	0.40
1:BY:2:ASN:HB2	1:BZ:124:VAL:HB	2.02	0.40
1:BY:20:PRO:HB3	1:CE:116:PHE:CE2	2.56	0.40
1:CH:5:MET:CG	1:CH:17:TRP:HB3	2.51	0.40
1:CH:37:LYS:NZ	1:CH:40:ILE:O	2.55	0.40
1:CK:14:LYS:NZ	1:CK:28:SER:HB2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:60:LYS:NZ	1:CL:65:ALA:HB3	2.35	0.40
1:CW:37:LYS:NZ	1:CW:39:GLY:O	2.54	0.40
1:CZ:68:CYS:CA	1:ID:64:CYS:H	2.33	0.40
1:DC:101:ARG:NH2	1:DC:124:VAL:HG21	2.36	0.40
1:DV:19:ASP:HB3	1:DV:22:ARG:O	2.20	0.40
1:EG:25:THR:O	1:EG:25:THR:OG1	2.34	0.40
1:EM:60:LYS:NZ	1:EM:65:ALA:H	2.19	0.40
1:ET:59:PRO:HG2	1:EU:87:GLU:HG3	2.03	0.40
1:EW:34:GLN:OE1	1:EW:36:VAL:HG13	2.21	0.40
1:FD:1:ALA:O	1:FE:129:THR:N	2.35	0.40
1:FJ:31:LEU:HD11	1:FK:117:LEU:HB3	2.03	0.40
1:FR:72:PRO:HG2	1:FS:38:VAL:HG22	2.02	0.40
1:GD:24:SER:HB2	1:GD:55:LYS:HG3	2.03	0.40
1:GO:101:ARG:HH21	1:GO:124:VAL:HG21	1.86	0.40
1:GZ:8:ILE:HG13	1:GZ:18:SER:HB2	2.02	0.40
1:HE:11:THR:HB	1:HE:14:LYS:H	1.85	0.40
1:HG:31:LEU:HD13	1:HI:115:GLY:HA2	2.03	0.40
1:HG:88:ASN:ND2	1:HI:74:GLU:OE2	2.44	0.40
1:HJ:5:MET:HB2	1:HJ:17:TRP:HB3	2.03	0.40
1:HT:31:LEU:HD13	1:HU:115:GLY:HA2	2.03	0.40
1:IJ:59:PRO:O	1:IJ:71:MET:HE1	2.20	0.40
1:IJ:60:LYS:HD2	1:IJ:71:MET:HE2	2.03	0.40
1:JI:3:LYS:HZ2	1:JJ:129:THR:HG23	1.86	0.40
1:JI:31:LEU:HD12	1:JJ:117:LEU:HD22	2.04	0.40
1:AI:56:ARG:O	1:AI:74:GLU:N	2.48	0.40
1:AL:102:ASN:HA	1:AL:105:THR:HG22	2.03	0.40
1:AW:72:PRO:HG2	1:AX:38:VAL:HG22	2.03	0.40
1:BE:58:ALA:HB3	1:BE:71:MET:HG3	2.03	0.40
1:BG:101:ARG:NH2	1:BG:124:VAL:HG21	2.36	0.40
1:BK:104:ASP:OD2	1:BL:100:LYS:NZ	2.51	0.40
1:BM:104:ASP:OD2	1:BN:100:LYS:NZ	2.54	0.40
1:BR:56:ARG:HD2	1:BR:76:GLN:HE22	1.85	0.40
1:CA:115:GLY:O	1:CB:33:ARG:HD3	2.21	0.40
1:CM:49:GLN:OE1	1:CM:79:ARG:NH2	2.38	0.40
1:CP:101:ARG:CZ	1:CP:124:VAL:HG21	2.50	0.40
1:CS:123:ILE:HG13	1:CT:17:TRP:CD2	2.56	0.40
1:CU:127:ASP:OD1	1:CU:127:ASP:N	2.52	0.40
1:CV:67:ALA:HA	1:HL:63:GLY:N	2.22	0.40
1:DN:8:ILE:HG13	1:DN:18:SER:HB3	2.03	0.40
1:DQ:62:GLU:O	1:DQ:62:GLU:HG2	2.21	0.40
1:ED:115:GLY:O	1:EE:33:ARG:HD3	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EG:69:VAL:H	1:HX:64:CYS:H	1.69	0.40
1:EH:101:ARG:NH2	1:EI:2:ASN:HD22	2.19	0.40
1:EM:25:THR:O	1:EM:25:THR:OG1	2.35	0.40
1:EM:62:GLU:O	1:EM:62:GLU:HG2	2.21	0.40
1:EO:102:ASN:HA	1:EO:105:THR:HG22	2.04	0.40
1:ET:113:GLY:O	1:EU:46:VAL:HG11	2.21	0.40
1:FB:31:LEU:HD11	1:FC:117:LEU:HB3	2.03	0.40
1:FE:5:MET:SD	1:FE:5:MET:N	2.94	0.40
1:FF:56:ARG:O	1:FF:74:GLU:HG2	2.22	0.40
1:FK:3:LYS:HD2	1:FK:21:THR:HG21	2.03	0.40
1:FU:22:ARG:NH2	1:FU:55:LYS:O	2.46	0.40
1:FY:38:VAL:HG22	1:FY:39:GLY:H	1.87	0.40
1:GF:35:ARG:HH12	1:GF:44:ASN:CG	2.24	0.40
1:GT:8:ILE:N	1:GT:16:VAL:O	2.41	0.40
1:GY:106:LEU:HA	1:GY:106:LEU:HD23	1.82	0.40
1:HD:106:LEU:HD11	1:HD:123:ILE:HD11	2.03	0.40
1:HE:60:LYS:HD2	1:HE:71:MET:HE2	2.04	0.40
1:HI:5:MET:N	1:HI:5:MET:SD	2.95	0.40
1:HW:94:ALA:O	1:HW:98:THR:HG23	2.22	0.40
1:HY:102:ASN:O	1:HY:105:THR:HG22	2.21	0.40
1:HZ:11:THR:N	1:HZ:14:LYS:O	2.54	0.40
1:HZ:31:LEU:HD11	1:IA:117:LEU:HB3	2.04	0.40
1:IG:23:LEU:O	1:IG:24:SER:OG	2.32	0.40
1:IG:62:GLU:HG2	1:IG:62:GLU:O	2.21	0.40
1:IH:113:GLY:O	1:II:46:VAL:HG11	2.22	0.40
1:IV:32:LEU:HG	1:IV:34:GLN:NE2	2.37	0.40
1:IX:101:ARG:NH2	1:IX:124:VAL:HG21	2.36	0.40
1:JE:8:ILE:HB	1:JJ:116:PHE:HE1	1.86	0.40
1:AD:12:ALA:HB2	1:AE:10:SER:H	1.86	0.40
1:AD:68:CYS:HA	1:IV:61:PRO:O	2.21	0.40
1:AE:1:ALA:HB1	1:AF:128:THR:HG23	2.03	0.40
1:AH:67:ALA:H	1:JE:65:ALA:CB	2.34	0.40
1:AK:117:LEU:HB3	1:AL:15:ILE:HD11	2.03	0.40
1:AY:19:ASP:HB3	1:AY:22:ARG:O	2.21	0.40
1:BD:93:LYS:O	1:BD:97:GLU:OE1	2.40	0.40
1:BM:128:THR:HA	1:BN:2:ASN:HA	2.02	0.40
1:BZ:36:VAL:O	1:BZ:43:LEU:N	2.44	0.40
1:CA:58:ALA:HB3	1:CA:71:MET:HG3	2.03	0.40
1:CY:3:LYS:HZ2	1:CZ:129:THR:HG23	1.86	0.40
1:CY:89:LEU:HG	1:CY:93:LYS:HE3	2.03	0.40
1:DG:116:PHE:CE2	1:FU:20:PRO:HA	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DR:11:THR:HB	1:DR:14:LYS:H	1.87	0.40
1:DY:37:LYS:NZ	1:DY:40:ILE:O	2.54	0.40
1:EB:101:ARG:CZ	1:EB:124:VAL:HG21	2.52	0.40
1:EI:74:GLU:OE2	1:EI:76:GLN:NE2	2.42	0.40
1:FP:98:THR:HA	1:FP:101:ARG:HG2	2.04	0.40
1:FQ:64:CYS:SG	1:FS:68:CYS:HA	2.61	0.40
1:FR:19:ASP:HB3	1:FR:22:ARG:O	2.22	0.40
1:FX:9:THR:O	1:FX:15:ILE:HA	2.21	0.40
1:GH:11:THR:N	1:GH:14:LYS:O	2.54	0.40
1:GX:68:CYS:SG	1:GX:69:VAL:HG13	2.61	0.40
1:GZ:56:ARG:O	1:GZ:74:GLU:N	2.27	0.40
1:HD:87:GLU:HG2	1:HD:88:ASN:N	2.35	0.40
1:HF:9:THR:O	1:HF:15:ILE:HA	2.21	0.40
1:HJ:65:ALA:N	1:HL:68:CYS:HB3	2.36	0.40
1:HJ:92:LEU:HD22	1:HK:76:GLN:HE21	1.85	0.40
1:HT:58:ALA:HB3	1:HT:71:MET:HE3	2.03	0.40
1:HT:60:LYS:NZ	1:HT:69:VAL:HG12	2.36	0.40
1:HT:123:ILE:HB	1:HU:5:MET:HB2	2.04	0.40
1:HZ:91:THR:HG21	1:IA:56:ARG:HD3	2.04	0.40
1:IN:5:MET:HB2	1:IN:17:TRP:HB3	2.03	0.40
1:IP:55:LYS:HZ2	1:IP:73:ASN:HB2	1.86	0.40
1:IR:5:MET:SD	1:IS:125:SER:HB2	2.61	0.40
1:IR:123:ILE:HB	1:IS:5:MET:HB2	2.03	0.40
1:JF:45:ASN:OD1	1:JF:46:VAL:N	2.55	0.40
1:JI:86:ALA:HB1	1:JJ:114:LEU:HD23	2.04	0.40
1:JJ:8:ILE:N	1:JJ:16:VAL:O	2.43	0.40
1:AB:67:ALA:HB1	1:EX:63:GLY:O	2.22	0.40
1:AC:104:ASP:OD2	1:AD:100:LYS:NZ	2.53	0.40
1:AH:68:CYS:O	1:JE:61:PRO:HG2	2.21	0.40
1:AN:68:CYS:SG	1:AN:69:VAL:HG13	2.61	0.40
1:AN:106:LEU:CD2	1:AN:123:ILE:HD11	2.47	0.40
1:AP:62:GLU:O	1:AP:62:GLU:HG2	2.21	0.40
1:AS:19:ASP:HB3	1:AS:22:ARG:O	2.22	0.40
1:BB:102:ASN:HA	1:BB:105:THR:HG22	2.04	0.40
1:BC:14:LYS:HZ1	1:BC:28:SER:CB	2.28	0.40
1:BH:5:MET:CG	1:BH:17:TRP:HB3	2.51	0.40
1:BK:19:ASP:HB3	1:BK:22:ARG:O	2.21	0.40
1:BM:62:GLU:HG2	1:BM:62:GLU:O	2.21	0.40
1:BR:67:ALA:O	1:FZ:65:ALA:HB2	2.21	0.40
1:CE:88:ASN:ND2	1:CF:74:GLU:OE1	2.37	0.40
1:CQ:5:MET:SD	1:CQ:5:MET:N	2.95	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:5:MET:HG3	1:CS:19:ASP:HA	2.04	0.40
1:CT:32:LEU:HB2	1:CT:47:SER:HB3	2.03	0.40
1:CW:56:ARG:O	1:CW:74:GLU:N	2.51	0.40
1:DA:101:ARG:NH2	1:DA:124:VAL:HG21	2.37	0.40
1:DG:62:GLU:O	1:DG:62:GLU:HG2	2.22	0.40
1:DI:60:LYS:HZ1	1:DI:65:ALA:HB3	1.86	0.40
1:DR:127:ASP:OD1	1:DR:127:ASP:N	2.52	0.40
1:DT:19:ASP:HB3	1:DT:22:ARG:O	2.21	0.40
1:DZ:19:ASP:HB3	1:DZ:22:ARG:O	2.21	0.40
1:EA:66:ASP:OD1	1:EA:66:ASP:N	2.53	0.40
1:ED:3:LYS:HZ3	1:EE:127:ASP:C	2.24	0.40
1:ED:101:ARG:HH21	1:EE:2:ASN:HD22	1.70	0.40
1:EW:9:THR:O	1:EW:15:ILE:HA	2.21	0.40
1:FB:91:THR:O	1:FB:95:GLU:HG2	2.22	0.40
1:FJ:1:ALA:O	1:FK:129:THR:N	2.45	0.40
1:FN:19:ASP:HB3	1:FN:22:ARG:O	2.22	0.40
1:FP:11:THR:N	1:FP:14:LYS:O	2.55	0.40
1:FQ:60:LYS:HE2	1:FQ:64:CYS:HB3	2.04	0.40
1:FR:5:MET:SD	1:FR:5:MET:N	2.94	0.40
1:FS:60:LYS:HG2	1:FS:71:MET:HE1	2.04	0.40
1:GG:56:ARG:O	1:GG:74:GLU:HG3	2.22	0.40
1:GH:31:LEU:HD12	1:GI:117:LEU:HD22	2.03	0.40
1:GZ:62:GLU:HG2	1:GZ:62:GLU:O	2.21	0.40
1:HD:89:LEU:HG	1:HD:93:LYS:HE3	2.03	0.40
1:HI:101:ARG:NH2	1:HI:124:VAL:HG21	2.29	0.40
1:HN:20:PRO:HB3	1:HS:116:PHE:HE2	1.85	0.40
1:IC:35:ARG:NH1	1:IC:35:ARG:HA	2.37	0.40
1:ID:96:TRP:NE1	1:ID:100:LYS:HE2	2.37	0.40
1:IK:8:ILE:N	1:IK:16:VAL:O	2.40	0.40
1:IL:14:LYS:CE	1:IL:28:SER:HB2	2.52	0.40
1:IN:24:SER:HB2	1:IN:55:LYS:HG3	2.04	0.40
1:IX:96:TRP:NE1	1:IX:100:LYS:HE2	2.36	0.40
1:JC:14:LYS:NZ	1:JC:28:SER:HB2	2.34	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	AB	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	AC	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	AD	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	AE	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	AF	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	AG	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	AH	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	AI	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	AJ	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	AK	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	AL	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	AM	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	AN	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	AO	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	AP	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	AQ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	AR	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	AS	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	AT	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	AU	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	AV	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	AW	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	AX	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	AY	127/129 (98%)	123 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AZ	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	BA	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	BB	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	BC	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	BD	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	BE	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	BF	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	BG	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	BH	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	BI	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	BJ	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	BK	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	BL	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	BM	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	BN	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	BO	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	BP	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	BQ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	BR	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	BS	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	BT	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	BU	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	BV	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	BW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	BX	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	BY	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	BZ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CA	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	CB	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	CC	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	CD	127/129 (98%)	125 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CE	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	CF	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	CG	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CH	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	CI	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CJ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CK	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	CL	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	CM	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	CN	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CO	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CP	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	CQ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CR	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CS	127/129 (98%)	127 (100%)	0	0	100	100
1	CT	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CU	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	CV	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	CW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	CX	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	CY	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	CZ	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	DA	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	DB	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	DC	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	DE	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	DF	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	DG	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	DH	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	DI	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	DJ	127/129 (98%)	125 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DK	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	DL	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	DM	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	DN	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	DO	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	DP	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	DQ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	DR	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	DS	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	DT	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	DU	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	DV	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	DW	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	DX	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	DY	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	DZ	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	EA	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	EB	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	EC	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	ED	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	EE	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	EF	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	EG	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	EH	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	EI	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	EJ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	EK	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	EL	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	EM	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	EN	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	EO	127/129 (98%)	126 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EP	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	EQ	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	ER	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	ES	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	ET	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	EU	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	EV	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	EW	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	EX	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	EY	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	EZ	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	FA	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
1	FB	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	FC	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	FD	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	FE	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	FF	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	FG	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	FH	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	FI	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	FJ	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	FK	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	FL	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	FM	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
1	FN	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	FO	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	FP	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	FQ	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	FR	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	FS	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
