



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:25 AM UTC

PDB ID : 6YFT / pdb_00006yft
Title : Virus-like particle of Wenzhou levi-like virus 1
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

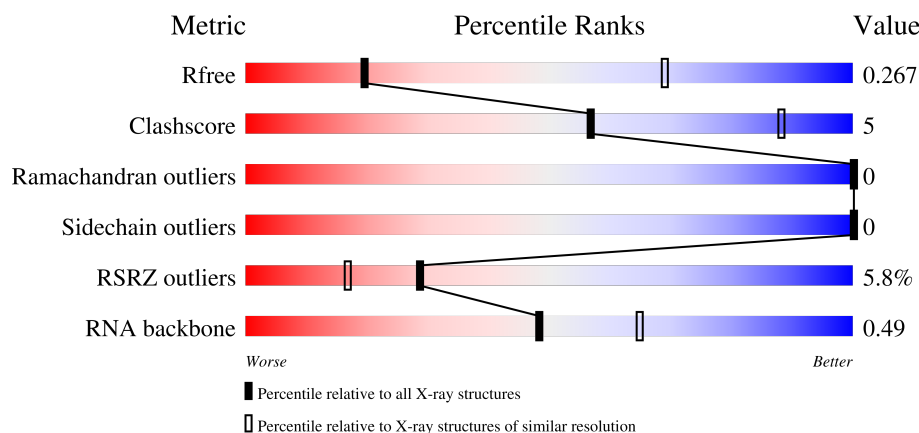
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)
RNA backbone	3983	1010 (3.98-3.02)

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

Mol	Chain	Length	Quality of chain
1	AA	113	6% 86% 14%
1	AB	113	2% 92% 8%
1	AC	113	4% 90% 10%
1	AD	113	5% 87% 13%

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Mol	Chain	Length	Quality of chain	
1	AE	113	5%	94% 6%
1	AF	113	4%	88% 12%
1	AG	113	3%	88% 12%
1	AH	113	5%	90% 10%
1	AI	113	13%	86% 14%
1	AJ	113	9%	88% 12%
1	AK	113	3%	94% 6%
1	AL	113	9%	84% 16%
1	AM	113	4%	88% 12%
1	AN	113	%	93% 7%
1	AO	113	4%	86% 14%
1	AP	113	11%	87% 13%
1	AQ	113	4%	92% 8%
1	AR	113	8%	86% 14%
1	AS	113	4%	86% 14%
1	AT	113	3%	90% 10%
1	AU	113	4%	88% 12%
1	AV	113	5%	88% 12%
1	AW	113	4%	91% 9%
1	AX	113	7%	88% 12%
1	AY	113	3%	88% 12%
1	AZ	113	5%	88% 12%
1	BA	113	7%	83% 17%
1	BB	113	7%	81% 19%
1	BC	113	4%	88% 12%

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Mol	Chain	Length	Quality of chain
1	BD	113	
1	BE	113	
1	BF	113	
1	BG	113	
1	BH	113	
1	BI	113	
1	BJ	113	
1	BK	113	
1	BL	113	
1	BM	113	
1	BN	113	
1	BO	113	
1	BP	113	
1	BQ	113	
1	BR	113	
1	BS	113	
1	BT	113	
1	BU	113	
1	BV	113	
1	BW	113	
1	BX	113	
1	BY	113	
1	BZ	113	
1	CA	113	
1	CB	113	

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Mol	Chain	Length	Quality of chain
1	CC	113	9% 86% 14%
1	CD	113	5% 94% 6%
1	CE	113	13% 88% 12%
1	CF	113	5% 88% 12%
1	CG	113	5% 93% 7%
1	CH	113	11% 87% 13%
1	CI	113	4% 88% 12%
1	CJ	113	5% 90% 10%
1	CK	113	4% 87% 13%
1	CL	113	5% 88% 12%
1	CM	113	4% 93% 7%
1	CN	113	10% 89% 11%
1	CO	113	4% 86% 14%
1	CP	113	12% 87% 13%
1	CQ	113	4% 87% 13%
1	CR	113	8% 89% 11%
1	CS	113	4% 90% 10%
1	CT	113	6% 86% 14%
1	CU	113	6% 87% 13%
1	CV	113	6% 90% 10%
1	CW	113	4% 88% 12%
1	CX	113	12% 81% 19%
1	CY	113	6% 90% 10%
1	CZ	113	12% 85% 15%
1	DA	113	4% 87% 13%

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Mol	Chain	Length	Quality of chain
1	DB	113	
1	DC	113	
1	DD	113	
1	DE	113	
1	DF	113	
1	DG	113	
1	DH	113	
1	DI	113	
1	DJ	113	
1	DK	113	
1	DL	113	
1	DM	113	
1	DN	113	
1	DO	113	
1	DP	113	
1	DQ	113	
1	DR	113	
1	DS	113	
1	DT	113	
1	DU	113	
1	DV	113	
1	DW	113	
1	DX	113	
1	DY	113	
1	DZ	113	

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Mol	Chain	Length	Quality of chain
1	EA	113	87% 13%
1	EB	113	8% 87% 13%
1	EC	113	9% 86% 14%
1	ED	113	5% 88% 12%
1	EE	113	9% 88% 12%
1	EF	113	92% 8%
1	EG	113	7% 89% 11%
1	EH	113	6% 87% 13%
1	EI	113	3% 90% 10%
1	EJ	113	6% 89% 11%
1	EK	113	7% 86% 14%
1	EL	113	10% 90% 10%
1	EM	113	8% 86% 14%
1	EN	113	4% 89% 11%
1	EO	113	7% 91% 9%
1	EP	113	10% 89% 11%
1	EQ	113	5% 86% 14%
1	ER	113	4% 89% 11%
1	ES	113	8% 85% 15%
1	ET	113	6% 88% 12%
1	EU	113	10% 90% 10%
1	EV	113	4% 89% 11%
1	EW	113	8% 86% 14%
1	EX	113	4% 88% 12%
1	EY	113	5% 88% 12%

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Mol	Chain	Length	Quality of chain
1	EZ	113	4% 88% 12%
1	FA	113	5% 91% 9%
1	FB	113	5% 88% 12%
1	FC	113	4% 88% 12%
1	FD	113	4% 93% 7%
1	FE	113	12% 87% 13%
1	FF	113	9% 88% 12%
1	FG	113	4% 93% 7%
1	FH	113	3% 86% 14%
1	FI	113	3% 87% 13%
1	FJ	113	4% 90% 10%
1	FK	113	4% 90% 10%
1	FL	113	5% 87% 13%
1	FM	113	2% 91% 9%
1	FN	113	% 89% 11%
1	FO	113	3% 90% 10%
1	FP	113	4% 89% 11%
1	FQ	113	5% 89% 11%
1	FR	113	6% 88% 12%
1	FS	113	6% 89% 11%
1	FT	113	5% 89% 11%
1	FU	113	5% 88% 12%
1	FV	113	3% 93% 7%
1	FW	113	4% 89% 11%
1	FX	113	4% 88% 12%

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Mol	Chain	Length	Quality of chain
1	FY	113	
1	FZ	113	
1	GA	113	
1	GB	113	
1	GC	113	
1	GD	113	
1	GE	113	
1	GF	113	
1	GG	113	
1	GH	113	
1	GI	113	
1	GJ	113	
1	GK	113	
1	GL	113	
1	GM	113	
1	GN	113	
1	GO	113	
1	GP	113	
1	GQ	113	
1	GR	113	
1	GS	113	
1	GT	113	
1	GU	113	
1	GV	113	
1	GW	113	

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Mol	Chain	Length	Quality of chain
1	GX	113	8% 82% 18%
1	GY	113	10% 88% 12%
1	GZ	113	4% 91% 9%
1	HA	113	7% 82% 18%
1	HB	113	4% 88% 12%
1	HC	113	7% 91% 9%
1	HD	113	4% 88% 12%
1	HE	113	8% 83% 17%
1	HF	113	2% 91% 9%
1	HG	113	5% 90% 10%
1	HH	113	9% 86% 14%
1	HI	113	10% 86% 14%
1	HJ	113	11% 88% 12%
1	HK	113	4% 88% 12%
1	HL	113	2% 91% 9%
1	HM	113	8% 83% 17%
1	HN	113	0% 88% 12%
1	HO	113	6% 89% 11%
1	HP	113	4% 87% 13%
1	HQ	113	2% 89% 11%
1	HR	113	10% 91% 9%
1	HS	113	4% 88% 12%
1	HT	113	2% 88% 12%
1	HU	113	2% 92% 8%
1	HV	113	4% 88% 12%

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Mol	Chain	Length	Quality of chain
1	HW	113	7% 88% 12%
1	HX	113	8% 91% 9%
1	HY	113	4% 88% 12%
1	HZ	113	7% 88% 12%
1	IA	113	7% 93% 7%
1	IB	113	7% 85% 15%
1	IC	113	16% 82% 18%
1	ID	113	5% 84% 16%
1	IE	113	7% 85% 15%
1	IF	113	5% 89% 11%
1	IG	113	4% 91% 9%
1	IH	113	6% 86% 14%
1	II	113	4% 86% 14%
1	IJ	113	6% 87% 13%
1	IK	113	4% 87% 13%
1	IL	113	6% 88% 12%
1	IM	113	3% 93% 7%
1	IN	113	15% 87% 13%
1	IO	113	5% 88% 12%
1	IP	113	4% 91% 9%
1	IQ	113	6% 85% 15%
1	IR	113	4% 86% 14%
1	IS	113	% 90% 10%
1	IT	113	5% 86% 14%
1	IU	113	7% 88% 12%

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Mol	Chain	Length	Quality of chain
1	IV	113	6% 90% 10%
1	IW	113	4% 88% 12%
1	IX	113	5% 87% 13%
1	IY	113	5% 89% 11%
1	IZ	113	5% 87% 13%
1	JA	113	10% 87% 13%
1	JB	113	4% 93% 7%
1	JC	113	3% 86% 14%
1	JD	113	5% 88% 12%
1	JE	113	3% 87% 13%
1	JF	113	14% 87% 13%
1	JG	113	4% 88% 12%
1	JH	113	4% 90% 10%
1	JI	113	5% 85% 15%
1	JJ	113	4% 84% 16%
1	JK	113	6% 90% 10%
1	JL	113	7% 88% 12%
1	JM	113	4% 87% 13%
1	JN	113	% 88% 12%
1	JO	113	4% 86% 14%
1	JP	113	4% 88% 12%
1	JQ	113	3% 91% 9%
1	JR	113	6% 88% 12%
1	JS	113	4% 87% 13%
1	JT	113	4% 91% 9%

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Mol	Chain	Length	Quality of chain
1	JU	113	4% 88% 12%
1	JV	113	4% 88% 12%
1	JW	113	4% 93% 7%
1	JX	113	10% 88% 12%
1	JY	113	5% 88% 12%
1	JZ	113	4% 93% 7%
1	KA	113	4% 88% 12%
1	KB	113	5% 88% 12%
1	KC	113	4% 92% 8%
1	KD	113	7% 87% 13%
1	KE	113	4% 87% 13%
1	KF	113	5% 89% 11%
1	KG	113	8% 88% 12%
1	KH	113	4% 85% 15%
1	KI	113	8% 91% 9%
1	KJ	113	11% 86% 14%
1	KK	113	3% 87% 13%
1	KL	113	4% 92% 8%
1	KM	113	7% 81% 19%
1	KN	113	10% 87% 13%
1	KO	113	4% 92% 8%
1	KP	113	2% 89% 11%
1	KQ	113	4% 87% 13%
1	KR	113	2% 89% 11%
1	KS	113	4% 89% 11%

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Mol	Chain	Length	Quality of chain	
1	KT	113	6%	88% 12%
1	KU	113	3%	89% 11%
1	KV	113	11%	87% 13%
1	KW	113	9%	83% 17%
1	KX	113	10%	92% 8%
1	KY	113	4%	84% 16%
1	KZ	113	5%	88% 12%
1	LA	113	5%	93% 7%
1	LB	113	11%	87% 13%
1	LC	113	2%	85% 15%
1	LD	113	4%	92% 8%
1	LE	113	6%	88% 12%
1	LF	113	4%	86% 14%
1	LG	113	2%	92% 8%
1	LH	113	11%	88% 12%
1	LI	113	7%	88% 12%
1	LJ	113	0%	93% 7%
1	LK	113	5%	90% 10%
1	LL	113	4%	88% 12%
1	LM	113	2%	90% 10%
1	LN	113	4%	86% 14%
1	LO	113	8%	88% 12%
1	LP	113	6%	92% 8%
1	LQ	113	10%	84% 16%
1	LR	113	3%	85% 15%

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Mol	Chain	Length	Quality of chain
1	LS	113	
1	LT	113	
1	LU	113	
1	LV	113	
1	LW	113	
1	LX	113	
1	LY	113	
1	LZ	113	
1	MA	113	
1	MB	113	
1	MC	113	
1	MD	113	
1	ME	113	
1	MF	113	
1	MG	113	
1	MH	113	
1	MI	113	
1	MJ	113	
1	MK	113	
1	ML	113	
1	MM	113	
1	MN	113	
1	MO	113	
1	MP	113	
1	MQ	113	

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Mol	Chain	Length	Quality of chain
1	MR	113	6% 85% 15%
1	MS	113	4% 84% 16%
1	MT	113	4% 89% 11%
1	MU	113	4% 85% 15%
1	MV	113	5% 87% 13%
1	MW	113	4% 88% 12%
1	MX	113	8% 88% 12%
1	MY	113	7% 87% 13%
1	MZ	113	7% 92% 8%
1	NA	113	6% 85% 15%
1	NB	113	3% 88% 12%
1	NC	113	5% 92% 8%
1	ND	113	4% 89% 11%
1	NE	113	8% 88% 12%
1	NF	113	4% 93% 7%
1	NG	113	4% 88% 12%
1	NH	113	4% 88% 12%
1	NI	113	3% 89% 11%
1	NJ	113	7% 88% 12%
1	NK	113	6% 88% 12%
1	NL	113	5% 91% 9%
1	NM	113	12% 88% 12%
1	NN	113	4% 87% 13%
1	NO	113	4% 89% 11%
1	NP	113	4% 89% 11%

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Mol	Chain	Length	Quality of chain
1	NQ	113	4% 86% 14%
1	NR	113	% 91% 9%
1	NS	113	6% 89% 11%
1	NT	113	4% 85% 15%
1	NU	113	4% 88% 12%
1	NV	113	14% 85% 15%
2	RA	30	10% 47% 20% 33%
2	RB	30	7% 47% 20% 33%
2	RC	30	7% 57% 10% 33%
2	RD	30	7% 57% 10% 33%
2	RE	30	3% 57% 10% 33%
2	RF	30	10% 50% 17% 33%
2	RG	30	3% 50% 17% 33%
2	RH	30	57% 10% 33%
2	RI	30	7% 47% 20% 33%
2	RJ	30	7% 47% 20% 33%
2	RK	30	10% 47% 20% 33%
2	RL	30	7% 50% 17% 33%
2	RM	30	7% 57% 10% 33%
2	RN	30	7% 53% 13% 33%
2	RO	30	17% 47% 20% 33%
2	RP	30	3% 57% 10% 33%
2	RQ	30	3% 57% 10% 33%
2	RR	30	10% 53% 13% 33%
2	RS	30	10% 53% 13% 33%

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Mol	Chain	Length	Quality of chain
2	RT	30	
2	RU	30	
2	RV	30	
2	RW	30	
2	RX	30	
2	RY	30	
2	RZ	30	
2	SA	30	
2	SB	30	
2	SC	30	
2	SD	30	
2	SE	30	
2	SF	30	
2	SG	30	
2	SH	30	
2	SI	30	
2	SJ	30	
2	SK	30	
2	SL	30	
2	SM	30	
2	SN	30	
2	SO	30	
2	SP	30	
2	SQ	30	
2	SR	30	

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Mol	Chain	Length	Quality of chain
2	SS	30	
2	ST	30	
2	SU	30	
2	SV	30	
2	SW	30	
2	SX	30	
2	SY	30	
2	SZ	30	
2	TA	30	
2	TB	30	
2	TC	30	
2	TD	30	
2	TE	30	
2	TF	30	
2	TG	30	
2	TH	30	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 327240 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called coat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	AZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	BZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	CZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	DZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	ED	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	ER	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	ES	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	ET	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	EZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	FM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	FZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	GH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	GZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	HC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	HX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	HZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	ID	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	II	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	IS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	IZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	JN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	JZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	KI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	KZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	LD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	LY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	LZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MD	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	ME	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	ML	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	MT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MW	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MX	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MY	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	MZ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NA	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NB	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NC	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	ND	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NE	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NF	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NG	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NH	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NI	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NJ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NK	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NL	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NM	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NN	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	NO	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NP	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NQ	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NR	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NS	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NT	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NU	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			
1	NV	113	Total	C	N	O	S	0	0	0
			839	529	146	163	1			

- Molecule 2 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	RA	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RB	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RC	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RD	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RE	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RF	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RG	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RH	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RI	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RJ	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			
2	RK	20	Total	C	N	O	P	0	0	0
			420	190	70	140	20			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	RL	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RM	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RN	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RO	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RP	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RQ	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RR	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RS	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RT	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RU	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RV	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RW	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RX	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RY	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	RZ	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SA	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SB	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SC	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SD	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SE	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SF	20	Total 420	C 190	N 70	O 140	P 20	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	SG	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SH	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SI	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SJ	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SK	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SL	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SM	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SN	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SO	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SP	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SQ	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SR	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SS	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	ST	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SU	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SV	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SW	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SX	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SY	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	SZ	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	TA	20	Total 420	C 190	N 70	O 140	P 20	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	TB	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	TC	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	TD	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	TE	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	TF	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	TG	20	Total 420	C 190	N 70	O 140	P 20	0	0	0
2	TH	20	Total 420	C 190	N 70	O 140	P 20	0	0	0

3 Residue-property plots [i](#)

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

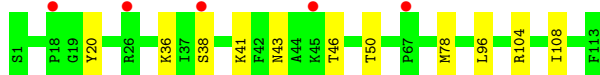
- Molecule 1: coat protein



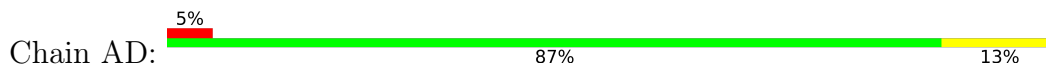
- Molecule 1: coat protein



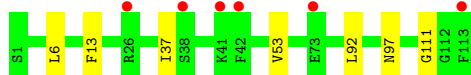
- Molecule 1: coat protein



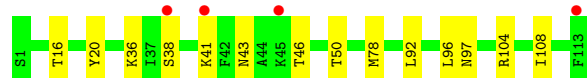
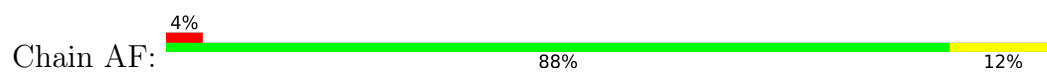
- Molecule 1: coat protein



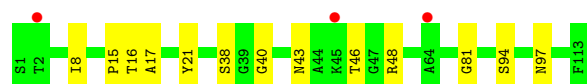
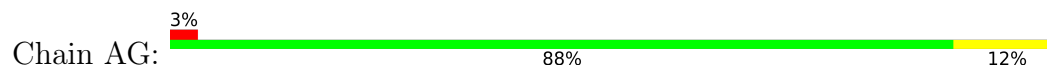
- Molecule 1: coat protein



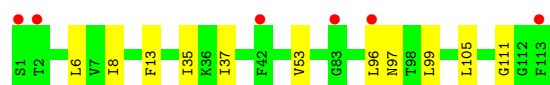
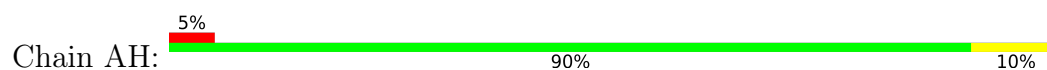
- Molecule 1: coat protein



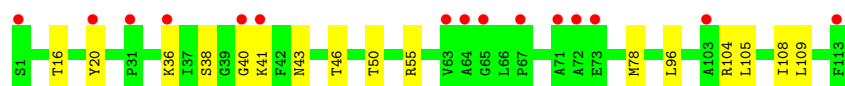
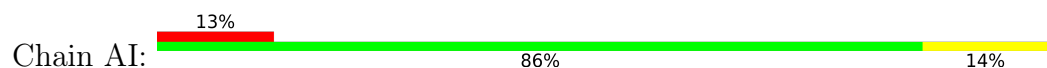
- Molecule 1: coat protein



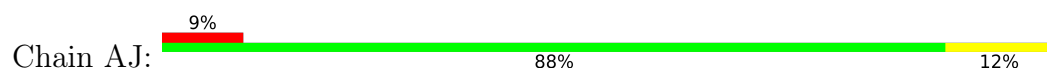
- Molecule 1: coat protein



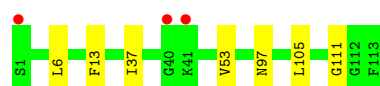
- Molecule 1: coat protein



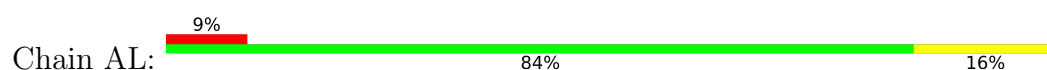
- Molecule 1: coat protein



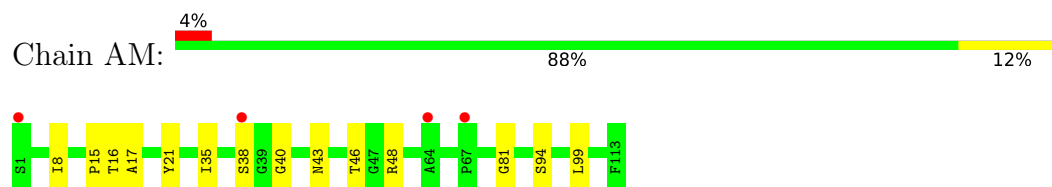
- Molecule 1: coat protein



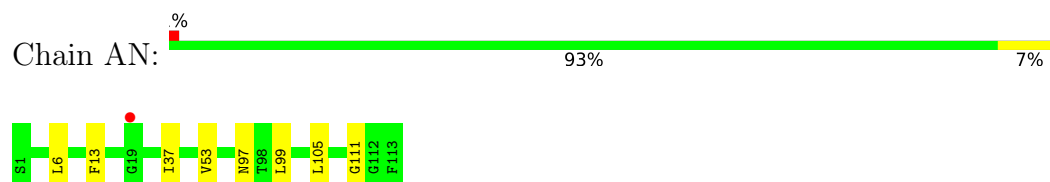
- Molecule 1: coat protein



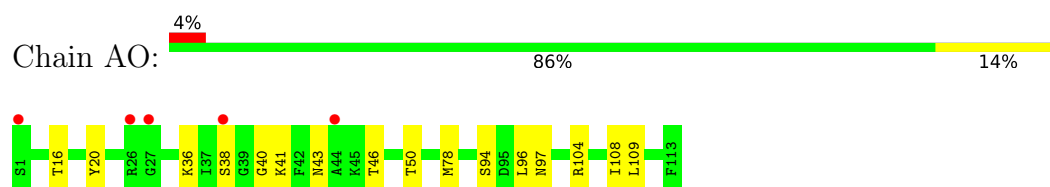
● Molecule 1: coat protein



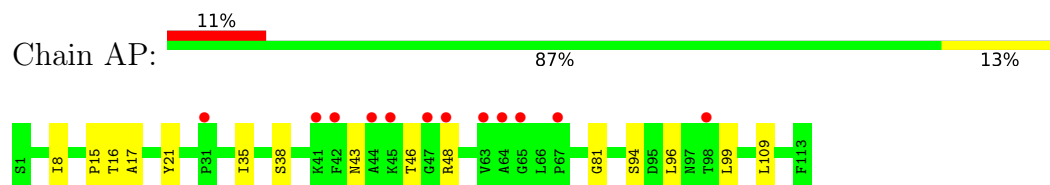
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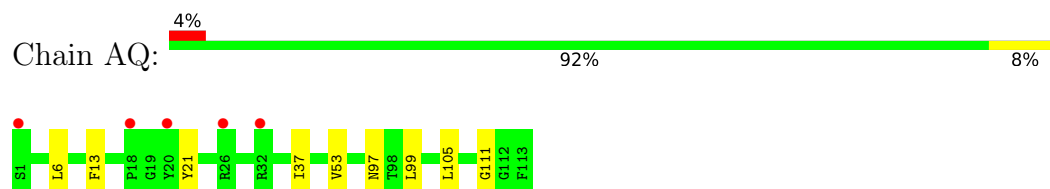
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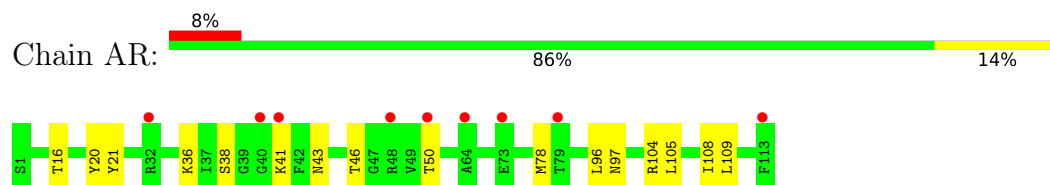
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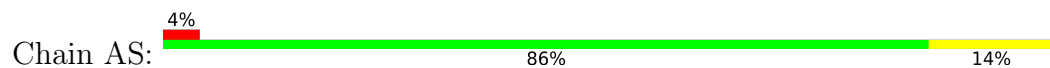
● Molecule 1: coat protein



● Molecule 1: coat protein



● Molecule 1: coat protein

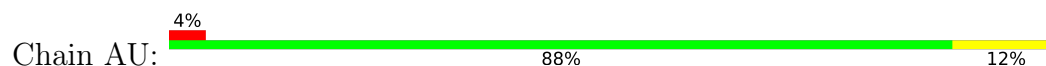




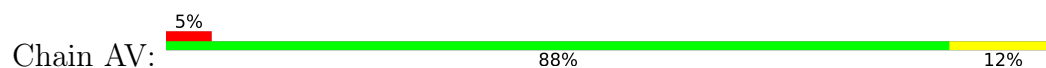
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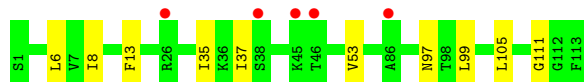
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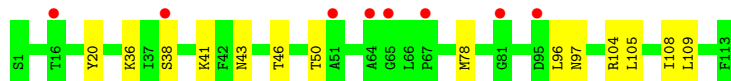
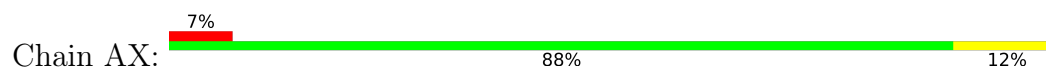
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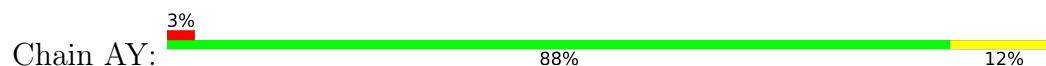
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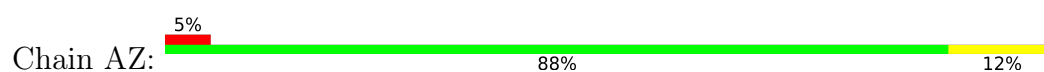
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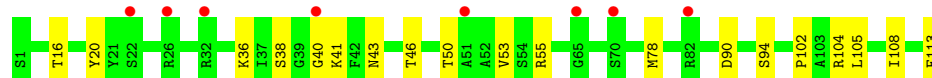
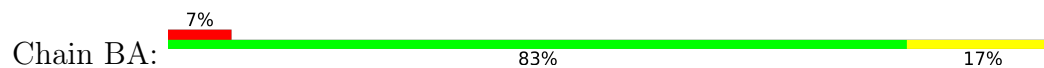
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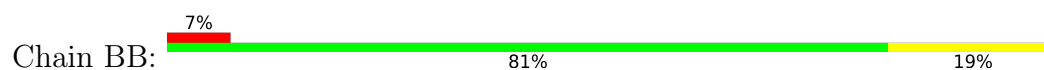
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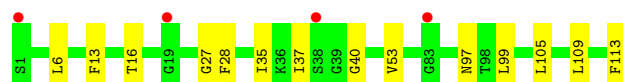
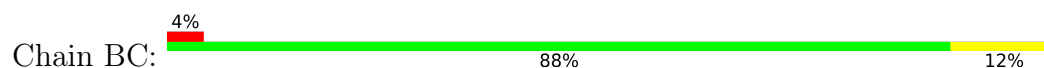
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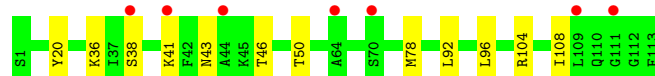
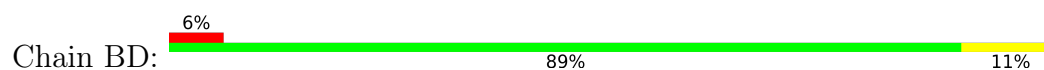
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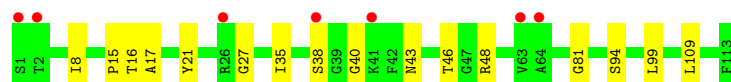
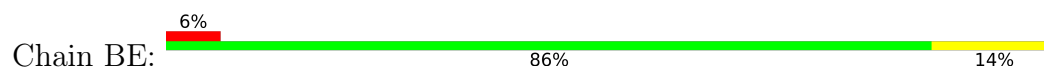
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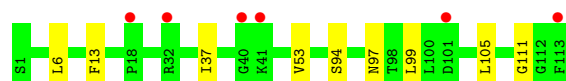
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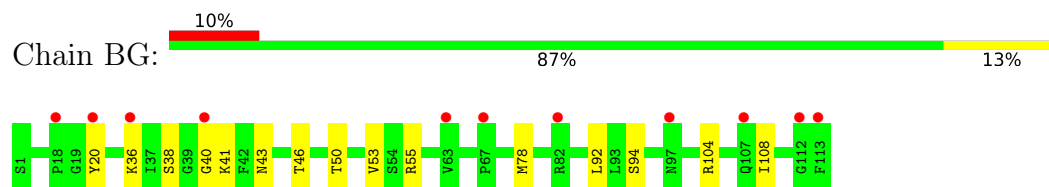
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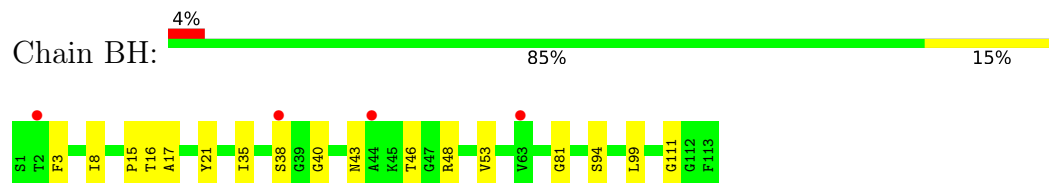
- Molecule 1: coat protein



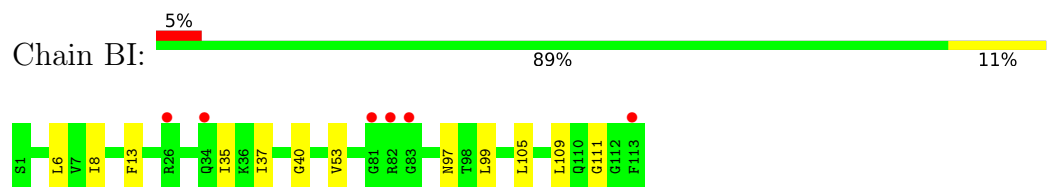
● Molecule 1: coat protein



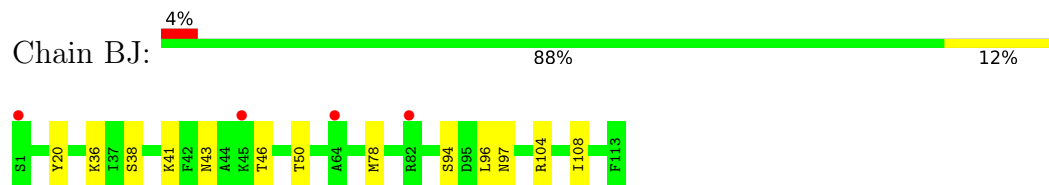
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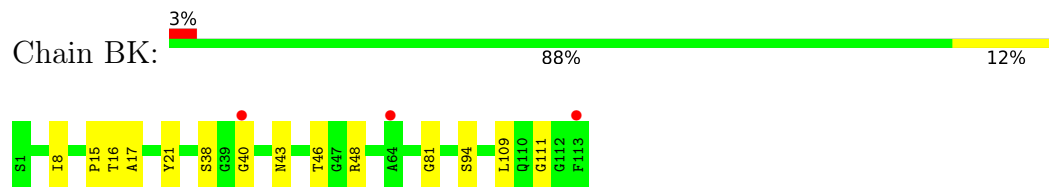
● Molecule 1: coat protein



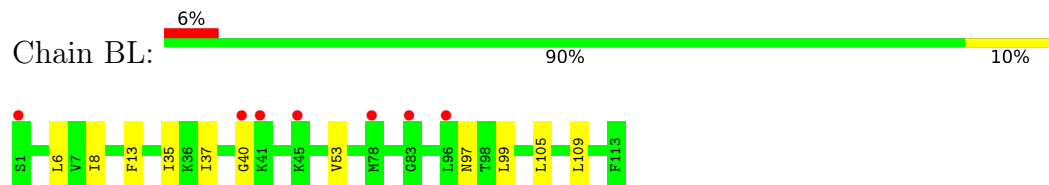
● Molecule 1: coat protein



● Molecule 1: coat protein

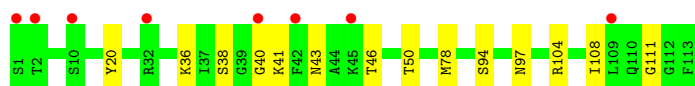


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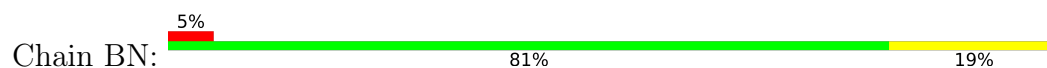


● Molecule 1: coat protein

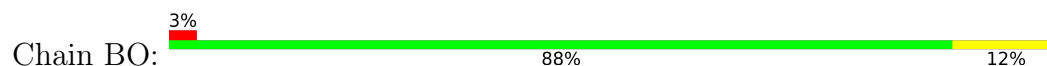




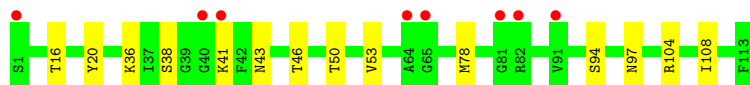
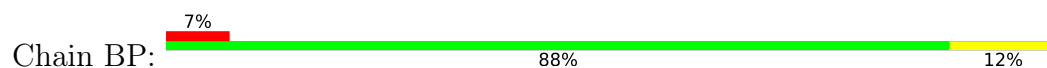
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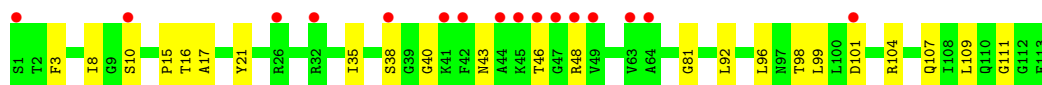
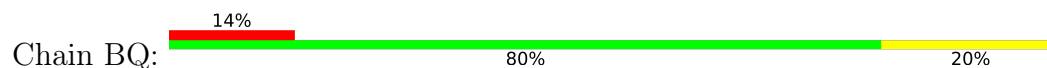
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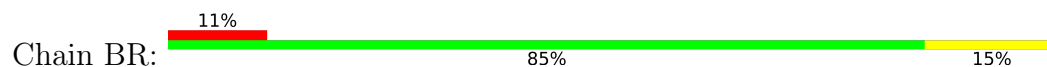
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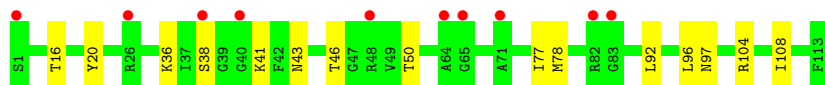
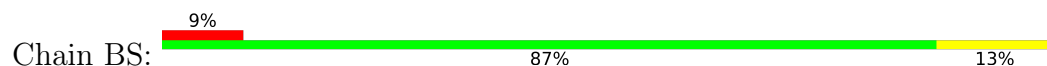
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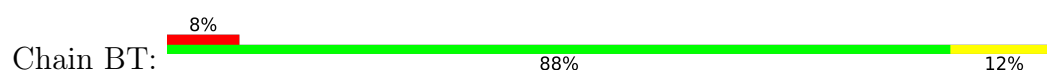
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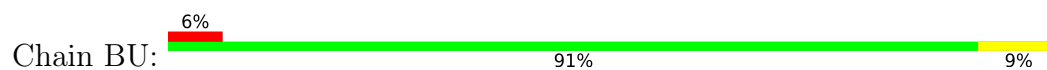
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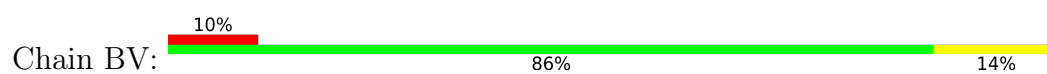
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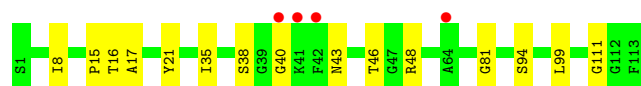
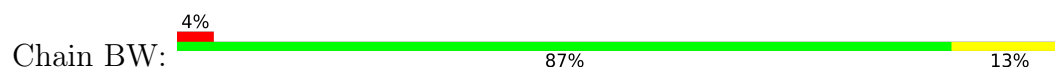
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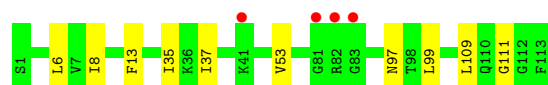
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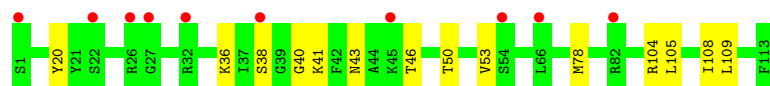
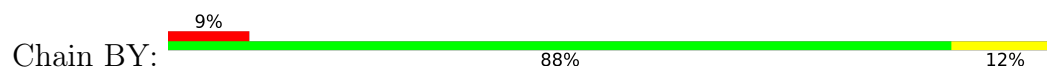
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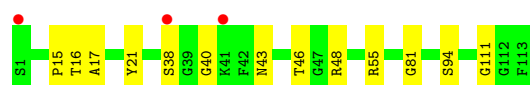
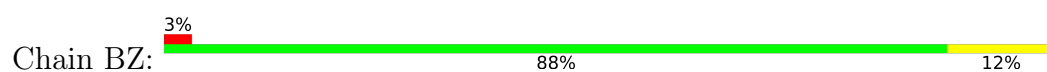
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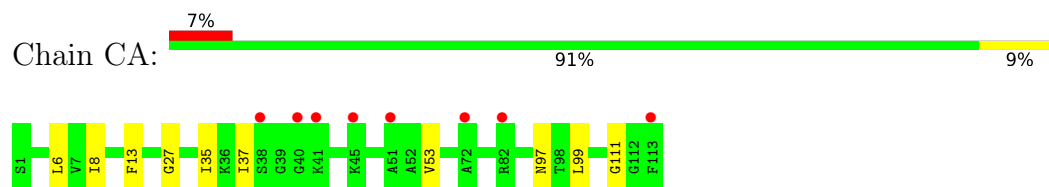
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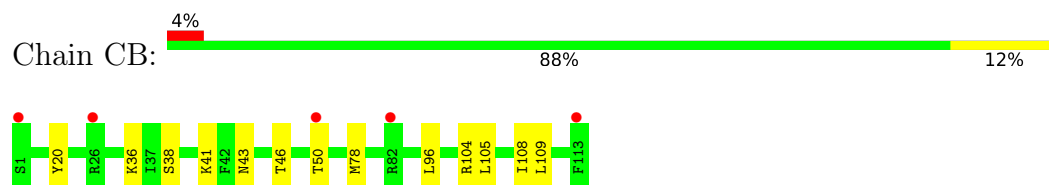
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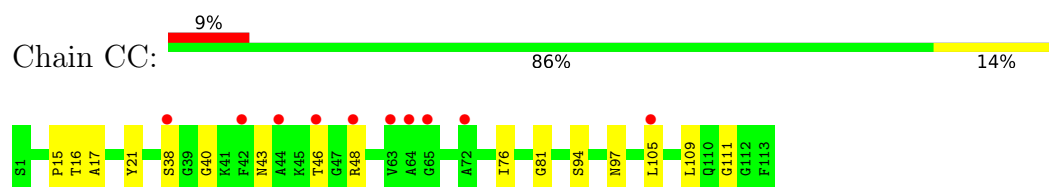
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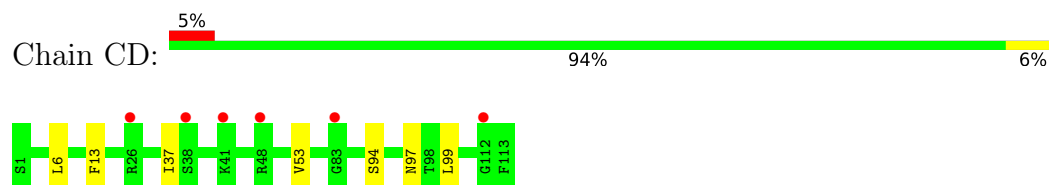
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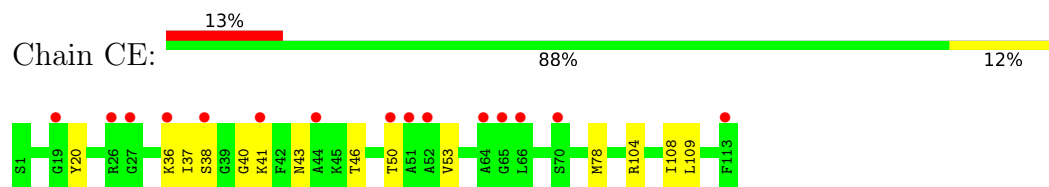
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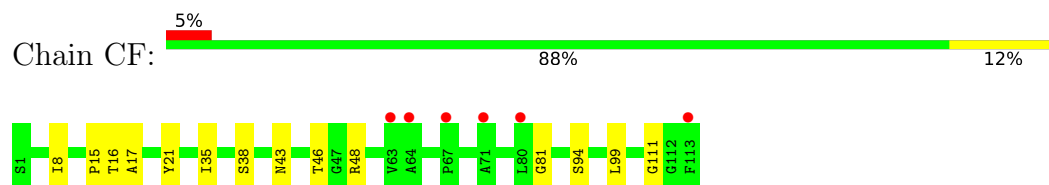
● Molecule 1: coat protein