1	FT	127/129 (98%)	125 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	FU	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	FV	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	FW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	FX	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	FY	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	FZ	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	GA	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	GB	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	GC	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	GD	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	GE	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	GF	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	GG	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	GH	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	GI	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	GK	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	GL	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
1	GM	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	GN	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
1	GO	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	GP	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	GQ	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	GR	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	GS	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	GT	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	GU	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	GV	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	GW	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	GX	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	GY	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	GZ	127/129 (98%)	119 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	HA	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	HB	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	HC	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	HD	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	HE	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	HF	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	HG	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	HI	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	HJ	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	HK	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	HL	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	HM	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	HN	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	HO	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	HP	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	HQ	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	HR	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	HS	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	HT	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	HU	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	HV	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	HW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	HX	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	HY	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	HZ	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	IA	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	IB	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	IC	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
1	ID	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	IE	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
1	IF	127/129 (98%)	122 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	IG	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	IH	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	II	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	IJ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	IK	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	IL	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	IM	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	IN	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
1	IO	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	IP	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	IQ	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	IR	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	IS	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	IT	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
1	IU	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
1	IV	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	IW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	IX	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	IZ	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	JA	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
1	JB	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	JC	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	JD	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
1	JE	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	JF	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
1	JG	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
1	JH	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
1	JI	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
1	JJ	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
All	All	30480/30960 (98%)	29335 (96%)	1145 (4%)	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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	108/108 (100%)	108 (100%)	0	100	100
1	AB	108/108 (100%)	108 (100%)	0	100	100
1	AC	108/108 (100%)	108 (100%)	0	100	100
1	AD	108/108 (100%)	108 (100%)	0	100	100
1	AE	108/108 (100%)	108 (100%)	0	100	100
1	AF	108/108 (100%)	108 (100%)	0	100	100
1	AG	108/108 (100%)	108 (100%)	0	100	100
1	AH	108/108 (100%)	108 (100%)	0	100	100
1	AI	108/108 (100%)	108 (100%)	0	100	100
1	AJ	108/108 (100%)	108 (100%)	0	100	100
1	AK	108/108 (100%)	108 (100%)	0	100	100
1	AL	108/108 (100%)	108 (100%)	0	100	100
1	AM	108/108 (100%)	108 (100%)	0	100	100
1	AN	108/108 (100%)	108 (100%)	0	100	100
1	AO	108/108 (100%)	108 (100%)	0	100	100
1	AP	108/108 (100%)	108 (100%)	0	100	100
1	AQ	108/108 (100%)	108 (100%)	0	100	100
1	AR	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	AS	108/108 (100%)	108 (100%)	0	100	100
1	AT	108/108 (100%)	108 (100%)	0	100	100
1	AU	108/108 (100%)	108 (100%)	0	100	100
1	AV	108/108 (100%)	108 (100%)	0	100	100
1	AW	108/108 (100%)	108 (100%)	0	100	100
1	AX	108/108 (100%)	108 (100%)	0	100	100
1	AY	108/108 (100%)	108 (100%)	0	100	100
1	AZ	108/108 (100%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	108/108 (100%)	108 (100%)	0	100	100
1	BB	108/108 (100%)	108 (100%)	0	100	100
1	BC	108/108 (100%)	108 (100%)	0	100	100
1	BD	108/108 (100%)	108 (100%)	0	100	100
1	BE	108/108 (100%)	108 (100%)	0	100	100
1	BF	108/108 (100%)	108 (100%)	0	100	100
1	BG	108/108 (100%)	108 (100%)	0	100	100
1	BH	108/108 (100%)	108 (100%)	0	100	100
1	BI	108/108 (100%)	108 (100%)	0	100	100
1	BJ	108/108 (100%)	108 (100%)	0	100	100
1	BK	108/108 (100%)	108 (100%)	0	100	100
1	BL	108/108 (100%)	108 (100%)	0	100	100
1	BM	108/108 (100%)	108 (100%)	0	100	100
1	BN	108/108 (100%)	108 (100%)	0	100	100
1	BO	108/108 (100%)	108 (100%)	0	100	100
1	BP	108/108 (100%)	108 (100%)	0	100	100
1	BQ	108/108 (100%)	108 (100%)	0	100	100
1	BR	108/108 (100%)	108 (100%)	0	100	100
1	BS	108/108 (100%)	108 (100%)	0	100	100
1	BT	108/108 (100%)	108 (100%)	0	100	100
1	BU	108/108 (100%)	108 (100%)	0	100	100
1	BV	108/108 (100%)	108 (100%)	0	100	100
1	BW	108/108 (100%)	108 (100%)	0	100	100
1	BX	108/108 (100%)	108 (100%)	0	100	100
1	BY	108/108 (100%)	108 (100%)	0	100	100
1	BZ	108/108 (100%)	108 (100%)	0	100	100
1	CA	108/108 (100%)	108 (100%)	0	100	100
1	CB	108/108 (100%)	108 (100%)	0	100	100
1	CC	108/108 (100%)	108 (100%)	0	100	100
1	CD	108/108 (100%)	108 (100%)	0	100	100
1	CE	108/108 (100%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CF	108/108 (100%)	108 (100%)	0	100	100
1	CG	108/108 (100%)	108 (100%)	0	100	100
1	CH	108/108 (100%)	108 (100%)	0	100	100
1	CI	108/108 (100%)	108 (100%)	0	100	100
1	CJ	108/108 (100%)	108 (100%)	0	100	100
1	CK	108/108 (100%)	108 (100%)	0	100	100
1	CL	108/108 (100%)	108 (100%)	0	100	100
1	CM	108/108 (100%)	108 (100%)	0	100	100
1	CN	108/108 (100%)	108 (100%)	0	100	100
1	CO	108/108 (100%)	108 (100%)	0	100	100
1	CP	108/108 (100%)	108 (100%)	0	100	100
1	CQ	108/108 (100%)	108 (100%)	0	100	100
1	CR	108/108 (100%)	108 (100%)	0	100	100
1	CS	108/108 (100%)	108 (100%)	0	100	100
1	CT	108/108 (100%)	108 (100%)	0	100	100
1	CU	108/108 (100%)	108 (100%)	0	100	100
1	CV	108/108 (100%)	108 (100%)	0	100	100
1	CW	108/108 (100%)	108 (100%)	0	100	100
1	CX	108/108 (100%)	108 (100%)	0	100	100
1	CY	108/108 (100%)	108 (100%)	0	100	100
1	CZ	108/108 (100%)	108 (100%)	0	100	100
1	DA	108/108 (100%)	108 (100%)	0	100	100
1	DB	108/108 (100%)	108 (100%)	0	100	100
1	DC	108/108 (100%)	108 (100%)	0	100	100
1	DE	108/108 (100%)	108 (100%)	0	100	100
1	DF	108/108 (100%)	108 (100%)	0	100	100
1	DG	108/108 (100%)	108 (100%)	0	100	100
1	DH	108/108 (100%)	108 (100%)	0	100	100
1	DI	108/108 (100%)	108 (100%)	0	100	100
1	DJ	108/108 (100%)	108 (100%)	0	100	100
1	DK	108/108 (100%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DL	108/108 (100%)	108 (100%)	0	100	100
1	DM	108/108 (100%)	108 (100%)	0	100	100
1	DN	108/108 (100%)	108 (100%)	0	100	100
1	DO	108/108 (100%)	108 (100%)	0	100	100
1	DP	108/108 (100%)	108 (100%)	0	100	100
1	DQ	108/108 (100%)	108 (100%)	0	100	100
1	DR	108/108 (100%)	108 (100%)	0	100	100
1	DS	108/108 (100%)	108 (100%)	0	100	100
1	DT	108/108 (100%)	108 (100%)	0	100	100
1	DU	108/108 (100%)	108 (100%)	0	100	100
1	DV	108/108 (100%)	108 (100%)	0	100	100
1	DW	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	DX	108/108 (100%)	108 (100%)	0	100	100
1	DY	108/108 (100%)	108 (100%)	0	100	100
1	DZ	108/108 (100%)	108 (100%)	0	100	100
1	EA	108/108 (100%)	108 (100%)	0	100	100
1	EB	108/108 (100%)	108 (100%)	0	100	100
1	EC	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	ED	108/108 (100%)	108 (100%)	0	100	100
1	EE	108/108 (100%)	108 (100%)	0	100	100
1	EF	108/108 (100%)	108 (100%)	0	100	100
1	EG	108/108 (100%)	108 (100%)	0	100	100
1	EH	108/108 (100%)	108 (100%)	0	100	100
1	EI	108/108 (100%)	108 (100%)	0	100	100
1	EJ	108/108 (100%)	108 (100%)	0	100	100
1	EK	108/108 (100%)	108 (100%)	0	100	100
1	EL	108/108 (100%)	108 (100%)	0	100	100
1	EM	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	EN	108/108 (100%)	108 (100%)	0	100	100
1	EO	108/108 (100%)	108 (100%)	0	100	100
1	EP	108/108 (100%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	EQ	108/108 (100%)	108 (100%)	0	100	100
1	ER	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	ES	108/108 (100%)	108 (100%)	0	100	100
1	ET	108/108 (100%)	108 (100%)	0	100	100
1	EU	108/108 (100%)	108 (100%)	0	100	100
1	EV	108/108 (100%)	108 (100%)	0	100	100
1	EW	108/108 (100%)	108 (100%)	0	100	100
1	EX	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	EY	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	EZ	108/108 (100%)	108 (100%)	0	100	100
1	FA	108/108 (100%)	108 (100%)	0	100	100
1	FB	108/108 (100%)	108 (100%)	0	100	100
1	FC	108/108 (100%)	108 (100%)	0	100	100
1	FD	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FE	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FF	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FG	108/108 (100%)	108 (100%)	0	100	100
1	FH	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FI	108/108 (100%)	108 (100%)	0	100	100
1	FJ	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FK	108/108 (100%)	108 (100%)	0	100	100
1	FL	108/108 (100%)	108 (100%)	0	100	100
1	FM	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FN	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FO	108/108 (100%)	108 (100%)	0	100	100
1	FP	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FQ	108/108 (100%)	108 (100%)	0	100	100
1	FR	108/108 (100%)	108 (100%)	0	100	100
1	FS	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FT	108/108 (100%)	106 (98%)	2 (2%)	52	71
1	FU	108/108 (100%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	FV	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	FW	108/108 (100%)	108 (100%)	0	100	100
1	FX	108/108 (100%)	108 (100%)	0	100	100
1	FY	108/108 (100%)	108 (100%)	0	100	100
1	FZ	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	GA	108/108 (100%)	108 (100%)	0	100	100
1	GB	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	GC	108/108 (100%)	108 (100%)	0	100	100
1	GD	108/108 (100%)	108 (100%)	0	100	100
1	GE	108/108 (100%)	108 (100%)	0	100	100
1	GF	108/108 (100%)	108 (100%)	0	100	100
1	GG	108/108 (100%)	108 (100%)	0	100	100
1	GH	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	GI	108/108 (100%)	108 (100%)	0	100	100
1	GK	108/108 (100%)	108 (100%)	0	100	100
1	GL	108/108 (100%)	108 (100%)	0	100	100
1	GM	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	GN	108/108 (100%)	108 (100%)	0	100	100
1	GO	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	GP	108/108 (100%)	108 (100%)	0	100	100
1	GQ	108/108 (100%)	108 (100%)	0	100	100
1	GR	108/108 (100%)	108 (100%)	0	100	100
1	GS	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	GT	108/108 (100%)	108 (100%)	0	100	100
1	GU	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	GV	108/108 (100%)	108 (100%)	0	100	100
1	GW	108/108 (100%)	108 (100%)	0	100	100
1	GX	108/108 (100%)	108 (100%)	0	100	100
1	GY	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	GZ	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	HA	108/108 (100%)	107 (99%)	1 (1%)	75	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	HB	108/108 (100%)	108 (100%)	0	100	100
1	HC	108/108 (100%)	108 (100%)	0	100	100
1	HD	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	HE	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	HF	108/108 (100%)	108 (100%)	0	100	100
1	HG	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	HI	108/108 (100%)	108 (100%)	0	100	100
1	HJ	108/108 (100%)	108 (100%)	0	100	100
1	HK	108/108 (100%)	108 (100%)	0	100	100
1	HL	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	HM	108/108 (100%)	108 (100%)	0	100	100
1	HN	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	HO	108/108 (100%)	108 (100%)	0	100	100
1	HP	108/108 (100%)	108 (100%)	0	100	100
1	HQ	108/108 (100%)	108 (100%)	0	100	100
1	HR	108/108 (100%)	108 (100%)	0	100	100
1	HS	108/108 (100%)	108 (100%)	0	100	100
1	HT	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	HU	108/108 (100%)	108 (100%)	0	100	100
1	HV	108/108 (100%)	108 (100%)	0	100	100
1	HW	108/108 (100%)	108 (100%)	0	100	100
1	HX	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	HY	108/108 (100%)	108 (100%)	0	100	100
1	HZ	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	IA	108/108 (100%)	108 (100%)	0	100	100
1	IB	108/108 (100%)	108 (100%)	0	100	100
1	IC	108/108 (100%)	108 (100%)	0	100	100
1	ID	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	IE	108/108 (100%)	108 (100%)	0	100	100
1	IF	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	IG	108/108 (100%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	IH	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	II	108/108 (100%)	108 (100%)	0	100	100
1	IJ	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	IK	108/108 (100%)	108 (100%)	0	100	100
1	IL	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	IM	108/108 (100%)	108 (100%)	0	100	100
1	IN	108/108 (100%)	108 (100%)	0	100	100
1	IO	108/108 (100%)	108 (100%)	0	100	100
1	IP	108/108 (100%)	108 (100%)	0	100	100
1	IQ	108/108 (100%)	108 (100%)	0	100	100
1	IR	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	IS	108/108 (100%)	108 (100%)	0	100	100
1	IT	108/108 (100%)	108 (100%)	0	100	100
1	IU	108/108 (100%)	108 (100%)	0	100	100
1	IV	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	IW	108/108 (100%)	108 (100%)	0	100	100
1	IX	108/108 (100%)	108 (100%)	0	100	100
1	IZ	108/108 (100%)	108 (100%)	0	100	100
1	JA	108/108 (100%)	108 (100%)	0	100	100
1	JB	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	JC	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	JD	108/108 (100%)	108 (100%)	0	100	100
1	JE	108/108 (100%)	108 (100%)	0	100	100
1	JF	108/108 (100%)	108 (100%)	0	100	100
1	JG	108/108 (100%)	108 (100%)	0	100	100
1	JH	108/108 (100%)	108 (100%)	0	100	100
1	JI	108/108 (100%)	107 (99%)	1 (1%)	75	86
1	JJ	108/108 (100%)	108 (100%)	0	100	100
All	All	25920/25920 (100%)	25873 (100%)	47 (0%)	91	96

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AR	5	MET
1	DW	5	MET
1	EC	5	MET
1	EM	5	MET
1	ER	33	ARG
1	EX	33	ARG
1	EY	71	MET
1	FD	33	ARG
1	FE	71	MET
1	FF	33	ARG
1	FH	33	ARG
1	FJ	33	ARG
1	FM	71	MET
1	FN	33	ARG
1	FP	33	ARG
1	FS	71	MET
1	FT	33	ARG
1	FT	71	MET
1	FV	33	ARG
1	FZ	33	ARG
1	GB	33	ARG
1	GH	33	ARG
1	GM	33	ARG
1	GO	33	ARG
1	GS	33	ARG
1	GU	33	ARG
1	GY	33	ARG
1	GZ	71	MET
1	HA	33	ARG
1	HD	71	MET
1	HE	33	ARG
1	HG	33	ARG
1	HL	33	ARG
1	HN	33	ARG
1	HT	33	ARG
1	HX	33	ARG
1	HZ	33	ARG
1	ID	33	ARG
1	IF	33	ARG
1	IH	33	ARG
1	IJ	33	ARG
1	IL	33	ARG
1	IR	33	ARG

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Mol	Chain	Res	Type
1	IV	33	ARG
1	JB	33	ARG
1	JC	33	ARG
1	JI	33	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	AD	34	GLN
1	AH	34	GLN
1	AI	13	ASN
1	AJ	34	GLN
1	AL	34	GLN
1	AO	13	ASN
1	AP	34	GLN
1	AV	34	GLN
1	AZ	34	GLN
1	BB	34	GLN
1	BF	34	GLN
1	BH	34	GLN
1	BJ	34	GLN
1	BP	34	GLN
1	BT	34	GLN
1	BV	34	GLN
1	BX	34	GLN
1	CB	34	GLN
1	CF	34	GLN
1	CH	34	GLN
1	CL	34	GLN
1	CP	34	GLN
1	CR	34	GLN
1	CT	34	GLN
1	CX	34	GLN
1	CZ	34	GLN
1	DB	34	GLN
1	DE	34	GLN
1	DI	34	GLN
1	DM	34	GLN
1	DO	34	GLN
1	DQ	34	GLN
1	DS	34	GLN
1	DU	34	GLN