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● Molecule 1: coat protein

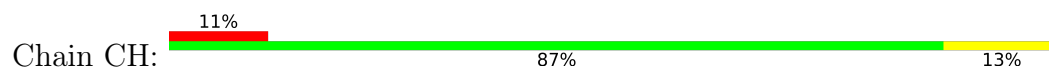


● Molecule 1: coat protein

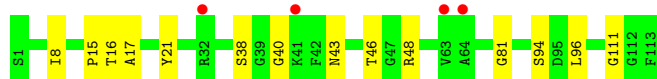
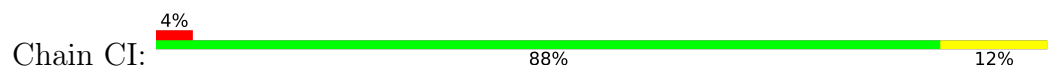




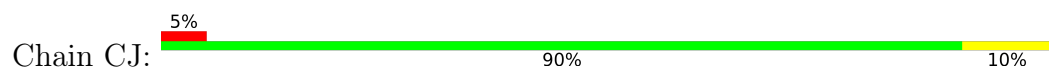
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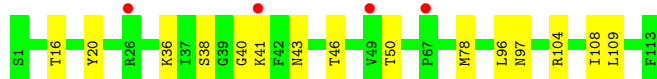
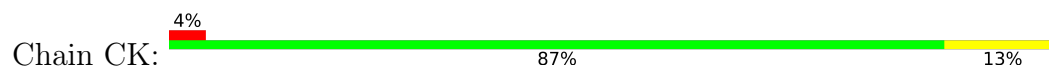
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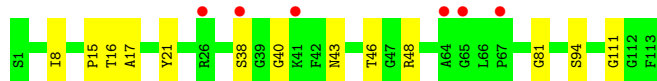
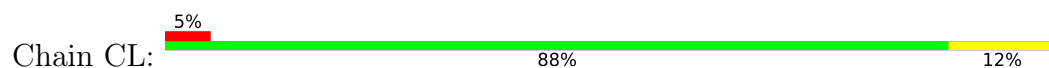
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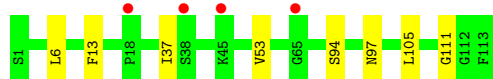
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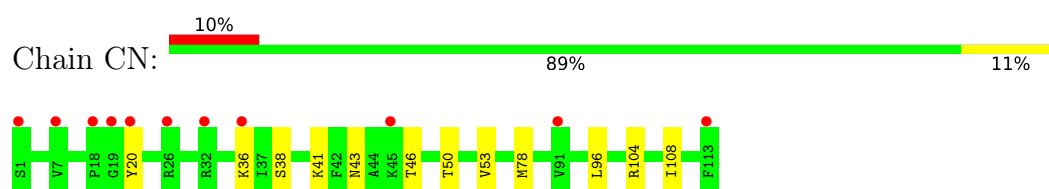
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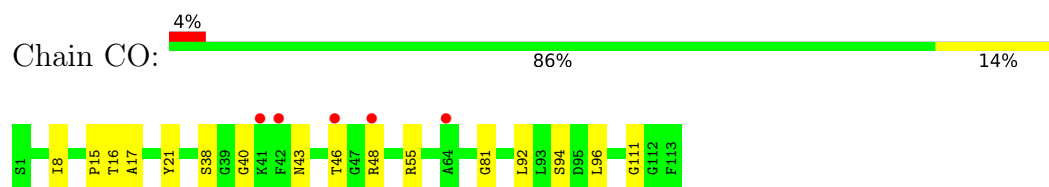
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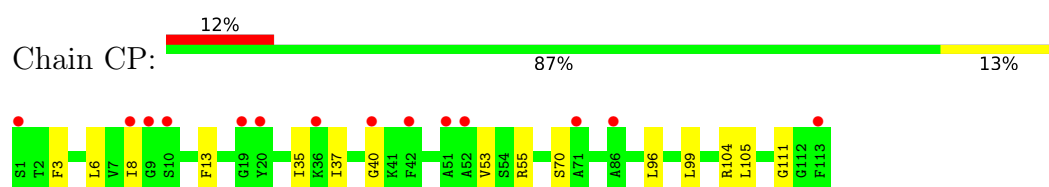
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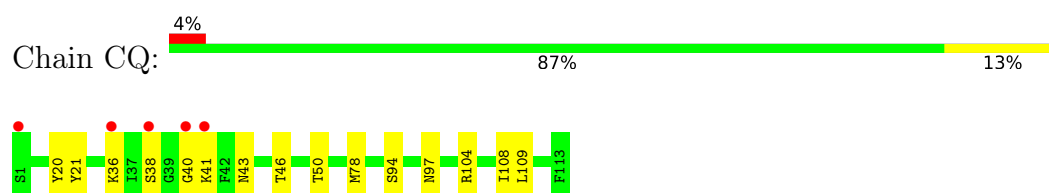
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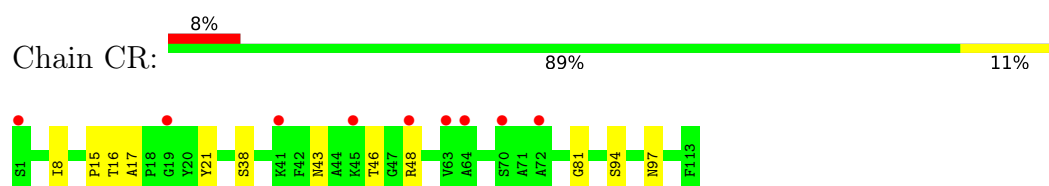
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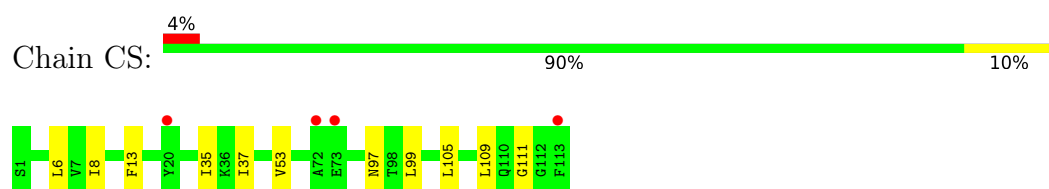
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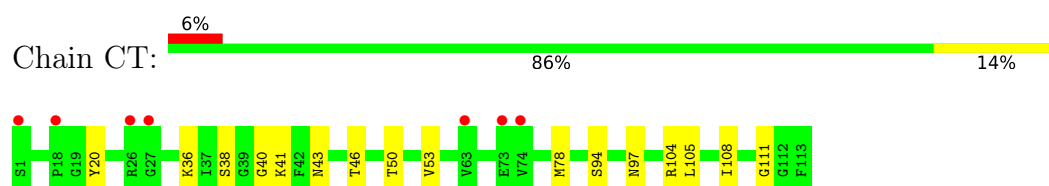
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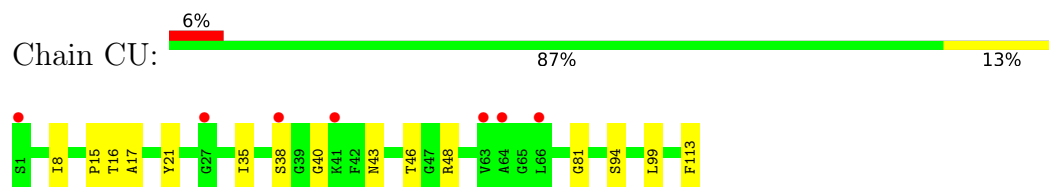
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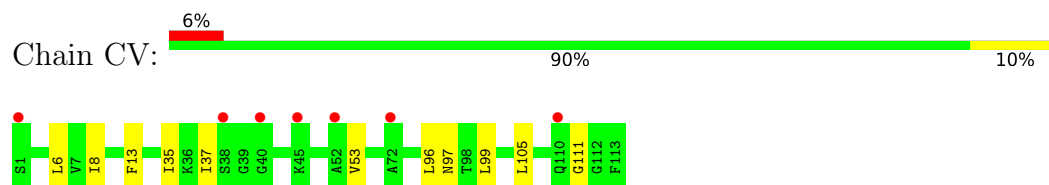
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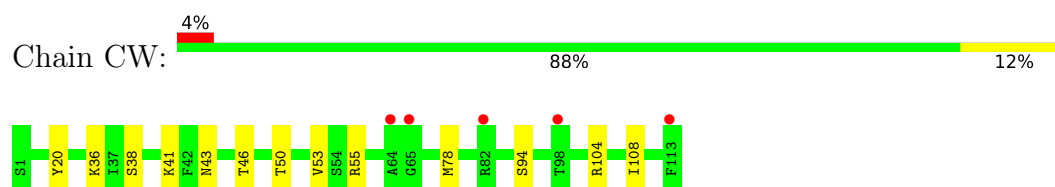
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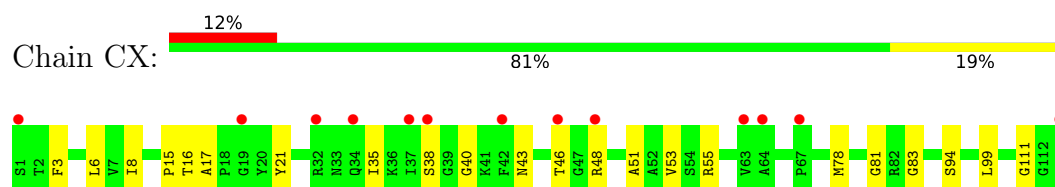
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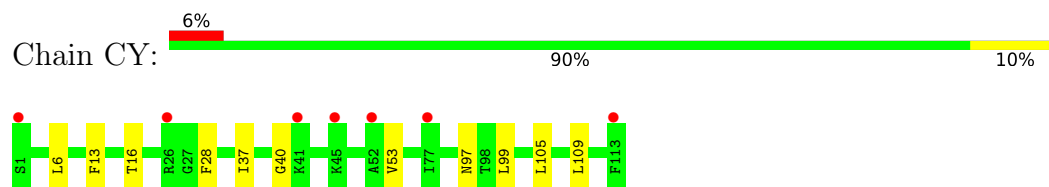
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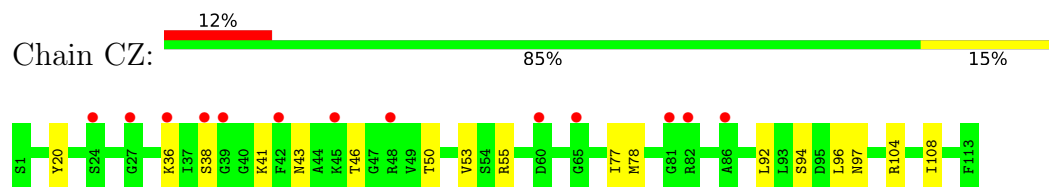
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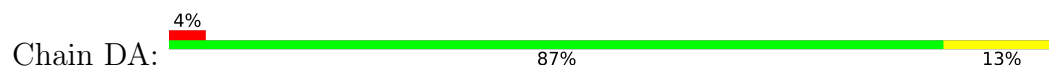
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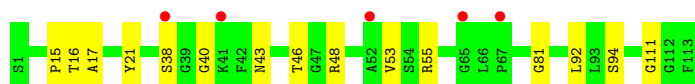


- Molecule 1: coat protein

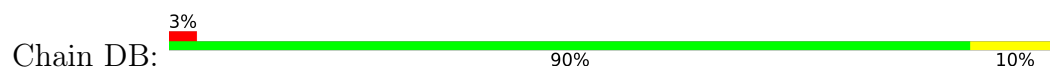


- Molecule 1: coat protein

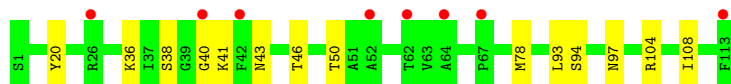
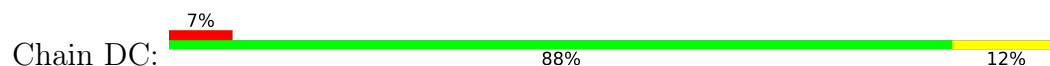




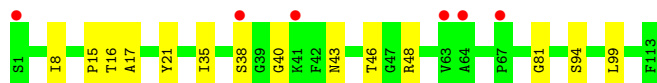
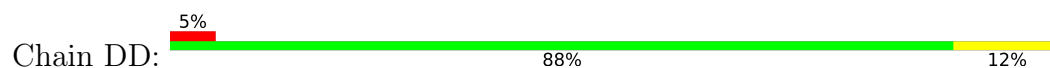
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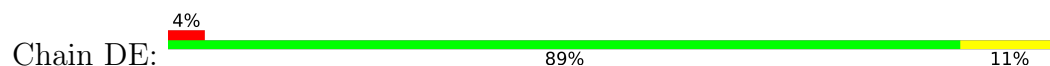
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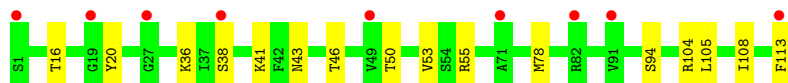
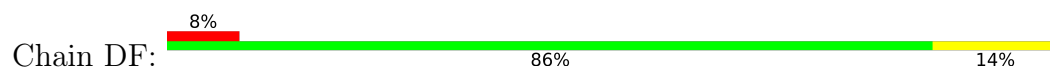
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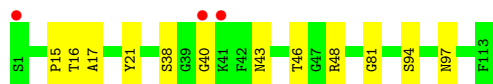
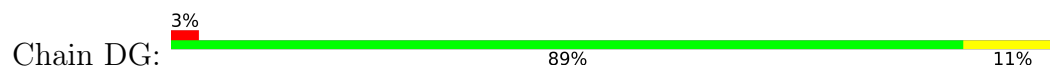
- Molecule 1: coat protein



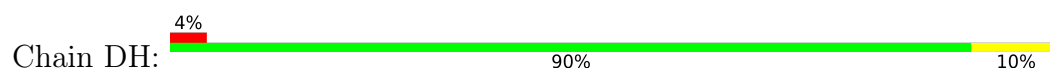
- Molecule 1: coat protein



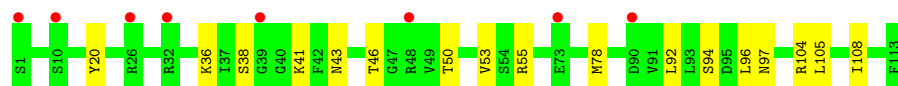
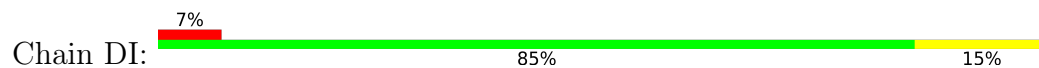
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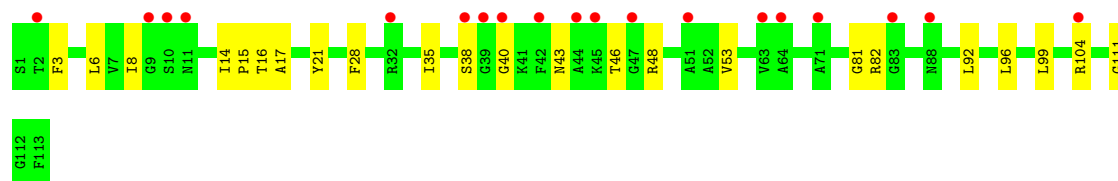
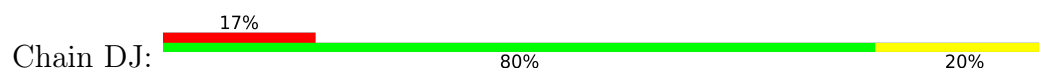
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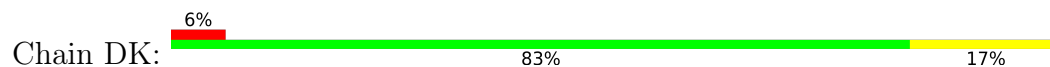
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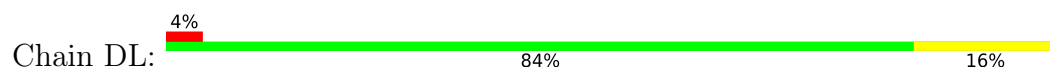
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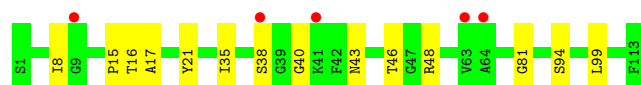
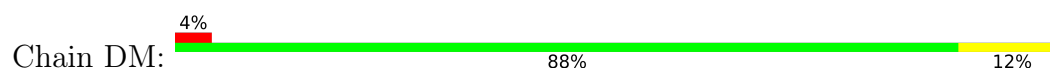
- Molecule 1: coat protein



- Molecule 1: coat protein

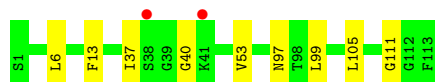


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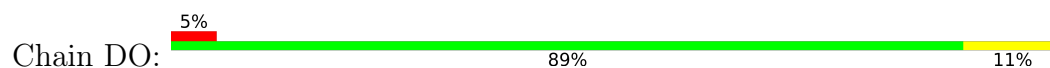


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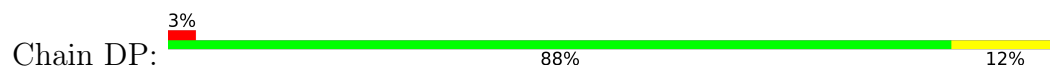




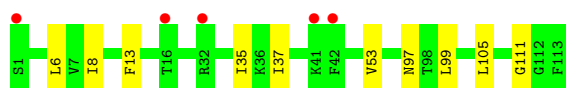
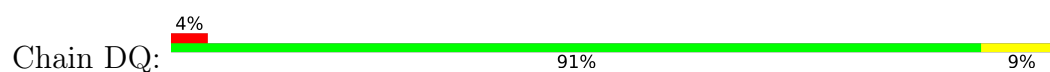
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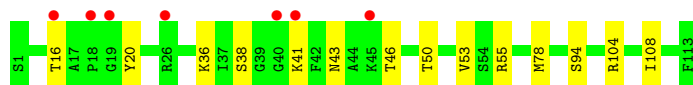
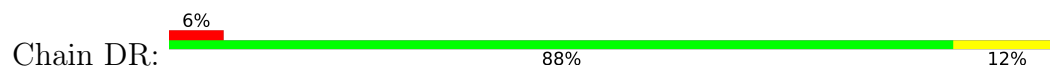
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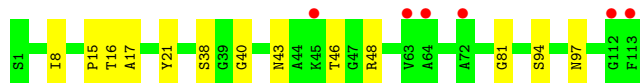
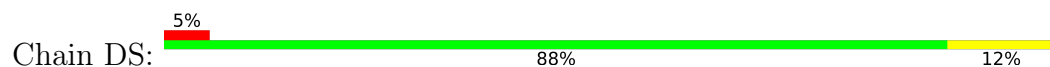
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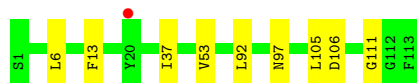
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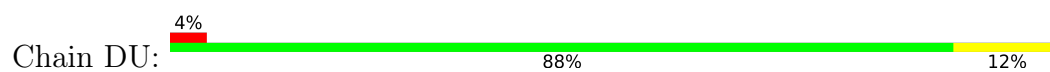
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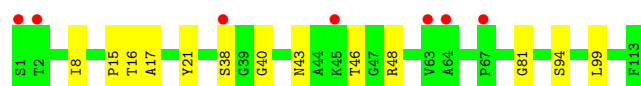
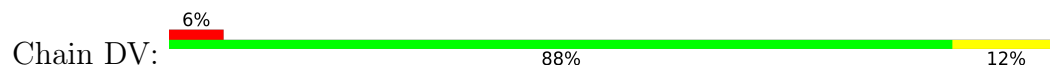
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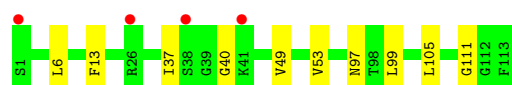
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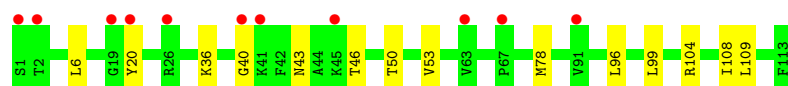
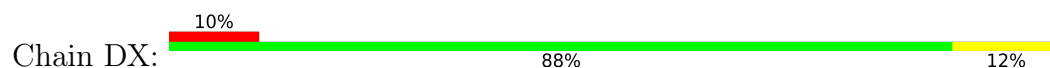
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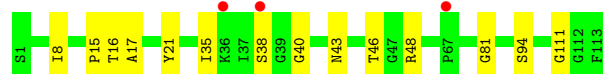
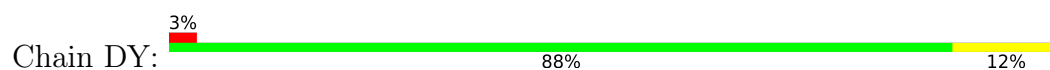
- Molecule 1: coat protein



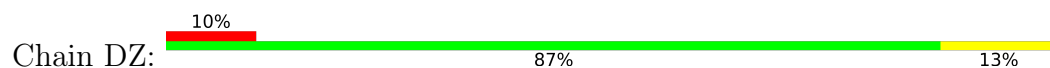
- Molecule 1: coat protein



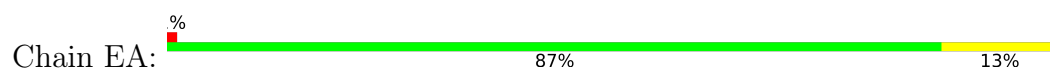
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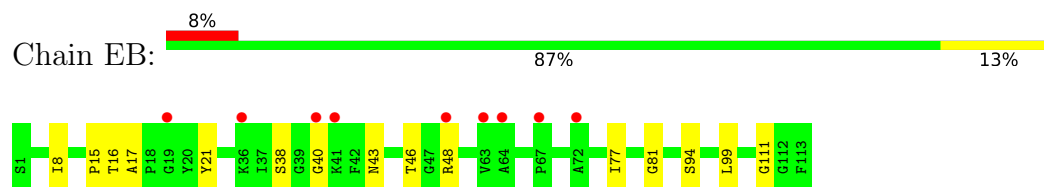
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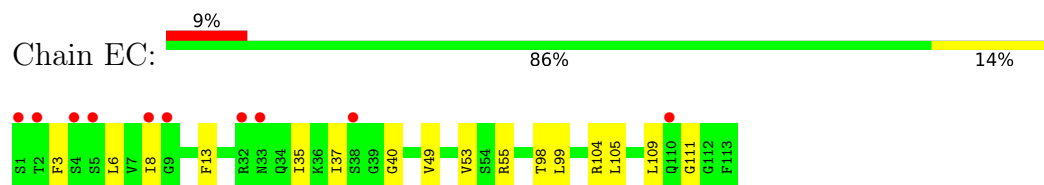
- Molecule 1: coat protein



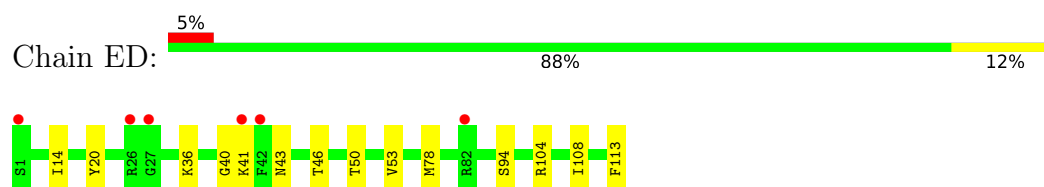
● Molecule 1: coat protein



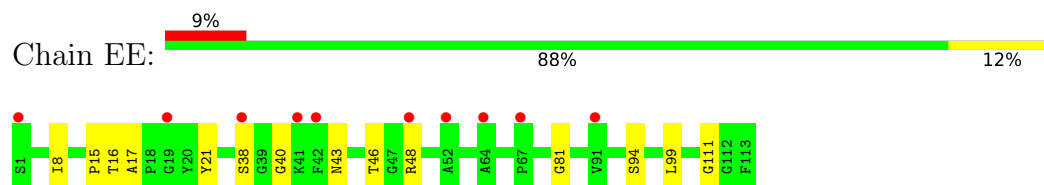
● Molecule 1: coat protein



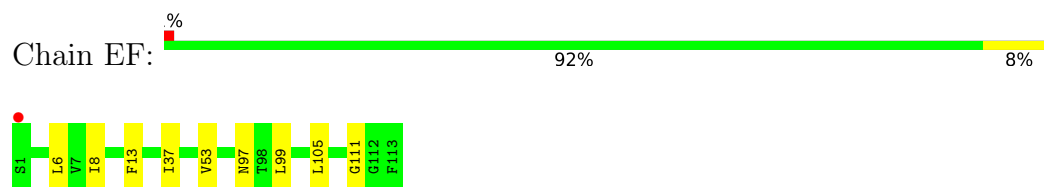
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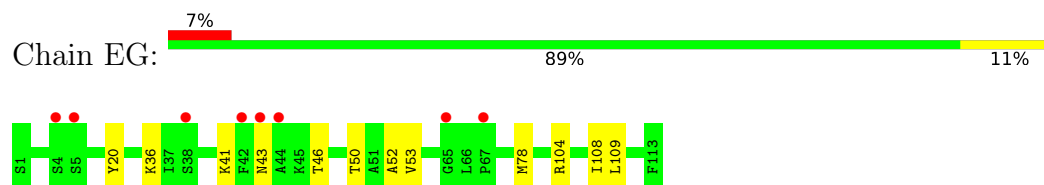
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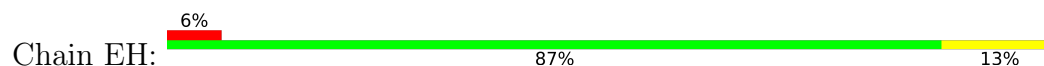
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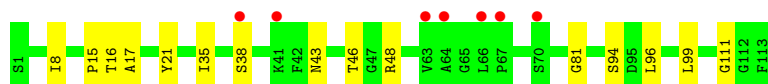


● Molecule 1: coat protein

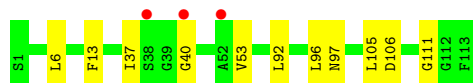
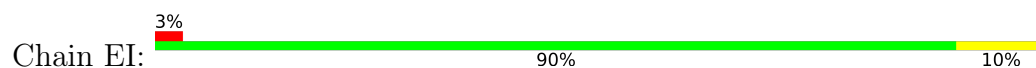


● Molecule 1: coat protein

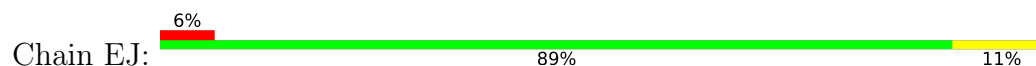




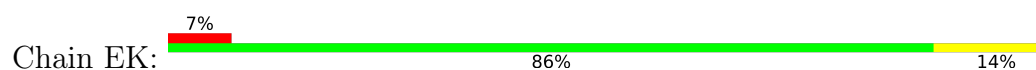
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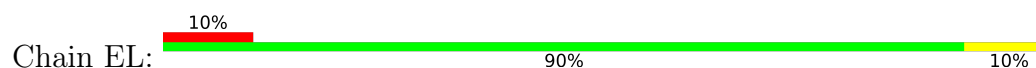
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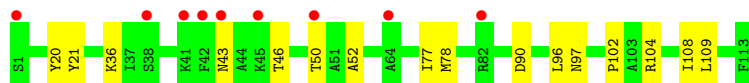
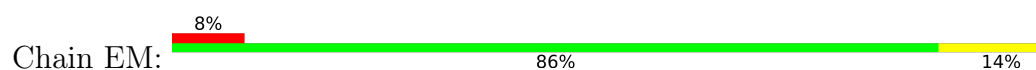
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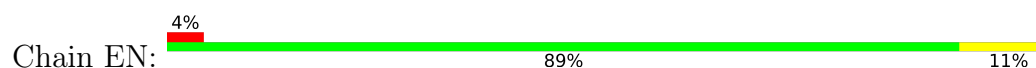
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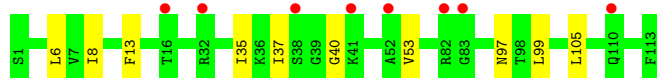
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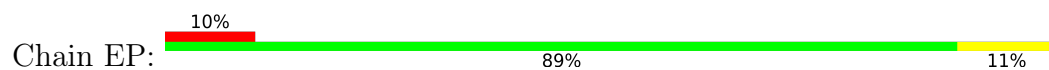
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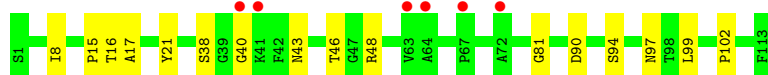
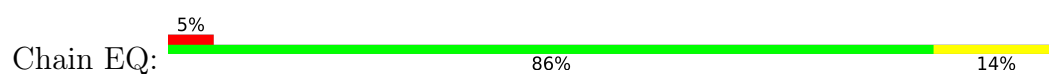
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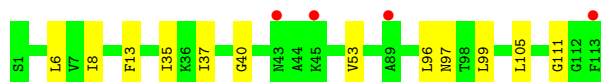
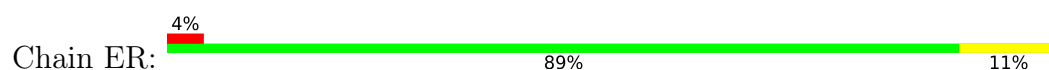
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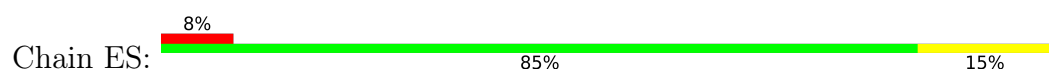
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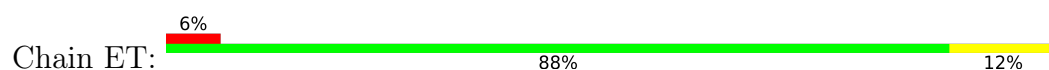
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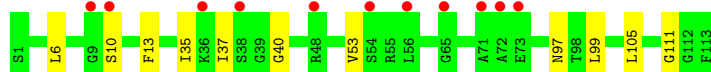
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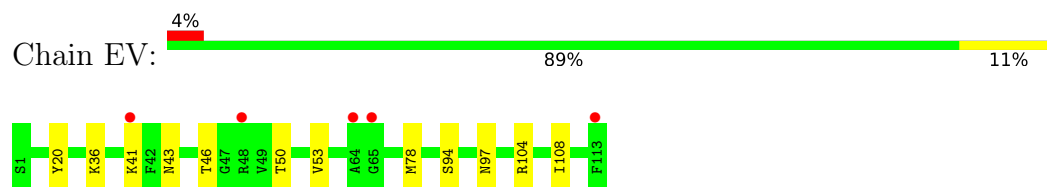
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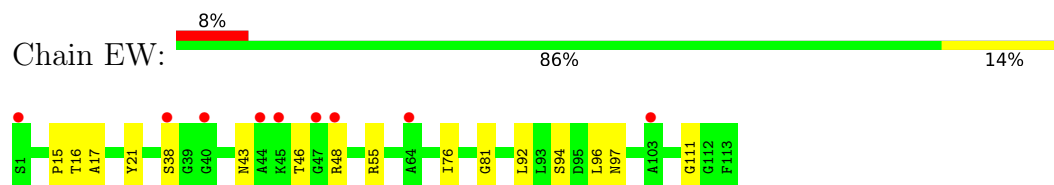
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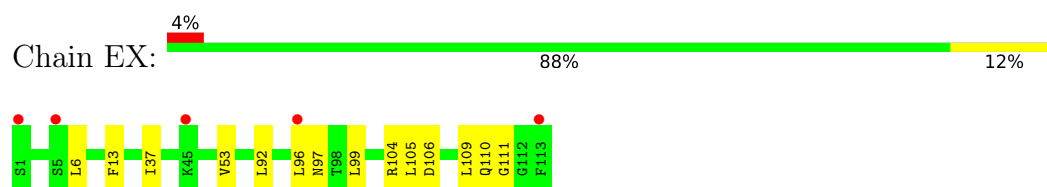
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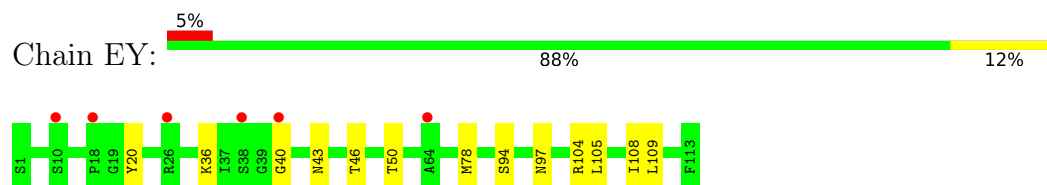
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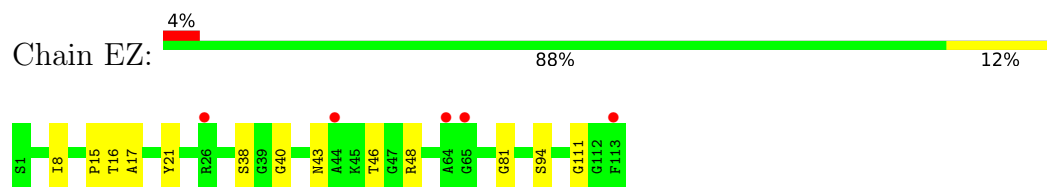
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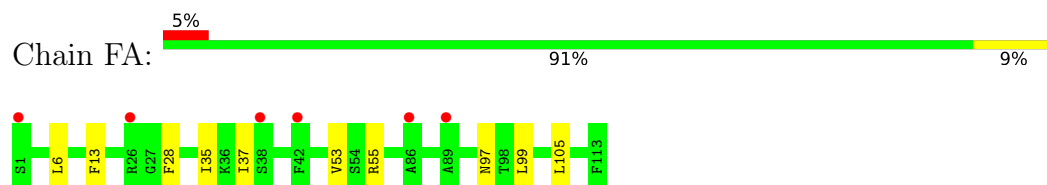
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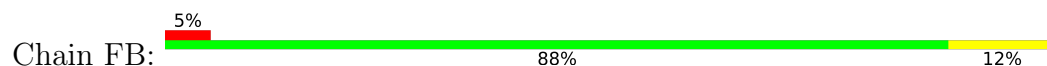
● Molecule 1: coat protein



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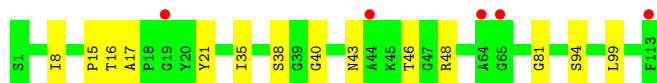
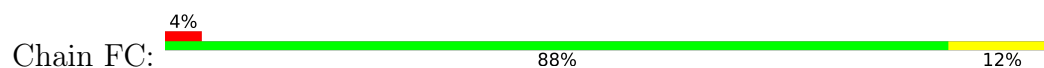


● Molecule 1: coat protein





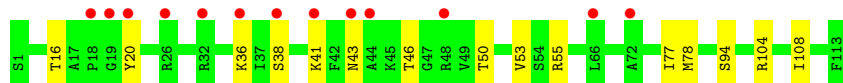
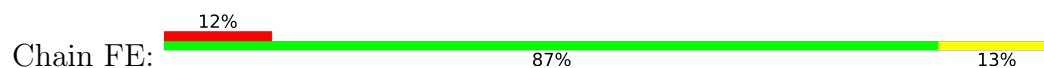
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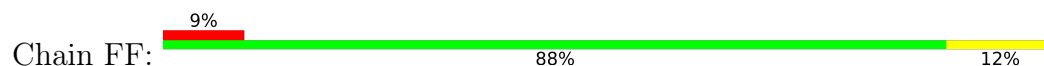
- Molecule 1: coat protein



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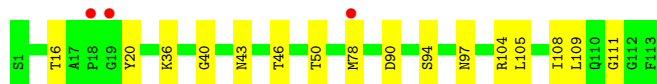
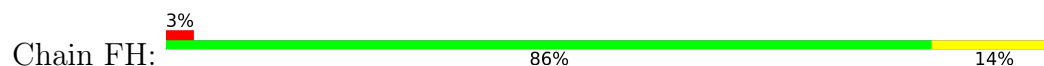
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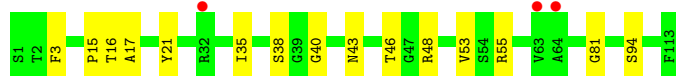
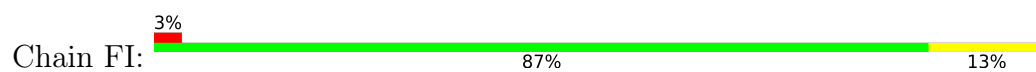
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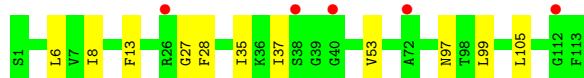
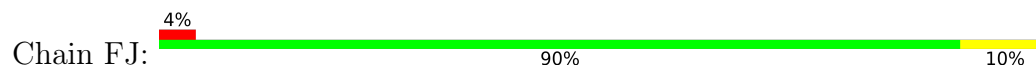
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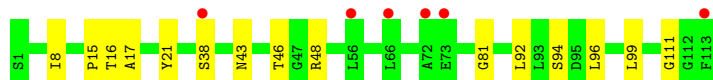
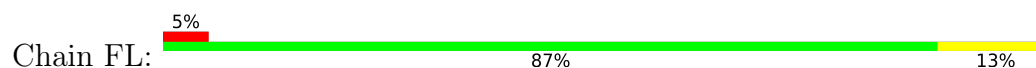
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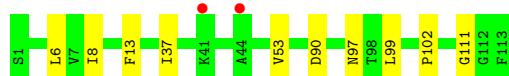
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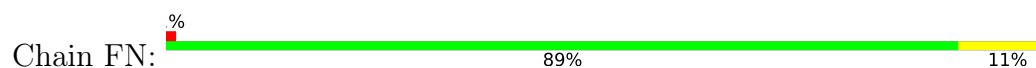
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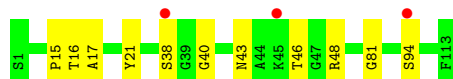
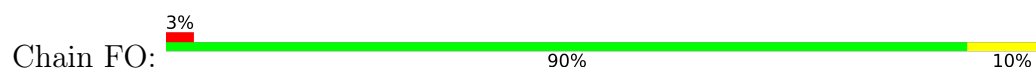
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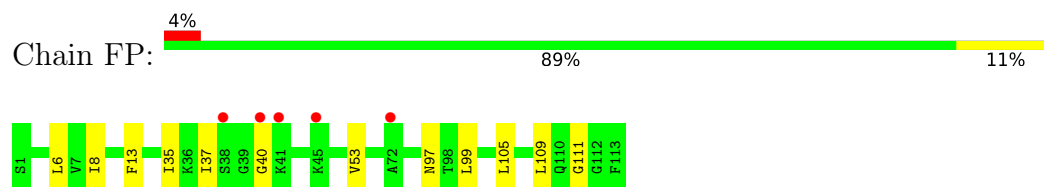
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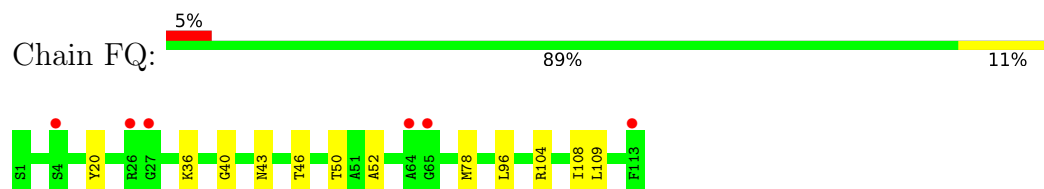
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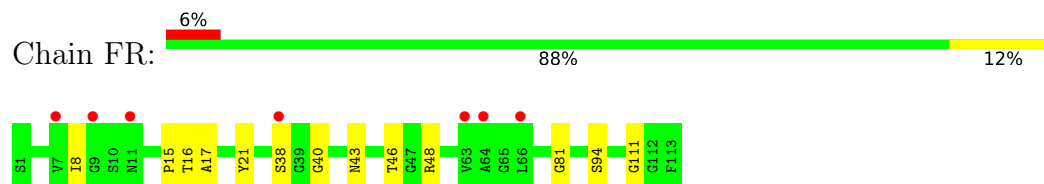
● Molecule 1: coat protein