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Mol	Chain	Res	Type
1	DY	34	GLN
1	EA	34	GLN
1	EE	34	GLN
1	EG	34	GLN
1	EI	34	GLN
1	EK	34	GLN
1	EQ	34	GLN
1	EV	44	ASN
1	FF	44	ASN
1	FL	88	ASN
1	FM	111	ASN
1	FR	88	ASN
1	FS	44	ASN
1	FS	111	ASN
1	GQ	44	ASN
1	GR	111	ASN
1	HC	44	ASN
1	HM	88	ASN
1	HT	2	ASN
1	IB	44	ASN
1	IR	2	ASN
1	IT	88	ASN
1	JB	111	ASN
1	JG	44	ASN
1	JH	111	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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.

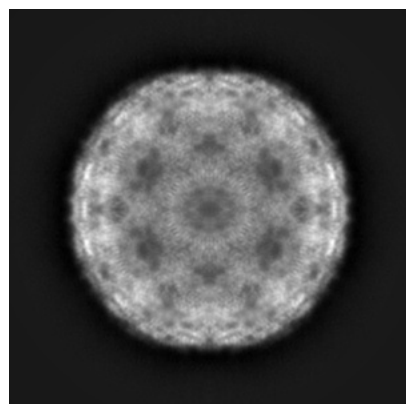
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41657. These allow visual inspection of the internal detail of the map and identification of artifacts.

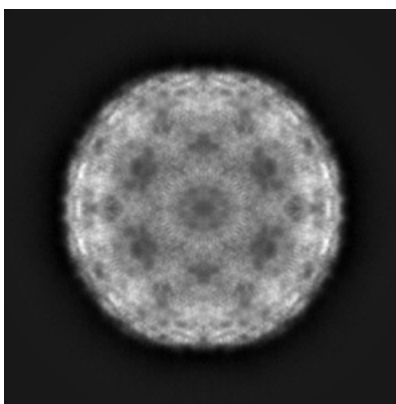
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

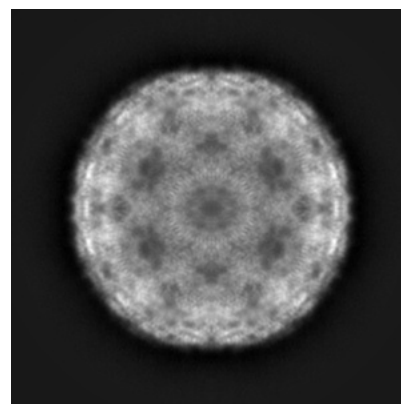
6.1.1 Primary map



X

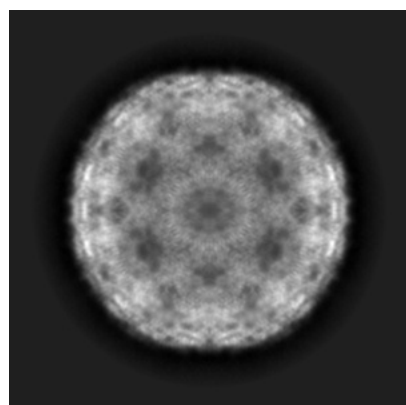


Y

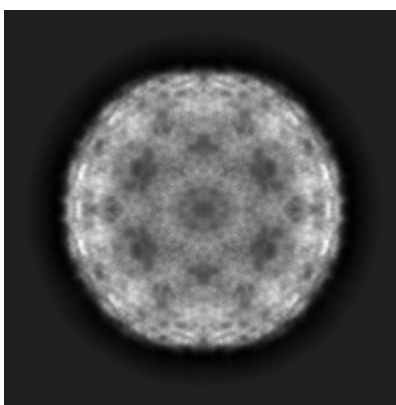


Z

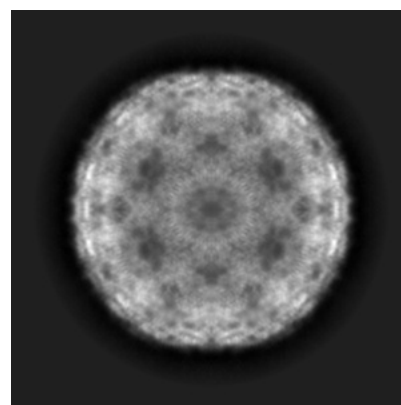
6.1.2 Raw map



X



Y

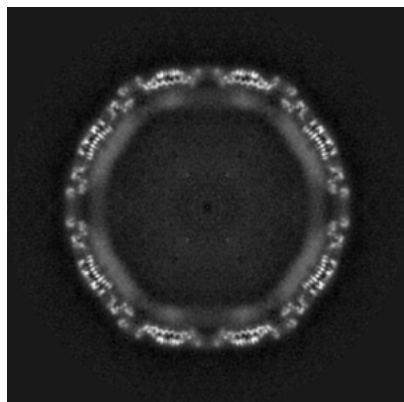


Z

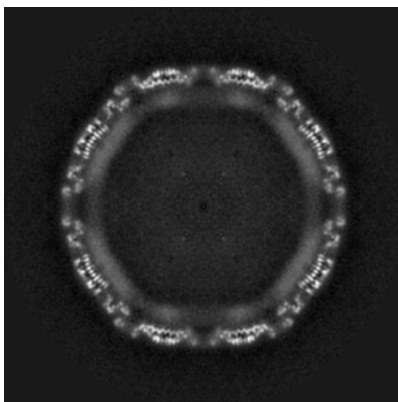
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

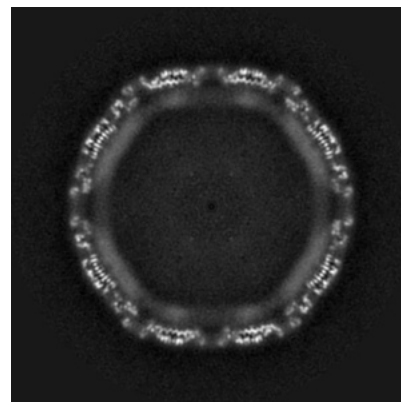
6.2.1 Primary map



X Index: 216

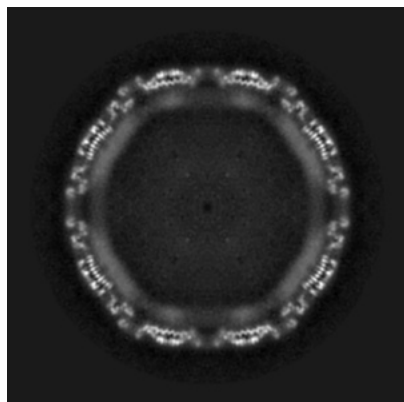


Y Index: 216

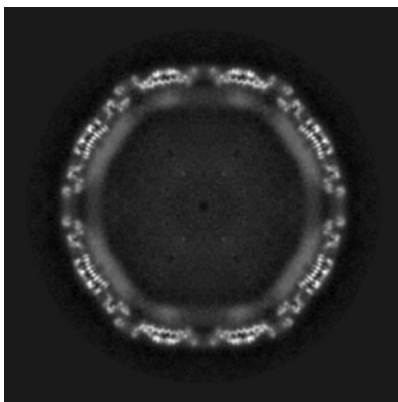


Z Index: 216

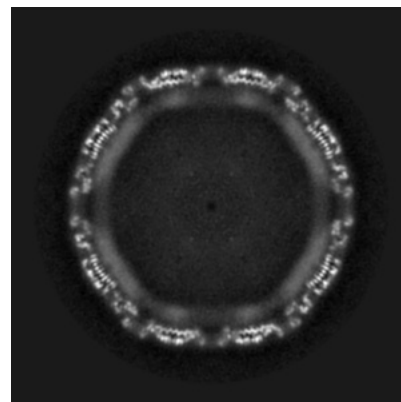
6.2.2 Raw map



X Index: 216



Y Index: 216

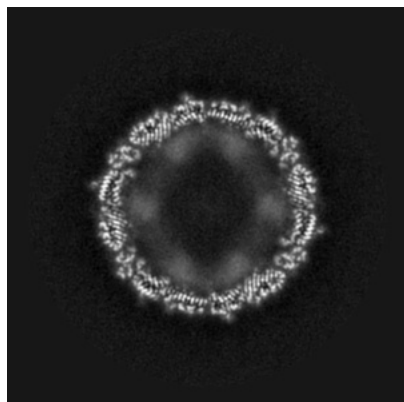


Z Index: 216

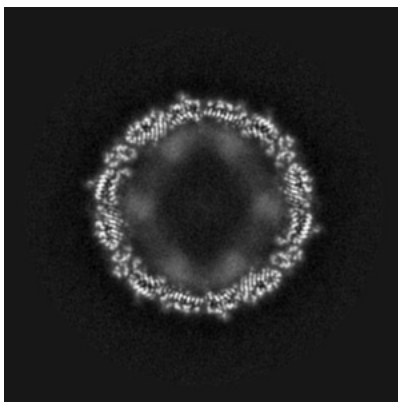
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