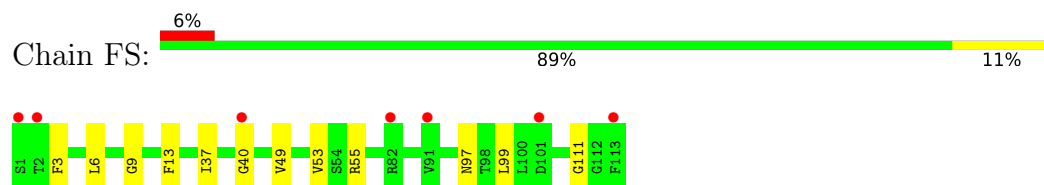
● Molecule 1: coat protein



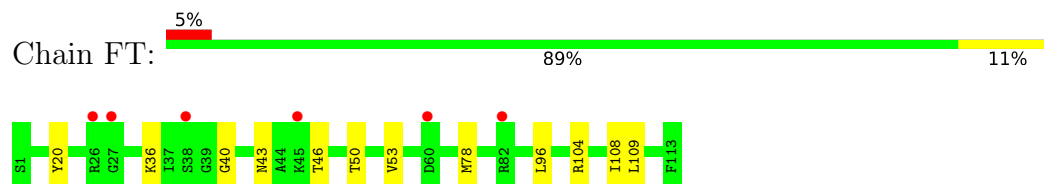
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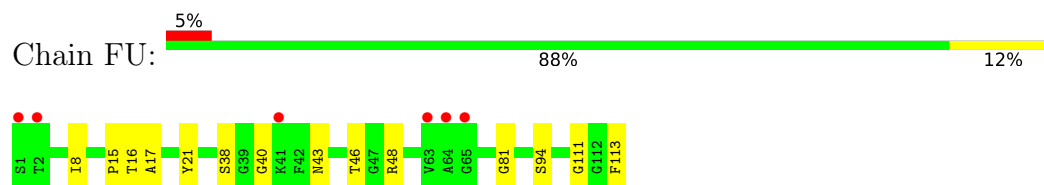
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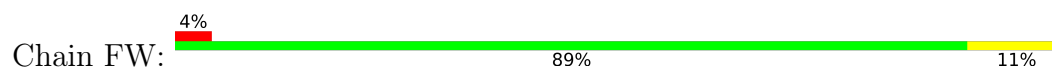


● Molecule 1: coat protein

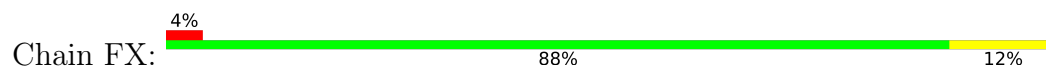




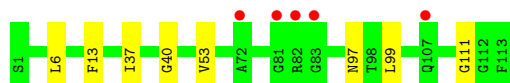
- Molecule 1: coat protein



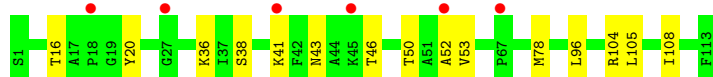
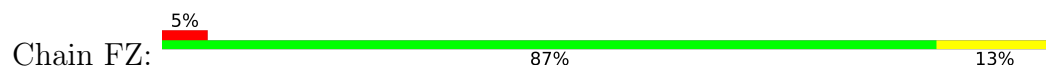
- Molecule 1: coat protein



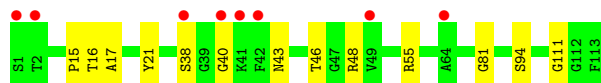
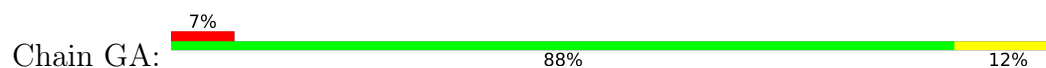
- Molecule 1: coat protein



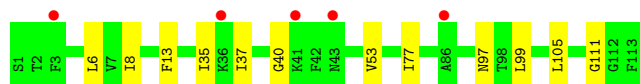
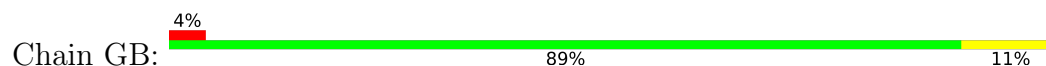
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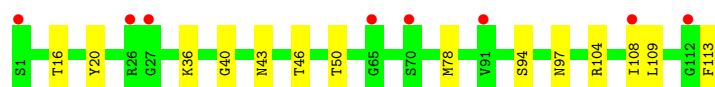
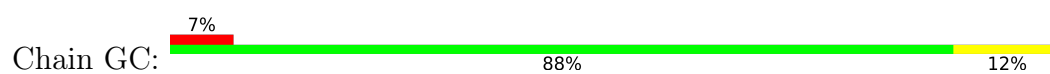
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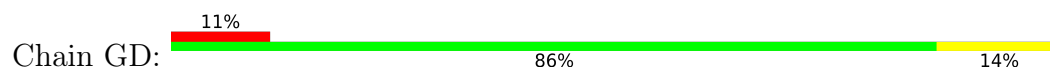
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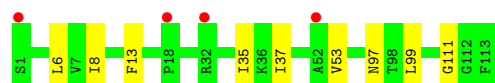
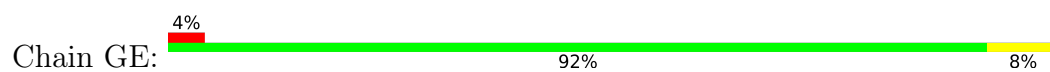
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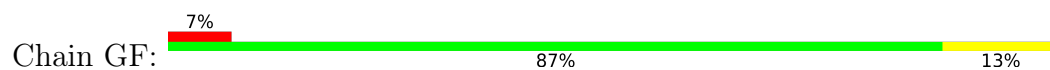
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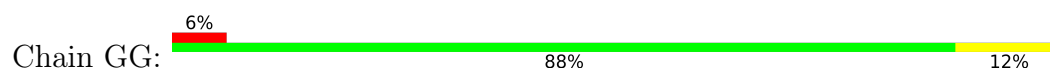
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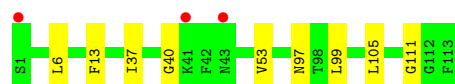
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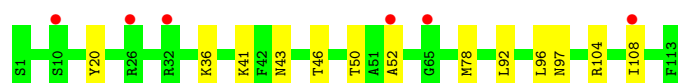
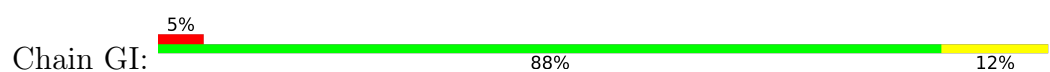
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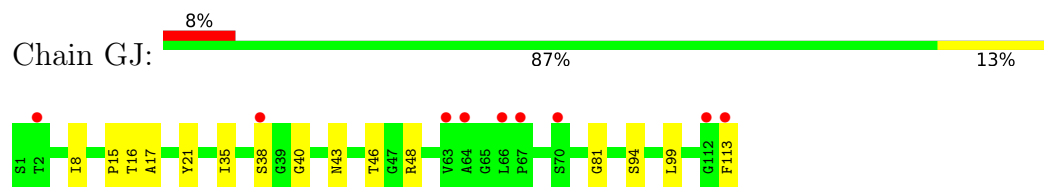
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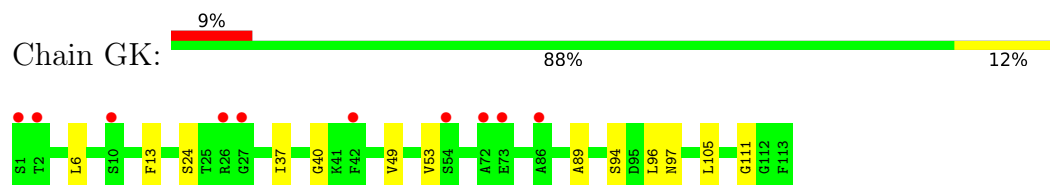
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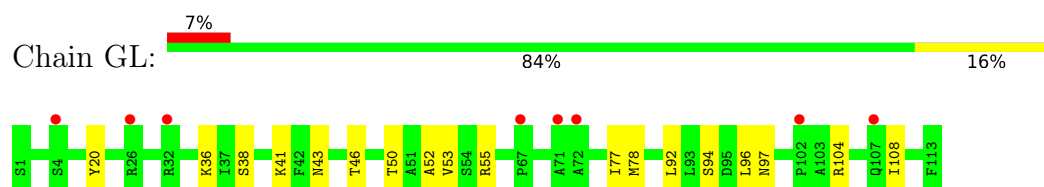
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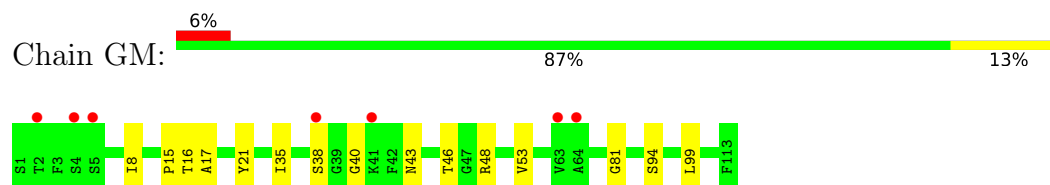
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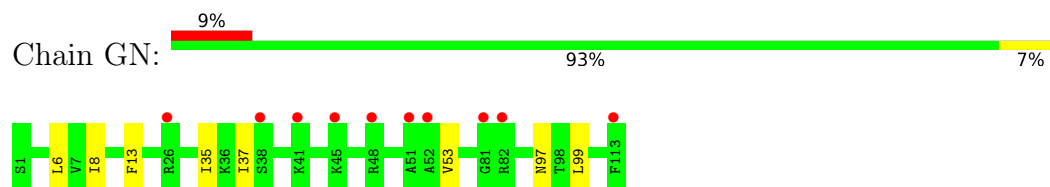
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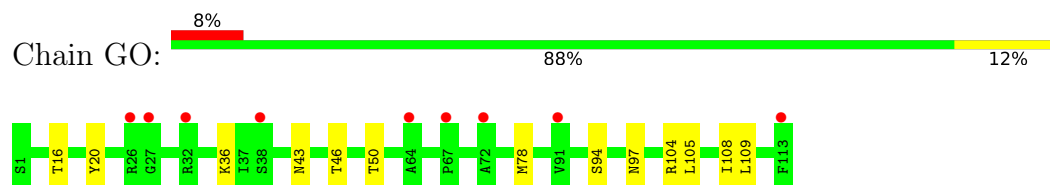
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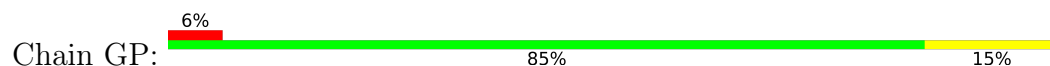
● Molecule 1: coat protein



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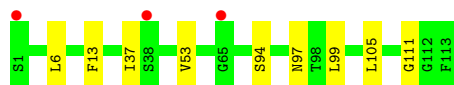


● Molecule 1: coat protein

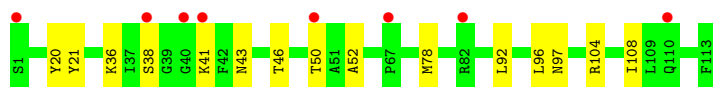




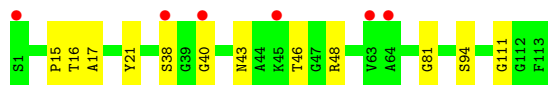
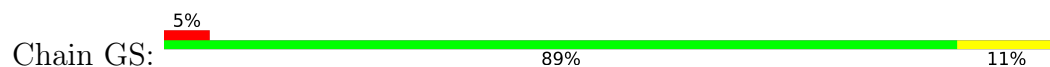
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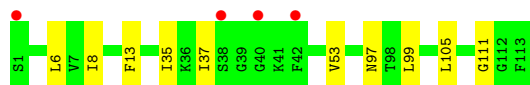
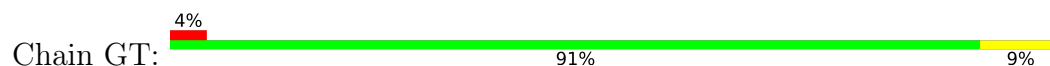
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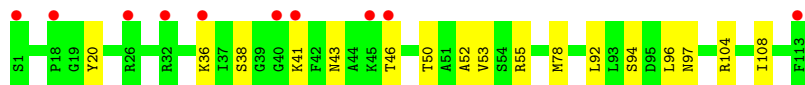
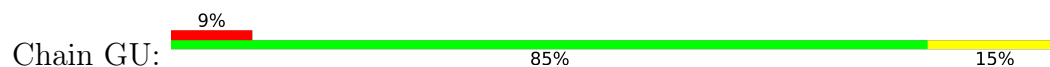
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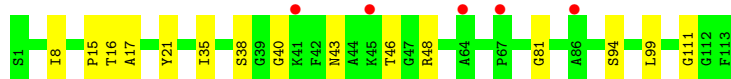
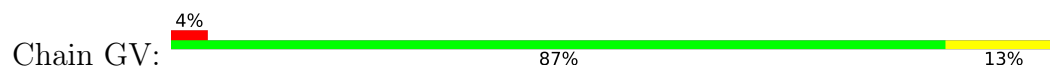
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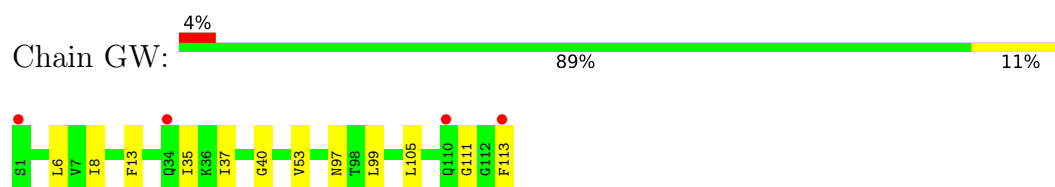
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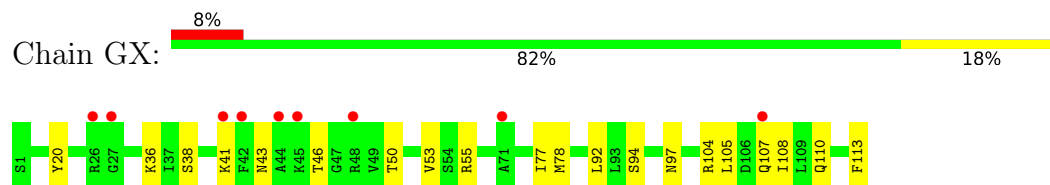
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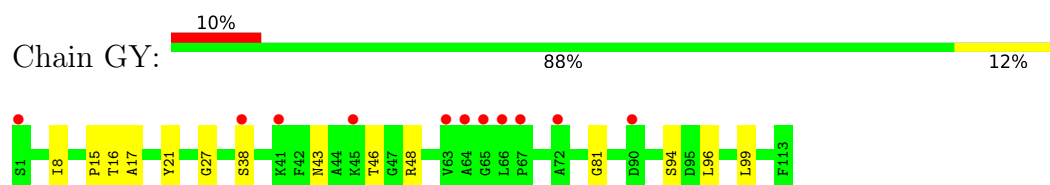
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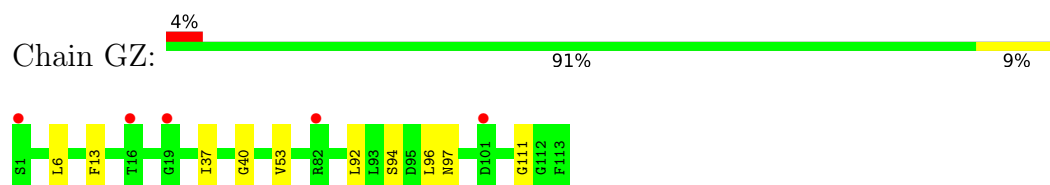
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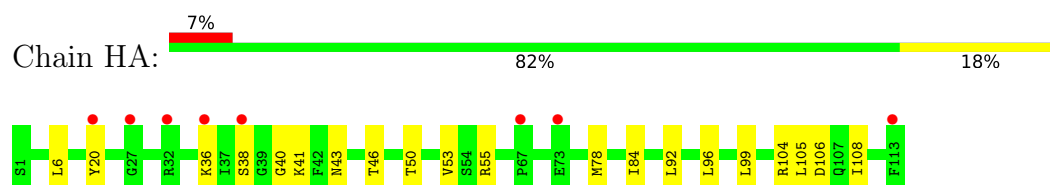
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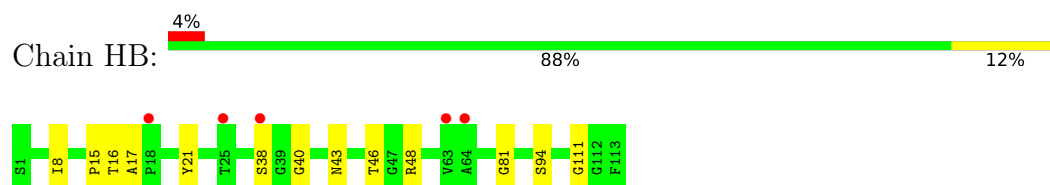
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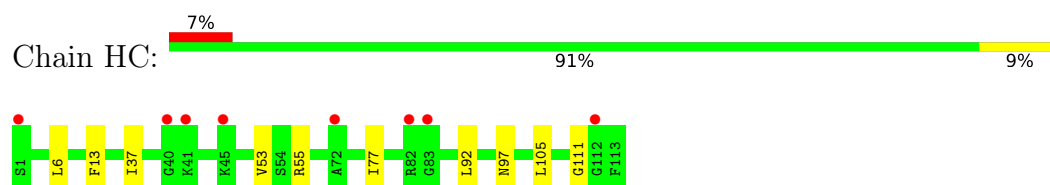
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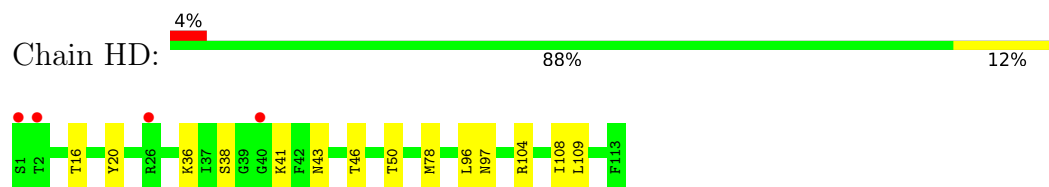
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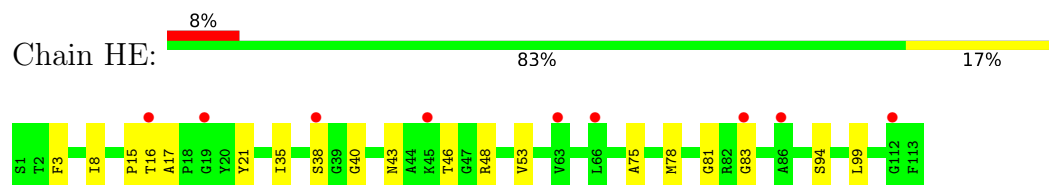
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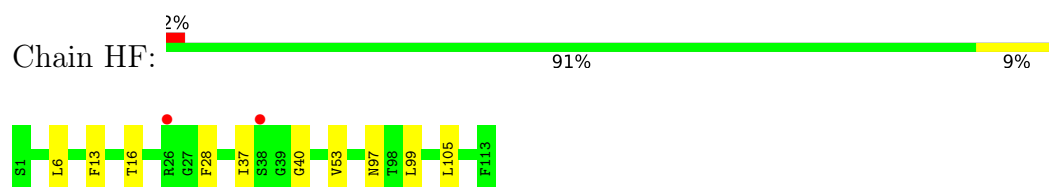
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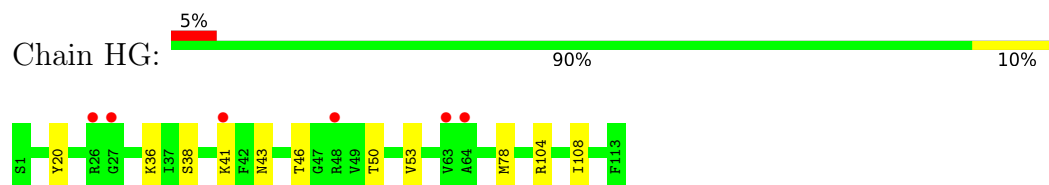
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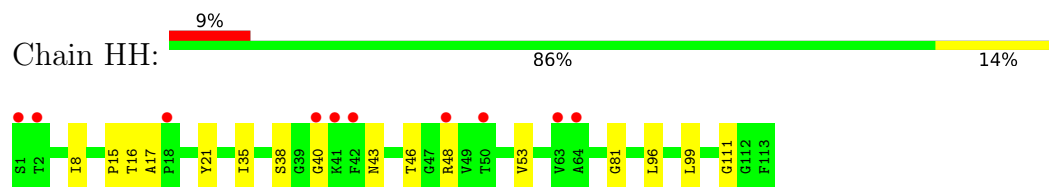
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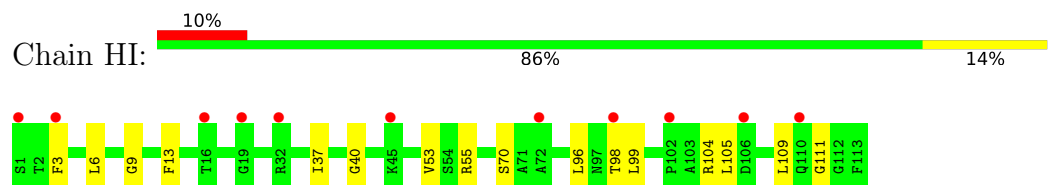
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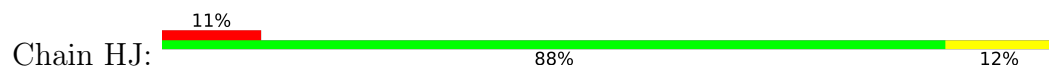
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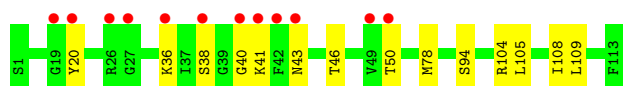


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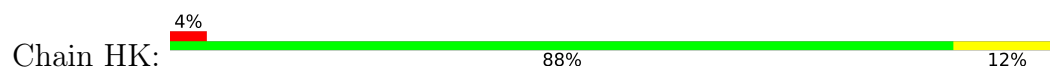


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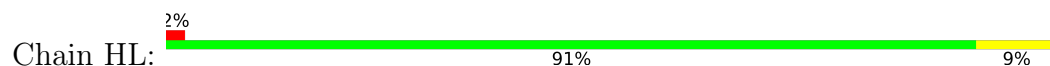




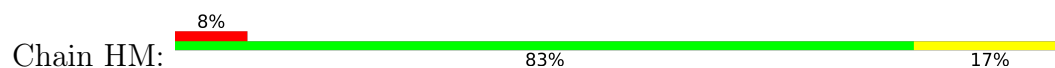
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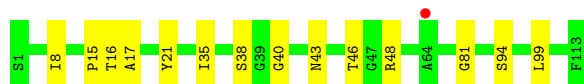
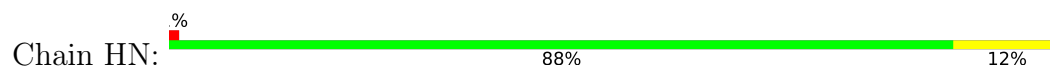
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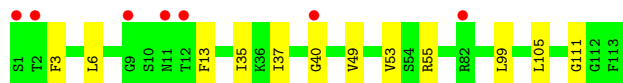
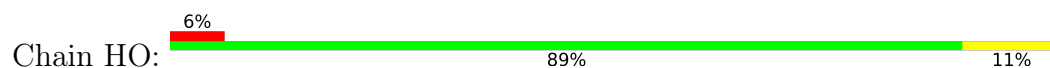
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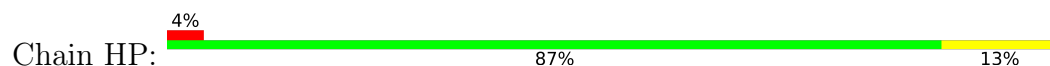
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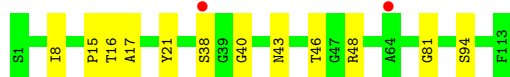
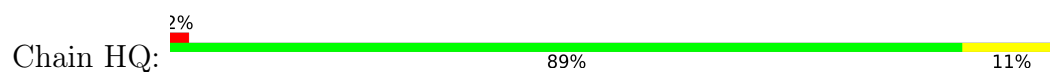
- Molecule 1: coat protein



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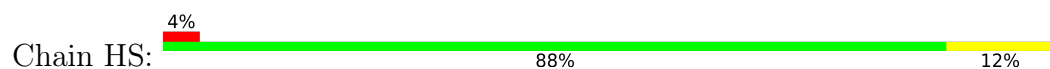
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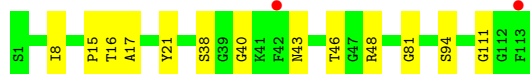
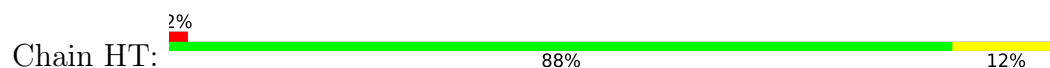
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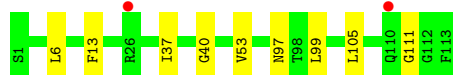
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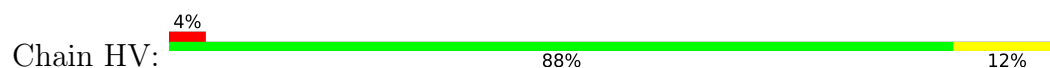
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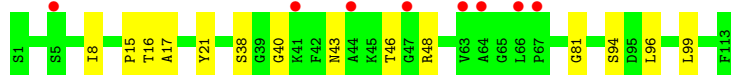
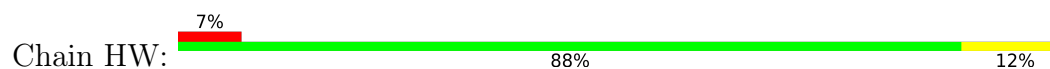
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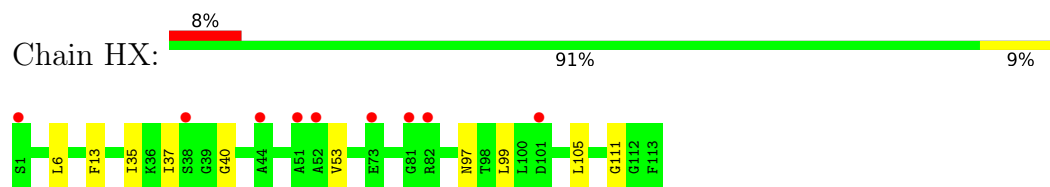
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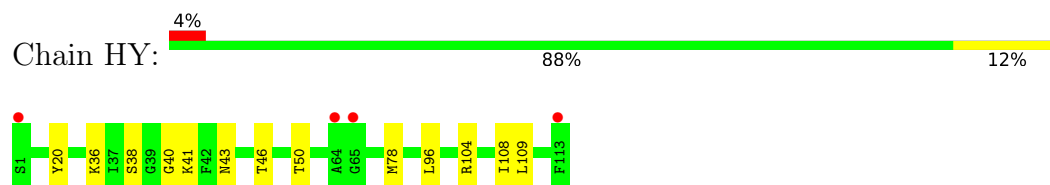
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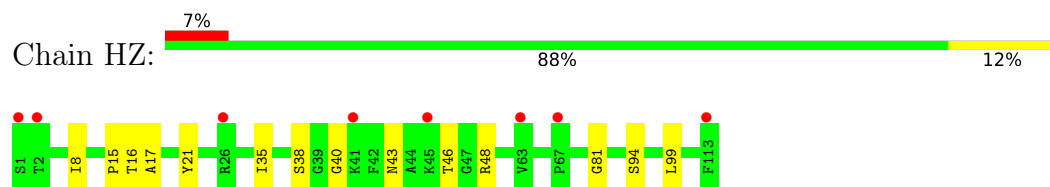
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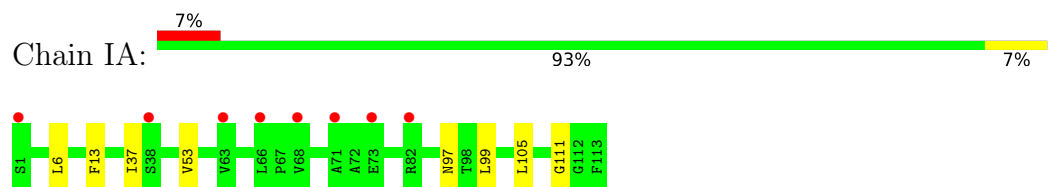
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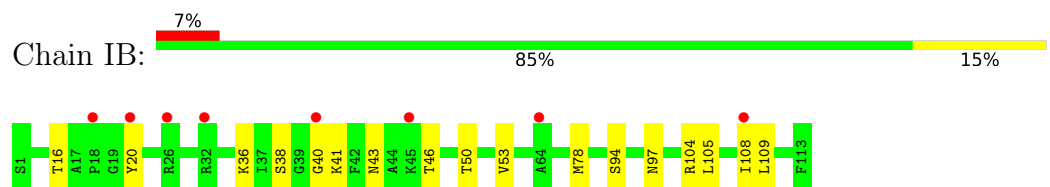
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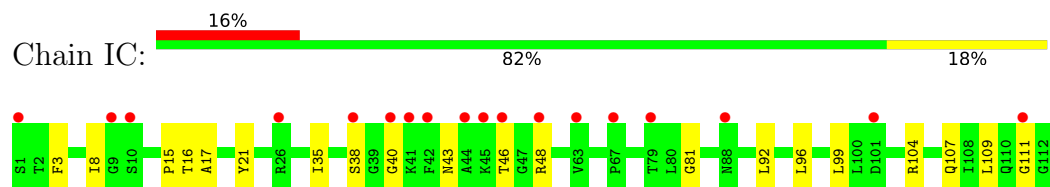
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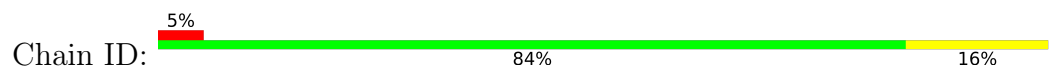
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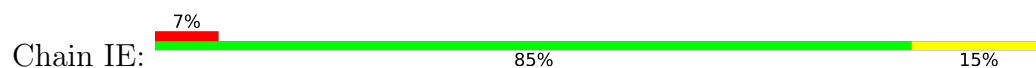


- Molecule 1: coat protein

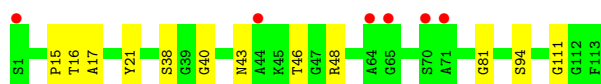
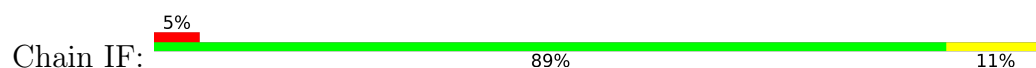




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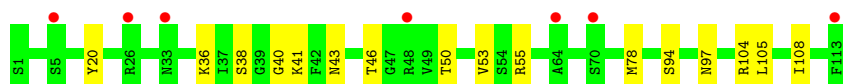
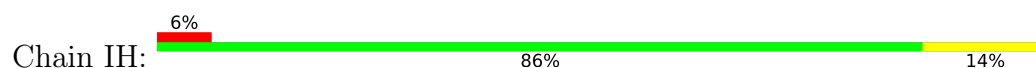
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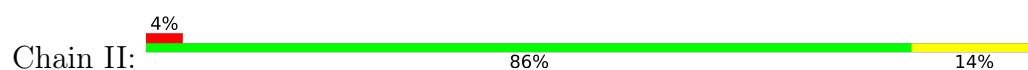
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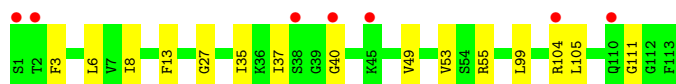
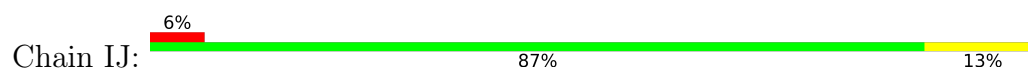
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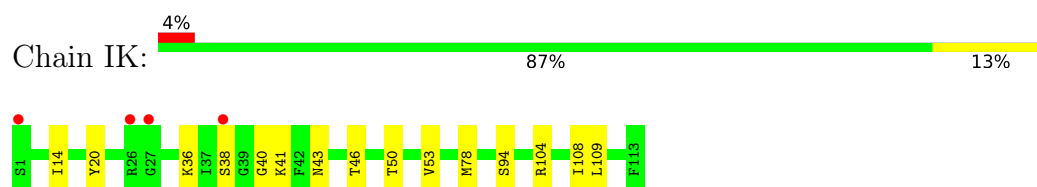
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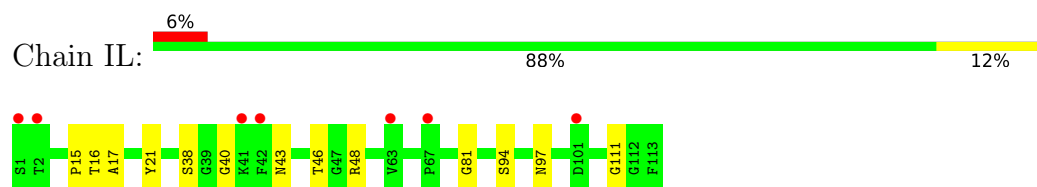
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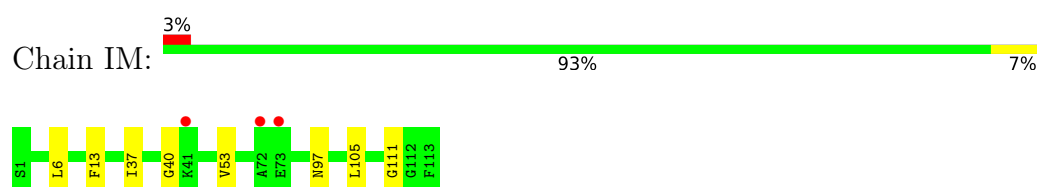
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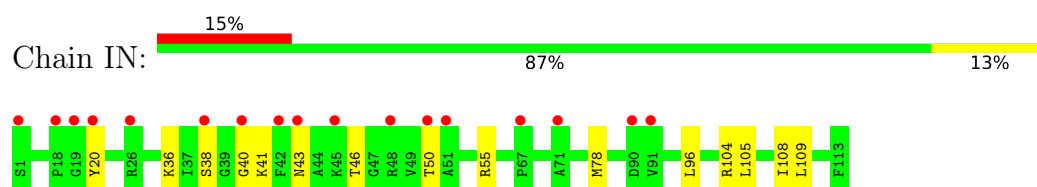
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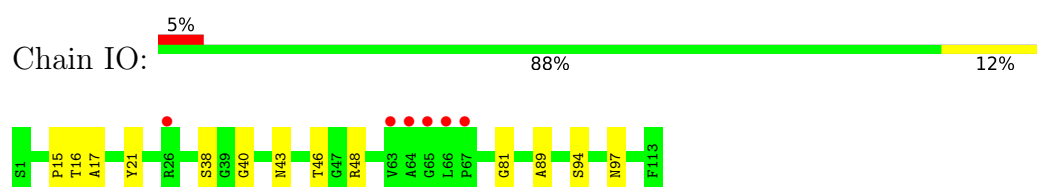
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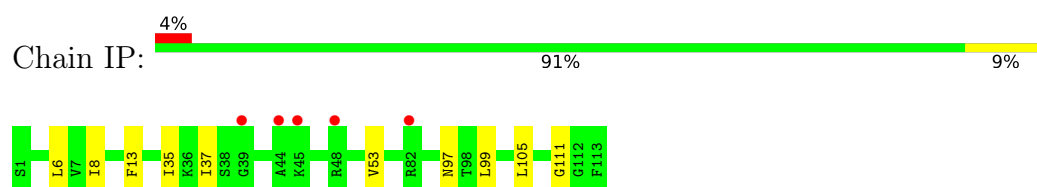
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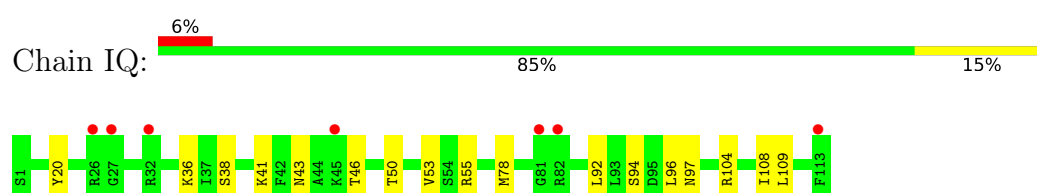
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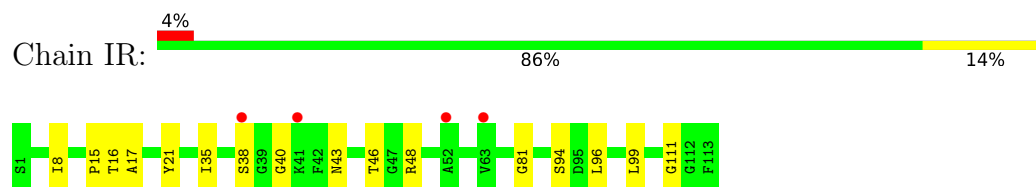
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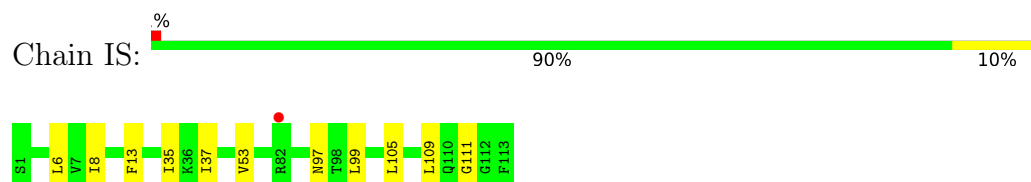
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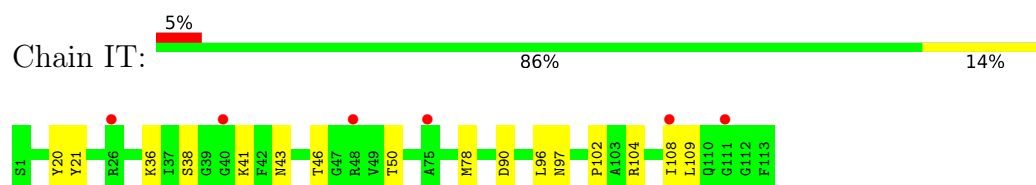
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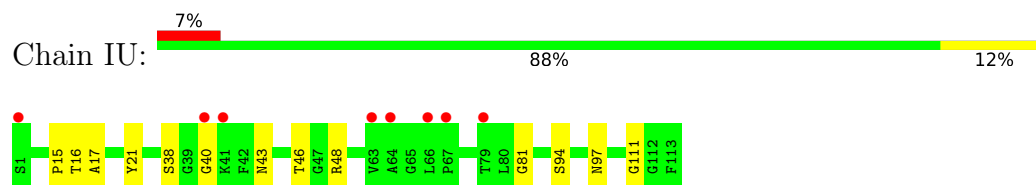
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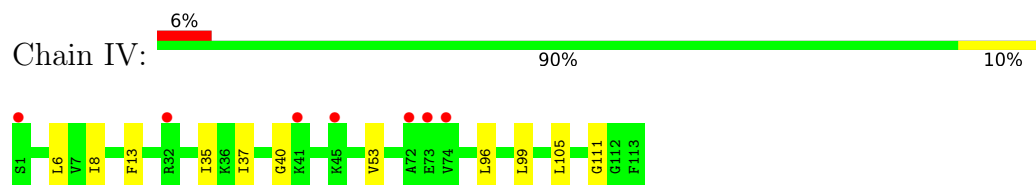
● Molecule 1: coat protein



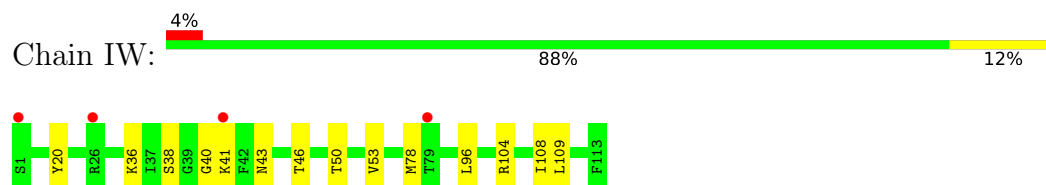
● Molecule 1: coat protein



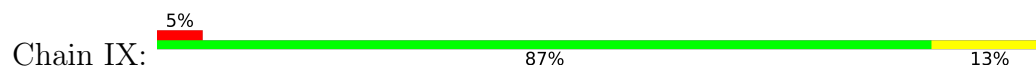
● Molecule 1: coat protein



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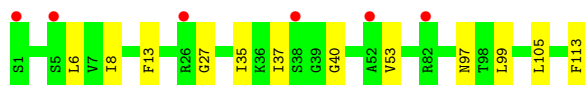
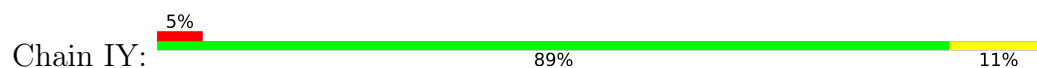


● Molecule 1: coat protein

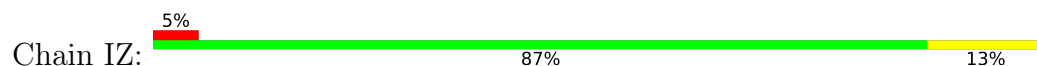




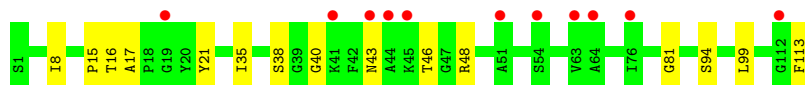
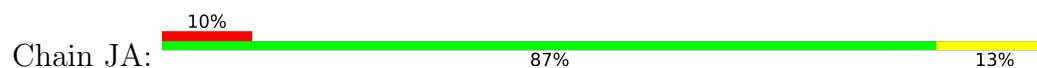
- Molecule 1: coat protein



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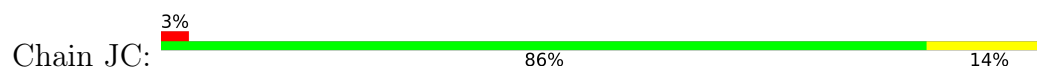
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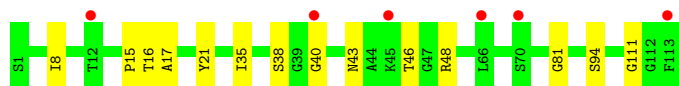
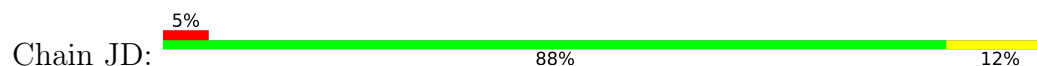
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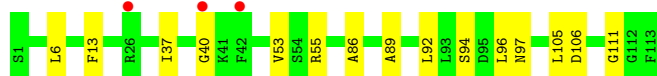
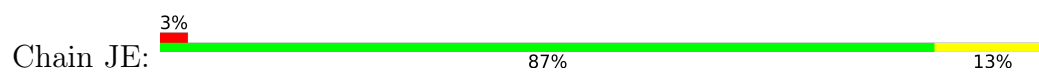
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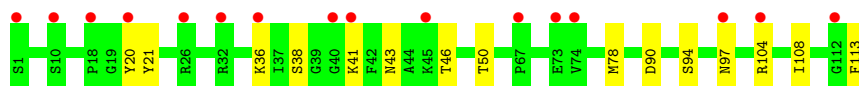
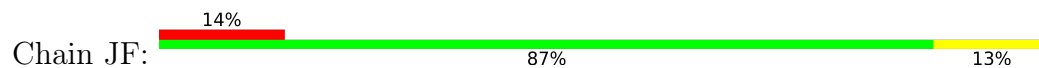
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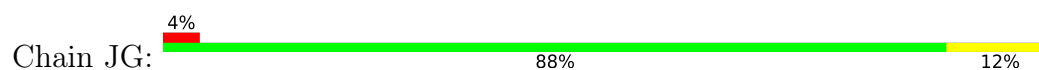
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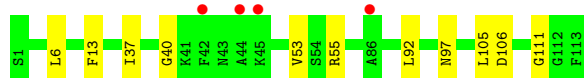
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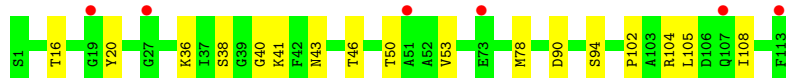
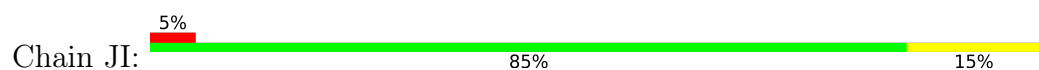
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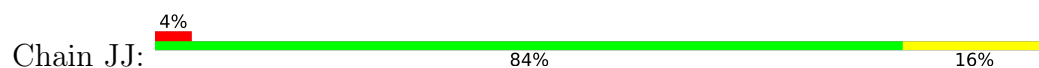
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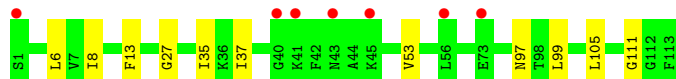
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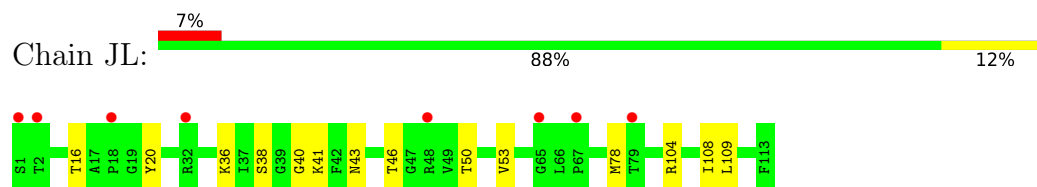
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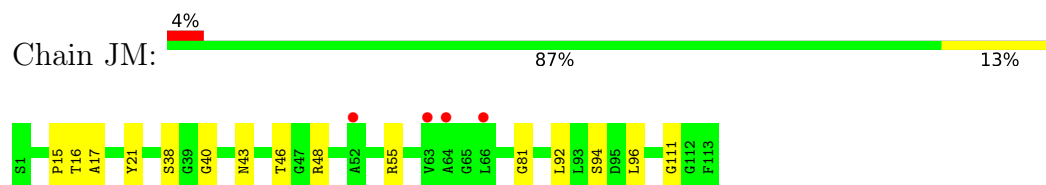
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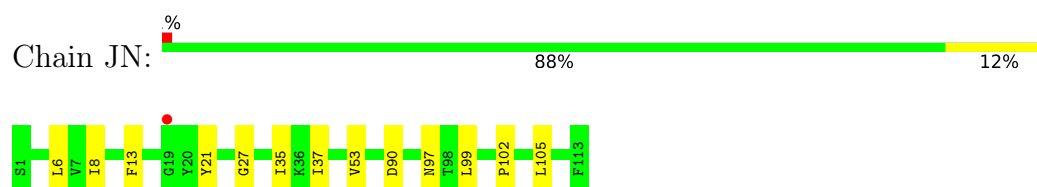
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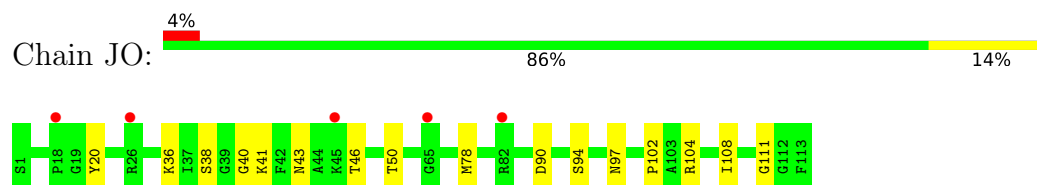
● Molecule 1: coat protein



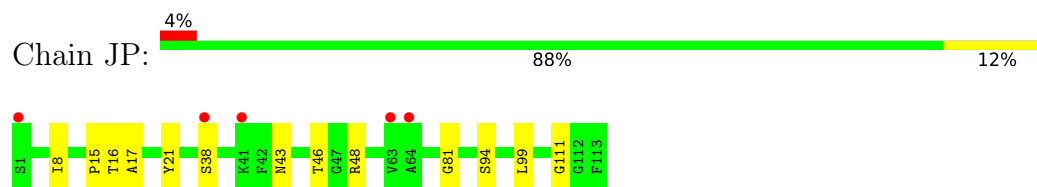
● Molecule 1: coat protein



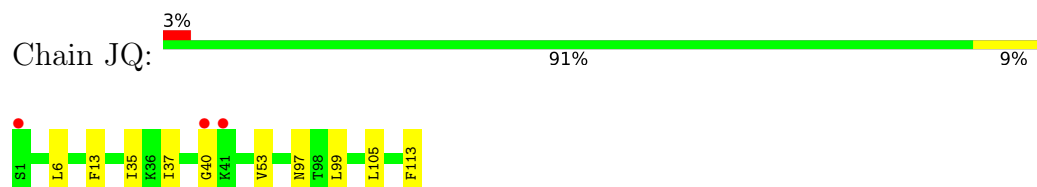
● Molecule 1: coat protein



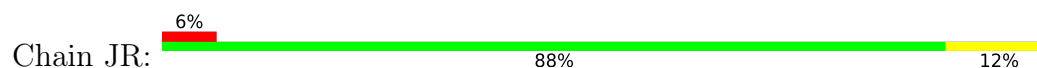
● Molecule 1: coat protein



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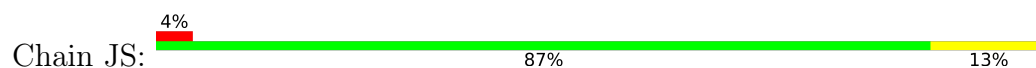


● Molecule 1: coat protein

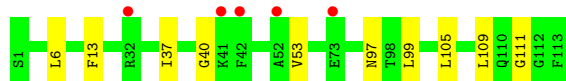




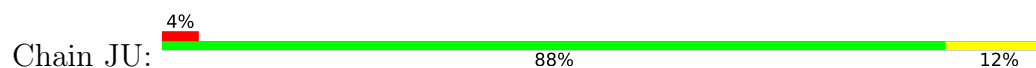
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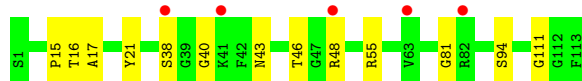
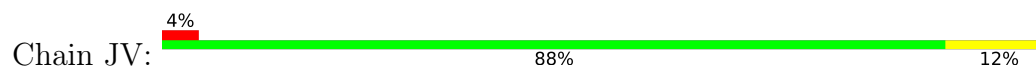
- Molecule 1: coat protein



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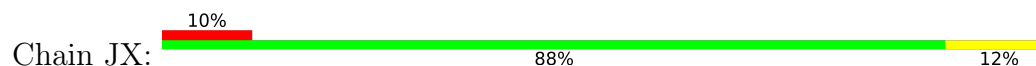
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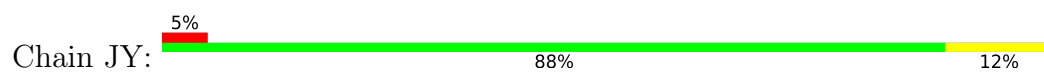
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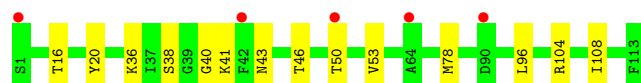
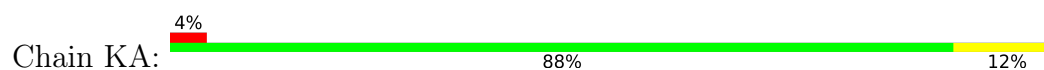
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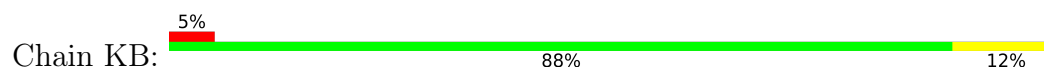
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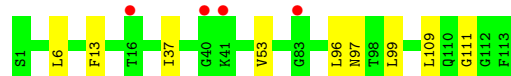
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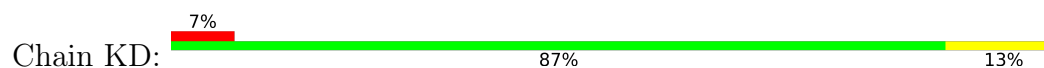
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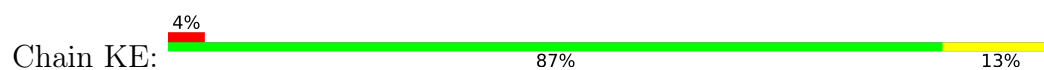
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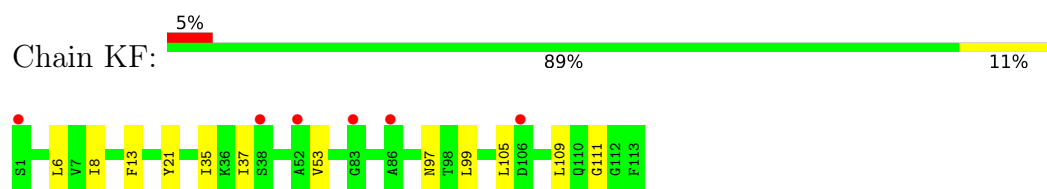
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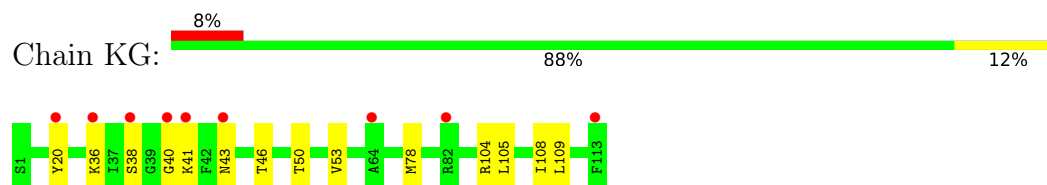
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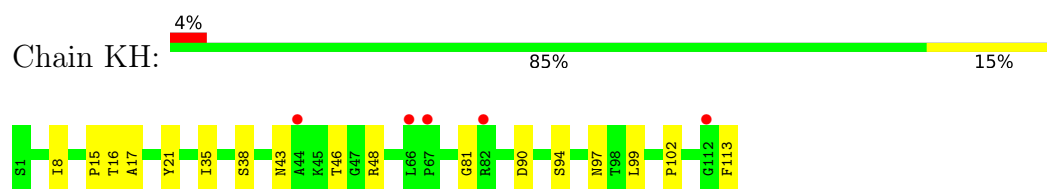
● Molecule 1: coat protein



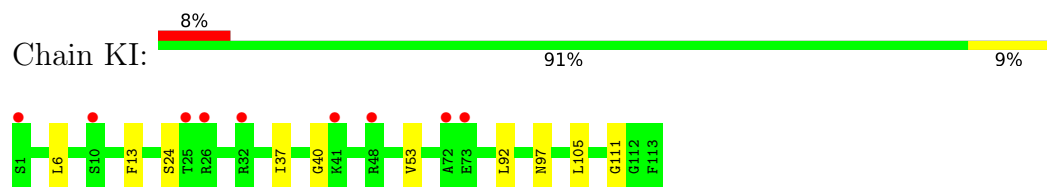
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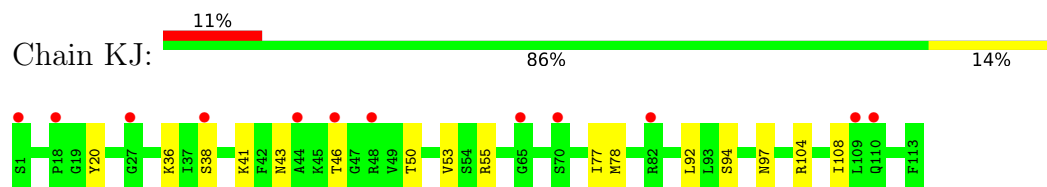
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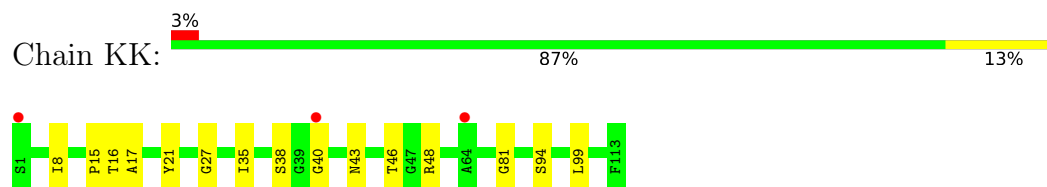
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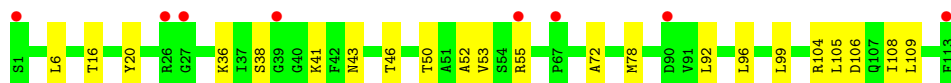
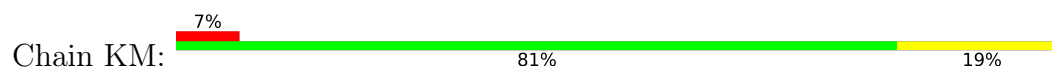


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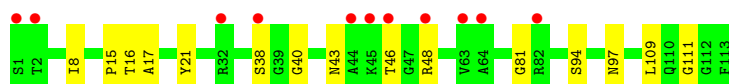
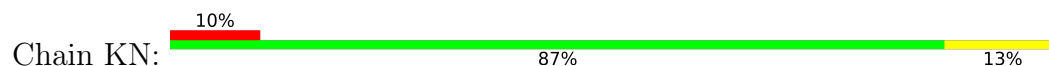




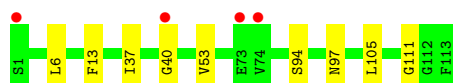
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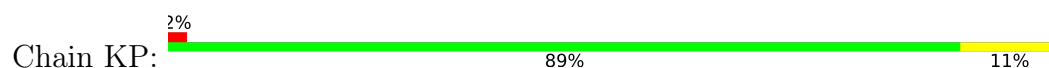
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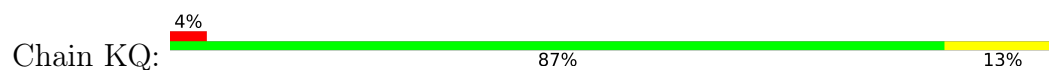
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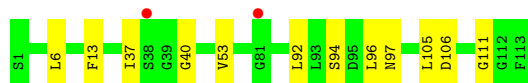
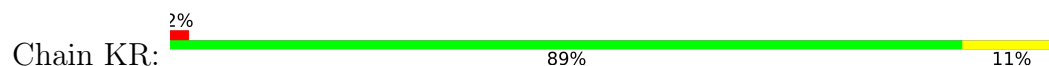
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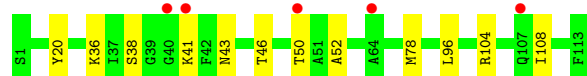
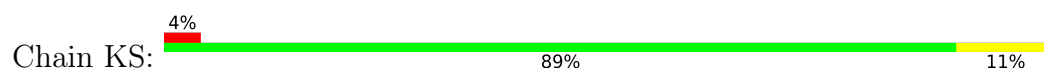
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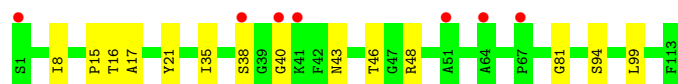
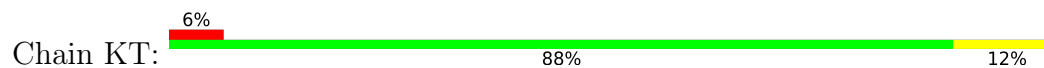
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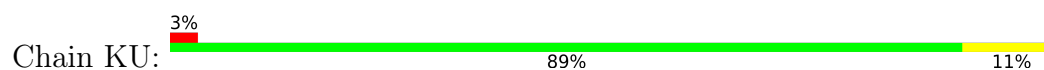
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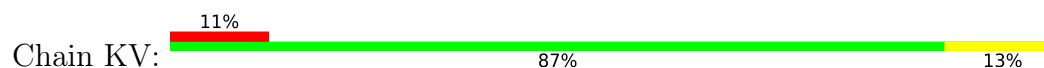
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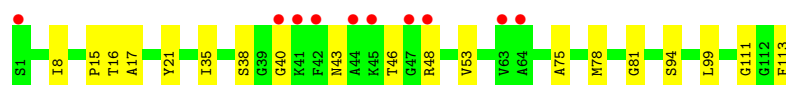
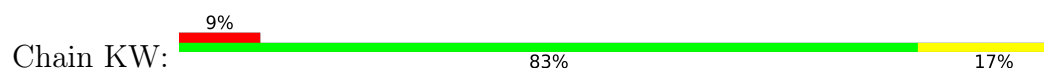
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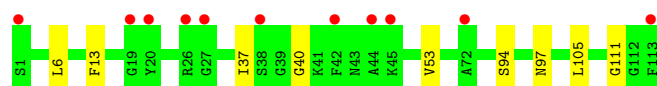
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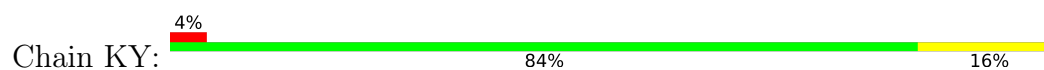
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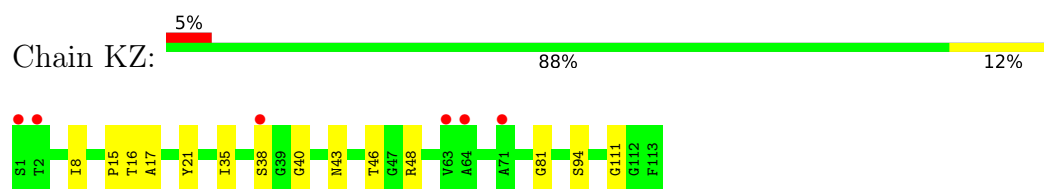
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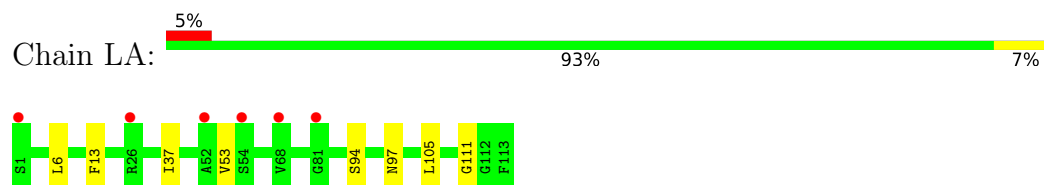
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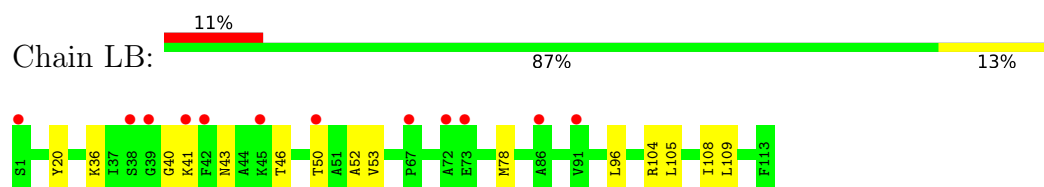
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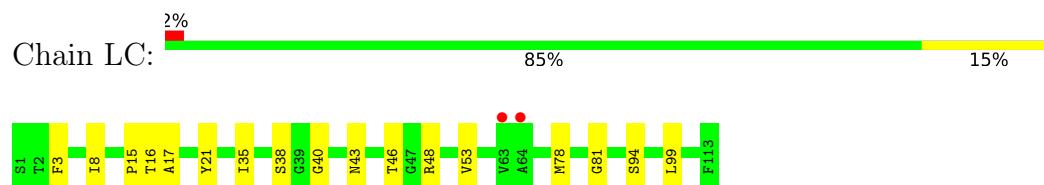
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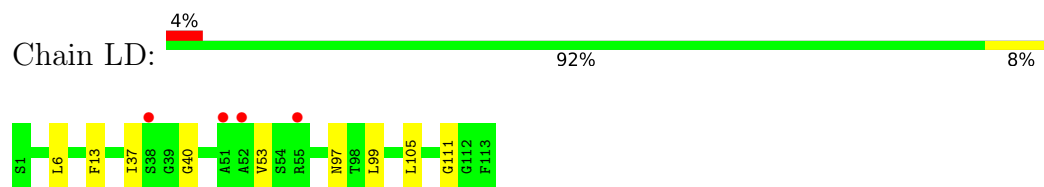
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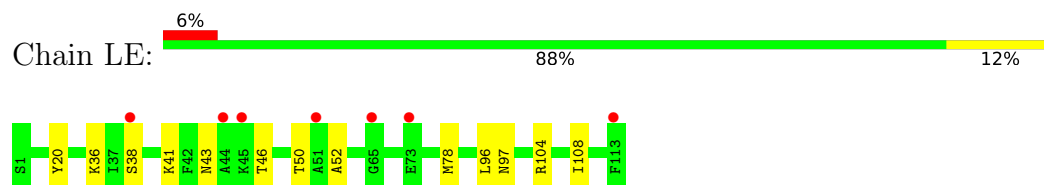
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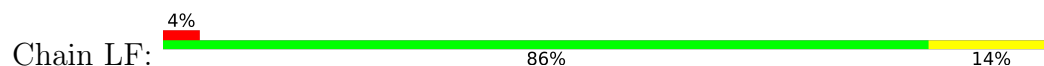
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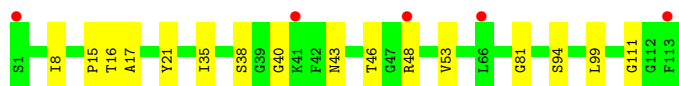


● Molecule 1: coat protein

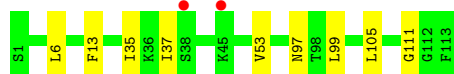


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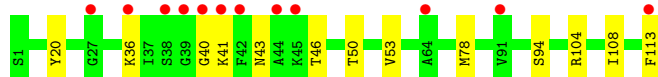
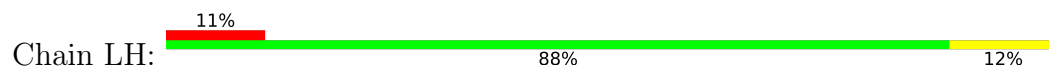




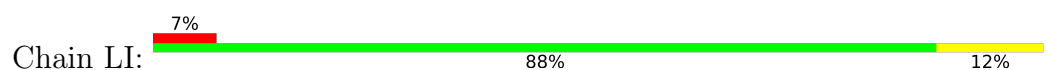
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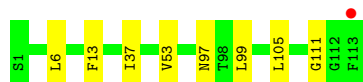
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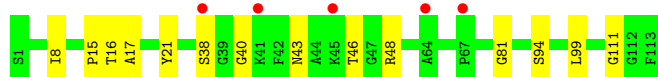
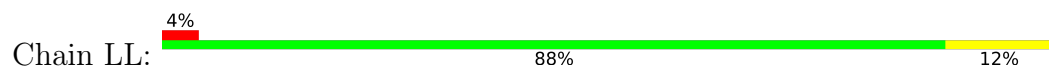
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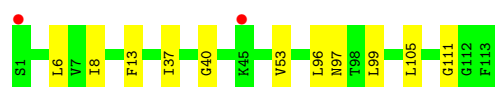
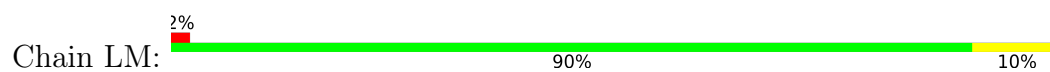
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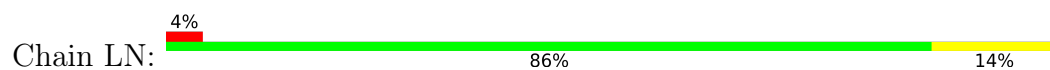
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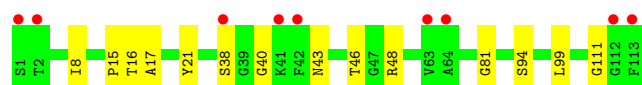
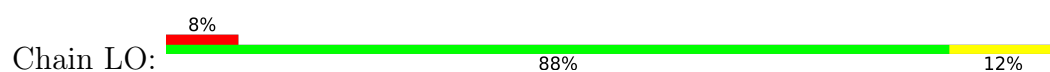
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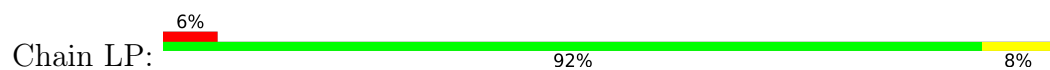
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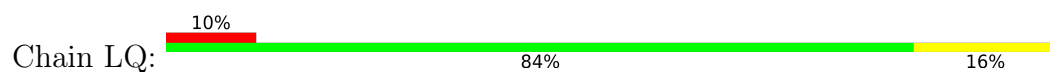
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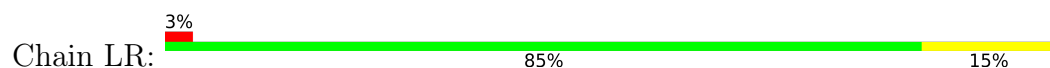
• Molecule 1: coat protein



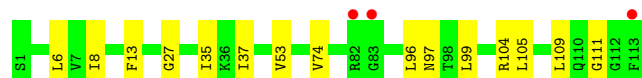
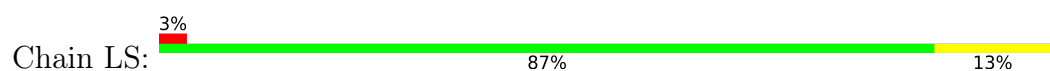
• Molecule 1: coat protein



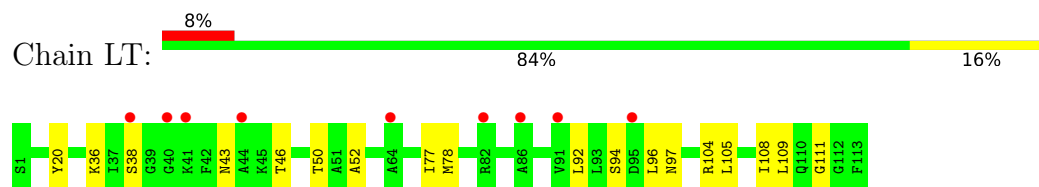
• Molecule 1: coat protein



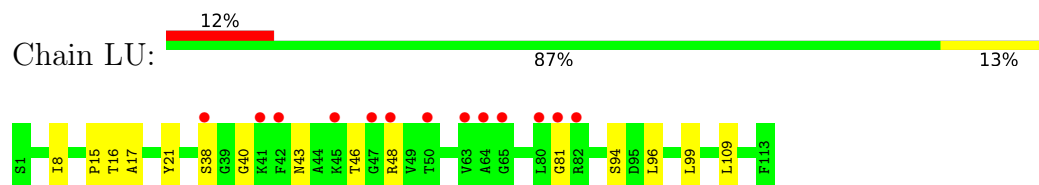
• Molecule 1: coat protein



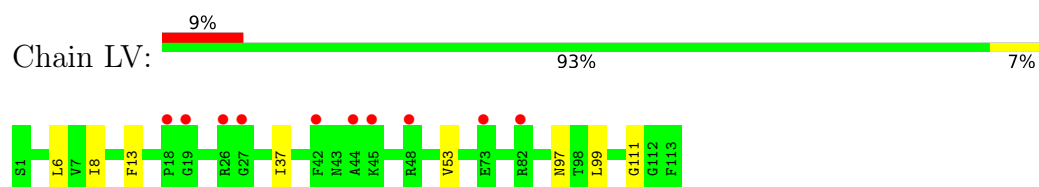
● Molecule 1: coat protein



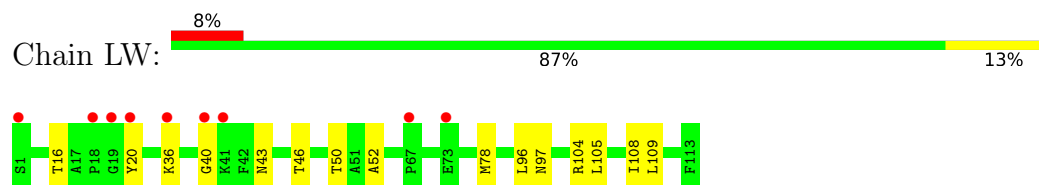
● Molecule 1: coat protein



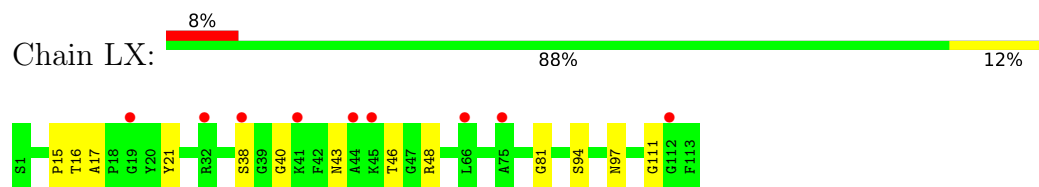
● Molecule 1: coat protein



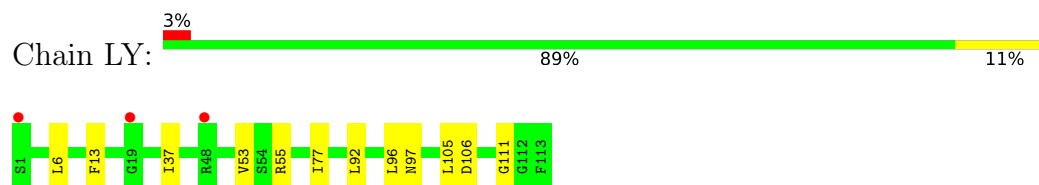
● Molecule 1: coat protein



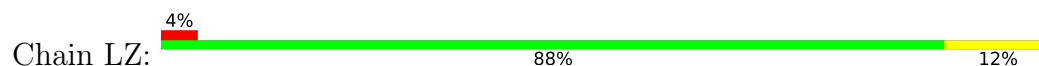
● Molecule 1: coat protein



● Molecule 1: coat protein

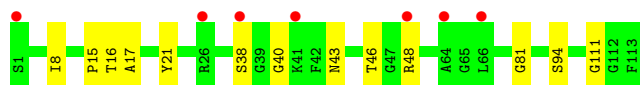
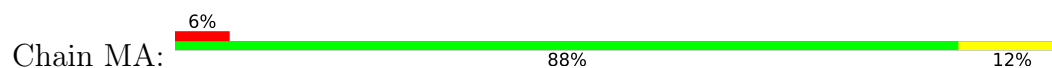


● Molecule 1: coat protein





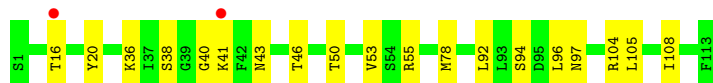
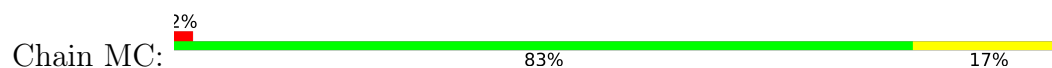
- Molecule 1: coat protein



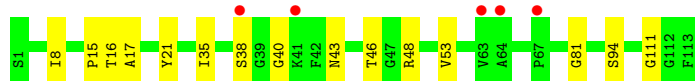
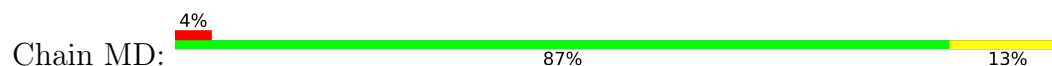
- Molecule 1: coat protein



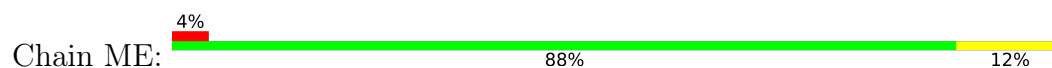
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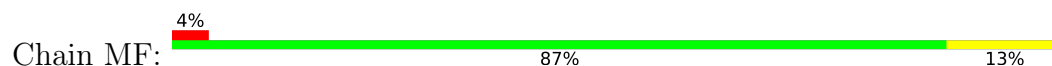
- Molecule 1: coat protein



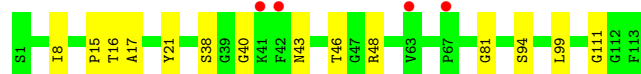
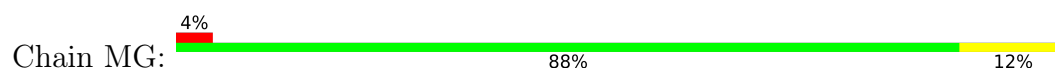
- Molecule 1: coat protein



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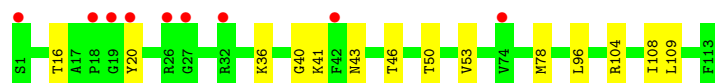
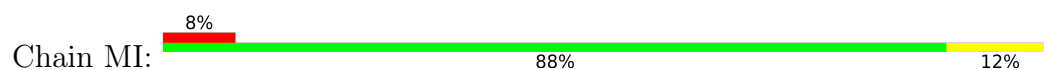
- Molecule 1: coat protein



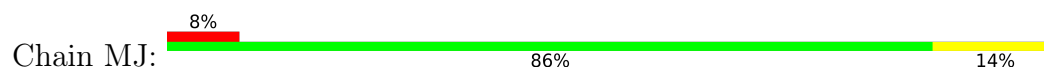
- Molecule 1: coat protein



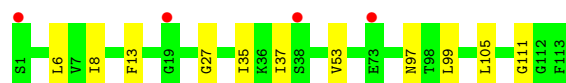
- Molecule 1: coat protein



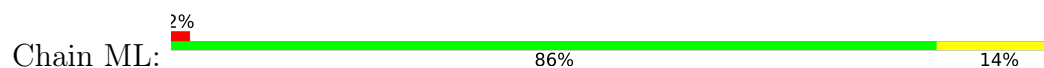
- Molecule 1: coat protein



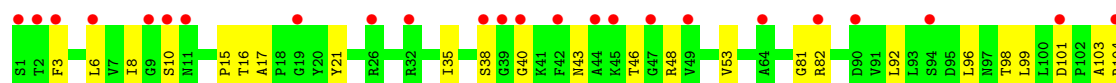
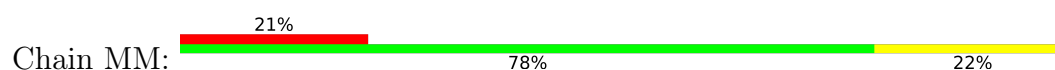
- Molecule 1: coat protein



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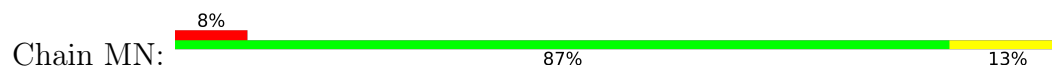


- Molecule 1: coat protein

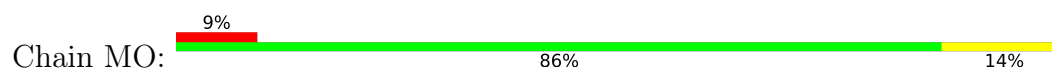




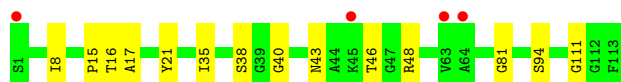
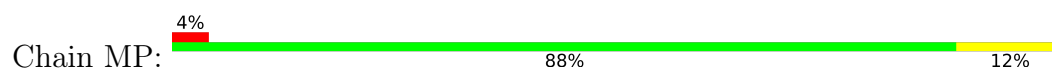
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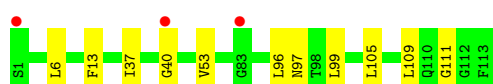
- Molecule 1: coat protein



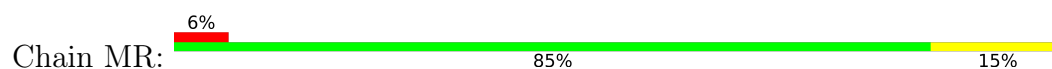
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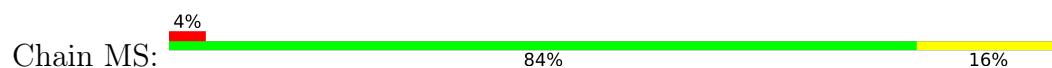
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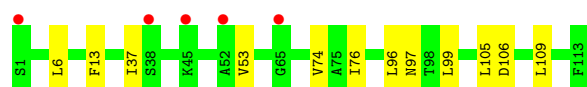
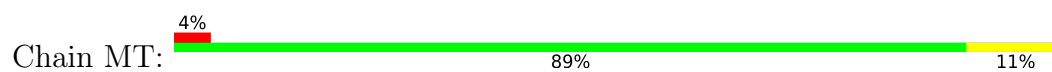
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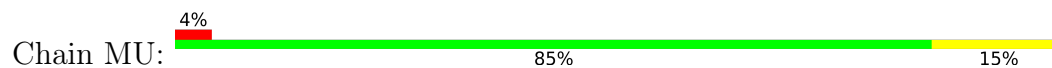
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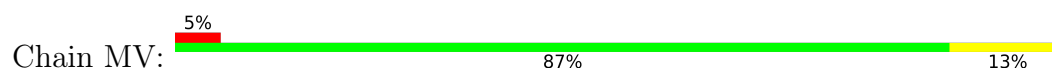
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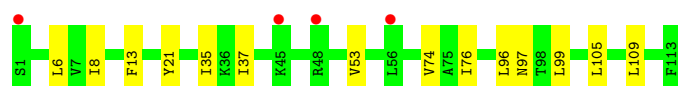
• Molecule 1: coat protein



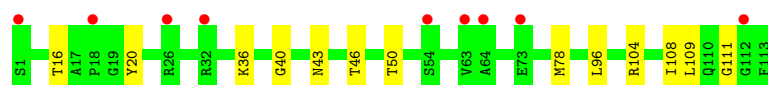
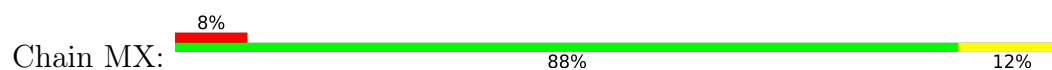
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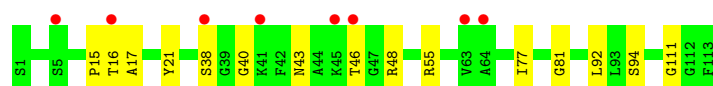
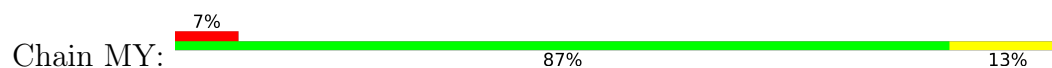
• Molecule 1: coat protein



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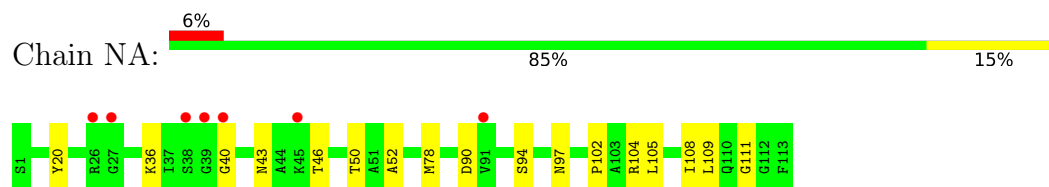
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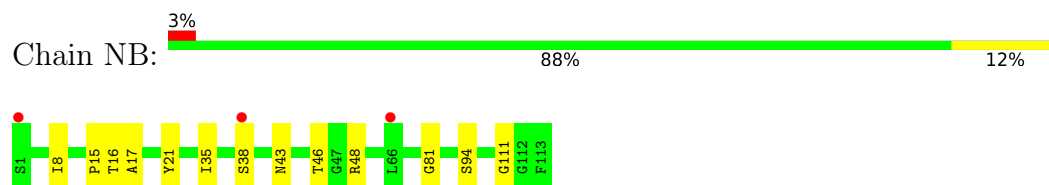
• Molecule 1: coat protein