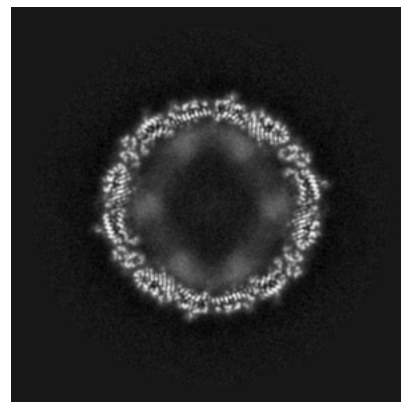
6.3.1 Primary map



X Index: 117

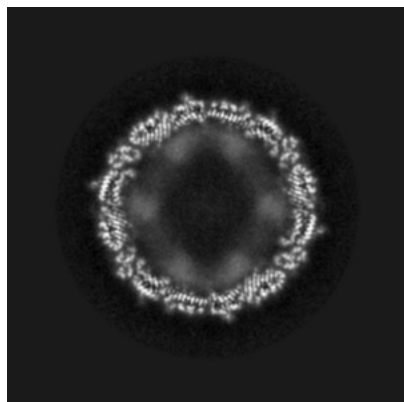


Y Index: 117

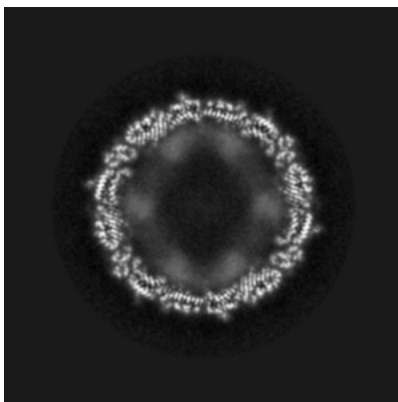


Z Index: 314

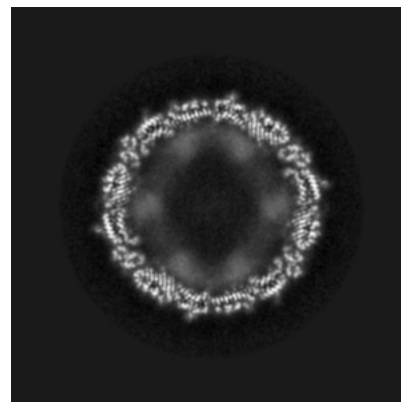
6.3.2 Raw map



X Index: 117



Y Index: 117

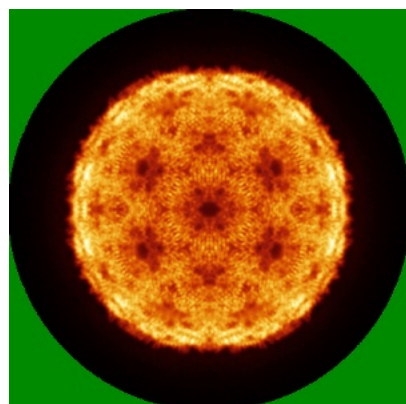


Z Index: 314

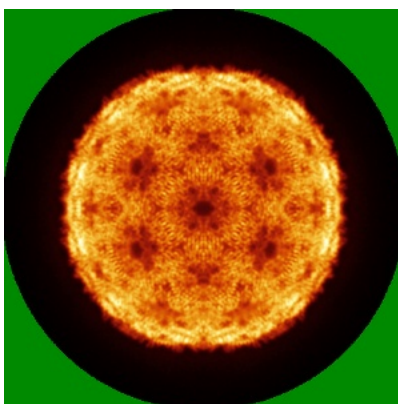
The images above show the largest variance slices of the map in three orthogonal directions.

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

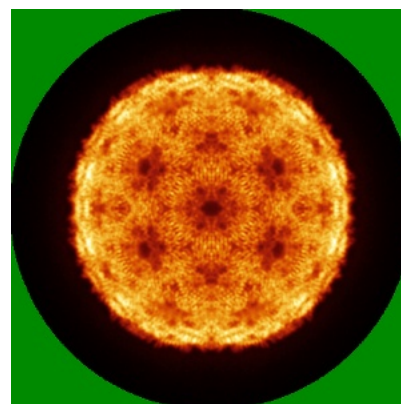
6.4.1 Primary map



X

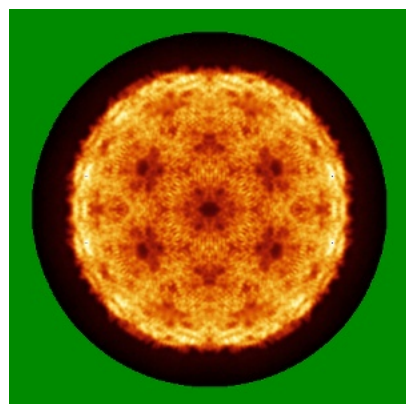


Y

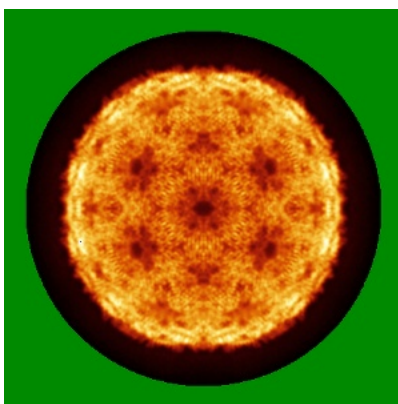


Z

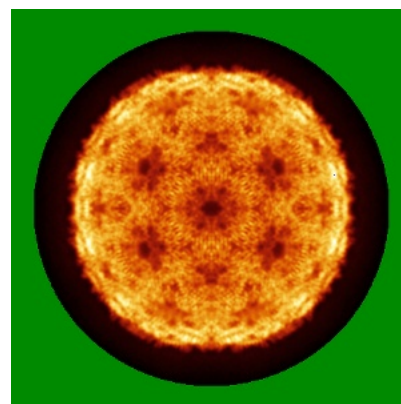
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

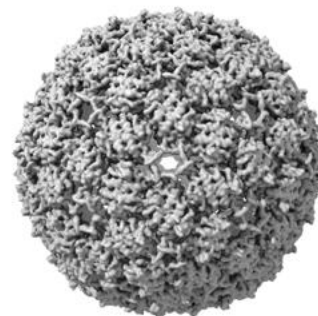
6.5.1 Primary map



X



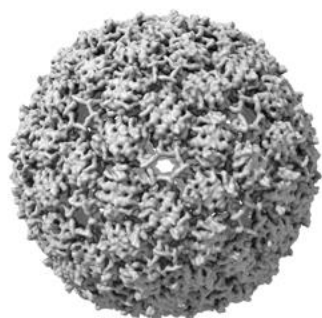
Y



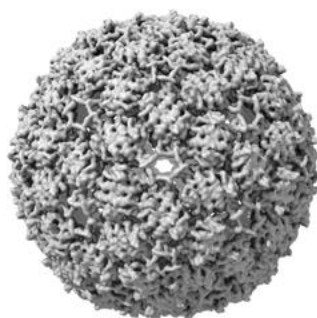
Z

The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

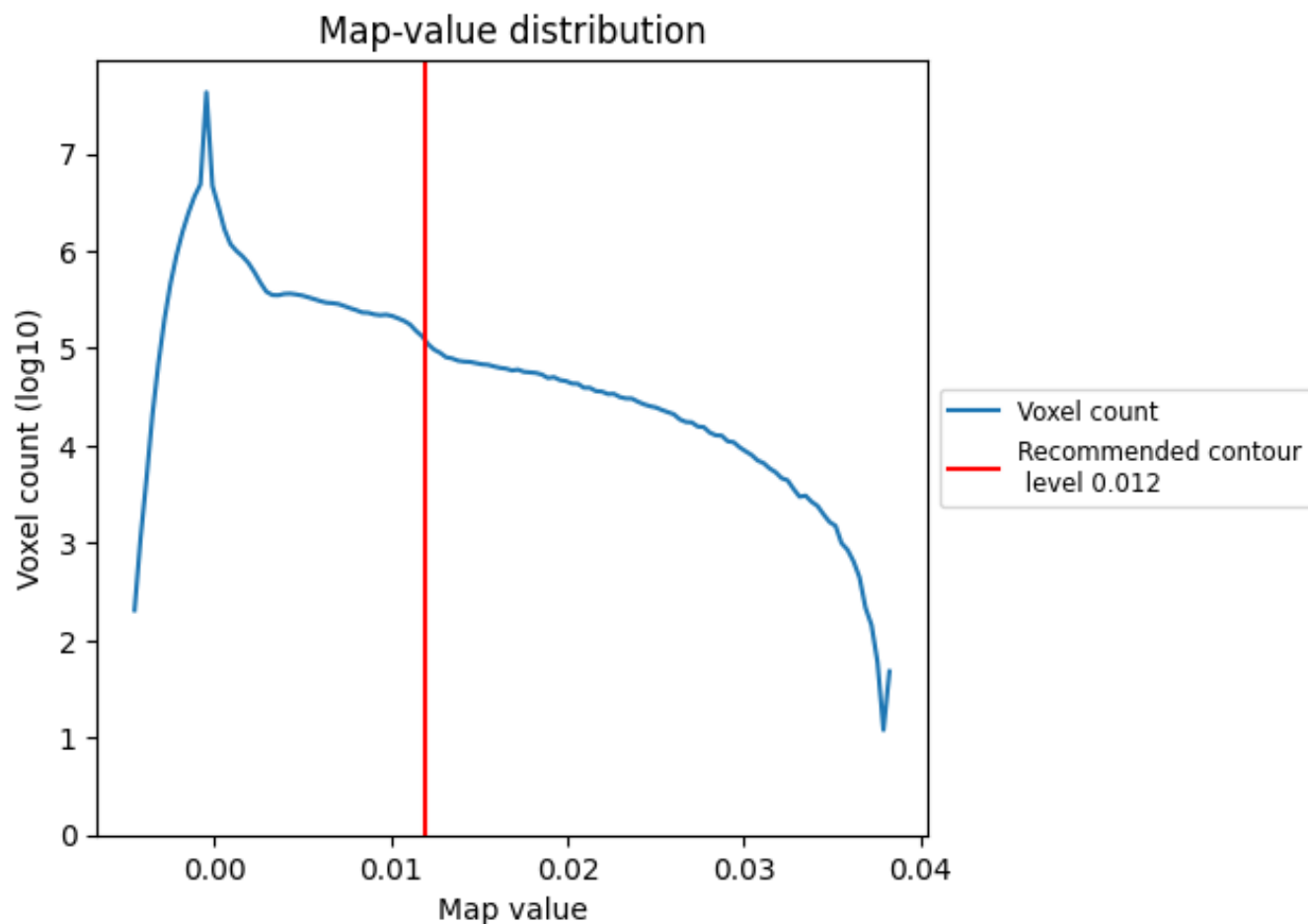
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