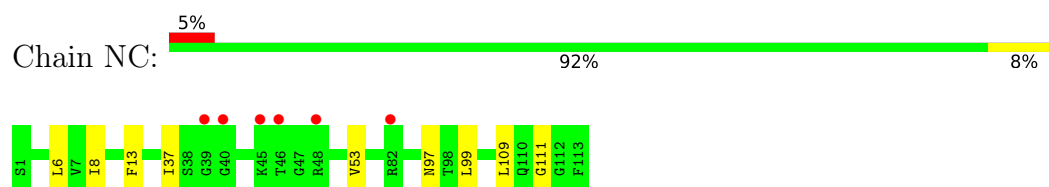
● Molecule 1: coat protein



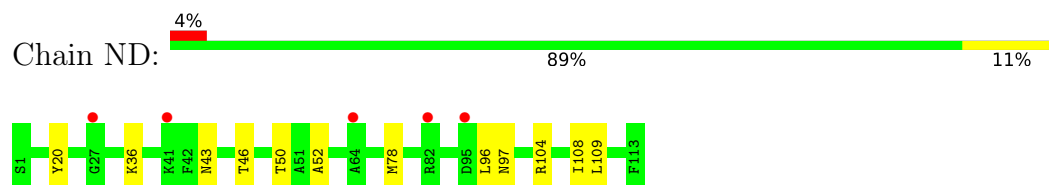
● Molecule 1: coat protein



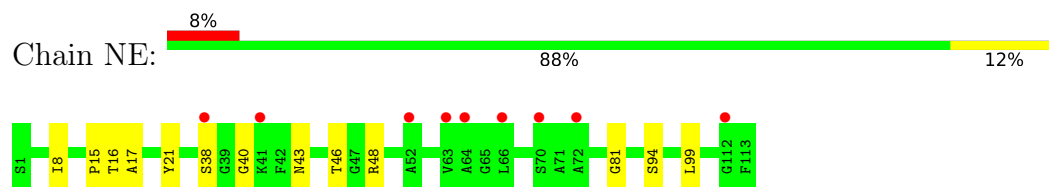
● Molecule 1: coat protein



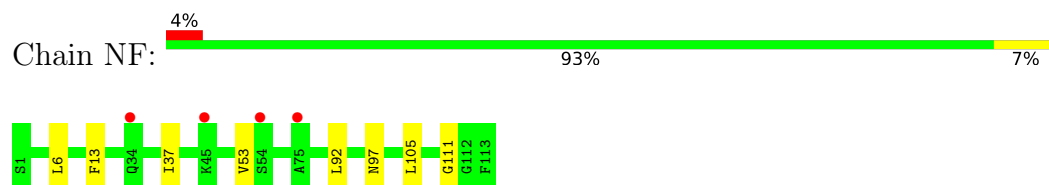
● Molecule 1: coat protein



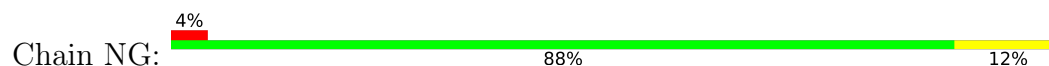
● Molecule 1: coat protein

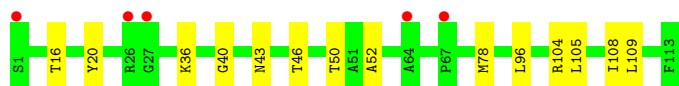


● Molecule 1: coat protein

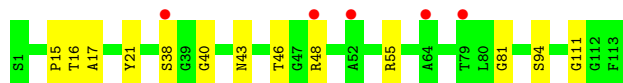
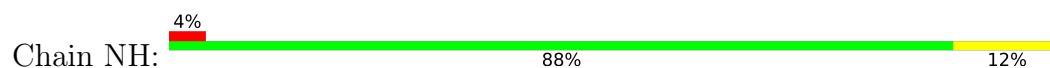


● Molecule 1: coat protein

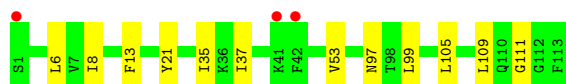
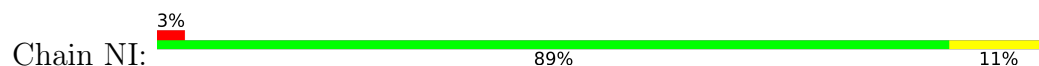




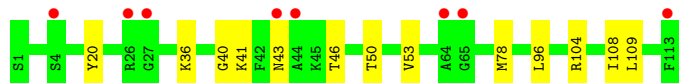
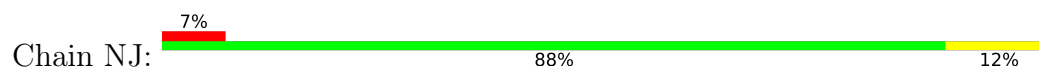
- Molecule 1: coat protein



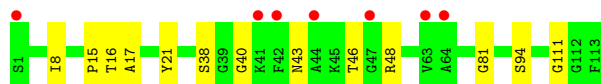
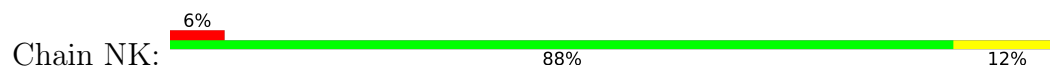
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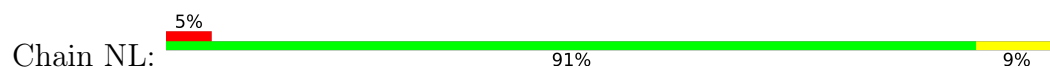
- Molecule 1: coat protein



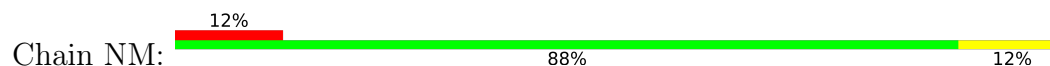
- Molecule 1: coat protein



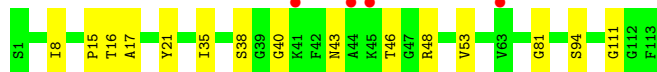
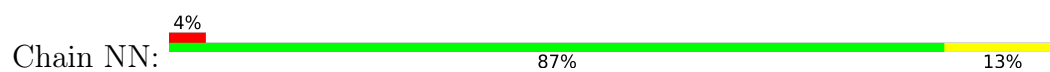
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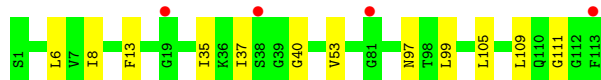
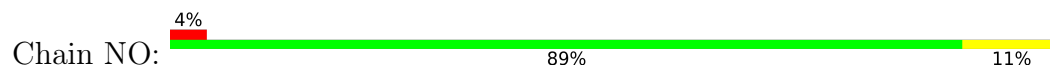
- Molecule 1: coat protein



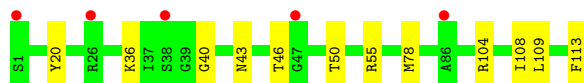
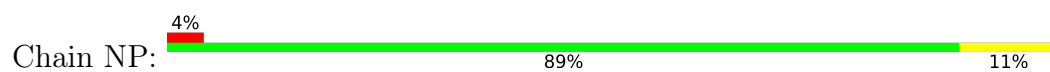
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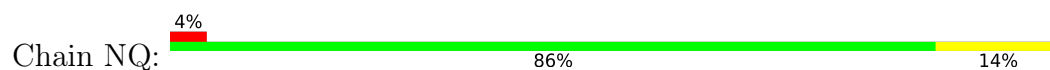
- Molecule 1: coat protein



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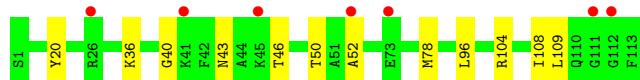
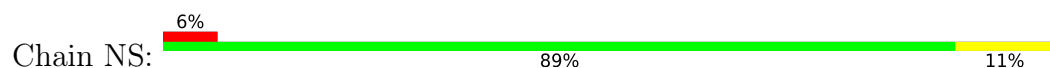
- Molecule 1: coat protein



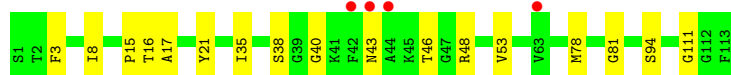
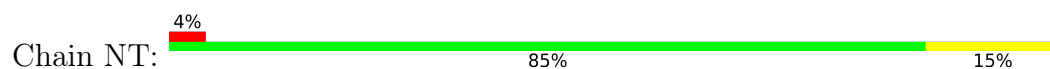
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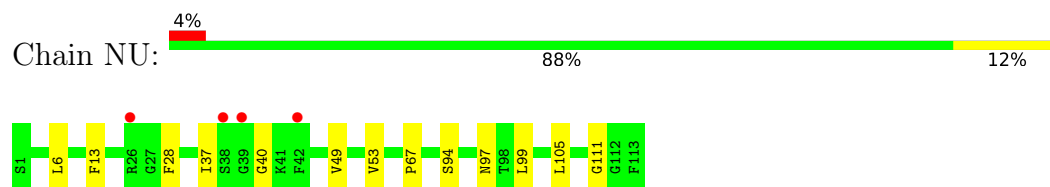
- Molecule 1: coat protein



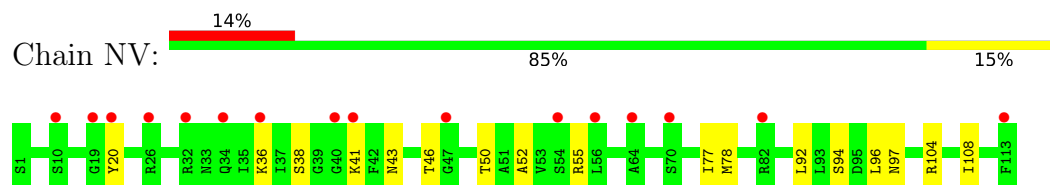
- Molecule 1: coat protein



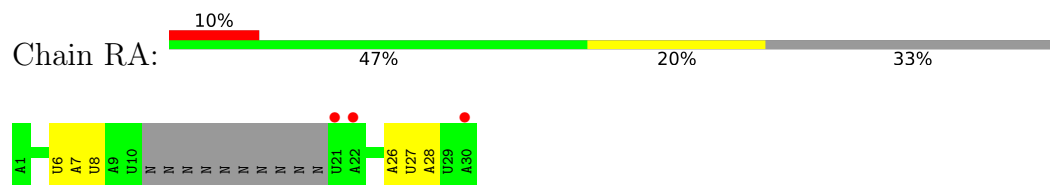
- Molecule 1: coat protein



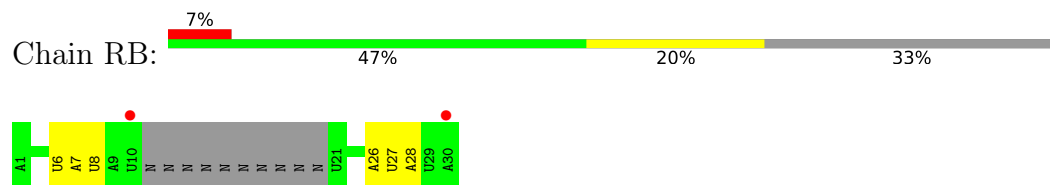
- Molecule 1: coat protein



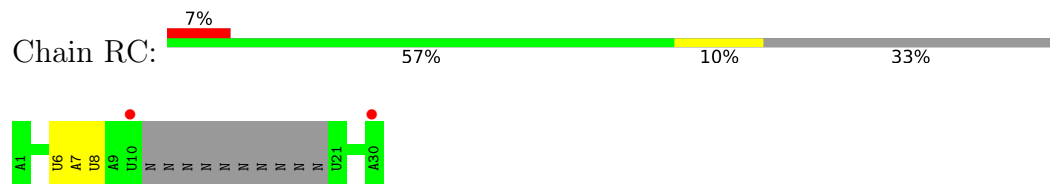
- Molecule 2: RNA



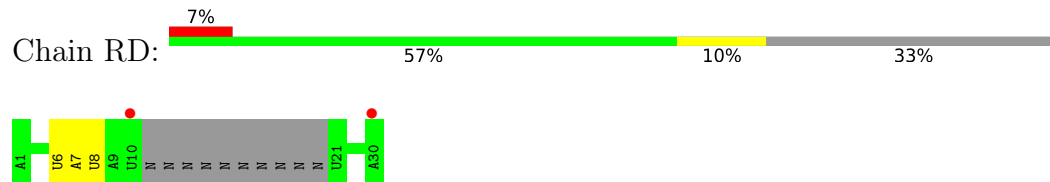
- Molecule 2: RNA



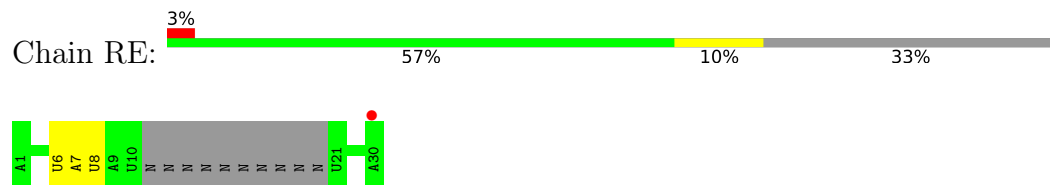
- Molecule 2: RNA



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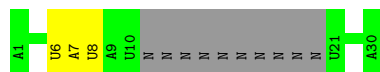
● Molecule 2: RNA



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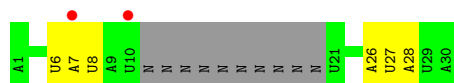
● Molecule 2: RNA



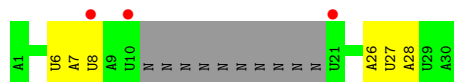
● Molecule 2: RNA



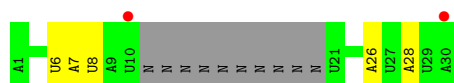
● Molecule 2: RNA



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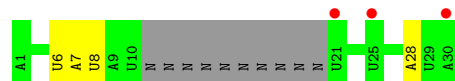
● Molecule 2: RNA



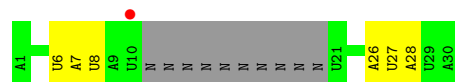
● Molecule 2: RNA



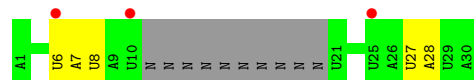
● Molecule 2: RNA



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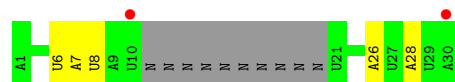
● Molecule 2: RNA



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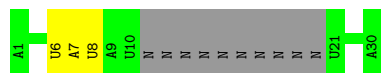
● Molecule 2: RNA



● Molecule 2: RNA



● Molecule 2: RNA

Chain SA:  57% 10% 33%

● Molecule 2: RNA

Chain SB:  10% 47% 20% 33%

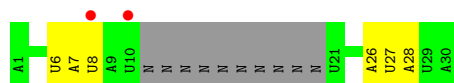
● Molecule 2: RNA

Chain SC:  3% 50% 17% 33%

● Molecule 2: RNA

Chain SD:  3% 47% 20% 33%

● Molecule 2: RNA

Chain SE:  7% 47% 20% 33%

● Molecule 2: RNA

Chain SF:  3% 50% 17% 33%

● Molecule 2: RNA

Chain SG:  3% 47% 20% 33%

● Molecule 2: RNA



● Molecule 2: RNA



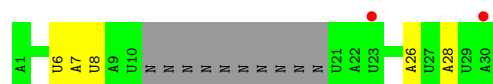
● Molecule 2: RNA



● Molecule 2: RNA



● Molecule 2: RNA



● Molecule 2: RNA



● Molecule 2: RNA



● Molecule 2: RNA



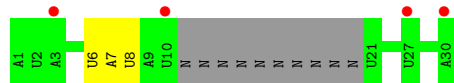
● Molecule 2: RNA



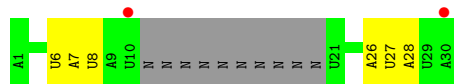
● Molecule 2: RNA



● Molecule 2: RNA



● Molecule 2: RNA



● Molecule 2: RNA



● Molecule 2: RNA



• Molecule 2: RNA

Chain SV:  7% 53% 13% 33%



• Molecule 2: RNA

Chain SW:  7% 47% 20% 33%



• Molecule 2: RNA

Chain SX:  10% 47% 20% 33%



• Molecule 2: RNA

Chain SY:  3% 53% 13% 33%



• Molecule 2: RNA

Chain SZ:  3% 57% 10% 33%



• Molecule 2: RNA

Chain TA:  7% 53% 13% 33%

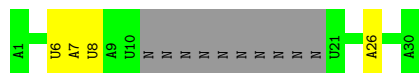


• Molecule 2: RNA

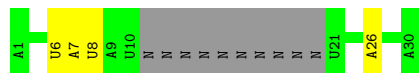
Chain TB:  13% 53% 13% 33%



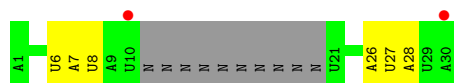
● Molecule 2: RNA

Chain TC:  53% 13% 33%

● Molecule 2: RNA

Chain TD:  53% 13% 33%

● Molecule 2: RNA

Chain TE:  7% 47% 20% 33%

● Molecule 2: RNA

Chain TF:  7% 53% 13% 33%

● Molecule 2: RNA

Chain TG:  7% 53% 13% 33%

● Molecule 2: RNA

Chain TH:  10% 47% 20% 33%

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	277.47Å 396.64Å 399.87Å 69.66° 83.65° 83.49°	Depositor
Resolution (Å)	61.15 – 3.50 61.15 – 3.50	Depositor EDS
% Data completeness (in resolution range)	87.2 (61.15-3.50) 87.6 (61.15-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.31	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 3.49Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.261 , 0.261 0.268 , 0.267	Depositor DCC
R_{free} test set	20000 reflections (1.14%)	wwPDB-VP
Wilson B-factor (Å ²)	72.4	Xtriage
Anisotropy	0.317	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 60.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.096 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	327240	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.13% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.38	0/852	0.60	2/1158 (0.2%)
1	AB	0.37	0/852	0.57	0/1158
1	AC	0.38	0/852	0.55	0/1158
1	AD	0.38	0/852	0.60	2/1158 (0.2%)
1	AE	0.37	0/852	0.57	0/1158
1	AF	0.38	0/852	0.55	0/1158
1	AG	0.38	0/852	0.60	2/1158 (0.2%)
1	AH	0.37	0/852	0.57	0/1158
1	AI	0.38	0/852	0.55	0/1158
1	AJ	0.38	0/852	0.60	2/1158 (0.2%)
1	AK	0.37	0/852	0.57	0/1158
1	AL	0.38	0/852	0.55	0/1158
1	AM	0.38	0/852	0.60	2/1158 (0.2%)
1	AN	0.37	0/852	0.58	0/1158
1	AO	0.38	0/852	0.55	0/1158
1	AP	0.38	0/852	0.60	2/1158 (0.2%)
1	AQ	0.37	0/852	0.57	0/1158
1	AR	0.38	0/852	0.55	0/1158
1	AS	0.38	0/852	0.60	2/1158 (0.2%)
1	AT	0.37	0/852	0.57	0/1158
1	AU	0.38	0/852	0.55	0/1158
1	AV	0.38	0/852	0.60	2/1158 (0.2%)
1	AW	0.37	0/852	0.57	0/1158
1	AX	0.38	0/852	0.55	0/1158
1	AY	0.38	0/852	0.60	2/1158 (0.2%)
1	AZ	0.37	0/852	0.57	0/1158
1	BA	0.38	0/852	0.55	0/1158
1	BB	0.38	0/852	0.60	2/1158 (0.2%)
1	BC	0.37	0/852	0.57	0/1158
1	BD	0.38	0/852	0.55	0/1158
1	BE	0.38	0/852	0.60	2/1158 (0.2%)
1	BF	0.37	0/852	0.57	0/1158
1	BG	0.38	0/852	0.55	0/1158
1	BH	0.38	0/852	0.60	2/1158 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.37	0/852	0.57	0/1158
1	BJ	0.38	0/852	0.55	0/1158
1	BK	0.38	0/852	0.60	2/1158 (0.2%)
1	BL	0.37	0/852	0.57	0/1158
1	BM	0.38	0/852	0.55	0/1158
1	BN	0.38	0/852	0.60	2/1158 (0.2%)
1	BO	0.37	0/852	0.57	0/1158
1	BP	0.38	0/852	0.55	0/1158
1	BQ	0.38	0/852	0.60	2/1158 (0.2%)
1	BR	0.37	0/852	0.57	0/1158
1	BS	0.38	0/852	0.55	0/1158
1	BT	0.38	0/852	0.60	2/1158 (0.2%)
1	BU	0.36	0/852	0.57	0/1158
1	BV	0.38	0/852	0.55	0/1158
1	BW	0.38	0/852	0.60	2/1158 (0.2%)
1	BX	0.37	0/852	0.57	0/1158
1	BY	0.38	0/852	0.55	0/1158
1	BZ	0.38	0/852	0.60	2/1158 (0.2%)
1	CA	0.37	0/852	0.57	0/1158
1	CB	0.38	0/852	0.55	0/1158
1	CC	0.38	0/852	0.60	2/1158 (0.2%)
1	CD	0.37	0/852	0.58	0/1158
1	CE	0.38	0/852	0.55	0/1158
1	CF	0.38	0/852	0.60	2/1158 (0.2%)
1	CG	0.37	0/852	0.57	0/1158
1	CH	0.38	0/852	0.55	0/1158
1	CI	0.38	0/852	0.60	2/1158 (0.2%)
1	CJ	0.37	0/852	0.57	0/1158
1	CK	0.38	0/852	0.55	0/1158
1	CL	0.38	0/852	0.60	2/1158 (0.2%)
1	CM	0.37	0/852	0.57	0/1158
1	CN	0.38	0/852	0.55	0/1158
1	CO	0.38	0/852	0.60	2/1158 (0.2%)
1	CP	0.37	0/852	0.57	0/1158
1	CQ	0.38	0/852	0.55	0/1158
1	CR	0.38	0/852	0.60	2/1158 (0.2%)
1	CS	0.37	0/852	0.57	0/1158
1	CT	0.38	0/852	0.55	0/1158
1	CU	0.38	0/852	0.60	2/1158 (0.2%)
1	CV	0.37	0/852	0.58	0/1158
1	CW	0.38	0/852	0.55	0/1158
1	CX	0.38	0/852	0.60	2/1158 (0.2%)
1	CY	0.37	0/852	0.57	0/1158

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CZ	0.38	0/852	0.55	0/1158
1	DA	0.38	0/852	0.60	2/1158 (0.2%)
1	DB	0.37	0/852	0.57	0/1158
1	DC	0.38	0/852	0.55	0/1158
1	DD	0.38	0/852	0.60	2/1158 (0.2%)
1	DE	0.37	0/852	0.57	0/1158
1	DF	0.38	0/852	0.55	0/1158
1	DG	0.38	0/852	0.60	2/1158 (0.2%)
1	DH	0.37	0/852	0.57	0/1158
1	DI	0.38	0/852	0.55	0/1158
1	DJ	0.38	0/852	0.60	2/1158 (0.2%)
1	DK	0.37	0/852	0.57	0/1158
1	DL	0.38	0/852	0.55	0/1158
1	DM	0.38	0/852	0.60	2/1158 (0.2%)
1	DN	0.37	0/852	0.57	0/1158
1	DO	0.38	0/852	0.55	0/1158
1	DP	0.38	0/852	0.60	2/1158 (0.2%)
1	DQ	0.37	0/852	0.57	0/1158
1	DR	0.38	0/852	0.55	0/1158
1	DS	0.38	0/852	0.60	2/1158 (0.2%)
1	DT	0.37	0/852	0.57	0/1158
1	DU	0.38	0/852	0.55	0/1158
1	DV	0.38	0/852	0.60	2/1158 (0.2%)
1	DW	0.37	0/852	0.57	0/1158
1	DX	0.38	0/852	0.55	0/1158
1	DY	0.38	0/852	0.60	2/1158 (0.2%)
1	DZ	0.37	0/852	0.57	0/1158
1	EA	0.38	0/852	0.55	0/1158
1	EB	0.38	0/852	0.60	2/1158 (0.2%)
1	EC	0.37	0/852	0.57	0/1158
1	ED	0.38	0/852	0.55	0/1158
1	EE	0.38	0/852	0.60	2/1158 (0.2%)
1	EF	0.37	0/852	0.57	0/1158
1	EG	0.38	0/852	0.55	0/1158
1	EH	0.38	0/852	0.60	2/1158 (0.2%)
1	EI	0.37	0/852	0.57	0/1158
1	EJ	0.38	0/852	0.55	0/1158
1	EK	0.38	0/852	0.60	2/1158 (0.2%)
1	EL	0.37	0/852	0.57	0/1158
1	EM	0.38	0/852	0.55	0/1158
1	EN	0.38	0/852	0.60	2/1158 (0.2%)
1	EO	0.37	0/852	0.57	0/1158
1	EP	0.38	0/852	0.55	0/1158

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	EQ	0.38	0/852	0.60	2/1158 (0.2%)
1	ER	0.37	0/852	0.57	0/1158
1	ES	0.38	0/852	0.55	0/1158
1	ET	0.38	0/852	0.60	2/1158 (0.2%)
1	EU	0.37	0/852	0.57	0/1158
1	EV	0.38	0/852	0.55	0/1158
1	EW	0.38	0/852	0.60	2/1158 (0.2%)
1	EX	0.37	0/852	0.57	0/1158
1	EY	0.38	0/852	0.55	0/1158
1	EZ	0.38	0/852	0.60	2/1158 (0.2%)
1	FA	0.37	0/852	0.57	0/1158
1	FB	0.38	0/852	0.55	0/1158
1	FC	0.38	0/852	0.60	2/1158 (0.2%)
1	FD	0.37	0/852	0.57	0/1158
1	FE	0.38	0/852	0.55	0/1158
1	FF	0.38	0/852	0.60	2/1158 (0.2%)
1	FG	0.37	0/852	0.57	0/1158
1	FH	0.38	0/852	0.55	0/1158
1	FI	0.38	0/852	0.60	2/1158 (0.2%)
1	FJ	0.37	0/852	0.57	0/1158
1	FK	0.38	0/852	0.55	0/1158
1	FL	0.38	0/852	0.60	2/1158 (0.2%)
1	FM	0.37	0/852	0.57	0/1158
1	FN	0.38	0/852	0.55	0/1158
1	FO	0.38	0/852	0.60	2/1158 (0.2%)
1	FP	0.37	0/852	0.57	0/1158
1	FQ	0.38	0/852	0.55	0/1158
1	FR	0.38	0/852	0.60	2/1158 (0.2%)
1	FS	0.37	0/852	0.57	0/1158
1	FT	0.38	0/852	0.55	0/1158
1	FU	0.38	0/852	0.60	2/1158 (0.2%)
1	FV	0.37	0/852	0.57	0/1158
1	FW	0.38	0/852	0.55	0/1158
1	FX	0.38	0/852	0.60	2/1158 (0.2%)
1	FY	0.37	0/852	0.57	0/1158
1	FZ	0.38	0/852	0.55	0/1158
1	GA	0.38	0/852	0.60	2/1158 (0.2%)
1	GB	0.37	0/852	0.57	0/1158
1	GC	0.38	0/852	0.55	0/1158
1	GD	0.38	0/852	0.60	2/1158 (0.2%)
1	GE	0.37	0/852	0.57	0/1158
1	GF	0.38	0/852	0.55	0/1158
1	GG	0.38	0/852	0.60	2/1158 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GH	0.37	0/852	0.57	0/1158
1	GI	0.38	0/852	0.55	0/1158
1	GJ	0.38	0/852	0.60	2/1158 (0.2%)
1	GK	0.37	0/852	0.57	0/1158
1	GL	0.38	0/852	0.55	0/1158
1	GM	0.38	0/852	0.60	2/1158 (0.2%)
1	GN	0.37	0/852	0.57	0/1158
1	GO	0.38	0/852	0.55	0/1158
1	GP	0.38	0/852	0.60	2/1158 (0.2%)
1	GQ	0.37	0/852	0.57	0/1158
1	GR	0.38	0/852	0.55	0/1158
1	GS	0.38	0/852	0.60	2/1158 (0.2%)
1	GT	0.37	0/852	0.57	0/1158
1	GU	0.38	0/852	0.55	0/1158
1	GV	0.38	0/852	0.60	2/1158 (0.2%)
1	GW	0.37	0/852	0.57	0/1158
1	GX	0.38	0/852	0.55	0/1158
1	GY	0.38	0/852	0.60	2/1158 (0.2%)
1	GZ	0.37	0/852	0.57	0/1158
1	HA	0.38	0/852	0.55	0/1158
1	HB	0.38	0/852	0.60	2/1158 (0.2%)
1	HC	0.37	0/852	0.57	0/1158
1	HD	0.38	0/852	0.55	0/1158
1	HE	0.38	0/852	0.60	2/1158 (0.2%)
1	HF	0.37	0/852	0.58	0/1158
1	HG	0.38	0/852	0.55	0/1158
1	HH	0.38	0/852	0.60	2/1158 (0.2%)
1	HI	0.37	0/852	0.57	0/1158
1	HJ	0.38	0/852	0.55	0/1158
1	HK	0.38	0/852	0.60	2/1158 (0.2%)
1	HL	0.37	0/852	0.57	0/1158
1	HM	0.38	0/852	0.55	0/1158
1	HN	0.38	0/852	0.60	2/1158 (0.2%)
1	HO	0.37	0/852	0.57	0/1158
1	HP	0.38	0/852	0.55	0/1158
1	HQ	0.38	0/852	0.60	2/1158 (0.2%)
1	HR	0.37	0/852	0.58	0/1158
1	HS	0.38	0/852	0.55	0/1158
1	HT	0.38	0/852	0.60	2/1158 (0.2%)
1	HU	0.37	0/852	0.57	0/1158
1	HV	0.38	0/852	0.55	0/1158
1	HW	0.38	0/852	0.60	2/1158 (0.2%)
1	HX	0.37	0/852	0.57	0/1158

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	HY	0.38	0/852	0.55	0/1158
1	HZ	0.38	0/852	0.60	2/1158 (0.2%)
1	IA	0.37	0/852	0.57	0/1158
1	IB	0.38	0/852	0.55	0/1158
1	IC	0.38	0/852	0.60	2/1158 (0.2%)
1	ID	0.37	0/852	0.57	0/1158
1	IE	0.38	0/852	0.55	0/1158
1	IF	0.38	0/852	0.60	2/1158 (0.2%)
1	IG	0.37	0/852	0.57	0/1158
1	IH	0.38	0/852	0.55	0/1158
1	II	0.38	0/852	0.60	2/1158 (0.2%)
1	IJ	0.37	0/852	0.57	0/1158
1	IK	0.38	0/852	0.55	0/1158
1	IL	0.38	0/852	0.60	2/1158 (0.2%)
1	IM	0.37	0/852	0.57	0/1158
1	IN	0.38	0/852	0.55	0/1158
1	IO	0.38	0/852	0.60	2/1158 (0.2%)
1	IP	0.37	0/852	0.57	0/1158
1	IQ	0.38	0/852	0.55	0/1158
1	IR	0.38	0/852	0.60	2/1158 (0.2%)
1	IS	0.37	0/852	0.57	0/1158
1	IT	0.38	0/852	0.55	0/1158
1	IU	0.38	0/852	0.60	2/1158 (0.2%)
1	IV	0.37	0/852	0.57	0/1158
1	IW	0.38	0/852	0.55	0/1158
1	IX	0.38	0/852	0.60	2/1158 (0.2%)
1	IY	0.37	0/852	0.57	0/1158
1	IZ	0.38	0/852	0.55	0/1158
1	JA	0.38	0/852	0.60	2/1158 (0.2%)
1	JB	0.37	0/852	0.58	0/1158
1	JC	0.38	0/852	0.55	0/1158
1	JD	0.38	0/852	0.60	2/1158 (0.2%)
1	JE	0.37	0/852	0.57	0/1158
1	JF	0.38	0/852	0.55	0/1158
1	JG	0.38	0/852	0.60	2/1158 (0.2%)
1	JH	0.37	0/852	0.57	0/1158
1	JI	0.38	0/852	0.55	0/1158
1	JJ	0.38	0/852	0.60	2/1158 (0.2%)
1	JK	0.37	0/852	0.58	0/1158
1	JL	0.38	0/852	0.55	0/1158
1	JM	0.38	0/852	0.60	2/1158 (0.2%)
1	JN	0.37	0/852	0.57	0/1158
1	JO	0.38	0/852	0.55	0/1158

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	JP	0.38	0/852	0.60	2/1158 (0.2%)
1	JQ	0.37	0/852	0.57	0/1158
1	JR	0.38	0/852	0.55	0/1158
1	JS	0.38	0/852	0.60	2/1158 (0.2%)
1	JT	0.37	0/852	0.57	0/1158
1	JU	0.38	0/852	0.55	0/1158
1	JV	0.38	0/852	0.60	2/1158 (0.2%)
1	JW	0.37	0/852	0.57	0/1158
1	JX	0.38	0/852	0.55	0/1158
1	JY	0.38	0/852	0.60	2/1158 (0.2%)
1	JZ	0.37	0/852	0.57	0/1158
1	KA	0.38	0/852	0.55	0/1158
1	KB	0.38	0/852	0.60	2/1158 (0.2%)
1	KC	0.37	0/852	0.58	0/1158
1	KD	0.38	0/852	0.55	0/1158
1	KE	0.38	0/852	0.60	2/1158 (0.2%)
1	KF	0.37	0/852	0.57	0/1158
1	KG	0.38	0/852	0.55	0/1158
1	KH	0.38	0/852	0.60	2/1158 (0.2%)
1	KI	0.37	0/852	0.58	0/1158
1	KJ	0.38	0/852	0.55	0/1158
1	KK	0.38	0/852	0.60	2/1158 (0.2%)
1	KL	0.37	0/852	0.57	0/1158
1	KM	0.38	0/852	0.55	0/1158
1	KN	0.38	0/852	0.60	2/1158 (0.2%)
1	KO	0.37	0/852	0.57	0/1158
1	KP	0.38	0/852	0.55	0/1158
1	KQ	0.38	0/852	0.60	2/1158 (0.2%)
1	KR	0.37	0/852	0.57	0/1158
1	KS	0.38	0/852	0.55	0/1158
1	KT	0.38	0/852	0.60	2/1158 (0.2%)
1	KU	0.37	0/852	0.57	0/1158
1	KV	0.38	0/852	0.55	0/1158
1	KW	0.38	0/852	0.60	2/1158 (0.2%)
1	KX	0.37	0/852	0.57	0/1158
1	KY	0.38	0/852	0.55	0/1158
1	KZ	0.38	0/852	0.60	2/1158 (0.2%)
1	LA	0.37	0/852	0.57	0/1158
1	LB	0.38	0/852	0.55	0/1158
1	LC	0.38	0/852	0.60	2/1158 (0.2%)
1	LD	0.37	0/852	0.57	0/1158
1	LE	0.38	0/852	0.55	0/1158
1	LF	0.38	0/852	0.60	2/1158 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	LG	0.37	0/852	0.57	0/1158
1	LH	0.38	0/852	0.55	0/1158
1	LI	0.38	0/852	0.60	2/1158 (0.2%)
1	LJ	0.37	0/852	0.57	0/1158
1	LK	0.38	0/852	0.55	0/1158
1	LL	0.38	0/852	0.60	2/1158 (0.2%)
1	LM	0.37	0/852	0.57	0/1158
1	LN	0.38	0/852	0.55	0/1158
1	LO	0.38	0/852	0.60	2/1158 (0.2%)
1	LP	0.37	0/852	0.57	0/1158
1	LQ	0.38	0/852	0.55	0/1158
1	LR	0.38	0/852	0.60	2/1158 (0.2%)
1	LS	0.37	0/852	0.57	0/1158
1	LT	0.38	0/852	0.55	0/1158
1	LU	0.38	0/852	0.60	2/1158 (0.2%)
1	LV	0.37	0/852	0.57	0/1158
1	LW	0.38	0/852	0.55	0/1158
1	LX	0.38	0/852	0.60	2/1158 (0.2%)
1	LY	0.37	0/852	0.57	0/1158
1	LZ	0.38	0/852	0.55	0/1158
1	MA	0.38	0/852	0.60	2/1158 (0.2%)
1	MB	0.37	0/852	0.57	0/1158
1	MC	0.38	0/852	0.55	0/1158
1	MD	0.38	0/852	0.60	2/1158 (0.2%)
1	ME	0.37	0/852	0.57	0/1158
1	MF	0.38	0/852	0.55	0/1158
1	MG	0.38	0/852	0.60	2/1158 (0.2%)
1	MH	0.37	0/852	0.57	0/1158
1	MI	0.38	0/852	0.55	0/1158
1	MJ	0.38	0/852	0.60	2/1158 (0.2%)
1	MK	0.37	0/852	0.57	0/1158
1	ML	0.38	0/852	0.55	0/1158
1	MM	0.38	0/852	0.60	2/1158 (0.2%)
1	MN	0.37	0/852	0.57	0/1158
1	MO	0.38	0/852	0.55	0/1158
1	MP	0.38	0/852	0.60	2/1158 (0.2%)
1	MQ	0.37	0/852	0.57	0/1158
1	MR	0.38	0/852	0.55	0/1158
1	MS	0.38	0/852	0.60	2/1158 (0.2%)
1	MT	0.37	0/852	0.57	0/1158
1	MU	0.38	0/852	0.55	0/1158
1	MV	0.38	0/852	0.60	2/1158 (0.2%)
1	MW	0.37	0/852	0.57	0/1158

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	MX	0.38	0/852	0.55	0/1158
1	MY	0.38	0/852	0.60	2/1158 (0.2%)
1	MZ	0.37	0/852	0.57	0/1158
1	NA	0.38	0/852	0.55	0/1158
1	NB	0.38	0/852	0.60	2/1158 (0.2%)
1	NC	0.37	0/852	0.57	0/1158
1	ND	0.38	0/852	0.55	0/1158
1	NE	0.38	0/852	0.60	2/1158 (0.2%)
1	NF	0.37	0/852	0.57	0/1158
1	NG	0.38	0/852	0.55	0/1158
1	NH	0.38	0/852	0.60	2/1158 (0.2%)
1	NI	0.37	0/852	0.57	0/1158
1	NJ	0.38	0/852	0.55	0/1158
1	NK	0.38	0/852	0.60	2/1158 (0.2%)
1	NL	0.37	0/852	0.57	0/1158
1	NM	0.38	0/852	0.55	0/1158
1	NN	0.38	0/852	0.60	2/1158 (0.2%)
1	NO	0.37	0/852	0.57	0/1158
1	NP	0.38	0/852	0.55	0/1158
1	NQ	0.38	0/852	0.60	2/1158 (0.2%)
1	NR	0.37	0/852	0.57	0/1158
1	NS	0.38	0/852	0.55	0/1158
1	NT	0.38	0/852	0.60	2/1158 (0.2%)
1	NU	0.37	0/852	0.57	0/1158
1	NV	0.38	0/852	0.55	0/1158
2	RA	0.35	0/468	0.45	0/722
2	RB	0.35	0/468	0.45	0/722
2	RC	0.35	0/468	0.45	0/722
2	RD	0.35	0/468	0.45	0/722
2	RE	0.35	0/468	0.45	0/722
2	RF	0.35	0/468	0.45	0/722
2	RG	0.35	0/468	0.45	0/722
2	RH	0.35	0/468	0.45	0/722
2	RI	0.35	0/468	0.45	0/722
2	RJ	0.35	0/468	0.45	0/722
2	RK	0.35	0/468	0.45	0/722
2	RL	0.35	0/468	0.45	0/722
2	RM	0.35	0/468	0.45	0/722
2	RN	0.35	0/468	0.45	0/722
2	RO	0.35	0/468	0.45	0/722
2	RP	0.35	0/468	0.45	0/722
2	RQ	0.35	0/468	0.45	0/722
2	RR	0.35	0/468	0.45	0/722

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	RS	0.35	0/468	0.45	0/722
2	RT	0.35	0/468	0.45	0/722
2	RU	0.35	0/468	0.45	0/722
2	RV	0.35	0/468	0.45	0/722
2	RW	0.35	0/468	0.45	0/722
2	RX	0.35	0/468	0.45	0/722
2	RY	0.35	0/468	0.45	0/722
2	RZ	0.35	0/468	0.45	0/722
2	SA	0.35	0/468	0.45	0/722
2	SB	0.35	0/468	0.45	0/722
2	SC	0.35	0/468	0.45	0/722
2	SD	0.35	0/468	0.45	0/722
2	SE	0.35	0/468	0.45	0/722
2	SF	0.35	0/468	0.45	0/722
2	SG	0.35	0/468	0.45	0/722
2	SH	0.35	0/468	0.45	0/722
2	SI	0.35	0/468	0.45	0/722
2	SJ	0.35	0/468	0.45	0/722
2	SK	0.35	0/468	0.45	0/722
2	SL	0.35	0/468	0.45	0/722
2	SM	0.35	0/468	0.45	0/722
2	SN	0.35	0/468	0.45	0/722
2	SO	0.35	0/468	0.45	0/722
2	SP	0.35	0/468	0.45	0/722
2	SQ	0.35	0/468	0.45	0/722
2	SR	0.35	0/468	0.45	0/722
2	SS	0.35	0/468	0.45	0/722
2	ST	0.35	0/468	0.45	0/722
2	SU	0.35	0/468	0.45	0/722
2	SV	0.35	0/468	0.45	0/722
2	SW	0.35	0/468	0.45	0/722
2	SX	0.35	0/468	0.45	0/722
2	SY	0.35	0/468	0.45	0/722
2	SZ	0.35	0/468	0.45	0/722
2	TA	0.35	0/468	0.45	0/722
2	TB	0.35	0/468	0.45	0/722
2	TC	0.35	0/468	0.45	0/722
2	TD	0.35	0/468	0.45	0/722
2	TE	0.35	0/468	0.45	0/722
2	TF	0.35	0/468	0.45	0/722
2	TG	0.35	0/468	0.45	0/722
2	TH	0.35	0/468	0.45	0/722
All	All	0.37	0/334800	0.56	240/460200 (0.1%)

There are no bond length outliers.