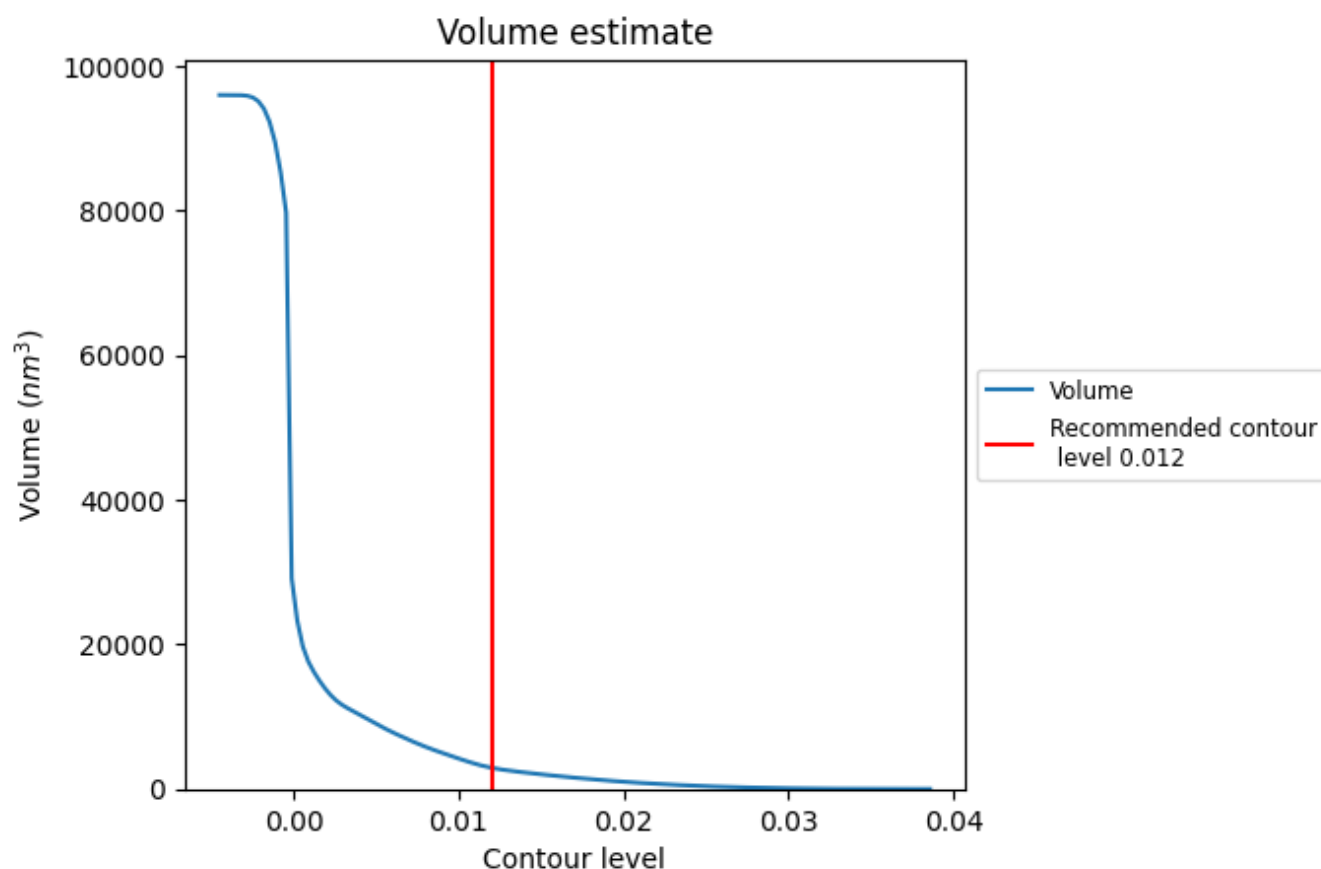
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

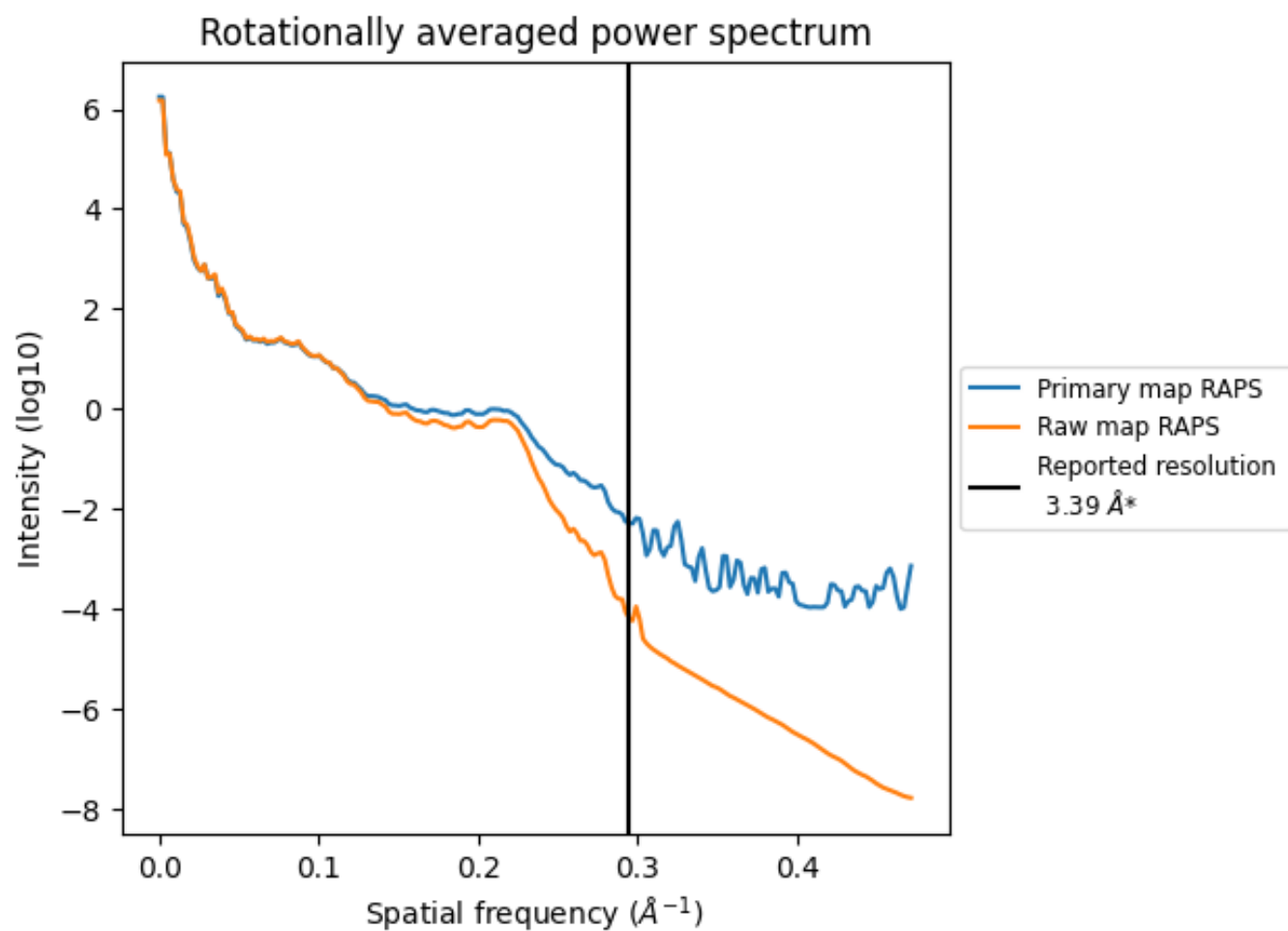
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2923 nm^3 ; this corresponds to an approximate mass of 2640 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