All (240) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	GJ	38	SER	CA-C-N	-5.56	112.07	121.47
1	GJ	38	SER	C-N-CA	-5.56	112.07	121.47
1	DM	38	SER	CA-C-N	-5.56	112.08	121.47
1	DM	38	SER	C-N-CA	-5.56	112.08	121.47
1	KQ	38	SER	CA-C-N	-5.55	112.08	121.47
1	KQ	38	SER	C-N-CA	-5.55	112.08	121.47
1	BW	38	SER	CA-C-N	-5.55	112.09	121.47
1	BW	38	SER	C-N-CA	-5.55	112.09	121.47
1	IL	38	SER	CA-C-N	-5.55	112.09	121.47
1	IL	38	SER	C-N-CA	-5.55	112.09	121.47
1	CC	38	SER	CA-C-N	-5.54	112.11	121.47
1	CC	38	SER	C-N-CA	-5.54	112.11	121.47
1	HE	38	SER	CA-C-N	-5.54	112.10	121.47
1	HE	38	SER	C-N-CA	-5.54	112.10	121.47
1	JA	38	SER	CA-C-N	-5.54	112.11	121.47
1	JA	38	SER	C-N-CA	-5.54	112.11	121.47
1	NN	38	SER	CA-C-N	-5.54	112.11	121.47
1	NN	38	SER	C-N-CA	-5.54	112.11	121.47
1	KZ	38	SER	CA-C-N	-5.54	112.11	121.47
1	KZ	38	SER	C-N-CA	-5.54	112.11	121.47
1	CU	38	SER	CA-C-N	-5.54	112.11	121.47
1	CU	38	SER	C-N-CA	-5.54	112.11	121.47
1	DV	38	SER	CA-C-N	-5.54	112.11	121.47
1	DV	38	SER	C-N-CA	-5.54	112.11	121.47
1	EN	38	SER	CA-C-N	-5.54	112.11	121.47
1	EN	38	SER	C-N-CA	-5.54	112.11	121.47
1	MD	38	SER	CA-C-N	-5.54	112.11	121.47
1	MD	38	SER	C-N-CA	-5.54	112.11	121.47
1	MY	38	SER	CA-C-N	-5.54	112.11	121.47
1	MY	38	SER	C-N-CA	-5.54	112.11	121.47
1	LI	38	SER	CA-C-N	-5.54	112.11	121.47
1	LI	38	SER	C-N-CA	-5.54	112.11	121.47
1	FU	38	SER	CA-C-N	-5.54	112.12	121.47
1	FU	38	SER	C-N-CA	-5.54	112.12	121.47
1	HK	38	SER	CA-C-N	-5.54	112.12	121.47
1	HK	38	SER	C-N-CA	-5.54	112.12	121.47
1	IU	38	SER	CA-C-N	-5.54	112.11	121.47
1	IU	38	SER	C-N-CA	-5.54	112.11	121.47
1	EW	38	SER	CA-C-N	-5.53	112.12	121.47
1	EW	38	SER	C-N-CA	-5.53	112.12	121.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	JJ	38	SER	CA-C-N	-5.53	112.12	121.47
1	JJ	38	SER	C-N-CA	-5.53	112.12	121.47
1	MA	38	SER	CA-C-N	-5.53	112.12	121.47
1	MA	38	SER	C-N-CA	-5.53	112.12	121.47
1	AG	38	SER	CA-C-N	-5.53	112.12	121.47
1	AG	38	SER	C-N-CA	-5.53	112.12	121.47
1	FO	38	SER	CA-C-N	-5.53	112.12	121.47
1	FO	38	SER	C-N-CA	-5.53	112.12	121.47
1	GD	38	SER	CA-C-N	-5.53	112.12	121.47
1	GD	38	SER	C-N-CA	-5.53	112.12	121.47
1	HZ	38	SER	CA-C-N	-5.53	112.12	121.47
1	HZ	38	SER	C-N-CA	-5.53	112.12	121.47
1	KT	38	SER	CA-C-N	-5.53	112.12	121.47
1	KT	38	SER	C-N-CA	-5.53	112.12	121.47
1	MJ	38	SER	CA-C-N	-5.53	112.12	121.47
1	MJ	38	SER	C-N-CA	-5.53	112.12	121.47
1	MP	38	SER	CA-C-N	-5.53	112.12	121.47
1	MP	38	SER	C-N-CA	-5.53	112.12	121.47
1	DD	38	SER	CA-C-N	-5.53	112.13	121.47
1	DD	38	SER	C-N-CA	-5.53	112.13	121.47
1	DS	38	SER	CA-C-N	-5.53	112.13	121.47
1	DS	38	SER	C-N-CA	-5.53	112.13	121.47
1	JG	38	SER	CA-C-N	-5.53	112.13	121.47
1	JG	38	SER	C-N-CA	-5.53	112.13	121.47
1	KW	38	SER	CA-C-N	-5.53	112.13	121.47
1	KW	38	SER	C-N-CA	-5.53	112.13	121.47
1	MS	38	SER	CA-C-N	-5.53	112.12	121.47
1	MS	38	SER	C-N-CA	-5.53	112.12	121.47
1	BT	38	SER	CA-C-N	-5.53	112.13	121.47
1	BT	38	SER	C-N-CA	-5.53	112.13	121.47
1	CR	38	SER	CA-C-N	-5.53	112.13	121.47
1	CR	38	SER	C-N-CA	-5.53	112.13	121.47
1	GP	38	SER	CA-C-N	-5.53	112.13	121.47
1	GP	38	SER	C-N-CA	-5.53	112.13	121.47
1	KN	38	SER	CA-C-N	-5.53	112.13	121.47
1	KN	38	SER	C-N-CA	-5.53	112.13	121.47
1	LX	38	SER	CA-C-N	-5.53	112.13	121.47
1	LX	38	SER	C-N-CA	-5.53	112.13	121.47
1	BE	38	SER	CA-C-N	-5.53	112.13	121.47
1	BE	38	SER	C-N-CA	-5.53	112.13	121.47
1	BN	38	SER	CA-C-N	-5.53	112.13	121.47
1	BN	38	SER	C-N-CA	-5.53	112.13	121.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CI	38	SER	CA-C-N	-5.53	112.13	121.47
1	CI	38	SER	C-N-CA	-5.53	112.13	121.47
1	GA	38	SER	CA-C-N	-5.53	112.13	121.47
1	GA	38	SER	C-N-CA	-5.53	112.13	121.47
1	KK	38	SER	CA-C-N	-5.53	112.13	121.47
1	KK	38	SER	C-N-CA	-5.53	112.13	121.47
1	LR	38	SER	CA-C-N	-5.53	112.13	121.47
1	LR	38	SER	C-N-CA	-5.53	112.13	121.47
1	AJ	38	SER	CA-C-N	-5.52	112.14	121.47
1	AJ	38	SER	C-N-CA	-5.52	112.14	121.47
1	BB	38	SER	CA-C-N	-5.52	112.13	121.47
1	BB	38	SER	C-N-CA	-5.52	112.13	121.47
1	BK	38	SER	CA-C-N	-5.52	112.14	121.47
1	BK	38	SER	C-N-CA	-5.52	112.14	121.47
1	DP	38	SER	CA-C-N	-5.52	112.14	121.47
1	DP	38	SER	C-N-CA	-5.52	112.14	121.47
1	HT	38	SER	CA-C-N	-5.52	112.14	121.47
1	HT	38	SER	C-N-CA	-5.52	112.14	121.47
1	JV	38	SER	CA-C-N	-5.52	112.14	121.47
1	JV	38	SER	C-N-CA	-5.52	112.14	121.47
1	LL	38	SER	CA-C-N	-5.52	112.14	121.47
1	LL	38	SER	C-N-CA	-5.52	112.14	121.47
1	LO	38	SER	CA-C-N	-5.52	112.14	121.47
1	LO	38	SER	C-N-CA	-5.52	112.14	121.47
1	AY	38	SER	CA-C-N	-5.52	112.14	121.47
1	AY	38	SER	C-N-CA	-5.52	112.14	121.47
1	HQ	38	SER	CA-C-N	-5.52	112.14	121.47
1	HQ	38	SER	C-N-CA	-5.52	112.14	121.47
1	JM	38	SER	CA-C-N	-5.52	112.14	121.47
1	JM	38	SER	C-N-CA	-5.52	112.14	121.47
1	AA	38	SER	CA-C-N	-5.52	112.14	121.47
1	AA	38	SER	C-N-CA	-5.52	112.14	121.47
1	CO	38	SER	CA-C-N	-5.52	112.14	121.47
1	CO	38	SER	C-N-CA	-5.52	112.14	121.47
1	DY	38	SER	CA-C-N	-5.52	112.14	121.47
1	DY	38	SER	C-N-CA	-5.52	112.14	121.47
1	EE	38	SER	CA-C-N	-5.52	112.14	121.47
1	EE	38	SER	C-N-CA	-5.52	112.14	121.47
1	HN	38	SER	CA-C-N	-5.52	112.14	121.47
1	HN	38	SER	C-N-CA	-5.52	112.14	121.47
1	JS	38	SER	CA-C-N	-5.52	112.14	121.47
1	JS	38	SER	C-N-CA	-5.52	112.14	121.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	LF	38	SER	CA-C-N	-5.52	112.14	121.47
1	LF	38	SER	C-N-CA	-5.52	112.14	121.47
1	BQ	38	SER	CA-C-N	-5.52	112.15	121.47
1	BQ	38	SER	C-N-CA	-5.52	112.15	121.47
1	BZ	38	SER	CA-C-N	-5.52	112.14	121.47
1	BZ	38	SER	C-N-CA	-5.52	112.14	121.47
1	DA	38	SER	CA-C-N	-5.52	112.15	121.47
1	DA	38	SER	C-N-CA	-5.52	112.15	121.47
1	FX	38	SER	CA-C-N	-5.52	112.15	121.47
1	FX	38	SER	C-N-CA	-5.52	112.15	121.47
1	HB	38	SER	CA-C-N	-5.52	112.14	121.47
1	HB	38	SER	C-N-CA	-5.52	112.14	121.47
1	IC	38	SER	CA-C-N	-5.52	112.14	121.47
1	IC	38	SER	C-N-CA	-5.52	112.14	121.47
1	LU	38	SER	CA-C-N	-5.52	112.14	121.47
1	LU	38	SER	C-N-CA	-5.52	112.14	121.47
1	AS	38	SER	CA-C-N	-5.52	112.15	121.47
1	AS	38	SER	C-N-CA	-5.52	112.15	121.47
1	BH	38	SER	CA-C-N	-5.52	112.15	121.47
1	BH	38	SER	C-N-CA	-5.52	112.15	121.47
1	FI	38	SER	CA-C-N	-5.52	112.15	121.47
1	FI	38	SER	C-N-CA	-5.52	112.15	121.47
1	HW	38	SER	CA-C-N	-5.52	112.15	121.47
1	HW	38	SER	C-N-CA	-5.52	112.15	121.47
1	JP	38	SER	CA-C-N	-5.51	112.15	121.47
1	JP	38	SER	C-N-CA	-5.51	112.15	121.47
1	JY	38	SER	CA-C-N	-5.51	112.15	121.47
1	JY	38	SER	C-N-CA	-5.51	112.15	121.47
1	KB	38	SER	CA-C-N	-5.51	112.15	121.47
1	KB	38	SER	C-N-CA	-5.51	112.15	121.47
1	MM	38	SER	CA-C-N	-5.51	112.15	121.47
1	MM	38	SER	C-N-CA	-5.51	112.15	121.47
1	NB	38	SER	CA-C-N	-5.51	112.15	121.47
1	NB	38	SER	C-N-CA	-5.51	112.15	121.47
1	NE	38	SER	CA-C-N	-5.51	112.15	121.47
1	NE	38	SER	C-N-CA	-5.51	112.15	121.47
1	GS	38	SER	CA-C-N	-5.51	112.15	121.47
1	GS	38	SER	C-N-CA	-5.51	112.15	121.47
1	FC	38	SER	CA-C-N	-5.51	112.16	121.47
1	FC	38	SER	C-N-CA	-5.51	112.16	121.47
1	FR	38	SER	CA-C-N	-5.51	112.16	121.47
1	FR	38	SER	C-N-CA	-5.51	112.16	121.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	GG	38	SER	CA-C-N	-5.51	112.16	121.47
1	GG	38	SER	C-N-CA	-5.51	112.16	121.47
1	GV	38	SER	CA-C-N	-5.51	112.16	121.47
1	GV	38	SER	C-N-CA	-5.51	112.16	121.47
1	II	38	SER	CA-C-N	-5.51	112.16	121.47
1	II	38	SER	C-N-CA	-5.51	112.16	121.47
1	AD	38	SER	CA-C-N	-5.51	112.16	121.47
1	AD	38	SER	C-N-CA	-5.51	112.16	121.47
1	ET	38	SER	CA-C-N	-5.51	112.16	121.47
1	ET	38	SER	C-N-CA	-5.51	112.16	121.47
1	HH	38	SER	CA-C-N	-5.51	112.16	121.47
1	HH	38	SER	C-N-CA	-5.51	112.16	121.47
1	JD	38	SER	CA-C-N	-5.51	112.16	121.47
1	JD	38	SER	C-N-CA	-5.51	112.16	121.47
1	NH	38	SER	CA-C-N	-5.51	112.16	121.47
1	NH	38	SER	C-N-CA	-5.51	112.16	121.47
1	AP	38	SER	CA-C-N	-5.51	112.16	121.47
1	AP	38	SER	C-N-CA	-5.51	112.16	121.47
1	EH	38	SER	CA-C-N	-5.51	112.16	121.47
1	EH	38	SER	C-N-CA	-5.51	112.16	121.47
1	IO	38	SER	CA-C-N	-5.51	112.16	121.47
1	IO	38	SER	C-N-CA	-5.51	112.16	121.47
1	NK	38	SER	CA-C-N	-5.51	112.16	121.47
1	NK	38	SER	C-N-CA	-5.51	112.16	121.47
1	AM	38	SER	CA-C-N	-5.51	112.16	121.47
1	AM	38	SER	C-N-CA	-5.51	112.16	121.47
1	CX	38	SER	CA-C-N	-5.51	112.17	121.47
1	CX	38	SER	C-N-CA	-5.51	112.17	121.47
1	DG	38	SER	CA-C-N	-5.51	112.17	121.47
1	DG	38	SER	C-N-CA	-5.51	112.17	121.47
1	DJ	38	SER	CA-C-N	-5.51	112.16	121.47
1	DJ	38	SER	C-N-CA	-5.51	112.16	121.47
1	EQ	38	SER	CA-C-N	-5.51	112.16	121.47
1	EQ	38	SER	C-N-CA	-5.51	112.16	121.47
1	EZ	38	SER	CA-C-N	-5.51	112.16	121.47
1	EZ	38	SER	C-N-CA	-5.51	112.16	121.47
1	NQ	38	SER	CA-C-N	-5.51	112.17	121.47
1	NQ	38	SER	C-N-CA	-5.51	112.17	121.47
1	CF	38	SER	CA-C-N	-5.50	112.17	121.47
1	CF	38	SER	C-N-CA	-5.50	112.17	121.47
1	LC	38	SER	CA-C-N	-5.50	112.17	121.47
1	LC	38	SER	C-N-CA	-5.50	112.17	121.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	MG	38	SER	CA-C-N	-5.50	112.17	121.47
1	MG	38	SER	C-N-CA	-5.50	112.17	121.47
1	GM	38	SER	CA-C-N	-5.50	112.17	121.47
1	GM	38	SER	C-N-CA	-5.50	112.17	121.47
1	KH	38	SER	CA-C-N	-5.50	112.17	121.47
1	KH	38	SER	C-N-CA	-5.50	112.17	121.47
1	FF	38	SER	CA-C-N	-5.50	112.17	121.47
1	FF	38	SER	C-N-CA	-5.50	112.17	121.47
1	CL	38	SER	CA-C-N	-5.50	112.18	121.47
1	CL	38	SER	C-N-CA	-5.50	112.18	121.47
1	EK	38	SER	CA-C-N	-5.50	112.18	121.47
1	EK	38	SER	C-N-CA	-5.50	112.18	121.47
1	GY	38	SER	CA-C-N	-5.50	112.18	121.47
1	GY	38	SER	C-N-CA	-5.50	112.18	121.47
1	NT	38	SER	CA-C-N	-5.50	112.18	121.47
1	NT	38	SER	C-N-CA	-5.50	112.18	121.47
1	AV	38	SER	CA-C-N	-5.50	112.18	121.47
1	AV	38	SER	C-N-CA	-5.50	112.18	121.47
1	IR	38	SER	CA-C-N	-5.50	112.18	121.47
1	IR	38	SER	C-N-CA	-5.50	112.18	121.47
1	MV	38	SER	CA-C-N	-5.50	112.18	121.47
1	MV	38	SER	C-N-CA	-5.50	112.18	121.47
1	EB	38	SER	CA-C-N	-5.49	112.19	121.47
1	EB	38	SER	C-N-CA	-5.49	112.19	121.47
1	IF	38	SER	CA-C-N	-5.49	112.19	121.47
1	IF	38	SER	C-N-CA	-5.49	112.19	121.47
1	KE	38	SER	CA-C-N	-5.49	112.19	121.47
1	KE	38	SER	C-N-CA	-5.49	112.19	121.47
1	FL	38	SER	CA-C-N	-5.49	112.19	121.47
1	FL	38	SER	C-N-CA	-5.49	112.19	121.47
1	IX	38	SER	CA-C-N	-5.49	112.19	121.47
1	IX	38	SER	C-N-CA	-5.49	112.19	121.47

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	839	0	858	14	0
1	AB	839	0	858	8	0
1	AC	839	0	858	8	0
1	AD	839	0	858	12	0
1	AE	839	0	858	6	0
1	AF	839	0	858	13	0
1	AG	839	0	858	9	0
1	AH	839	0	858	12	0
1	AI	839	0	858	14	0
1	AJ	839	0	858	12	0
1	AK	839	0	858	6	0
1	AL	839	0	858	15	0
1	AM	839	0	858	11	0
1	AN	839	0	858	7	0
1	AO	839	0	858	15	0
1	AP	839	0	858	11	0
1	AQ	839	0	858	8	0
1	AR	839	0	858	14	0
1	AS	839	0	858	12	0
1	AT	839	0	858	10	0
1	AU	839	0	858	10	0
1	AV	839	0	858	10	0
1	AW	839	0	858	10	0
1	AX	839	0	858	12	0
1	AY	839	0	858	12	0
1	AZ	839	0	858	14	2
1	BA	839	0	858	18	0
1	BB	839	0	858	20	0
1	BC	839	0	858	14	0
1	BD	839	0	858	10	0
1	BE	839	0	858	12	0
1	BF	839	0	858	8	0
1	BG	839	0	858	16	0
1	BH	839	0	858	16	0
1	BI	839	0	858	13	0
1	BJ	839	0	858	11	0
1	BK	839	0	858	10	0
1	BL	839	0	858	10	0
1	BM	839	0	858	13	0
1	BN	839	0	858	25	0
1	BO	839	0	858	15	0
1	BP	839	0	858	13	0
1	BQ	839	0	858	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BR	839	0	858	21	0
1	BS	839	0	858	16	0
1	BT	839	0	858	9	0
1	BU	839	0	858	10	0
1	BV	839	0	858	16	0
1	BW	839	0	858	12	0
1	BX	839	0	858	10	0
1	BY	839	0	858	11	0
1	BZ	839	0	858	9	0
1	CA	839	0	858	10	0
1	CB	839	0	858	10	0
1	CC	839	0	858	12	0
1	CD	839	0	858	6	0
1	CE	839	0	858	11	0
1	CF	839	0	858	11	0
1	CG	839	0	858	7	0
1	CH	839	0	858	12	0
1	CI	839	0	858	10	0
1	CJ	839	0	858	12	0
1	CK	839	0	858	13	0
1	CL	839	0	858	9	0
1	CM	839	0	858	7	0
1	CN	839	0	858	9	0
1	CO	839	0	858	14	0
1	CP	839	0	858	18	0
1	CQ	839	0	858	15	0
1	CR	839	0	858	8	0
1	CS	839	0	858	11	0
1	CT	839	0	858	16	0
1	CU	839	0	858	12	0
1	CV	839	0	858	11	0
1	CW	839	0	858	11	0
1	CX	839	0	858	23	0
1	CY	839	0	858	11	0
1	CZ	839	0	858	16	0
1	DA	839	0	858	13	0
1	DB	839	0	858	11	0
1	DC	839	0	858	13	0
1	DD	839	0	858	12	0
1	DE	839	0	858	12	0
1	DF	839	0	858	14	0
1	DG	839	0	858	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DH	839	0	858	11	0
1	DI	839	0	858	16	0
1	DJ	839	0	858	21	0
1	DK	839	0	858	24	0
1	DL	839	0	858	17	0
1	DM	839	0	858	11	0
1	DN	839	0	858	8	0
1	DO	839	0	858	9	0
1	DP	839	0	858	12	0
1	DQ	839	0	858	10	0
1	DR	839	0	858	13	0
1	DS	839	0	858	9	0
1	DT	839	0	858	8	0
1	DU	839	0	858	10	0
1	DV	839	0	858	10	0
1	DW	839	0	858	9	0
1	DX	839	0	858	12	0
1	DY	839	0	858	11	0
1	DZ	839	0	858	23	0
1	EA	839	0	858	13	0
1	EB	839	0	858	13	0
1	EC	839	0	858	23	0
1	ED	839	0	858	12	0
1	EE	839	0	858	10	0
1	EF	839	0	858	9	0
1	EG	839	0	858	9	0
1	EH	839	0	858	11	0
1	EI	839	0	858	11	0
1	EJ	839	0	858	9	0
1	EK	839	0	858	13	0
1	EL	839	0	858	11	0
1	EM	839	0	858	18	0
1	EN	839	0	858	9	0
1	EO	839	0	858	10	0
1	EP	839	0	858	10	0
1	EQ	839	0	858	12	0
1	ER	839	0	858	12	0
1	ES	839	0	858	18	0
1	ET	839	0	858	9	0
1	EU	839	0	858	9	1
1	EV	839	0	858	10	0
1	EW	839	0	858	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	EX	839	0	858	14	0
1	EY	839	0	858	11	0
1	EZ	839	0	858	10	0
1	FA	839	0	858	10	0
1	FB	839	0	858	11	0
1	FC	839	0	858	11	0
1	FD	839	0	858	7	0
1	FE	839	0	858	16	0
1	FF	839	0	858	9	0
1	FG	839	0	858	7	0
1	FH	839	0	858	15	0
1	FI	839	0	858	13	0
1	FJ	839	0	858	10	0
1	FK	839	0	858	7	0
1	FL	839	0	858	11	0
1	FM	839	0	858	10	0
1	FN	839	0	858	8	0
1	FO	839	0	858	7	0
1	FP	839	0	858	12	0
1	FQ	839	0	858	9	0
1	FR	839	0	858	9	0
1	FS	839	0	858	12	1
1	FT	839	0	858	9	0
1	FU	839	0	858	10	0
1	FV	839	0	858	7	0
1	FW	839	0	858	10	0
1	FX	839	0	858	9	0
1	FY	839	0	858	8	0
1	FZ	839	0	858	12	0
1	GA	839	0	858	9	0
1	GB	839	0	858	11	0
1	GC	839	0	858	15	0
1	GD	839	0	858	14	0
1	GE	839	0	858	8	0
1	GF	839	0	858	13	0
1	GG	839	0	858	10	0
1	GH	839	0	858	9	0
1	GI	839	0	858	11	0
1	GJ	839	0	858	11	0
1	GK	839	0	858	11	1
1	GL	839	0	858	17	0
1	GM	839	0	858	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GN	839	0	858	8	0
1	GO	839	0	858	11	0
1	GP	839	0	858	14	0
1	GQ	839	0	858	8	0
1	GR	839	0	858	13	0
1	GS	839	0	858	8	0
1	GT	839	0	858	10	0
1	GU	839	0	858	15	0
1	GV	839	0	858	13	0
1	GW	839	0	858	11	0
1	GX	839	0	858	19	0
1	GY	839	0	858	12	0
1	GZ	839	0	858	9	0
1	HA	839	0	858	21	0
1	HB	839	0	858	9	0
1	HC	839	0	858	9	0
1	HD	839	0	858	11	0
1	HE	839	0	858	18	0
1	HF	839	0	858	10	0
1	HG	839	0	858	8	0
1	HH	839	0	858	12	0
1	HI	839	0	858	25	0
1	HJ	839	0	858	11	0
1	HK	839	0	858	12	0
1	HL	839	0	858	10	0
1	HM	839	0	858	20	0
1	HN	839	0	858	12	0
1	HO	839	0	858	16	0
1	HP	839	0	858	12	0
1	HQ	839	0	858	8	0
1	HR	839	0	858	8	1
1	HS	839	0	858	11	0
1	HT	839	0	858	9	0
1	HU	839	0	858	8	0
1	HV	839	0	858	11	0
1	HW	839	0	858	10	0
1	HX	839	0	858	10	0
1	HY	839	0	858	10	0
1	HZ	839	0	858	10	0
1	IA	839	0	858	7	0
1	IB	839	0	858	17	0
1	IC	839	0	858	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	ID	839	0	858	19	0
1	IE	839	0	858	16	0
1	IF	839	0	858	8	0
1	IG	839	0	858	10	0
1	IH	839	0	858	16	0
1	II	839	0	858	12	0
1	IJ	839	0	858	21	0
1	IK	839	0	858	12	0
1	IL	839	0	858	9	0
1	IM	839	0	858	7	0
1	IN	839	0	858	13	0
1	IO	839	0	858	9	0
1	IP	839	0	858	9	0
1	IQ	839	0	858	15	0
1	IR	839	0	858	13	0
1	IS	839	0	858	11	0
1	IT	839	0	858	14	0
1	IU	839	0	858	9	0
1	IV	839	0	858	11	0
1	IW	839	0	858	11	0
1	IX	839	0	858	11	0
1	IY	839	0	858	12	0
1	IZ	839	0	858	13	0
1	JA	839	0	858	13	0
1	JB	839	0	858	7	0
1	JC	839	0	858	15	0
1	JD	839	0	858	10	0
1	JE	839	0	858	17	0
1	JF	839	0	858	15	0
1	JG	839	0	858	9	0
1	JH	839	0	858	11	0
1	JI	839	0	858	16	0
1	JJ	839	0	858	17	0
1	JK	839	0	858	11	0
1	JL	839	0	858	12	0
1	JM	839	0	858	12	0
1	JN	839	0	858	17	0
1	JO	839	0	858	16	0
1	JP	839	0	858	9	0
1	JQ	839	0	858	10	0
1	JR	839	0	858	11	0
1	JS	839	0	858	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	JT	839	0	858	9	0
1	JU	839	0	858	11	0
1	JV	839	0	858	9	0
1	JW	839	0	858	7	0
1	JX	839	0	858	11	0
1	JY	839	0	858	11	0
1	JZ	839	0	858	7	0
1	KA	839	0	858	11	0
1	KB	839	0	858	11	0
1	KC	839	0	858	9	0
1	KD	839	0	858	13	0
1	KE	839	0	858	12	0
1	KF	839	0	858	12	0
1	KG	839	0	858	11	0
1	KH	839	0	858	17	0
1	KI	839	0	858	8	1
1	KJ	839	0	858	16	0
1	KK	839	0	858	11	0
1	KL	839	0	858	10	0
1	KM	839	0	858	23	0
1	KN	839	0	858	11	0
1	KO	839	0	858	8	0
1	KP	839	0	858	9	0
1	KQ	839	0	858	13	0
1	KR	839	0	858	11	0
1	KS	839	0	858	9	0
1	KT	839	0	858	11	0
1	KU	839	0	858	11	0
1	KV	839	0	858	13	0
1	KW	839	0	858	15	0
1	KX	839	0	858	8	0
1	KY	839	0	858	19	0
1	KZ	839	0	858	12	0
1	LA	839	0	858	8	0
1	LB	839	0	858	12	0
1	LC	839	0	858	14	0
1	LD	839	0	858	8	0
1	LE	839	0	858	11	0
1	LF	839	0	858	13	0
1	LG	839	0	858	9	0
1	LH	839	0	858	10	0
1	LI	839	0	858	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LJ	839	0	858	7	0
1	LK	839	0	858	7	0
1	LL	839	0	858	10	0
1	LM	839	0	858	12	0
1	LN	839	0	858	14	0
1	LO	839	0	858	11	0
1	LP	839	0	858	8	0
1	LQ	839	0	858	17	0
1	LR	839	0	858	17	0
1	LS	839	0	858	14	0
1	LT	839	0	858	16	0
1	LU	839	0	858	11	0
1	LV	839	0	858	7	0
1	LW	839	0	858	12	0
1	LX	839	0	858	10	0
1	LY	839	0	858	12	0
1	LZ	839	0	858	10	0
1	MA	839	0	858	9	0
1	MB	839	0	858	8	0
1	MC	839	0	858	17	0
1	MD	839	0	858	11	0
1	ME	839	0	858	16	1
1	MF	839	0	858	13	0
1	MG	839	0	858	10	0
1	MH	839	0	858	8	0
1	MI	839	0	858	10	0
1	MJ	839	0	858	13	0
1	MK	839	0	858	10	0
1	ML	839	0	858	14	0
1	MM	839	0	858	32	0
1	MN	839	0	858	17	0
1	MO	839	0	858	15	0
1	MP	839	0	858	11	0
1	MQ	839	0	858	11	0
1	MR	839	0	858	20	0
1	MS	839	0	858	17	0
1	MT	839	0	858	11	0
1	MU	839	0	858	14	0
1	MV	839	0	858	11	0
1	MW	839	0	858	13	0
1	MX	839	0	858	9	0
1	MY	839	0	858	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	MZ	839	0	858	9	0
1	NA	839	0	858	15	0
1	NB	839	0	858	9	0
1	NC	839	0	858	9	0
1	ND	839	0	858	9	0
1	NE	839	0	858	9	0
1	NF	839	0	858	7	0
1	NG	839	0	858	10	0
1	NH	839	0	858	9	0
1	NI	839	0	858	12	0
1	NJ	839	0	858	9	0
1	NK	839	0	858	10	0
1	NL	839	0	858	9	2
1	NM	839	0	858	10	0
1	NN	839	0	858	12	0
1	NO	839	0	858	12	0
1	NP	839	0	858	10	0
1	NQ	839	0	858	12	0
1	NR	839	0	858	10	0
1	NS	839	0	858	8	0
1	NT	839	0	858	16	0
1	NU	839	0	858	12	0
1	NV	839	0	858	17	0
2	RA	420	0	212	7	0
2	RB	420	0	212	6	0
2	RC	420	0	212	3	0
2	RD	420	0	212	3	0
2	RE	420	0	212	3	0
2	RF	420	0	212	5	0
2	RG	420	0	212	6	0
2	RH	420	0	212	3	0
2	RI	420	0	212	8	0
2	RJ	420	0	212	6	0
2	RK	420	0	212	7	0
2	RL	420	0	212	5	0
2	RM	420	0	212	3	0
2	RN	420	0	212	4	0
2	RO	420	0	212	6	0
2	RP	420	0	212	3	0
2	RQ	420	0	212	3	0
2	RR	420	0	212	4	0
2	RS	420	0	212	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	RT	420	0	212	4	0
2	RU	420	0	212	4	0
2	RV	420	0	212	7	0
2	RW	420	0	212	5	0
2	RX	420	0	212	3	0
2	RY	420	0	212	6	0
2	RZ	420	0	212	7	0
2	SA	420	0	212	3	0
2	SB	420	0	212	7	0
2	SC	420	0	212	6	0
2	SD	420	0	212	6	0
2	SE	420	0	212	7	0
2	SF	420	0	212	5	0
2	SG	420	0	212	7	0
2	SH	420	0	212	7	0
2	SI	420	0	212	6	0
2	SJ	420	0	212	6	0
2	SK	420	0	212	7	0
2	SL	420	0	212	5	0
2	SM	420	0	212	3	0
2	SN	420	0	212	4	0
2	SO	420	0	212	6	0
2	SP	420	0	212	6	0
2	SQ	420	0	212	5	0
2	SR	420	0	212	3	0
2	SS	420	0	212	6	0
2	ST	420	0	212	4	0
2	SU	420	0	212	4	0
2	SV	420	0	212	5	0
2	SW	420	0	212	7	0
2	SX	420	0	212	10	0
2	SY	420	0	212	5	0
2	SZ	420	0	212	3	0
2	TA	420	0	212	4	0
2	TB	420	0	212	4	0
2	TC	420	0	212	4	0
2	TD	420	0	212	4	0
2	TE	420	0	212	6	0
2	TF	420	0	212	4	0
2	TG	420	0	212	4	0
2	TH	420	0	212	7	0
All	All	327240	0	321600	2967	5

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 5.