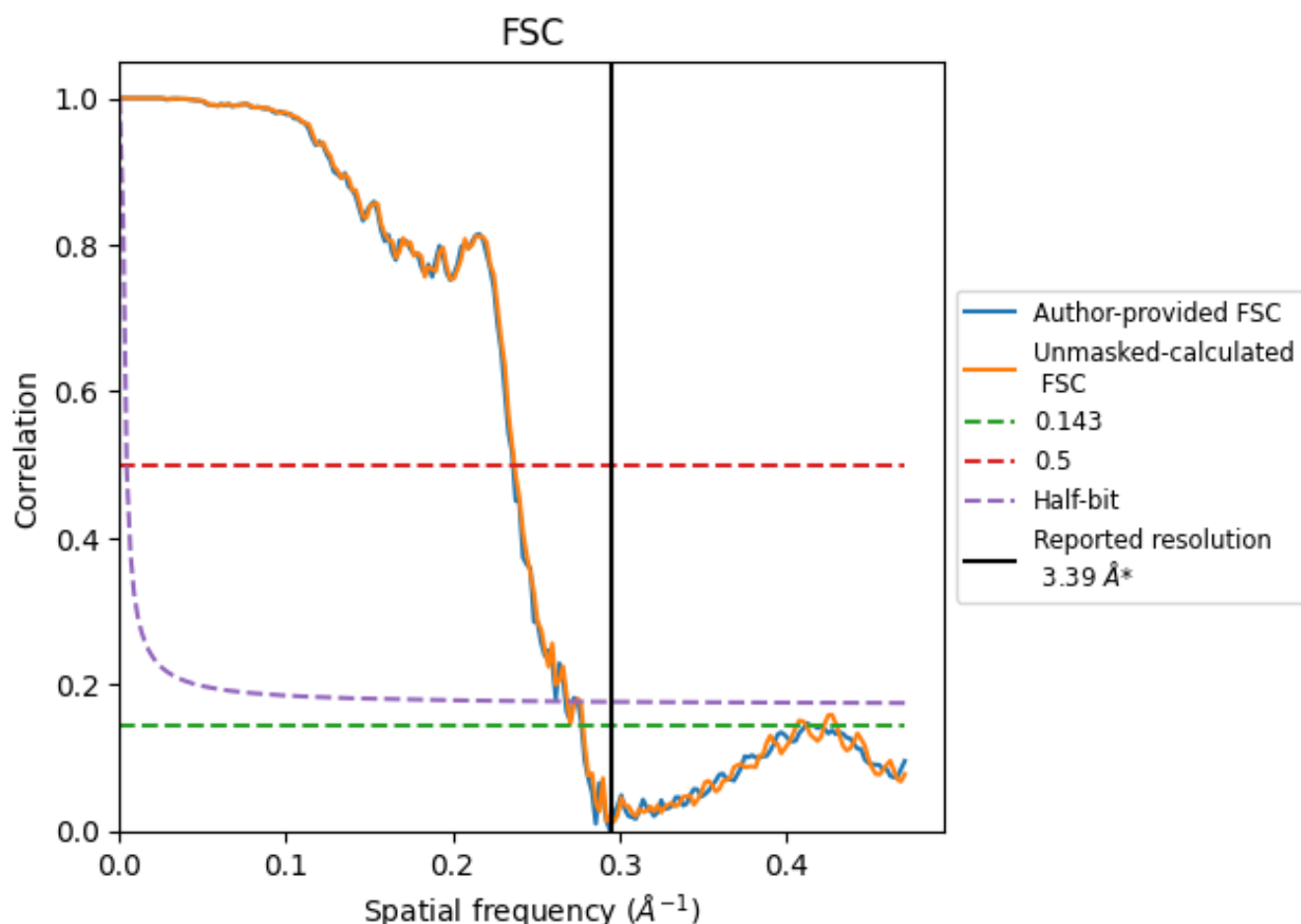


*Reported resolution corresponds to spatial frequency of 0.295 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.295 Å⁻¹

8.2 Resolution estimates [i](#)

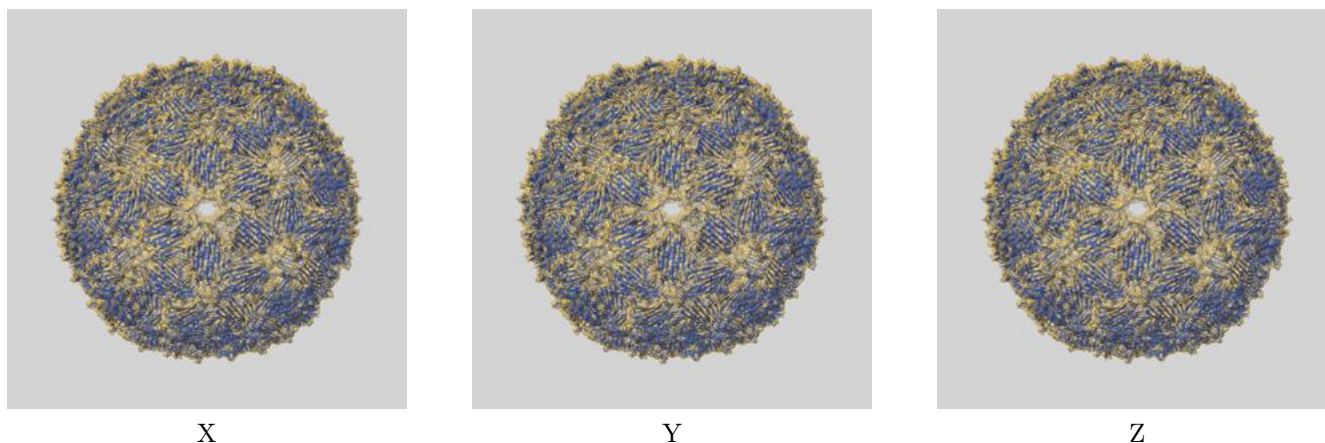
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.39	-	-
Author-provided FSC curve	3.60	4.23	3.73
Unmasked-calculated*	3.59	4.21	3.72

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

9 Map-model fit [i](#)

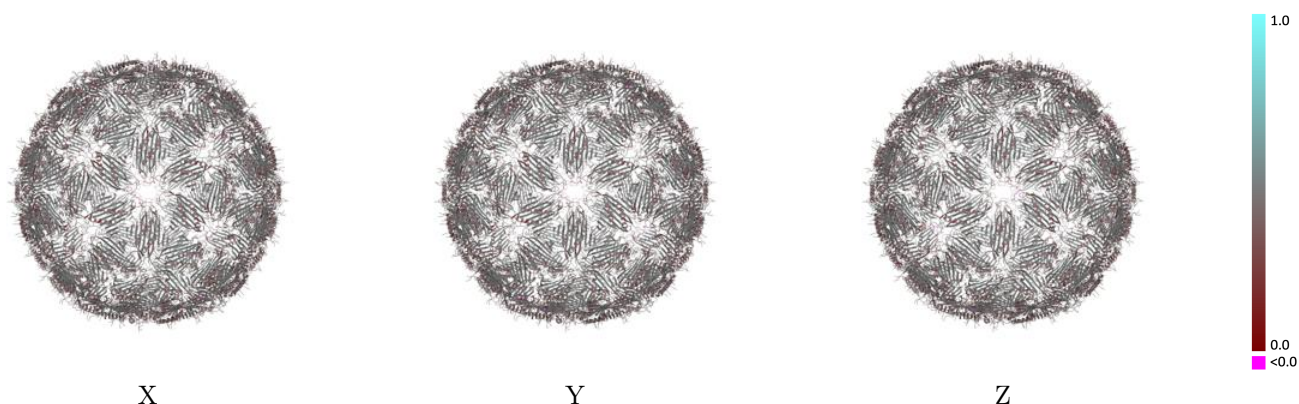
This section contains information regarding the fit between EMDB map EMD-41657 and PDB model 8TW2. Per-residue inclusion information can be found in section [3](#) on page [25](#).

9.1 Map-model overlay [i](#)



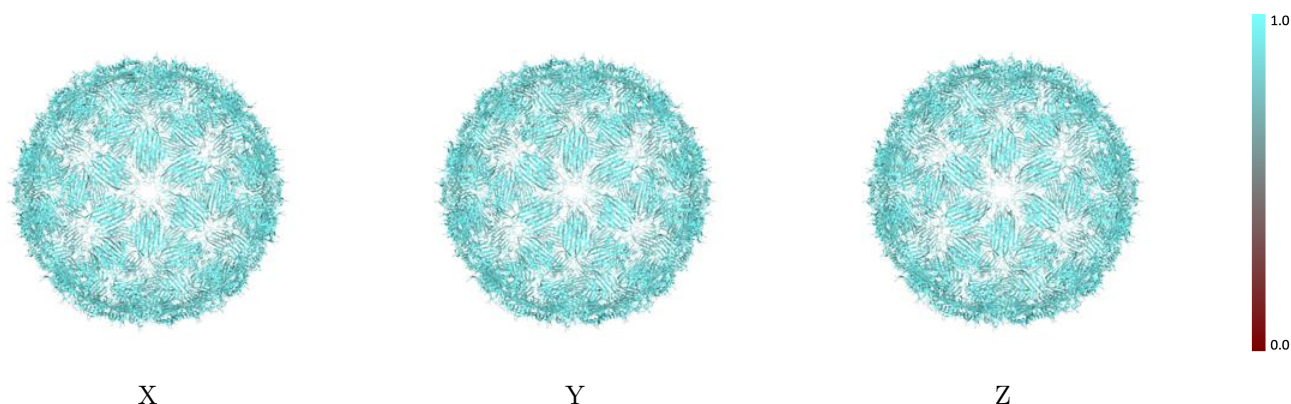
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