All (2967) 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:EC:98:THR:HG23	1:MM:98:THR:HG23	1.36	1.05
1:EC:98:THR:CG2	1:MM:98:THR:HG23	1.95	0.96
1:CX:40:GLY:HA2	1:DK:109:LEU:O	1.71	0.90
1:EC:98:THR:HG23	1:MM:98:THR:CG2	2.06	0.83
1:HE:40:GLY:HA2	1:ID:109:LEU:O	1.78	0.83
1:IO:94:SER:HA	1:LA:97:ASN:HD21	1.44	0.82
1:BQ:98:THR:HG23	1:HI:98:THR:HG23	1.62	0.81
1:MN:109:LEU:O	1:NT:40:GLY:HA2	1.83	0.79
1:CX:35:ILE:HD13	1:DK:99:LEU:HD22	1.66	0.78
1:BB:40:GLY:HA2	1:BR:109:LEU:O	1.86	0.76
1:AK:97:ASN:HD21	1:FO:94:SER:HA	1.50	0.76
1:BQ:10:SER:HB3	1:MM:101:ASP:OD2	1.86	0.76
1:JE:97:ASN:ND2	1:JJ:94:SER:HA	2.00	0.75
1:AI:109:LEU:O	1:DU:40:GLY:HA2	1.87	0.75
1:AY:94:SER:HA	1:EI:97:ASN:HD21	1.53	0.74
1:AQ:97:ASN:HD21	1:FU:94:SER:HA	1.53	0.73
1:BQ:10:SER:CB	1:MM:101:ASP:OD2	2.36	0.73
1:HR:97:ASN:HD21	1:LX:94:SER:HA	1.54	0.73
1:GZ:97:ASN:HD21	1:MV:94:SER:HA	1.54	0.73
1:JE:97:ASN:HD21	1:JJ:94:SER:HA	1.52	0.72
1:IL:94:SER:HA	1:KX:97:ASN:HD21	1.55	0.72
1:BQ:8:ILE:HD11	1:EC:99:LEU:HB2	1.72	0.72
1:EM:52:ALA:HB2	2:RI:26:A:H4'	1.72	0.72
1:HE:35:ILE:HD13	1:ID:99:LEU:HD22	1.72	0.71
1:IO:94:SER:HA	1:LA:97:ASN:ND2	2.04	0.71
1:AG:94:SER:HA	1:BF:97:ASN:HD21	1.55	0.71
1:EQ:94:SER:HA	1:FM:97:ASN:HD21	1.56	0.71
1:EP:20:TYR:OH	2:RJ:28:A:OP1	2.06	0.70
1:KS:20:TYR:OH	2:SG:28:A:OP1	2.09	0.70
1:IX:94:SER:HA	1:KR:97:ASN:HD21	1.57	0.70
1:CC:94:SER:HA	1:GK:97:ASN:HD21	1.57	0.69
1:JW:97:ASN:HD21	1:NE:94:SER:HA	1.58	0.69
1:GL:20:TYR:OH	2:RZ:28:A:OP1	2.08	0.69
1:IC:8:ILE:HD11	1:IJ:99:LEU:HB2	1.74	0.69
1:BQ:10:SER:N	1:MM:101:ASP:OD2	2.26	0.69
1:CM:97:ASN:HD21	1:DG:94:SER:HA	1.58	0.69
1:BG:53:VAL:HG12	1:ES:96:LEU:HD22	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:97:ASN:HD21	1:GA:94:SER:HA	1.58	0.68
1:AT:97:ASN:HD21	1:EZ:94:SER:HA	1.57	0.68
1:DL:97:ASN:HD21	1:GX:94:SER:HA	1.58	0.68
1:HB:94:SER:HA	1:IA:97:ASN:HD21	1.59	0.68
1:AB:97:ASN:HD21	1:FX:94:SER:HA	1.58	0.68
1:KK:94:SER:HA	1:NR:97:ASN:HD21	1.58	0.67
1:DS:94:SER:HA	1:GQ:97:ASN:HD21	1.58	0.67
1:CC:94:SER:HA	1:GK:97:ASN:ND2	2.10	0.67
1:HL:97:ASN:HD21	1:MP:94:SER:HA	1.57	0.67
1:LY:97:ASN:HD21	1:MJ:94:SER:HA	1.59	0.67
1:HH:8:ILE:HD11	1:IV:99:LEU:HB2	1.76	0.67
1:IX:40:GLY:HA3	1:KR:111:GLY:HA2	1.76	0.67
1:EX:111:GLY:HA2	1:FI:40:GLY:HA3	1.76	0.67
1:IH:94:SER:HA	1:LT:97:ASN:HD21	1.60	0.67
1:IN:109:LEU:O	1:LZ:40:GLY:HA2	1.95	0.67
1:IF:94:SER:HA	1:IM:97:ASN:HD21	1.59	0.67
1:GZ:97:ASN:ND2	1:MV:94:SER:HA	2.09	0.67
1:AK:97:ASN:ND2	1:FO:94:SER:HA	2.10	0.66
1:DL:97:ASN:ND2	1:GX:94:SER:HA	2.10	0.66
1:BQ:35:ILE:HD13	1:EC:99:LEU:HD22	1.78	0.66
1:LQ:20:TYR:OH	2:SO:28:A:OP1	2.10	0.66
1:LL:94:SER:HA	1:MH:97:ASN:HD21	1.59	0.66
1:BT:94:SER:HA	1:DN:97:ASN:HD21	1.60	0.66
1:IN:40:GLY:HA2	1:LZ:109:LEU:O	1.96	0.66
1:IC:96:LEU:HD22	1:IJ:53:VAL:HG12	1.78	0.66
1:HR:97:ASN:ND2	1:LX:94:SER:HA	2.11	0.66
1:IH:94:SER:HA	1:LT:97:ASN:ND2	2.11	0.66
1:MR:20:TYR:OH	2:SX:28:A:OP1	2.12	0.66
1:LC:35:ILE:HD13	1:LS:99:LEU:HD22	1.78	0.66
1:JY:94:SER:HA	1:KC:97:ASN:HD21	1.60	0.65
1:JN:21:TYR:HH	1:KH:113:PHE:C	2.04	0.65
1:AV:94:SER:HA	1:EF:97:ASN:HD21	1.61	0.65
1:GR:52:ALA:HB2	2:SB:26:A:H4'	1.79	0.65
1:JF:113:PHE:C	1:MR:21:TYR:HH	2.04	0.65
1:CC:40:GLY:HA3	1:GK:111:GLY:HA2	1.79	0.65
1:JN:97:ASN:HD21	1:KH:94:SER:HA	1.62	0.65
1:CD:97:ASN:HD21	1:CR:94:SER:HA	1.62	0.65
1:IX:94:SER:HA	1:KR:97:ASN:ND2	2.12	0.65
1:JL:40:GLY:HA2	1:MX:109:LEU:O	1.97	0.65
1:LV:97:ASN:HD21	1:MG:94:SER:HA	1.62	0.65
1:AY:94:SER:HA	1:EI:97:ASN:ND2	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:94:SER:HA	1:DT:97:ASN:HD21	1.60	0.65
1:EH:8:ILE:HD11	1:EO:99:LEU:HB2	1.79	0.64
1:IL:94:SER:HA	1:KX:97:ASN:ND2	2.12	0.64
1:IU:94:SER:HA	1:KO:97:ASN:HD21	1.60	0.64
1:CM:97:ASN:ND2	1:DG:94:SER:HA	2.13	0.64
1:EC:104:ARG:NH2	1:HI:9:GLY:O	2.30	0.64
1:MR:52:ALA:HB2	2:SX:26:A:H4'	1.79	0.64
1:CX:3:PHE:CE1	1:DK:104:ARG:HG2	2.32	0.64
1:JT:97:ASN:HD21	1:NK:94:SER:HA	1.61	0.64
1:BB:35:ILE:HD13	1:BR:99:LEU:HD22	1.80	0.64
1:IZ:40:GLY:HA2	1:ML:109:LEU:O	1.98	0.64
1:AM:94:SER:HA	1:CA:97:ASN:HD21	1.63	0.64
1:CY:97:ASN:HD21	1:GG:94:SER:HA	1.62	0.64
1:HL:111:GLY:HA2	1:MP:40:GLY:HA3	1.80	0.64
1:BQ:99:LEU:HD22	1:EC:35:ILE:HD13	1.80	0.64
1:BS:96:LEU:HD22	1:FE:53:VAL:HG12	1.80	0.64
1:FE:20:TYR:OH	2:RO:28:A:OP1	2.13	0.64
1:HQ:94:SER:HA	1:LJ:97:ASN:HD21	1.63	0.64
1:CU:8:ILE:HD11	1:DH:99:LEU:HB2	1.79	0.63
1:FS:40:GLY:HA3	1:GP:111:GLY:HA2	1.80	0.63
1:BK:94:SER:HA	1:DW:97:ASN:HD21	1.63	0.63
1:JS:8:ILE:HD11	1:KF:99:LEU:HB2	1.80	0.63
1:MT:97:ASN:HD21	1:NQ:94:SER:HA	1.63	0.63
1:BB:53:VAL:HG12	1:BR:96:LEU:HD22	1.81	0.63
1:FV:97:ASN:HD21	1:GS:94:SER:HA	1.64	0.63
1:EE:94:SER:HA	1:EU:97:ASN:HD21	1.63	0.63
1:LY:97:ASN:ND2	1:MJ:94:SER:HA	2.14	0.63
1:AL:40:GLY:HA2	1:DX:109:LEU:O	1.99	0.63
1:DB:97:ASN:HD21	1:GJ:94:SER:HA	1.62	0.63
1:EX:97:ASN:HD21	1:FI:94:SER:HA	1.63	0.63
1:LI:94:SER:HA	1:LP:97:ASN:HD21	1.62	0.63
1:ES:20:TYR:OH	2:RK:28:A:OP1	2.16	0.63
1:JG:94:SER:HA	1:NF:97:ASN:HD21	1.63	0.63
1:DS:94:SER:HA	1:GQ:97:ASN:ND2	2.14	0.63
1:AG:94:SER:HA	1:BF:97:ASN:ND2	2.13	0.63
1:DV:94:SER:HA	1:GE:97:ASN:HD21	1.63	0.63
1:JV:40:GLY:HA3	1:KI:111:GLY:HA2	1.81	0.63
1:NV:20:TYR:OH	2:TH:28:A:OP1	2.17	0.63
1:IC:99:LEU:HD22	1:IJ:35:ILE:HD13	1.81	0.62
1:LC:8:ILE:HD11	1:LS:99:LEU:HB2	1.80	0.62
1:CE:40:GLY:HA2	1:FQ:109:LEU:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:97:ASN:HD21	1:CL:94:SER:HA	1.64	0.62
1:DA:94:SER:HA	1:DE:97:ASN:HD21	1.64	0.62
1:HH:35:ILE:HD13	1:IV:99:LEU:HD22	1.82	0.62
1:IK:40:GLY:HA2	1:LW:109:LEU:O	1.98	0.62
1:AQ:97:ASN:ND2	1:FU:94:SER:HA	2.15	0.62
1:JZ:97:ASN:HD21	1:NH:94:SER:HA	1.64	0.62
1:AB:97:ASN:ND2	1:FX:94:SER:HA	2.14	0.62
1:AN:97:ASN:HD21	1:FR:94:SER:HA	1.65	0.62
1:BQ:98:THR:HG23	1:HI:98:THR:CG2	2.28	0.62
1:HE:8:ILE:HD11	1:ID:99:LEU:HB2	1.82	0.62
1:LF:40:GLY:HA3	1:LM:111:GLY:HA2	1.82	0.62
1:CX:8:ILE:HD11	1:DK:99:LEU:HB2	1.81	0.62
1:HU:97:ASN:HD21	1:MA:94:SER:HA	1.64	0.62
1:IU:94:SER:HA	1:KO:97:ASN:ND2	2.15	0.62
1:DY:94:SER:HA	1:FY:97:ASN:HD21	1.65	0.61
1:GX:41:LYS:HD2	2:SD:26:A:OP1	1.99	0.61
1:BZ:94:SER:HA	1:DT:97:ASN:ND2	2.16	0.61
1:AA:8:ILE:HD11	1:BI:99:LEU:HB2	1.83	0.61
1:AE:97:ASN:ND2	1:GA:94:SER:HA	2.16	0.61
1:AI:40:GLY:HA2	1:DU:109:LEU:O	2.00	0.61
1:HZ:8:ILE:HD11	1:IP:99:LEU:HB2	1.82	0.61
1:DR:20:TYR:OH	2:RB:28:A:OP1	2.15	0.61
1:HA:53:VAL:HG12	1:KM:96:LEU:HD22	1.83	0.61
1:AZ:97:ASN:ND2	1:EW:94:SER:HA	2.16	0.61
1:MN:97:ASN:HD21	1:NT:94:SER:HA	1.65	0.61
1:IC:35:ILE:HD13	1:IJ:99:LEU:HD22	1.83	0.61
1:BQ:101:ASP:OD2	1:MM:10:SER:N	2.34	0.61
1:ET:94:SER:HA	1:FG:97:ASN:HD21	1.64	0.61
1:BE:8:ILE:HD11	1:BL:99:LEU:HB2	1.83	0.61
1:CC:111:GLY:HA2	1:GK:40:GLY:HA3	1.83	0.60
1:CS:99:LEU:HB2	1:DD:8:ILE:HD11	1.82	0.60
1:GZ:111:GLY:HA2	1:MV:40:GLY:HA3	1.82	0.60
1:JH:97:ASN:HD21	1:JM:94:SER:HA	1.66	0.60
1:JV:94:SER:HA	1:KI:97:ASN:HD21	1.65	0.60
1:KN:111:GLY:HA2	1:NU:40:GLY:HA3	1.84	0.60
1:LQ:38:SER:OG	2:SO:27:U:OP1	2.17	0.60
1:HO:40:GLY:HA3	1:MS:111:GLY:HA2	1.83	0.60
1:AX:109:LEU:O	1:EJ:40:GLY:HA2	2.02	0.60
1:AJ:94:SER:HA	1:BX:97:ASN:HD21	1.66	0.60
1:BK:111:GLY:HA2	1:DW:40:GLY:HA3	1.83	0.60
1:IF:40:GLY:HA3	1:IM:111:GLY:HA2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:II:94:SER:HA	1:KU:97:ASN:HD21	1.67	0.60
1:JD:94:SER:HA	1:NL:97:ASN:HD21	1.66	0.60
1:BB:3:PHE:CE1	1:BR:104:ARG:HG2	2.37	0.60
1:DF:53:VAL:HG12	1:GR:96:LEU:HD22	1.82	0.60
1:BQ:96:LEU:HD22	1:EC:53:VAL:HG12	1.84	0.60
1:FZ:20:TYR:OH	2:RV:28:A:OP1	2.12	0.60
1:KZ:94:SER:HA	1:MZ:97:ASN:HD21	1.66	0.60
1:BD:96:LEU:HD22	1:EP:53:VAL:HG12	1.84	0.60
1:GL:38:SER:OG	2:RZ:27:U:OP1	2.16	0.60
1:LO:94:SER:HA	1:MK:97:ASN:HD21	1.67	0.60
1:MQ:111:GLY:HA2	1:NN:40:GLY:HA3	1.84	0.60
1:AT:97:ASN:ND2	1:EZ:94:SER:HA	2.16	0.59
1:JE:94:SER:HA	1:JJ:97:ASN:ND2	2.16	0.59
1:JG:94:SER:HA	1:NF:97:ASN:ND2	2.17	0.59
1:LQ:41:LYS:HD2	2:SO:26:A:OP1	2.02	0.59
1:MQ:97:ASN:HD21	1:NN:94:SER:HA	1.67	0.59
1:AD:94:SER:HA	1:BC:97:ASN:HD21	1.66	0.59
1:BQ:101:ASP:OD2	1:MM:10:SER:HB3	2.02	0.59
1:IC:104:ARG:NH1	1:IJ:3:PHE:CD1	2.70	0.59
1:CD:97:ASN:ND2	1:CR:94:SER:HA	2.18	0.59
1:ES:52:ALA:HB2	2:RK:26:A:H4'	1.84	0.59
1:JB:97:ASN:HD21	1:JP:94:SER:HA	1.66	0.59
1:JL:109:LEU:O	1:MX:40:GLY:HA2	2.03	0.59
1:KM:20:TYR:OH	2:SE:28:A:OP1	2.13	0.59
1:KT:94:SER:HA	1:NC:97:ASN:HD21	1.66	0.59
1:IF:94:SER:HA	1:IM:97:ASN:ND2	2.16	0.59
1:BB:3:PHE:CD1	1:BR:104:ARG:NH1	2.71	0.59
1:JA:94:SER:HA	1:NI:97:ASN:HD21	1.67	0.59
1:KD:109:LEU:O	1:NP:40:GLY:HA2	2.03	0.59
1:LF:94:SER:HA	1:LM:97:ASN:HD21	1.68	0.59
1:CX:3:PHE:CD1	1:DK:104:ARG:NH1	2.71	0.59
1:DO:20:TYR:OH	2:RA:28:A:OP1	2.15	0.59
1:JN:99:LEU:HB2	1:KH:8:ILE:HD11	1.84	0.59
1:AF:96:LEU:HD22	1:DR:53:VAL:HG12	1.85	0.59
1:BQ:111:GLY:HA2	1:EC:40:GLY:HA3	1.83	0.59
1:HI:40:GLY:HA3	1:MM:111:GLY:HA2	1.85	0.59
1:KN:94:SER:HA	1:NU:97:ASN:HD21	1.67	0.59
1:HC:97:ASN:HD21	1:MY:94:SER:HA	1.68	0.59
1:JZ:97:ASN:ND2	1:NH:94:SER:HA	2.18	0.59
1:AZ:97:ASN:HD21	1:EW:94:SER:HA	1.67	0.59
1:FE:41:LYS:HD2	2:RO:26:A:OP1	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IO:40:GLY:HA3	1:LA:111:GLY:HA2	1.85	0.59
1:JS:35:ILE:HD13	1:KF:99:LEU:HD22	1.84	0.59
1:BT:94:SER:HA	1:DN:97:ASN:ND2	2.18	0.58
1:DM:8:ILE:HD11	1:GT:99:LEU:HB2	1.85	0.58
1:HN:8:ILE:HD11	1:IS:99:LEU:HB2	1.84	0.58
1:BK:40:GLY:HA3	1:DW:111:GLY:HA2	1.85	0.58
1:BZ:40:GLY:HA3	1:DT:111:GLY:HA2	1.85	0.58
1:KW:8:ILE:HD11	1:MW:99:LEU:HB2	1.85	0.58
1:IE:96:LEU:HD22	1:LQ:53:VAL:HG12	1.85	0.58
1:JS:94:SER:HA	1:KF:97:ASN:HD21	1.69	0.58
1:MN:99:LEU:HD22	1:NT:35:ILE:HD13	1.85	0.58
1:AT:111:GLY:HA2	1:EZ:40:GLY:HA3	1.84	0.58
1:GI:20:TYR:OH	2:RY:28:A:OP1	2.19	0.58
1:GX:20:TYR:OH	2:SD:28:A:OP1	2.16	0.58
1:JF:94:SER:HA	1:MR:97:ASN:HD21	1.67	0.58
1:BN:40:GLY:HA3	1:DZ:111:GLY:HA2	1.84	0.58
1:BN:92:LEU:HD22	1:DZ:55:ARG:CG	2.34	0.58
1:IT:109:LEU:O	1:MF:40:GLY:HA2	2.04	0.58
1:AW:97:ASN:HD21	1:FC:94:SER:HA	1.69	0.58
1:CP:99:LEU:HB2	1:DJ:8:ILE:HD11	1.86	0.58
1:DL:94:SER:HA	1:GX:97:ASN:ND2	2.18	0.58
1:FP:111:GLY:HA2	1:GV:40:GLY:HA3	1.85	0.58
1:LY:111:GLY:HA2	1:MJ:40:GLY:HA3	1.86	0.58
1:MN:111:GLY:HA2	1:NT:40:GLY:HA3	1.86	0.58
1:EP:41:LYS:HD2	2:RJ:26:A:OP1	2.03	0.57
1:HA:96:LEU:HD22	1:KM:53:VAL:HG12	1.86	0.57
1:AS:111:GLY:HA2	1:EL:40:GLY:HA3	1.85	0.57
1:BA:113:PHE:OXT	1:EM:21:TYR:OH	2.20	0.57
1:BN:96:LEU:HD22	1:DZ:53:VAL:HG12	1.85	0.57
1:GR:20:TYR:OH	2:SB:28:A:OP1	2.16	0.57
1:HO:53:VAL:HG12	1:MS:96:LEU:HD22	1.85	0.57
1:BA:113:PHE:C	1:EM:21:TYR:HH	2.12	0.57
1:BW:94:SER:HA	1:DQ:97:ASN:HD21	1.68	0.57
1:FP:97:ASN:HD21	1:GV:94:SER:HA	1.70	0.57
1:HB:94:SER:HA	1:IA:97:ASN:ND2	2.17	0.57
1:LE:52:ALA:HB2	2:SK:26:A:H4'	1.87	0.57
1:CT:94:SER:HA	1:GF:97:ASN:ND2	2.19	0.57
1:EK:40:GLY:HA3	1:ER:111:GLY:HA2	1.86	0.57
1:LT:52:ALA:HB2	2:SP:26:A:H4'	1.87	0.57
1:AK:111:GLY:HA2	1:FO:40:GLY:HA3	1.86	0.57
1:CI:94:SER:HA	1:GH:97:ASN:HD21	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JT:97:ASN:ND2	1:NK:94:SER:HA	2.19	0.57
1:LH:20:TYR:OH	2:SL:28:A:OP1	2.17	0.57
1:NV:38:SER:OG	2:TH:27:U:OP1	2.22	0.57
1:BK:94:SER:HA	1:DW:97:ASN:ND2	2.20	0.57
1:EE:40:GLY:HA3	1:EU:111:GLY:HA2	1.86	0.57
1:FE:38:SER:OG	2:RO:27:U:OP1	2.21	0.57
1:GX:38:SER:OG	2:SD:27:U:OP1	2.19	0.57
1:HK:8:ILE:HD11	1:IY:99:LEU:HB2	1.85	0.57
1:IC:111:GLY:HA2	1:IJ:40:GLY:HA3	1.85	0.57
1:JT:111:GLY:HA2	1:NK:40:GLY:HA3	1.85	0.57
1:JW:97:ASN:ND2	1:NE:94:SER:HA	2.19	0.57
1:DA:94:SER:HA	1:DE:97:ASN:ND2	2.19	0.57
1:ES:38:SER:OG	2:RK:27:U:OP1	2.22	0.57
1:FV:111:GLY:HA2	1:GS:40:GLY:HA3	1.86	0.57
1:HI:99:LEU:HD22	1:MM:35:ILE:HD13	1.86	0.57
1:IH:97:ASN:ND2	1:LT:94:SER:HA	2.19	0.57
1:KM:38:SER:OG	2:SE:27:U:OP1	2.22	0.57
1:AO:109:LEU:O	1:EA:40:GLY:HA2	2.05	0.57
1:JH:97:ASN:ND2	1:JM:94:SER:HA	2.20	0.57
1:CS:99:LEU:HD22	1:DD:35:ILE:HD13	1.86	0.57
1:FV:97:ASN:ND2	1:GS:94:SER:HA	2.20	0.57
1:EK:8:ILE:HD11	1:ER:99:LEU:HB2	1.85	0.56
1:CY:97:ASN:ND2	1:GG:94:SER:HA	2.20	0.56
1:JA:8:ILE:HD11	1:NI:99:LEU:HB2	1.86	0.56
1:CH:40:GLY:HA2	1:FT:109:LEU:O	2.05	0.56
1:DP:94:SER:HA	1:GW:97:ASN:HD21	1.70	0.56
1:HE:3:PHE:CE1	1:ID:104:ARG:HG2	2.40	0.56
1:JN:21:TYR:OH	1:KH:113:PHE:OXT	2.22	0.56
1:KK:94:SER:HA	1:NR:97:ASN:ND2	2.20	0.56
1:EQ:94:SER:HA	1:FM:97:ASN:ND2	2.19	0.56
1:FD:97:ASN:HD21	1:FF:94:SER:HA	1.70	0.56
1:KQ:94:SER:HA	1:NO:97:ASN:HD21	1.70	0.56
1:AL:109:LEU:O	1:DX:40:GLY:HA2	2.04	0.56
1:BH:35:ILE:HD13	1:BO:99:LEU:HD22	1.87	0.56
1:BN:111:GLY:HA2	1:DZ:40:GLY:HA3	1.87	0.56
1:CS:97:ASN:HD21	1:DD:94:SER:HA	1.70	0.56
1:CU:99:LEU:HB2	1:DH:8:ILE:HD11	1.87	0.56
1:HO:99:LEU:HB2	1:MS:8:ILE:HD11	1.88	0.56
1:HT:94:SER:HA	1:LD:97:ASN:HD21	1.71	0.56
1:IC:99:LEU:HD11	1:IJ:6:LEU:HD22	1.88	0.56
1:BQ:104:ARG:NH1	1:EC:3:PHE:CD1	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FS:111:GLY:HA2	1:GP:40:GLY:HA3	1.86	0.56
1:HI:104:ARG:HG2	1:MM:3:PHE:CE1	2.41	0.56
1:HQ:94:SER:HA	1:LJ:97:ASN:ND2	2.21	0.56
1:IX:111:GLY:HA2	1:KR:40:GLY:HA3	1.86	0.56
1:JF:94:SER:HA	1:MR:97:ASN:ND2	2.20	0.56
1:JF:113:PHE:OXT	1:MR:21:TYR:OH	2.21	0.56
1:BN:104:ARG:NH1	1:DZ:3:PHE:CD1	2.73	0.56
1:CT:94:SER:HA	1:GF:97:ASN:HD21	1.69	0.56
1:DA:40:GLY:HA3	1:DE:111:GLY:HA2	1.87	0.56
1:EE:94:SER:HA	1:EU:97:ASN:ND2	2.21	0.56
1:HH:99:LEU:HD22	1:IV:35:ILE:HD13	1.88	0.56
1:HL:97:ASN:ND2	1:MP:94:SER:HA	2.21	0.56
1:AR:96:LEU:HD22	1:ED:53:VAL:HG12	1.86	0.56
1:CV:97:ASN:HD21	1:GM:94:SER:HA	1.70	0.56
1:EK:35:ILE:HD13	1:ER:99:LEU:HD22	1.87	0.56
1:DV:94:SER:HA	1:GE:97:ASN:ND2	2.21	0.56
1:KS:52:ALA:HB2	2:SG:26:A:H4'	1.87	0.56
1:DO:41:LYS:HD2	2:RA:26:A:OP1	2.06	0.56
1:JO:94:SER:HA	1:NA:97:ASN:HD21	1.70	0.56
1:KN:94:SER:HA	1:NU:97:ASN:ND2	2.21	0.56
1:AM:8:ILE:HD11	1:CA:99:LEU:HB2	1.88	0.55
1:BA:94:SER:HA	1:EM:97:ASN:HD21	1.70	0.55
1:CG:97:ASN:ND2	1:CL:94:SER:HA	2.21	0.55
1:LL:94:SER:HA	1:MH:97:ASN:ND2	2.21	0.55
1:AJ:8:ILE:HD11	1:BX:99:LEU:HB2	1.86	0.55
1:CI:94:SER:HA	1:GH:97:ASN:ND2	2.21	0.55
1:CQ:109:LEU:O	1:GC:40:GLY:HA2	2.06	0.55
1:CX:53:VAL:HG12	1:DK:96:LEU:HD22	1.88	0.55
1:JV:94:SER:HA	1:KI:97:ASN:ND2	2.21	0.55
1:BH:94:SER:HA	1:BO:97:ASN:HD21	1.71	0.55
1:CU:35:ILE:HD13	1:DH:99:LEU:HD22	1.89	0.55
1:GL:41:LYS:HD2	2:RZ:26:A:OP1	2.06	0.55
1:GY:21:TYR:HH	1:IG:113:PHE:C	2.14	0.55
1:HU:97:ASN:ND2	1:MA:94:SER:HA	2.21	0.55
1:HX:97:ASN:HD21	1:LU:94:SER:HA	1.72	0.55
1:MB:97:ASN:HD21	1:MD:94:SER:HA	1.72	0.55
1:HI:3:PHE:CD1	1:MM:104:ARG:NH1	2.75	0.55
1:HZ:99:LEU:HB2	1:IP:8:ILE:HD11	1.89	0.55
1:BM:97:ASN:ND2	1:EY:94:SER:HA	2.22	0.55
1:CT:97:ASN:ND2	1:GF:94:SER:HA	2.22	0.55
1:CX:40:GLY:HA3	1:DK:111:GLY:HA2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EP:38:SER:OG	2:RJ:27:U:OP1	2.20	0.55
1:HJ:20:TYR:OH	2:SH:8:U:OP1	2.21	0.55
1:JH:111:GLY:HA2	1:JM:40:GLY:HA3	1.88	0.55
1:LC:99:LEU:HB2	1:LS:8:ILE:HD11	1.89	0.55
1:GY:8:ILE:HD11	1:IG:99:LEU:HB2	1.88	0.55
1:IQ:96:LEU:HD22	1:MC:53:VAL:HG12	1.89	0.55
1:JO:94:SER:HA	1:NA:97:ASN:ND2	2.22	0.55
1:JY:94:SER:HA	1:KC:97:ASN:ND2	2.21	0.55
1:LH:41:LYS:HD2	2:SL:26:A:OP1	2.07	0.55
1:LV:97:ASN:ND2	1:MG:94:SER:HA	2.22	0.55
1:BH:40:GLY:HA3	1:BO:111:GLY:HA2	1.89	0.55
1:CK:109:LEU:O	1:FW:40:GLY:HA2	2.07	0.55
1:DM:94:SER:HA	1:GT:97:ASN:HD21	1.71	0.55
1:MT:97:ASN:ND2	1:NQ:94:SER:HA	2.22	0.55
1:BQ:98:THR:CG2	1:HI:98:THR:HG23	2.36	0.55
1:CH:109:LEU:O	1:FT:40:GLY:HA2	2.07	0.55
1:EN:94:SER:HA	1:FJ:97:ASN:HD21	1.71	0.55
1:DB:99:LEU:HB2	1:GJ:8:ILE:HD11	1.88	0.55
1:MO:38:SER:OG	2:SW:27:U:OP1	2.23	0.55
1:BM:94:SER:HA	1:EY:97:ASN:ND2	2.22	0.55
1:CF:8:ILE:HD11	1:GN:99:LEU:HB2	1.89	0.55
1:HM:92:LEU:HD22	1:KY:55:ARG:HG2	1.89	0.55
1:EM:20:TYR:OH	2:RI:28:A:OP1	2.24	0.54
1:NV:52:ALA:HB2	2:TH:26:A:H4'	1.88	0.54
1:AR:109:LEU:O	1:ED:40:GLY:HA2	2.07	0.54
1:AS:94:SER:HA	1:EL:97:ASN:HD21	1.71	0.54
1:BE:99:LEU:HB2	1:BL:8:ILE:HD11	1.90	0.54
1:BM:94:SER:HA	1:EY:97:ASN:HD21	1.71	0.54
1:IH:20:TYR:OH	2:SP:8:U:OP1	2.21	0.54
1:KQ:8:ILE:HD11	1:NO:99:LEU:HB2	1.89	0.54
1:KY:38:SER:OG	2:SI:27:U:OP1	2.23	0.54
1:MO:20:TYR:OH	2:SW:28:A:OP1	2.18	0.54
1:BT:40:GLY:HA3	1:DN:111:GLY:HA2	1.88	0.54
1:HM:55:ARG:HG2	1:KY:92:LEU:HD22	1.89	0.54
1:HN:94:SER:HA	1:IS:97:ASN:HD21	1.72	0.54
1:AY:40:GLY:HA3	1:EI:111:GLY:HA2	1.90	0.54
1:BM:97:ASN:HD21	1:EY:94:SER:HA	1.72	0.54
1:II:94:SER:HA	1:KU:97:ASN:ND2	2.23	0.54
1:LI:94:SER:HA	1:LP:97:ASN:ND2	2.22	0.54
1:DD:43:ASN:OD1	1:DD:46:THR:OG1	2.24	0.54
1:JD:8:ILE:HD11	1:NL:99:LEU:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LR:94:SER:HA	1:ME:97:ASN:HD21	1.71	0.54
1:BH:40:GLY:HA2	1:BO:109:LEU:O	2.07	0.54
1:BH:53:VAL:HG12	1:BO:96:LEU:HD22	1.90	0.54
1:CI:111:GLY:HA2	1:GH:40:GLY:HA3	1.88	0.54
1:JU:53:VAL:HG12	1:NG:96:LEU:HD22	1.90	0.54
1:BV:97:ASN:HD21	1:FH:94:SER:HA	1.72	0.54
1:HM:96:LEU:HD22	1:KY:53:VAL:HG12	1.90	0.54
1:IW:109:LEU:O	1:MI:40:GLY:HA2	2.08	0.54
1:JE:40:GLY:HA3	1:JJ:111:GLY:HA2	1.90	0.54
1:LC:40:GLY:HA2	1:LS:109:LEU:O	2.07	0.54
1:AV:8:ILE:HD11	1:EF:99:LEU:HB2	1.90	0.54
1:EB:94:SER:HA	1:GB:97:ASN:HD21	1.73	0.54
1:IB:40:GLY:HA2	1:LN:109:LEU:O	2.08	0.54
1:JE:111:GLY:HA2	1:JJ:40:GLY:HA3	1.90	0.54
1:KZ:8:ILE:HD11	1:MZ:99:LEU:HB2	1.90	0.54
1:EN:8:ILE:HD11	1:FJ:99:LEU:HB2	1.88	0.54
1:HF:97:ASN:HD21	1:NB:94:SER:HA	1.72	0.54
1:JO:97:ASN:ND2	1:NA:94:SER:HA	2.23	0.54
1:KJ:53:VAL:HG12	1:NV:96:LEU:HD22	1.90	0.54
1:NV:41:LYS:HD2	2:TH:26:A:OP1	2.07	0.54
1:AP:8:ILE:HD11	1:BU:99:LEU:HB2	1.90	0.54
1:FP:99:LEU:HB2	1:GV:8:ILE:HD11	1.90	0.54
1:KJ:55:ARG:HG2	1:NV:92:LEU:HD22	1.90	0.54
1:KW:35:ILE:HD13	1:MW:99:LEU:HD22	1.90	0.54
1:MR:41:LYS:HD2	2:SX:26:A:OP1	2.08	0.54
1:AA:40:GLY:HA2	1:BI:109:LEU:O	2.08	0.53
1:AD:8:ILE:HD11	1:BC:99:LEU:HB2	1.90	0.53
1:LE:20:TYR:OH	2:SK:28:A:OP1	2.18	0.53
1:AS:94:SER:HA	1:EL:97:ASN:ND2	2.23	0.53
1:BB:78:MET:HG2	1:BR:74:VAL:HG22	1.90	0.53
1:BG:55:ARG:HG2	1:ES:92:LEU:HD22	1.89	0.53
1:BN:92:LEU:HD22	1:DZ:55:ARG:HG3	1.90	0.53
1:HE:53:VAL:HG12	1:ID:96:LEU:HD22	1.90	0.53
1:HW:94:SER:HA	1:LG:97:ASN:HD21	1.73	0.53
1:IT:20:TYR:OH	2:ST:8:U:OP1	2.21	0.53
1:AH:99:LEU:HB2	1:GD:8:ILE:HD11	1.90	0.53
1:AN:97:ASN:ND2	1:FR:94:SER:HA	2.23	0.53
1:CV:99:LEU:HB2	1:GM:8:ILE:HD11	1.89	0.53
1:HL:99:LEU:HD22	1:MP:35:ILE:HD13	1.91	0.53
1:AD:94:SER:HA	1:BC:97:ASN:ND2	2.23	0.53
1:AL:20:TYR:OH	2:RD:8:U:OP1	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:20:TYR:OH	2:RE:8:U:OP1	2.21	0.53
1:BG:40:GLY:HA2	1:ES:109:LEU:O	2.09	0.53
1:BN:55:ARG:HG2	1:DZ:92:LEU:HD22	1.90	0.53
1:BQ:10:SER:HB3	1:MM:103:ALA:HB3	1.91	0.53
1:BQ:99:LEU:HD11	1:EC:6:LEU:HD22	1.91	0.53
1:ET:94:SER:HA	1:FG:97:ASN:ND2	2.23	0.53
1:HI:96:LEU:HD22	1:MM:53:VAL:HG12	1.89	0.53
1:HK:94:SER:HA	1:IY:97:ASN:HD21	1.74	0.53
1:EK:94:SER:HA	1:ER:97:ASN:HD21	1.74	0.53
1:EX:96:LEU:HD22	1:FI:53:VAL:HG12	1.91	0.53
1:HH:99:LEU:HB2	1:IV:8:ILE:HD11	1.90	0.53
1:HP:53:VAL:HG12	1:LB:96:LEU:HD22	1.90	0.53
1:HZ:99:LEU:HD22	1:IP:35:ILE:HD13	1.91	0.53
1:AP:43:ASN:OD1	1:AP:46:THR:OG1	2.24	0.53
1:BB:94:SER:HA	1:BR:97:ASN:HD21	1.73	0.53
1:GY:48:ARG:HG2	1:GY:81:GLY:HA2	1.91	0.53
1:HG:38:SER:OG	2:SG:7:A:OP1	2.26	0.53
1:KA:20:TYR:OH	2:TE:8:U:OP1	2.21	0.53
1:AB:40:GLY:HA3	1:FX:111:GLY:HA2	1.91	0.53
1:ED:20:TYR:OH	2:RF:28:A:OP1	2.16	0.53
1:EX:97:ASN:ND2	1:FI:94:SER:HA	2.23	0.53
1:FL:48:ARG:HG2	1:FL:81:GLY:HA2	1.91	0.53
1:GV:43:ASN:OD1	1:GV:46:THR:OG1	2.24	0.53
1:HI:99:LEU:HB2	1:MM:8:ILE:HD11	1.90	0.53
1:IH:53:VAL:HG12	1:LT:96:LEU:HD22	1.91	0.53
1:JB:97:ASN:ND2	1:JP:94:SER:HA	2.23	0.53
1:JW:99:LEU:HB2	1:NE:8:ILE:HD11	1.91	0.53
1:KM:41:LYS:HD2	2:SE:26:A:OP1	2.09	0.53
1:LX:48:ARG:HG2	1:LX:81:GLY:HA2	1.91	0.53
1:MN:104:ARG:NH1	1:NT:3:PHE:CD1	2.77	0.53
1:CS:8:ILE:HD11	1:DD:99:LEU:HB2	1.90	0.53
1:EE:48:ARG:HG2	1:EE:81:GLY:HA2	1.91	0.53
1:HA:92:LEU:HD22	1:KM:55:ARG:HG2	1.91	0.53
1:HO:3:PHE:CD1	1:MS:104:ARG:NH1	2.77	0.53
1:KG:40:GLY:HA2	1:NS:109:LEU:O	2.09	0.53
1:MG:48:ARG:HG2	1:MG:81:GLY:HA2	1.91	0.53
1:MY:48:ARG:HG2	1:MY:81:GLY:HA2	1.91	0.53
1:AL:53:VAL:HG12	1:DX:96:LEU:HD22	1.91	0.53
1:ET:48:ARG:HG2	1:ET:81:GLY:HA2	1.91	0.53
1:FU:48:ARG:HG2	1:FU:81:GLY:HA2	1.91	0.53
1:GM:48:ARG:HG2	1:GM:81:GLY:HA2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HI:55:ARG:CG	1:MM:92:LEU:HD22	2.39	0.53
1:HQ:48:ARG:HG2	1:HQ:81:GLY:HA2	1.91	0.53
1:II:77:ILE:HD12	1:KU:77:ILE:HD12	1.91	0.53
1:MC:41:LYS:HD2	2:SS:26:A:OP1	2.08	0.53
1:BB:48:ARG:HG2	1:BB:81:GLY:HA2	1.91	0.53
1:BS:92:LEU:HD22	1:FE:55:ARG:HG2	1.90	0.53
1:CF:94:SER:HA	1:GN:97:ASN:HD21	1.73	0.53
1:CP:99:LEU:HD22	1:DJ:35:ILE:HD13	1.90	0.53
1:CR:48:ARG:HG2	1:CR:81:GLY:HA2	1.91	0.53
1:CT:97:ASN:HD21	1:GF:94:SER:HA	1.74	0.53
1:CU:94:SER:HA	1:DH:97:ASN:HD21	1.73	0.53
1:DP:8:ILE:HD11	1:GW:99:LEU:HB2	1.90	0.53
1:DY:94:SER:HA	1:FY:97:ASN:ND2	2.24	0.53
1:FC:48:ARG:HG2	1:FC:81:GLY:HA2	1.91	0.53
1:FF:48:ARG:HG2	1:FF:81:GLY:HA2	1.91	0.53
1:GD:48:ARG:HG2	1:GD:81:GLY:HA2	1.91	0.53
1:JX:20:TYR:OH	2:TD:8:U:OP1	2.21	0.53
1:KZ:40:GLY:HA2	1:MZ:109:LEU:O	2.08	0.53
1:LI:48:ARG:HG2	1:LI:81:GLY:HA2	1.91	0.53
1:NE:48:ARG:HG2	1:NE:81:GLY:HA2	1.91	0.53
1:AP:48:ARG:HG2	1:AP:81:GLY:HA2	1.91	0.52
1:DG:48:ARG:HG2	1:DG:81:GLY:HA2	1.91	0.52
1:DR:38:SER:OG	2:RB:27:U:OP1	2.24	0.52
1:EH:99:LEU:HD22	1:EO:35:ILE:HD13	1.92	0.52
1:EQ:48:ARG:HG2	1:EQ:81:GLY:HA2	1.91	0.52
1:HK:48:ARG:HG2	1:HK:81:GLY:HA2	1.91	0.52
1:HZ:48:ARG:HG2	1:HZ:81:GLY:HA2	1.91	0.52
1:IC:48:ARG:HG2	1:IC:81:GLY:HA2	1.91	0.52
1:IE:92:LEU:HD22	1:LQ:55:ARG:HG2	1.90	0.52
1:JS:48:ARG:HG2	1:JS:81:GLY:HA2	1.91	0.52
1:KS:41:LYS:HD2	2:SG:26:A:OP1	2.10	0.52
1:LO:48:ARG:HG2	1:LO:81:GLY:HA2	1.91	0.52
1:AR:38:SER:OG	2:RF:7:A:OP1	2.26	0.52
1:AY:48:ARG:HG2	1:AY:81:GLY:HA2	1.91	0.52
1:BQ:48:ARG:HG2	1:BQ:81:GLY:HA2	1.91	0.52
1:BT:48:ARG:HG2	1:BT:81:GLY:HA2	1.91	0.52
1:DY:48:ARG:HG2	1:DY:81:GLY:HA2	1.91	0.52
1:HE:48:ARG:HG2	1:HE:81:GLY:HA2	1.91	0.52
1:HI:104:ARG:NH1	1:MM:3:PHE:CD1	2.77	0.52
1:HW:48:ARG:HG2	1:HW:81:GLY:HA2	1.91	0.52
1:IL:40:GLY:HA3	1:KX:111:GLY:HA2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DJ:48:ARG:HG2	1:DJ:81:GLY:HA2	1.91	0.52
1:HI:53:VAL:HG12	1:MM:96:LEU:HD22	1.90	0.52
1:HV:96:LEU:HD22	1:LH:53:VAL:HG12	1.91	0.52
1:JV:111:GLY:HA2	1:KI:40:GLY:HA3	1.92	0.52
1:LR:94:SER:HA	1:ME:97:ASN:ND2	2.24	0.52
1:LR:111:GLY:HA3	1:MF:16:THR:HB	1.91	0.52
1:MD:48:ARG:HG2	1:MD:81:GLY:HA2	1.91	0.52
1:MM:48:ARG:HG2	1:MM:81:GLY:HA2	1.91	0.52
1:MV:48:ARG:HG2	1:MV:81:GLY:HA2	1.91	0.52
1:NT:48:ARG:HG2	1:NT:81:GLY:HA2	1.91	0.52
1:BZ:48:ARG:HG2	1:BZ:81:GLY:HA2	1.91	0.52
1:CO:48:ARG:HG2	1:CO:81:GLY:HA2	1.91	0.52
1:CU:48:ARG:HG2	1:CU:81:GLY:HA2	1.91	0.52
1:CX:48:ARG:HG2	1:CX:81:GLY:HA2	1.91	0.52
1:DL:92:LEU:HD22	1:GX:55:ARG:HG2	1.91	0.52
1:EH:48:ARG:HG2	1:EH:81:GLY:HA2	1.91	0.52
1:HB:48:ARG:HG2	1:HB:81:GLY:HA2	1.91	0.52
1:HL:99:LEU:HB2	1:MP:8:ILE:HD11	1.92	0.52
1:IX:48:ARG:HG2	1:IX:81:GLY:HA2	1.91	0.52
1:JD:94:SER:HA	1:NL:97:ASN:ND2	2.25	0.52
1:KE:48:ARG:HG2	1:KE:81:GLY:HA2	1.91	0.52
1:KJ:94:SER:HA	1:NV:97:ASN:HD21	1.75	0.52
1:KJ:94:SER:HA	1:NV:97:ASN:ND2	2.23	0.52
1:KK:48:ARG:HG2	1:KK:81:GLY:HA2	1.91	0.52
1:LU:48:ARG:HG2	1:LU:81:GLY:HA2	1.91	0.52
1:NK:48:ARG:HG2	1:NK:81:GLY:HA2	1.91	0.52
1:NN:43:ASN:OD1	1:NN:46:THR:OG1	2.24	0.52
1:AH:111:GLY:HA2	1:GD:40:GLY:HA3	1.90	0.52
1:CC:48:ARG:HG2	1:CC:81:GLY:HA2	1.91	0.52
1:CH:20:TYR:OH	2:RT:8:U:OP1	2.21	0.52
1:DG:43:ASN:OD1	1:DG:46:THR:OG1	2.24	0.52
1:HJ:38:SER:OG	2:SH:7:A:OP1	2.26	0.52
1:HK:99:LEU:HD22	1:IY:35:ILE:HD13	1.92	0.52
1:HZ:43:ASN:OD1	1:HZ:46:THR:OG1	2.24	0.52
1:IB:94:SER:HA	1:LN:97:ASN:HD21	1.74	0.52
1:IF:48:ARG:HG2	1:IF:81:GLY:HA2	1.91	0.52
1:IN:20:TYR:OH	2:SR:8:U:OP1	2.21	0.52
1:JR:38:SER:OG	2:TB:7:A:OP1	2.26	0.52
1:KW:94:SER:HA	1:MW:97:ASN:HD21	1.74	0.52
1:MC:20:TYR:OH	2:SS:28:A:OP1	2.17	0.52