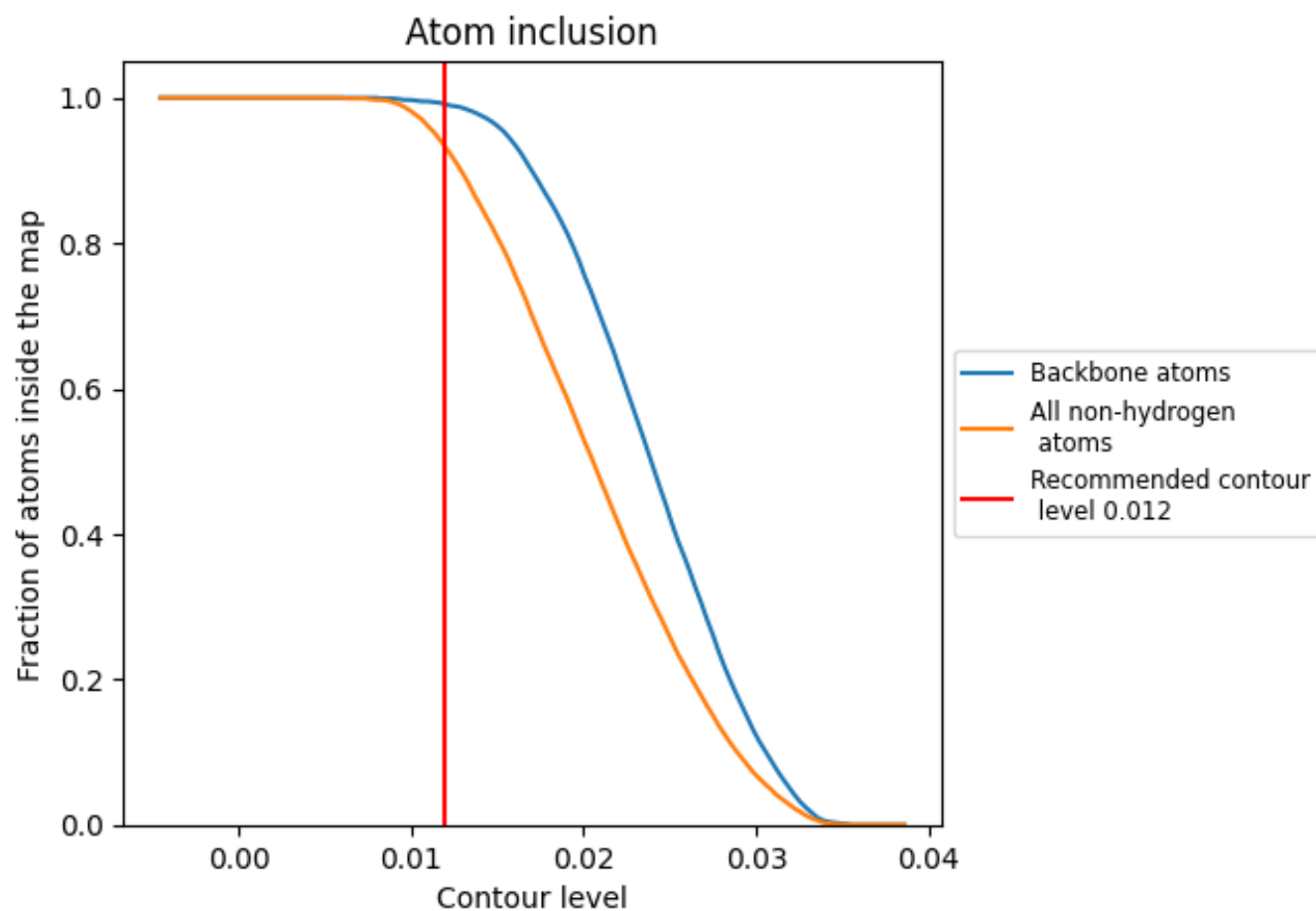
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.012).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 99% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9320	 0.4320
AA	 0.9300	 0.4360
AB	 0.9310	 0.4380
AC	 0.9290	 0.4380
AD	 0.9260	 0.4340
AE	 0.9320	 0.4380
AF	 0.9320	 0.4370
AG	 0.9320	 0.4390
AH	 0.9320	 0.4350
AI	 0.9300	 0.4360
AJ	 0.9340	 0.4360
AK	 0.9260	 0.4360
AL	 0.9300	 0.4330
AM	 0.9290	 0.4370
AN	 0.9300	 0.4350
AO	 0.9220	 0.4360
AP	 0.9420	 0.4380
AQ	 0.9270	 0.4370
AR	 0.9300	 0.4370
AS	 0.9340	 0.4370
AT	 0.9360	 0.4380
AU	 0.9330	 0.4390
AV	 0.9340	 0.4370
AW	 0.9290	 0.4300
AX	 0.9240	 0.4380
AY	 0.9310	 0.4370
AZ	 0.9330	 0.4340
BA	 0.9250	 0.4340
BB	 0.9410	 0.4380
BC	 0.9290	 0.4370
BD	 0.9420	 0.4360
BE	 0.9260	 0.4340
BF	 0.9380	 0.4340
BG	 0.9340	 0.4390
BH	 0.9410	 0.4400




















































































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Chain	Atom inclusion	Q-score
BI	 0.9300	 0.4390
BJ	 0.9320	 0.4380
BK	 0.9320	 0.4340
BL	 0.9300	 0.4420
BM	 0.9300	 0.4370
BN	 0.9320	 0.4390
BO	 0.9320	 0.4370
BP	 0.9380	 0.4380
BQ	 0.9300	 0.4370
BR	 0.9240	 0.4400
BS	 0.9310	 0.4370
BT	 0.9340	 0.4360
BU	 0.9320	 0.4360
BV	 0.9330	 0.4350
BW	 0.9290	 0.4370
BX	 0.9310	 0.4380
BY	 0.9310	 0.4370
BZ	 0.9290	 0.4410
CA	 0.9240	 0.4320
CB	 0.9290	 0.4340
CC	 0.9330	 0.4370
CD	 0.9340	 0.4370
CE	 0.9310	 0.4410
CF	 0.9300	 0.4350
CG	 0.9220	 0.4390
CH	 0.9320	 0.4330
CI	 0.9310	 0.4320
CJ	 0.9300	 0.4390
CK	 0.9270	 0.4390
CL	 0.9240	 0.4330
CM	 0.9270	 0.4330
CN	 0.9410	 0.4340
CO	 0.9330	 0.4380
CP	 0.9250	 0.4340
CQ	 0.9330	 0.4360
CR	 0.9440	 0.4360
CS	 0.9320	 0.4380
CT	 0.9330	 0.4380
CU	 0.9270	 0.4350
CV	 0.9240	 0.4370
CW	 0.9300	 0.4370
CX	 0.9320	 0.4330





















































































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Chain	Atom inclusion	Q-score
CY	 0.9320	 0.4380
CZ	 0.9330	 0.4360
DA	 0.9290	 0.4350
DB	 0.9340	 0.4380
DC	 0.9250	 0.4410
DE	 0.9320	 0.4340
DF	 0.9300	 0.4380
DG	 0.9430	 0.4360
DH	 0.9330	 0.4360
DI	 0.9330	 0.4350
DJ	 0.9270	 0.4340
DK	 0.9360	 0.4410
DL	 0.9320	 0.4380
DM	 0.9300	 0.4340
DN	 0.9270	 0.4380
DO	 0.9310	 0.4360
DP	 0.9210	 0.4370
DQ	 0.9410	 0.4380
DR	 0.9350	 0.4380
DS	 0.9420	 0.4390
DT	 0.9240	 0.4350
DU	 0.9290	 0.4300
DV	 0.9300	 0.4350
DW	 0.9310	 0.4370
DX	 0.9230	 0.4360
DY	 0.9420	 0.4370
DZ	 0.9330	 0.4380
EA	 0.9390	 0.4390
EB	 0.9340	 0.4340
EC	 0.9320	 0.4390
ED	 0.9310	 0.4360
EE	 0.9310	 0.4360
EF	 0.9270	 0.4330
EG	 0.9250	 0.4360
EH	 0.9310	 0.4360
EI	 0.9370	 0.4360
EJ	 0.9310	 0.4390
EK	 0.9270	 0.4340
EL	 0.9320	 0.4370
EM	 0.9370	 0.4420
EN	 0.9330	 0.4390
EO	 0.9380	 0.4370





















































































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Chain	Atom inclusion	Q-score
EP	 0.9240	 0.4380
EQ	 0.9330	 0.4310
ER	 0.9340	 0.4240
ES	 0.9350	 0.4300
ET	 0.9290	 0.4260
EU	 0.9310	 0.4280
EV	 0.9250	 0.4230
EW	 0.9400	 0.4290
EX	 0.9400	 0.4230
EY	 0.9340	 0.4320
EZ	 0.9300	 0.4230
FA	 0.9350	 0.4270
FB	 0.9240	 0.4260
FC	 0.9380	 0.4340
FD	 0.9350	 0.4250
FE	 0.9340	 0.4330
FF	 0.9230	 0.4210
FG	 0.9340	 0.4300
FH	 0.9240	 0.4160
FI	 0.9340	 0.4350
FJ	 0.9290	 0.4240
FK	 0.9320	 0.4380
FL	 0.9310	 0.4220
FM	 0.9380	 0.4330
FN	 0.9270	 0.4220
FO	 0.9360	 0.4370
FP	 0.9300	 0.4210
FQ	 0.9370	 0.4360
FR	 0.9380	 0.4230
FS	 0.9350	 0.4320
FT	 0.9360	 0.4230
FU	 0.9350	 0.4330
FV	 0.9360	 0.4270
FW	 0.9360	 0.4250
FX	 0.9370	 0.4250
FY	 0.9370	 0.4360
FZ	 0.9300	 0.4230
GA	 0.9320	 0.4290
GB	 0.9380	 0.4250
GC	 0.9330	 0.4320
GD	 0.9360	 0.4260
GE	 0.9310	 0.4310













































































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Chain	Atom inclusion	Q-score
GF	 0.9340	 0.4260
GG	 0.9390	 0.4360
GH	 0.9250	 0.4230
GI	 0.9350	 0.4340
GK	 0.9270	 0.4250
GL	 0.9240	 0.4310
GM	 0.9250	 0.4210
GN	 0.9340	 0.4360
GO	 0.9370	 0.4260
GP	 0.9380	 0.4330
GQ	 0.9170	 0.4160
GR	 0.9390	 0.4330
GS	 0.9230	 0.4250
GT	 0.9330	 0.4320
GU	 0.9230	 0.4270
GV	 0.9340	 0.4290
GW	 0.9340	 0.4240
GX	 0.9410	 0.4300
GY	 0.9310	 0.4230
GZ	 0.9330	 0.4300
HA	 0.9270	 0.4260
HB	 0.9370	 0.4340
HC	 0.9310	 0.4260
HD	 0.9290	 0.4260
HE	 0.9320	 0.4230
HF	 0.9330	 0.4350
HG	 0.9370	 0.4280
HI	 0.9340	 0.4270
HJ	 0.9320	 0.4240
HK	 0.9350	 0.4330
HL	 0.9300	 0.4260
HM	 0.9350	 0.4320
HN	 0.9330	 0.4300
HO	 0.9310	 0.4360
HP	 0.9300	 0.4250
HQ	 0.9320	 0.4310
HR	 0.9320	 0.4250
HS	 0.9360	 0.4340
HT	 0.9380	 0.4240
HU	 0.9340	 0.4350
HV	 0.9340	 0.4220
HW	 0.9400	 0.4350

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Chain	Atom inclusion	Q-score
HX	 0.9260	 0.4220
HY	 0.9370	 0.4330
HZ	 0.9310	 0.4210
IA	 0.9360	 0.4350
IB	 0.9290	 0.4290
IC	 0.9350	 0.4270
ID	 0.9230	 0.4190
IE	 0.9320	 0.4330
IF	 0.9360	 0.4260
IG	 0.9370	 0.4310
IH	 0.9330	 0.4240
II	 0.9370	 0.4250
IJ	 0.9360	 0.4290
IK	 0.9290	 0.4250
IL	 0.9390	 0.4220
IM	 0.9310	 0.4280
IN	 0.9320	 0.4240
IO	 0.9320	 0.4290
IP	 0.9210	 0.4230
IQ	 0.9380	 0.4290
IR	 0.9380	 0.4250
IS	 0.9320	 0.4360
IT	 0.9330	 0.4250
IU	 0.9400	 0.4320
IV	 0.9260	 0.4210
IW	 0.9370	 0.4370
IX	 0.9380	 0.4270
IZ	 0.9410	 0.4330
JA	 0.9190	 0.4170
JB	 0.9390	 0.4300
JC	 0.9300	 0.4220
JD	 0.9350	 0.4310
JE	 0.9290	 0.4280
JF	 0.9380	 0.4330
JG	 0.9180	 0.4180
JH	 0.9380	 0.4320
JI	 0.9270	 0.4180
JJ	 0.9380	 0.4330