1:AA:48:ARG:HG2	1:AA:81:GLY:HA2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:38:SER:OG	2:RA:7:A:OP1	2.26	0.52
1:DM:48:ARG:HG2	1:DM:81:GLY:HA2	1.91	0.52
1:HH:48:ARG:HG2	1:HH:81:GLY:HA2	1.91	0.52
1:HV:38:SER:OG	2:SL:7:A:OP1	2.26	0.52
1:KA:53:VAL:HG12	1:NM:96:LEU:HD22	1.92	0.52
1:KK:8:ILE:HD11	1:NR:99:LEU:HB2	1.91	0.52
1:MN:104:ARG:HG2	1:NT:3:PHE:CE1	2.45	0.52
1:NN:48:ARG:HG2	1:NN:81:GLY:HA2	1.91	0.52
1:AG:48:ARG:HG2	1:AG:81:GLY:HA2	1.91	0.52
1:AM:94:SER:HA	1:CA:97:ASN:ND2	2.24	0.52
1:BH:48:ARG:HG2	1:BH:81:GLY:HA2	1.91	0.52
1:DV:48:ARG:HG2	1:DV:81:GLY:HA2	1.91	0.52
1:EZ:48:ARG:HG2	1:EZ:81:GLY:HA2	1.91	0.52
1:GL:52:ALA:HB2	2:RZ:26:A:H4'	1.92	0.52
1:HA:20:TYR:OH	2:SE:8:U:OP1	2.21	0.52
1:HT:48:ARG:HG2	1:HT:81:GLY:HA2	1.91	0.52
1:KT:8:ILE:HD11	1:NC:99:LEU:HB2	1.91	0.52
1:LC:48:ARG:HG2	1:LC:81:GLY:HA2	1.91	0.52
1:AH:99:LEU:HD22	1:GD:35:ILE:HD13	1.90	0.52
1:BW:48:ARG:HG2	1:BW:81:GLY:HA2	1.91	0.52
1:BY:40:GLY:HA2	1:FK:109:LEU:O	2.09	0.52
1:CJ:40:GLY:HA3	1:CO:111:GLY:HA2	1.91	0.52
1:FS:97:ASN:HD21	1:GP:94:SER:HA	1.75	0.52
1:JF:97:ASN:ND2	1:MR:94:SER:HA	2.24	0.52
1:JS:99:LEU:HB2	1:KF:8:ILE:HD11	1.92	0.52
1:JV:48:ARG:HG2	1:JV:81:GLY:HA2	1.91	0.52
1:DD:48:ARG:HG2	1:DD:81:GLY:HA2	1.91	0.52
1:DF:38:SER:OG	2:SB:7:A:OP1	2.26	0.52
1:EK:48:ARG:HG2	1:EK:81:GLY:HA2	1.91	0.52
1:FB:16:THR:HB	1:FL:111:GLY:HA3	1.90	0.52
1:FE:16:THR:HB	1:FF:111:GLY:HA3	1.92	0.52
1:FI:48:ARG:HG2	1:FI:81:GLY:HA2	1.91	0.52
1:FX:48:ARG:HG2	1:FX:81:GLY:HA2	1.91	0.52
1:GG:48:ARG:HG2	1:GG:81:GLY:HA2	1.91	0.52
1:HF:99:LEU:HB2	1:NB:8:ILE:HD11	1.91	0.52
1:IR:8:ILE:HD11	1:KL:99:LEU:HB2	1.91	0.52
1:IX:43:ASN:OD1	1:IX:46:THR:OG1	2.24	0.52
1:JM:48:ARG:HG2	1:JM:81:GLY:HA2	1.91	0.52
1:JO:97:ASN:HD21	1:NA:94:SER:HA	1.74	0.52
1:KB:48:ARG:HG2	1:KB:81:GLY:HA2	1.91	0.52
1:KK:40:GLY:HA3	1:NR:111:GLY:HA2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KZ:94:SER:HA	1:MZ:97:ASN:ND2	2.25	0.52
1:LF:48:ARG:HG2	1:LF:81:GLY:HA2	1.91	0.52
1:MP:48:ARG:HG2	1:MP:81:GLY:HA2	1.91	0.52
1:MU:16:THR:HB	1:NQ:111:GLY:HA3	1.91	0.52
1:AM:48:ARG:HG2	1:AM:81:GLY:HA2	1.91	0.52
1:BS:38:SER:OG	2:RO:7:A:OP1	2.26	0.52
1:CF:48:ARG:HG2	1:CF:81:GLY:HA2	1.91	0.52
1:HI:111:GLY:HA2	1:MM:40:GLY:HA3	1.92	0.52
1:IR:48:ARG:HG2	1:IR:81:GLY:HA2	1.91	0.52
1:JG:48:ARG:HG2	1:JG:81:GLY:HA2	1.91	0.52
1:KZ:48:ARG:HG2	1:KZ:81:GLY:HA2	1.91	0.52
1:MN:96:LEU:HD22	1:NT:53:VAL:HG12	1.92	0.52
1:ND:52:ALA:HB2	2:TB:26:A:H4'	1.92	0.52
1:BB:53:VAL:HG12	1:BR:96:LEU:CD2	2.40	0.51
1:BG:20:TYR:OH	2:RK:8:U:OP1	2.21	0.51
1:BV:97:ASN:ND2	1:FH:94:SER:HA	2.25	0.51
1:CI:40:GLY:HA3	1:GH:111:GLY:HA2	1.92	0.51
1:DA:43:ASN:OD1	1:DA:46:THR:OG1	2.24	0.51
1:DS:48:ARG:HG2	1:DS:81:GLY:HA2	1.91	0.51
1:EH:43:ASN:OD1	1:EH:46:THR:OG1	2.24	0.51
1:EQ:8:ILE:HD11	1:FM:99:LEU:HB2	1.91	0.51
1:GG:43:ASN:OD1	1:GG:46:THR:OG1	2.24	0.51
1:GS:48:ARG:HG2	1:GS:81:GLY:HA2	1.91	0.51
1:HA:38:SER:OG	2:SE:7:A:OP1	2.26	0.51
1:HI:55:ARG:HG3	1:MM:92:LEU:HD22	1.92	0.51
1:HN:48:ARG:HG2	1:HN:81:GLY:HA2	1.91	0.51
1:HP:38:SER:OG	2:SJ:7:A:OP1	2.26	0.51
1:IE:38:SER:OG	2:SO:7:A:OP1	2.26	0.51
1:II:111:GLY:HA3	1:KV:16:THR:HB	1.91	0.51
1:IL:48:ARG:HG2	1:IL:81:GLY:HA2	1.91	0.51
1:JU:40:GLY:HA2	1:NG:109:LEU:O	2.10	0.51
1:LL:48:ARG:HG2	1:LL:81:GLY:HA2	1.91	0.51
1:MA:48:ARG:HG2	1:MA:81:GLY:HA2	1.91	0.51
1:MS:48:ARG:HG2	1:MS:81:GLY:HA2	1.91	0.51
1:AS:48:ARG:HG2	1:AS:81:GLY:HA2	1.91	0.51
1:AW:99:LEU:HB2	1:FC:8:ILE:HD11	1.92	0.51
1:AX:20:TYR:OH	2:RH:8:U:OP1	2.21	0.51
1:BE:35:ILE:HD13	1:BL:99:LEU:HD22	1.91	0.51
1:CK:38:SER:OG	2:RU:7:A:OP1	2.26	0.51
1:DA:48:ARG:HG2	1:DA:81:GLY:HA2	1.91	0.51
1:DL:96:LEU:HD22	1:GX:53:VAL:HG12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:99:LEU:HD22	1:GW:35:ILE:HD13	1.92	0.51
1:EB:48:ARG:HG2	1:EB:81:GLY:HA2	1.91	0.51
1:GP:48:ARG:HG2	1:GP:81:GLY:HA2	1.91	0.51
1:HA:55:ARG:HG2	1:KM:92:LEU:HD22	1.91	0.51
1:II:48:ARG:HG2	1:II:81:GLY:HA2	1.91	0.51
1:IW:38:SER:OG	2:SU:7:A:OP1	2.26	0.51
1:JI:20:TYR:OH	2:SY:8:U:OP1	2.21	0.51
1:JJ:43:ASN:OD1	1:JJ:46:THR:OG1	2.24	0.51
1:JP:48:ARG:HG2	1:JP:81:GLY:HA2	1.91	0.51
1:KN:48:ARG:HG2	1:KN:81:GLY:HA2	1.91	0.51
1:NB:48:ARG:HG2	1:NB:81:GLY:HA2	1.91	0.51
1:NQ:48:ARG:HG2	1:NQ:81:GLY:HA2	1.91	0.51
1:AD:48:ARG:HG2	1:AD:81:GLY:HA2	1.91	0.51
1:AI:20:TYR:OH	2:RC:8:U:OP1	2.21	0.51
1:AJ:48:ARG:HG2	1:AJ:81:GLY:HA2	1.91	0.51
1:AX:97:ASN:HD21	1:EJ:94:SER:HA	1.75	0.51
1:BB:8:ILE:HD11	1:BR:99:LEU:HB2	1.92	0.51
1:BE:99:LEU:HD22	1:BL:35:ILE:HD13	1.92	0.51
1:BN:48:ARG:HG2	1:BN:81:GLY:HA2	1.91	0.51
1:BQ:40:GLY:HA2	1:EC:109:LEU:O	2.10	0.51
1:DP:48:ARG:HG2	1:DP:81:GLY:HA2	1.91	0.51
1:EW:48:ARG:HG2	1:EW:81:GLY:HA2	1.91	0.51
1:FR:48:ARG:HG2	1:FR:81:GLY:HA2	1.91	0.51
1:HC:97:ASN:ND2	1:MY:94:SER:HA	2.24	0.51
1:JY:48:ARG:HG2	1:JY:81:GLY:HA2	1.91	0.51
1:KG:20:TYR:OH	2:TG:8:U:OP1	2.21	0.51
1:AA:94:SER:HA	1:BI:97:ASN:HD21	1.74	0.51
1:BP:38:SER:OG	2:RN:7:A:OP1	2.26	0.51
1:DR:41:LYS:HD2	2:RB:26:A:OP1	2.11	0.51
1:EB:8:ILE:HD11	1:GB:99:LEU:HB2	1.92	0.51
1:FZ:41:LYS:HD2	2:RV:26:A:OP1	2.09	0.51
1:GA:48:ARG:HG2	1:GA:81:GLY:HA2	1.91	0.51
1:HD:109:LEU:O	1:KP:40:GLY:HA2	2.10	0.51
1:IB:94:SER:HA	1:LN:97:ASN:ND2	2.26	0.51
1:JM:43:ASN:OD1	1:JM:46:THR:OG1	2.24	0.51
1:KT:48:ARG:HG2	1:KT:81:GLY:HA2	1.91	0.51
1:KV:20:TYR:OH	2:SH:28:A:OP1	2.23	0.51
1:KW:48:ARG:HG2	1:KW:81:GLY:HA2	1.91	0.51
1:KW:99:LEU:HB2	1:MW:8:ILE:HD11	1.91	0.51
1:AD:21:TYR:HH	1:BC:113:PHE:C	2.19	0.51
1:AE:111:GLY:HA2	1:GA:40:GLY:HA3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:97:ASN:HD21	1:EA:94:SER:HA	1.76	0.51
1:BK:48:ARG:HG2	1:BK:81:GLY:HA2	1.91	0.51
1:CI:48:ARG:HG2	1:CI:81:GLY:HA2	1.91	0.51
1:CN:20:TYR:OH	2:RV:8:U:OP1	2.21	0.51
1:EN:48:ARG:HG2	1:EN:81:GLY:HA2	1.91	0.51
1:HC:111:GLY:HA2	1:MY:40:GLY:HA3	1.93	0.51
1:IO:43:ASN:OD1	1:IO:46:THR:OG1	2.24	0.51
1:JL:20:TYR:OH	2:SZ:8:U:OP1	2.21	0.51
1:JY:40:GLY:HA2	1:KC:109:LEU:O	2.10	0.51
1:KH:48:ARG:HG2	1:KH:81:GLY:HA2	1.91	0.51
1:KN:43:ASN:OD1	1:KN:46:THR:OG1	2.24	0.51
1:AV:94:SER:HA	1:EF:97:ASN:ND2	2.23	0.51
1:DC:38:SER:OG	2:SA:7:A:OP1	2.26	0.51
1:DJ:43:ASN:OD1	1:DJ:46:THR:OG1	2.24	0.51
1:GJ:48:ARG:HG2	1:GJ:81:GLY:HA2	1.91	0.51
1:HN:35:ILE:HD13	1:IS:99:LEU:HD22	1.93	0.51
1:HP:109:LEU:O	1:LB:40:GLY:HA2	2.11	0.51
1:IO:48:ARG:HG2	1:IO:81:GLY:HA2	1.91	0.51
1:JA:48:ARG:HG2	1:JA:81:GLY:HA2	1.91	0.51
1:JD:48:ARG:HG2	1:JD:81:GLY:HA2	1.91	0.51
1:JN:8:ILE:HD11	1:KH:99:LEU:HB2	1.90	0.51
1:KQ:48:ARG:HG2	1:KQ:81:GLY:HA2	1.91	0.51
1:LI:40:GLY:HA3	1:LP:111:GLY:HA2	1.92	0.51
1:MB:99:LEU:HB2	1:MD:8:ILE:HD11	1.93	0.51
1:MM:43:ASN:OD1	1:MM:46:THR:OG1	2.24	0.51
1:MO:52:ALA:HB2	2:SW:26:A:H4'	1.92	0.51
1:AA:35:ILE:HD13	1:BI:99:LEU:HD22	1.92	0.51
1:AX:96:LEU:HD22	1:EJ:53:VAL:HG12	1.92	0.51
1:BM:40:GLY:HA2	1:EY:109:LEU:O	2.09	0.51
1:CL:48:ARG:HG2	1:CL:81:GLY:HA2	1.91	0.51
1:CS:111:GLY:HA2	1:DD:40:GLY:HA3	1.93	0.51
1:DB:97:ASN:ND2	1:GJ:94:SER:HA	2.24	0.51
1:HE:3:PHE:CD1	1:ID:104:ARG:NH1	2.79	0.51
1:IQ:20:TYR:OH	2:SS:8:U:OP1	2.21	0.51
1:IU:48:ARG:HG2	1:IU:81:GLY:HA2	1.91	0.51
1:LL:8:ILE:HD11	1:MH:99:LEU:HB2	1.93	0.51
1:LX:43:ASN:OD1	1:LX:46:THR:OG1	2.24	0.51
1:LY:92:LEU:HD22	1:MJ:55:ARG:HG2	1.93	0.51
1:BE:48:ARG:HG2	1:BE:81:GLY:HA2	1.91	0.51
1:BV:109:LEU:O	1:FH:40:GLY:HA2	2.10	0.51
1:CJ:55:ARG:CG	1:CO:92:LEU:HD22	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:43:ASN:OD1	1:CL:46:THR:OG1	2.24	0.51
1:DL:20:TYR:OH	2:SD:8:U:OP1	2.21	0.51
1:DM:43:ASN:OD1	1:DM:46:THR:OG1	2.24	0.51
1:EE:43:ASN:OD1	1:EE:46:THR:OG1	2.24	0.51
1:GV:48:ARG:HG2	1:GV:81:GLY:HA2	1.91	0.51
1:JJ:48:ARG:HG2	1:JJ:81:GLY:HA2	1.91	0.51
1:KZ:40:GLY:HA3	1:MZ:111:GLY:HA2	1.91	0.51
1:LO:8:ILE:HD11	1:MK:99:LEU:HB2	1.93	0.51
1:LR:48:ARG:HG2	1:LR:81:GLY:HA2	1.91	0.51
1:MO:41:LYS:HD2	2:SW:26:A:OP1	2.10	0.51
1:AH:97:ASN:HD21	1:GD:94:SER:HA	1.75	0.51
1:AV:48:ARG:HG2	1:AV:81:GLY:HA2	1.91	0.51
1:BO:27:GLY:HA2	1:DZ:106:ASP:OD2	2.11	0.51
1:DF:20:TYR:OH	2:SB:8:U:OP1	2.21	0.51
1:KS:38:SER:OG	2:SG:27:U:OP1	2.24	0.51
1:MJ:48:ARG:HG2	1:MJ:81:GLY:HA2	1.91	0.51
1:BA:40:GLY:HA2	1:EM:109:LEU:O	2.11	0.51
1:DL:2:THR:OG1	1:GX:113:PHE:O	2.20	0.51
1:HR:111:GLY:HA2	1:LX:40:GLY:HA3	1.93	0.51
1:HS:38:SER:OG	2:SK:7:A:OP1	2.26	0.51
1:IU:43:ASN:OD1	1:IU:46:THR:OG1	2.24	0.51
1:BE:43:ASN:OD1	1:BE:46:THR:OG1	2.24	0.50
1:BG:38:SER:OG	2:RK:7:A:OP1	2.26	0.50
1:CB:96:LEU:HD22	1:FN:53:VAL:HG12	1.92	0.50
1:CI:43:ASN:OD1	1:CI:46:THR:OG1	2.24	0.50
1:EQ:40:GLY:HA3	1:FM:111:GLY:HA2	1.93	0.50
1:GR:38:SER:OG	2:SB:27:U:OP1	2.25	0.50
1:HB:40:GLY:HA3	1:IA:111:GLY:HA2	1.92	0.50
1:HE:94:SER:HA	1:ID:97:ASN:HD21	1.76	0.50
1:IH:55:ARG:HG2	1:LT:92:LEU:HD22	1.92	0.50
1:LF:43:ASN:OD1	1:LF:46:THR:OG1	2.24	0.50
1:AA:111:GLY:HA2	1:BI:40:GLY:HA3	1.93	0.50
1:AC:96:LEU:HD22	1:DO:53:VAL:HG12	1.93	0.50
1:BA:90:ASP:OD2	1:EM:102:PRO:HD3	2.11	0.50
1:BH:8:ILE:HD11	1:BO:99:LEU:HB2	1.92	0.50
1:CJ:97:ASN:HD21	1:CO:94:SER:HA	1.75	0.50
1:DY:8:ILE:HD11	1:FY:99:LEU:HB2	1.93	0.50
1:EN:99:LEU:HB2	1:FJ:8:ILE:HD11	1.92	0.50
1:HE:78:MET:HG2	1:ID:74:VAL:HG22	1.93	0.50
1:HL:40:GLY:HA3	1:MP:111:GLY:HA2	1.92	0.50
1:HT:43:ASN:OD1	1:HT:46:THR:OG1	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JN:97:ASN:ND2	1:KH:94:SER:HA	2.26	0.50
1:KN:40:GLY:HA3	1:NU:111:GLY:HA2	1.92	0.50
1:KY:41:LYS:HD2	2:SI:26:A:OP1	2.11	0.50
1:LR:55:ARG:HG2	1:ME:92:LEU:HD22	1.93	0.50
1:MN:40:GLY:HA3	1:NT:111:GLY:HA2	1.93	0.50
1:GJ:43:ASN:OD1	1:GJ:46:THR:OG1	2.24	0.50
1:HZ:35:ILE:HD13	1:IP:99:LEU:HD22	1.93	0.50
1:IC:107:GLN:CD	1:IK:14:ILE:HD13	2.36	0.50
1:IZ:38:SER:OG	2:SV:7:A:OP1	2.26	0.50
1:JL:38:SER:OG	2:SZ:7:A:OP1	2.26	0.50
1:JQ:99:LEU:HB2	1:KB:8:ILE:HD11	1.93	0.50
1:JR:53:VAL:HG12	1:ND:96:LEU:HD22	1.94	0.50
1:MC:38:SER:OG	2:SS:27:U:OP1	2.26	0.50
1:NH:48:ARG:HG2	1:NH:81:GLY:HA2	1.91	0.50
1:CE:53:VAL:HG12	1:FQ:96:LEU:HD22	1.93	0.50
1:EG:20:TYR:OH	2:RG:28:A:OP1	2.16	0.50
1:FD:97:ASN:ND2	1:FF:94:SER:HA	2.26	0.50
1:FO:48:ARG:HG2	1:FO:81:GLY:HA2	1.91	0.50
1:HJ:40:GLY:HA2	1:KV:109:LEU:O	2.12	0.50
1:HP:20:TYR:OH	2:SJ:8:U:OP1	2.21	0.50
1:JC:20:TYR:OH	2:SW:8:U:OP1	2.21	0.50
1:EW:43:ASN:OD1	1:EW:46:THR:OG1	2.24	0.50
1:GY:94:SER:HA	1:IG:97:ASN:HD21	1.77	0.50
1:HT:94:SER:HA	1:LD:97:ASN:ND2	2.26	0.50
1:JA:99:LEU:HB2	1:NI:8:ILE:HD11	1.93	0.50
1:MQ:97:ASN:ND2	1:NN:94:SER:HA	2.26	0.50
1:AA:43:ASN:OD1	1:AA:46:THR:OG1	2.24	0.50
1:AP:99:LEU:HD22	1:BU:35:ILE:HD13	1.93	0.50
1:CB:20:TYR:OH	2:RR:8:U:OP1	2.21	0.50
1:FF:43:ASN:OD1	1:FF:46:THR:OG1	2.24	0.50
1:JA:40:GLY:HA2	1:NI:109:LEU:O	2.12	0.50
1:JK:97:ASN:HD21	1:KE:94:SER:HA	1.76	0.50
1:JQ:97:ASN:HD21	1:KB:94:SER:HA	1.76	0.50
1:KH:43:ASN:OD1	1:KH:46:THR:OG1	2.24	0.50
1:KT:94:SER:HA	1:NC:97:ASN:ND2	2.27	0.50
1:KW:43:ASN:OD1	1:KW:46:THR:OG1	2.24	0.50
1:LI:43:ASN:OD1	1:LI:46:THR:OG1	2.24	0.50
1:BW:94:SER:HA	1:DQ:97:ASN:ND2	2.27	0.50
1:FA:97:ASN:HD21	1:FL:94:SER:HA	1.76	0.50
1:GI:41:LYS:HD2	2:RY:26:A:OP1	2.12	0.50
1:GI:52:ALA:HB2	2:RY:26:A:H4'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HD:16:THR:HB	1:MY:111:GLY:HA3	1.94	0.50
1:HI:99:LEU:HD11	1:MM:6:LEU:HD22	1.94	0.50
1:HX:97:ASN:ND2	1:LU:94:SER:HA	2.26	0.50
1:IK:109:LEU:O	1:LW:40:GLY:HA2	2.10	0.50
1:KA:16:THR:HB	1:NH:111:GLY:HA3	1.94	0.50
1:KZ:43:ASN:OD1	1:KZ:46:THR:OG1	2.24	0.50
1:LC:40:GLY:HA3	1:LS:111:GLY:HA2	1.94	0.50
1:LR:92:LEU:HD22	1:ME:55:ARG:CG	2.42	0.50
1:MN:97:ASN:ND2	1:NT:94:SER:HA	2.26	0.50
1:AL:96:LEU:HD22	1:DX:53:VAL:HG12	1.93	0.50
1:AU:38:SER:OG	2:RG:7:A:OP1	2.26	0.50
1:BM:38:SER:OG	2:RM:7:A:OP1	2.26	0.50
1:BQ:99:LEU:HB2	1:EC:8:ILE:HD11	1.94	0.50
1:CP:53:VAL:HG12	1:DJ:96:LEU:HD22	1.92	0.50
1:DI:38:SER:OG	2:SC:7:A:OP1	2.26	0.50
1:JF:97:ASN:HD21	1:MR:94:SER:HA	1.76	0.50
1:JR:20:TYR:OH	2:TB:8:U:OP1	2.21	0.50
1:BY:38:SER:OG	2:RQ:7:A:OP1	2.26	0.50
1:CF:43:ASN:OD1	1:CF:46:THR:OG1	2.24	0.50
1:CM:111:GLY:HA2	1:DG:40:GLY:HA3	1.93	0.50
1:GP:43:ASN:OD1	1:GP:46:THR:OG1	2.24	0.50
1:HI:6:LEU:HD22	1:MM:99:LEU:HD11	1.93	0.50
1:HM:53:VAL:HG12	1:KY:96:LEU:HD22	1.94	0.50
1:JF:38:SER:OG	2:SX:7:A:OP1	2.26	0.50
1:LC:53:VAL:HG12	1:LS:96:LEU:HD22	1.93	0.50
1:AD:43:ASN:OD1	1:AD:46:THR:OG1	2.24	0.49
1:BT:43:ASN:OD1	1:BT:46:THR:OG1	2.24	0.49
1:CY:16:THR:HG21	1:DK:110:GLN:OE1	2.12	0.49
1:EH:35:ILE:HD13	1:EO:99:LEU:HD22	1.92	0.49
1:KD:38:SER:OG	2:TF:7:A:OP1	2.26	0.49
1:LC:99:LEU:HD22	1:LS:35:ILE:HD13	1.93	0.49
1:LF:35:ILE:HD13	1:LM:99:LEU:HD22	1.94	0.49
1:AA:99:LEU:HD22	1:BI:35:ILE:HD13	1.94	0.49
1:AH:96:LEU:HD22	1:GD:53:VAL:HG12	1.94	0.49
1:AL:20:TYR:CZ	1:AL:36:LYS:HD3	2.48	0.49
1:BW:8:ILE:HD11	1:DQ:99:LEU:HB2	1.92	0.49
1:CG:111:GLY:HA2	1:CL:40:GLY:HA3	1.94	0.49
1:CJ:111:GLY:HA2	1:CO:40:GLY:HA3	1.93	0.49
1:CK:20:TYR:OH	2:RU:8:U:OP1	2.21	0.49
1:CX:111:GLY:HA2	1:DK:40:GLY:HA3	1.94	0.49
1:CY:28:PHE:HB3	1:DK:106:ASP:OD1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DC:20:TYR:CZ	1:DC:36:LYS:HD3	2.48	0.49
1:DI:94:SER:HA	1:GU:97:ASN:ND2	2.27	0.49
1:EN:43:ASN:OD1	1:EN:46:THR:OG1	2.24	0.49
1:FZ:20:TYR:CZ	1:FZ:36:LYS:HD3	2.48	0.49
1:GY:99:LEU:HD22	1:IG:35:ILE:HD13	1.94	0.49
1:HE:40:GLY:HA3	1:ID:111:GLY:HA2	1.94	0.49
1:HG:53:VAL:HG12	1:KS:96:LEU:HD22	1.94	0.49
1:IN:38:SER:OG	2:SR:7:A:OP1	2.26	0.49
1:KQ:40:GLY:HA3	1:NO:111:GLY:HA2	1.94	0.49
1:NB:43:ASN:OD1	1:NB:46:THR:OG1	2.24	0.49
1:AF:92:LEU:HD22	1:DR:55:ARG:HG2	1.92	0.49
1:CW:20:TYR:CZ	1:CW:36:LYS:HD3	2.48	0.49
1:GI:20:TYR:CZ	1:GI:36:LYS:HD3	2.48	0.49
1:HD:20:TYR:CZ	1:HD:36:LYS:HD3	2.48	0.49
1:HW:43:ASN:OD1	1:HW:46:THR:OG1	2.24	0.49
1:IW:20:TYR:OH	2:SU:8:U:OP1	2.21	0.49
1:JI:40:GLY:HA2	1:MU:109:LEU:O	2.12	0.49
1:KA:20:TYR:CZ	1:KA:36:LYS:HD3	2.48	0.49
1:KG:38:SER:OG	2:TG:7:A:OP1	2.26	0.49
1:KQ:43:ASN:OD1	1:KQ:46:THR:OG1	2.24	0.49
1:MC:20:TYR:CZ	1:MC:36:LYS:HD3	2.48	0.49
1:MR:20:TYR:CZ	1:MR:36:LYS:HD3	2.48	0.49
1:AF:20:TYR:CZ	1:AF:36:LYS:HD3	2.48	0.49
1:CQ:20:TYR:CZ	1:CQ:36:LYS:HD3	2.48	0.49
1:CZ:20:TYR:CZ	1:CZ:36:LYS:HD3	2.48	0.49
1:EK:43:ASN:OD1	1:EK:46:THR:OG1	2.24	0.49
1:EY:20:TYR:CZ	1:EY:36:LYS:HD3	2.48	0.49
1:FK:20:TYR:CZ	1:FK:36:LYS:HD3	2.48	0.49
1:FS:97:ASN:ND2	1:GP:94:SER:HA	2.28	0.49
1:FW:20:TYR:CZ	1:FW:36:LYS:HD3	2.48	0.49
1:HJ:20:TYR:CZ	1:HJ:36:LYS:HD3	2.48	0.49
1:HK:99:LEU:HB2	1:IY:8:ILE:HD11	1.93	0.49
1:JG:40:GLY:HA3	1:NF:111:GLY:HA2	1.95	0.49
1:JO:20:TYR:CZ	1:JO:36:LYS:HD3	2.48	0.49
1:KP:20:TYR:CZ	1:KP:36:LYS:HD3	2.48	0.49
1:LB:20:TYR:CZ	1:LB:36:LYS:HD3	2.48	0.49
1:MI:20:TYR:CZ	1:MI:36:LYS:HD3	2.48	0.49
1:MP:43:ASN:OD1	1:MP:46:THR:OG1	2.24	0.49
1:MS:43:ASN:OD1	1:MS:46:THR:OG1	2.24	0.49
1:ND:20:TYR:CZ	1:ND:36:LYS:HD3	2.48	0.49
1:NV:20:TYR:CZ	1:NV:36:LYS:HD3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:20:TYR:CZ	1:BA:36:LYS:HD3	2.48	0.49
1:BV:94:SER:HA	1:FH:97:ASN:ND2	2.27	0.49
1:CH:20:TYR:CZ	1:CH:36:LYS:HD3	2.48	0.49
1:CT:20:TYR:CZ	1:CT:36:LYS:HD3	2.48	0.49
1:HM:20:TYR:CZ	1:HM:36:LYS:HD3	2.48	0.49
1:IR:94:SER:HA	1:KL:97:ASN:HD21	1.77	0.49
1:KZ:111:GLY:HA2	1:MZ:40:GLY:HA3	1.94	0.49
1:NP:20:TYR:CZ	1:NP:36:LYS:HD3	2.48	0.49
1:DC:40:GLY:HA2	1:GO:109:LEU:O	2.13	0.49
1:DL:94:SER:HA	1:GX:97:ASN:HD21	1.77	0.49
1:IK:20:TYR:CZ	1:IK:36:LYS:HD3	2.48	0.49
1:JL:20:TYR:CZ	1:JL:36:LYS:HD3	2.48	0.49
1:JO:20:TYR:OH	2:TA:8:U:OP1	2.21	0.49
1:MN:106:ASP:OD1	1:NU:28:PHE:HB3	2.12	0.49
1:NG:20:TYR:CZ	1:NG:36:LYS:HD3	2.48	0.49
1:AI:38:SER:OG	2:RC:7:A:OP1	2.26	0.49
1:AX:20:TYR:CZ	1:AX:36:LYS:HD3	2.48	0.49
1:AZ:53:VAL:HG12	1:EW:96:LEU:HD22	1.93	0.49
1:BD:20:TYR:CZ	1:BD:36:LYS:HD3	2.48	0.49
1:BD:20:TYR:OH	2:RJ:8:U:OP1	2.21	0.49
1:BG:20:TYR:CZ	1:BG:36:LYS:HD3	2.48	0.49
1:BP:94:SER:HA	1:FB:97:ASN:ND2	2.28	0.49
1:CK:20:TYR:CZ	1:CK:36:LYS:HD3	2.48	0.49
1:CN:53:VAL:HG12	1:FZ:96:LEU:HD22	1.95	0.49
1:CV:99:LEU:HD22	1:GM:35:ILE:HD13	1.94	0.49
1:DF:20:TYR:CZ	1:DF:36:LYS:HD3	2.48	0.49
1:ED:20:TYR:CZ	1:ED:36:LYS:HD3	2.48	0.49
1:EE:111:GLY:HA2	1:EU:40:GLY:HA3	1.95	0.49
1:GO:20:TYR:CZ	1:GO:36:LYS:HD3	2.48	0.49
1:GU:20:TYR:CZ	1:GU:36:LYS:HD3	2.48	0.49
1:HG:20:TYR:CZ	1:HG:36:LYS:HD3	2.48	0.49
1:HG:20:TYR:OH	2:SG:8:U:OP1	2.21	0.49
1:IW:20:TYR:CZ	1:IW:36:LYS:HD3	2.48	0.49
1:JI:20:TYR:CZ	1:JI:36:LYS:HD3	2.48	0.49
1:JW:37:ILE:HG12	1:JW:53:VAL:HG22	1.95	0.49
1:JX:20:TYR:CZ	1:JX:36:LYS:HD3	2.48	0.49
1:JY:8:ILE:HD11	1:KC:99:LEU:HB2	1.94	0.49
1:KJ:38:SER:OG	2:TH:7:A:OP1	2.26	0.49
1:KM:20:TYR:CZ	1:KM:36:LYS:HD3	2.48	0.49
1:LF:53:VAL:HG12	1:LM:96:LEU:HD22	1.95	0.49
1:LN:20:TYR:CZ	1:LN:36:LYS:HD3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ML:20:TYR:CZ	1:ML:36:LYS:HD3	2.48	0.49
1:NJ:20:TYR:CZ	1:NJ:36:LYS:HD3	2.48	0.49
1:AT:37:ILE:HG12	1:AT:53:VAL:HG22	1.95	0.49
1:CD:37:ILE:HG12	1:CD:53:VAL:HG22	1.95	0.49
1:CE:20:TYR:CZ	1:CE:36:LYS:HD3	2.48	0.49
1:CJ:37:ILE:HG12	1:CJ:53:VAL:HG22	1.95	0.49
1:DH:37:ILE:HG12	1:DH:53:VAL:HG22	1.95	0.49
1:DY:40:GLY:HA3	1:FY:111:GLY:HA2	1.95	0.49
1:FO:43:ASN:OD1	1:FO:46:THR:OG1	2.24	0.49
1:FQ:20:TYR:CZ	1:FQ:36:LYS:HD3	2.48	0.49
1:HM:97:ASN:ND2	1:KY:94:SER:HA	2.27	0.49
1:IA:37:ILE:HG12	1:IA:53:VAL:HG22	1.95	0.49
1:IV:37:ILE:HG12	1:IV:53:VAL:HG22	1.95	0.49
1:JF:20:TYR:CZ	1:JF:36:LYS:HD3	2.48	0.49
1:MX:20:TYR:CZ	1:MX:36:LYS:HD3	2.48	0.49
1:NA:20:TYR:CZ	1:NA:36:LYS:HD3	2.48	0.49
1:NU:37:ILE:HG12	1:NU:53:VAL:HG22	1.95	0.49
1:AF:43:ASN:OD1	1:AF:46:THR:OG1	2.31	0.49
1:BN:96:LEU:HD22	1:DZ:53:VAL:CG1	2.43	0.49
1:BV:20:TYR:CZ	1:BV:36:LYS:HD3	2.48	0.49
1:CB:20:TYR:CZ	1:CB:36:LYS:HD3	2.48	0.49
1:CX:78:MET:HG2	1:DK:74:VAL:HG22	1.95	0.49
1:CY:37:ILE:HG12	1:CY:53:VAL:HG22	1.95	0.49
1:DK:37:ILE:HG12	1:DK:53:VAL:HG22	1.95	0.49
1:DO:20:TYR:CZ	1:DO:36:LYS:HD3	2.48	0.49
1:DU:20:TYR:CZ	1:DU:36:LYS:HD3	2.48	0.49
1:DX:20:TYR:CZ	1:DX:36:LYS:HD3	2.48	0.49
1:DY:43:ASN:OD1	1:DY:46:THR:OG1	2.24	0.49
1:ES:20:TYR:CZ	1:ES:36:LYS:HD3	2.48	0.49
1:EV:20:TYR:CZ	1:EV:36:LYS:HD3	2.48	0.49
1:EZ:43:ASN:OD1	1:EZ:46:THR:OG1	2.24	0.49
1:FJ:37:ILE:HG12	1:FJ:53:VAL:HG22	1.95	0.49
1:HS:20:TYR:CZ	1:HS:36:LYS:HD3	2.48	0.49
1:HT:8:ILE:HD11	1:LD:99:LEU:HB2	1.95	0.49
1:HY:20:TYR:CZ	1:HY:36:LYS:HD3	2.48	0.49
1:IM:37:ILE:HG12	1:IM:53:VAL:HG22	1.95	0.49
1:IW:43:ASN:OD1	1:IW:46:THR:OG1	2.31	0.49
1:JI:43:ASN:OD1	1:JI:46:THR:OG1	2.31	0.49
1:KG:53:VAL:HG12	1:NS:96:LEU:HD22	1.95	0.49
1:KY:20:TYR:CZ	1:KY:36:LYS:HD3	2.48	0.49
1:LS:37:ILE:HG12	1:LS:53:VAL:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LV:99:LEU:HB2	1:MG:8:ILE:HD11	1.94	0.49
1:MN:37:ILE:HG12	1:MN:53:VAL:HG22	1.95	0.49
1:ND:43:ASN:OD1	1:ND:46:THR:OG1	2.31	0.49
1:NO:37:ILE:HG12	1:NO:53:VAL:HG22	1.95	0.49
1:NS:20:TYR:CZ	1:NS:36:LYS:HD3	2.48	0.49
1:AI:20:TYR:CZ	1:AI:36:LYS:HD3	2.48	0.49
1:BE:40:GLY:HA2	1:BL:109:LEU:O	2.13	0.49
1:BM:20:TYR:CZ	1:BM:36:LYS:HD3	2.48	0.49
1:CK:43:ASN:OD1	1:CK:46:THR:OG1	2.31	0.49
1:CO:43:ASN:OD1	1:CO:46:THR:OG1	2.24	0.49
1:CP:35:ILE:HD13	1:DJ:99:LEU:HD22	1.93	0.49
1:CP:111:GLY:HA2	1:DJ:40:GLY:HA3	1.95	0.49
1:CY:99:LEU:HB2	1:GG:8:ILE:HD11	1.94	0.49
1:DF:43:ASN:OD1	1:DF:46:THR:OG1	2.31	0.49
1:EA:20:TYR:CZ	1:EA:36:LYS:HD3	2.48	0.49
1:EM:20:TYR:CZ	1:EM:36:LYS:HD3	2.48	0.49
1:EO:37:ILE:HG12	1:EO:53:VAL:HG22	1.95	0.49
1:FE:20:TYR:CZ	1:FE:36:LYS:HD3	2.48	0.49
1:FT:43:ASN:OD1	1:FT:46:THR:OG1	2.31	0.49
1:FY:37:ILE:HG12	1:FY:53:VAL:HG22	1.95	0.49
1:HD:38:SER:OG	2:SF:7:A:OP1	2.26	0.49
1:HF:97:ASN:ND2	1:NB:94:SER:HA	2.28	0.49
1:HJ:109:LEU:O	1:KV:40:GLY:HA2	2.13	0.49
1:HP:43:ASN:OD1	1:HP:46:THR:OG1	2.31	0.49
1:HV:43:ASN:OD1	1:HV:46:THR:OG1	2.31	0.49
1:IN:43:ASN:OD1	1:IN:46:THR:OG1	2.31	0.49
1:JE:94:SER:HA	1:JJ:97:ASN:HD21	1.77	0.49
1:KG:20:TYR:CZ	1:KG:36:LYS:HD3	2.48	0.49
1:KR:37:ILE:HG12	1:KR:53:VAL:HG22	1.95	0.49
1:LH:20:TYR:CZ	1:LH:36:LYS:HD3	2.48	0.49
1:MB:37:ILE:HG12	1:MB:53:VAL:HG22	1.95	0.49
1:MF:20:TYR:CZ	1:MF:36:LYS:HD3	2.48	0.49
1:MG:43:ASN:OD1	1:MG:46:THR:OG1	2.24	0.49
1:NM:20:TYR:CZ	1:NM:36:LYS:HD3	2.48	0.49
1:AC:43:ASN:OD1	1:AC:46:THR:OG1	2.31	0.48
1:AU:43:ASN:OD1	1:AU:46:THR:OG1	2.31	0.48
1:BC:37:ILE:HG12	1:BC:53:VAL:HG22	1.95	0.48
1:BO:37:ILE:HG12	1:BO:53:VAL:HG22	1.95	0.48
1:BP:94:SER:HA	1:FB:97:ASN:HD21	1.78	0.48
1:BS:43:ASN:OD1	1:BS:46:THR:OG1	2.31	0.48
1:BU:37:ILE:HG12	1:BU:53:VAL:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DC:20:TYR:OH	2:SA:8:U:OP1	2.21	0.48
1:DI:20:TYR:CZ	1:DI:36:LYS:HD3	2.48	0.48
1:DT:37:ILE:HG12	1:DT:53:VAL:HG22	1.95	0.48
1:DV:8:ILE:HD11	1:GE:99:LEU:HB2	1.95	0.48
1:ES:43:ASN:OD1	1:ES:46:THR:OG1	2.31	0.48
1:EX:37:ILE:HG12	1:EX:53:VAL:HG22	1.95	0.48
1:EX:96:LEU:CD2	1:FI:53:VAL:HG12	2.43	0.48
1:FN:20:TYR:CZ	1:FN:36:LYS:HD3	2.48	0.48
1:GC:20:TYR:CZ	1:GC:36:LYS:HD3	2.48	0.48
1:GI:43:ASN:OD1	1:GI:46:THR:OG1	2.31	0.48
1:GR:20:TYR:CZ	1:GR:36:LYS:HD3	2.48	0.48
1:GR:43:ASN:OD1	1:GR:46:THR:OG1	2.31	0.48
1:HA:20:TYR:CZ	1:HA:36:LYS:HD3	2.48	0.48
1:HS:53:VAL:HG12	1:LE:96:LEU:HD22	1.95	0.48
1:IB:20:TYR:CZ	1:IB:36:LYS:HD3	2.48	0.48
1:IE:43:ASN:OD1	1:IE:46:THR:OG1	2.31	0.48
1:IQ:20:TYR:CZ	1:IQ:36:LYS:HD3	2.48	0.48
1:IR:111:GLY:HA3	1:KM:16:THR:HB	1.95	0.48
1:IY:37:ILE:HG12	1:IY:53:VAL:HG22	1.95	0.48
1:JC:16:THR:HB	1:JP:111:GLY:HA3	1.95	0.48
1:JL:43:ASN:OD1	1:JL:46:THR:OG1	2.31	0.48
1:KA:43:ASN:OD1	1:KA:46:THR:OG1	2.31	0.48
1:KP:43:ASN:OD1	1:KP:46:THR:OG1	2.31	0.48
1:KV:20:TYR:CZ	1:KV:36:LYS:HD3	2.48	0.48
1:LA:37:ILE:HG12	1:LA:53:VAL:HG22	1.95	0.48
1:LP:37:ILE:HG12	1:LP:53:VAL:HG22	1.95	0.48
1:LQ:43:ASN:OD1	1:LQ:46:THR:OG1	2.31	0.48
1:MD:43:ASN:OD1	1:MD:46:THR:OG1	2.24	0.48
1:MI:43:ASN:OD1	1:MI:46:THR:OG1	2.31	0.48
1:MU:20:TYR:CZ	1:MU:36:LYS:HD3	2.48	0.48
1:MU:43:ASN:OD1	1:MU:46:THR:OG1	2.31	0.48
1:MW:37:ILE:HG12	1:MW:53:VAL:HG22	1.95	0.48
1:MX:43:ASN:OD1	1:MX:46:THR:OG1	2.31	0.48
1:NH:43:ASN:OD1	1:NH:46:THR:OG1	2.24	0.48
1:AB:111:GLY:HA2	1:FX:40:GLY:HA3	1.95	0.48
1:AC:20:TYR:CZ	1:AC:36:LYS:HD3	2.48	0.48
1:AH:37:ILE:HG12	1:AH:53:VAL:HG22	1.95	0.48
1:BY:20:TYR:CZ	1:BY:36:LYS:HD3	2.48	0.48
1:CE:38:SER:OG	2:RS:7:A:OP1	2.26	0.48
1:CG:37:ILE:HG12	1:CG:53:VAL:HG22	1.95	0.48
1:CJ:97:ASN:ND2	1:CO:94:SER:HA	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CT:40:GLY:HA3	1:GF:111:GLY:HA2	1.95	0.48
1:CV:111:GLY:HA2	1:GM:40:GLY:HA3	1.95	0.48
1:DB:37:ILE:HG12	1:DB:53:VAL:HG22	1.95	0.48
1:DR:43:ASN:OD1	1:DR:46:THR:OG1	2.31	0.48
1:EI:37:ILE:HG12	1:EI:53:VAL:HG22	1.95	0.48
1:EM:43:ASN:OD1	1:EM:46:THR:OG1	2.31	0.48
1:EP:20:TYR:CZ	1:EP:36:LYS:HD3	2.48	0.48
1:ER:37:ILE:HG12	1:ER:53:VAL:HG22	1.95	0.48
1:FD:37:ILE:HG12	1:FD:53:VAL:HG22	1.95	0.48
1:FE:43:ASN:OD1	1:FE:46:THR:OG1	2.31	0.48
1:GF:20:TYR:CZ	1:GF:36:LYS:HD3	2.48	0.48
1:GK:37:ILE:HG12	1:GK:53:VAL:HG22	1.95	0.48
1:GN:37:ILE:HG12	1:GN:53:VAL:HG22	1.95	0.48
1:HF:37:ILE:HG12	1:HF:53:VAL:HG22	1.95	0.48
1:HH:43:ASN:OD1	1:HH:46:THR:OG1	2.24	0.48
1:HP:40:GLY:HA2	1:LB:109:LEU:O	2.14	0.48
1:HV:20:TYR:CZ	1:HV:36:LYS:HD3	2.48	0.48
1:HW:94:SER:HA	1:LG:97:ASN:ND2	2.28	0.48
1:HX:37:ILE:HG12	1:HX:53:VAL:HG22	1.95	0.48
1:IF:43:ASN:OD1	1:IF:46:THR:OG1	2.23	0.48
1:JC:94:SER:HA	1:MO:97:ASN:ND2	2.29	0.48
1:JE:37:ILE:HG12	1:JE:53:VAL:HG22	1.95	0.48
1:JR:43:ASN:OD1	1:JR:46:THR:OG1	2.31	0.48
1:KD:20:TYR:CZ	1:KD:36:LYS:HD3	2.48	0.48
1:KF:37:ILE:HG12	1:KF:53:VAL:HG22	1.95	0.48
1:KI:37:ILE:HG12	1:KI:53:VAL:HG22	1.95	0.48
1:KP:20:TYR:OH	2:SF:28:A:OP1	2.28	0.48
1:KS:20:TYR:CZ	1:KS:36:LYS:HD3	2.48	0.48
1:LQ:20:TYR:CZ	1:LQ:36:LYS:HD3	2.48	0.48
1:LZ:16:THR:HB	1:MJ:111:GLY:HA3	1.95	0.48
1:AJ:43:ASN:OD1	1:AJ:46:THR:OG1	2.24	0.48
1:AJ:94:SER:HA	1:BX:97:ASN:ND2	2.27	0.48
1:AO:43:ASN:OD1	1:AO:46:THR:OG1	2.31	0.48
1:AO:97:ASN:ND2	1:EA:94:SER:HA	2.28	0.48
1:AU:20:TYR:OH	2:RG:8:U:OP1	2.21	0.48
1:AW:37:ILE:HG12	1:AW:53:VAL:HG22	1.95	0.48
1:BB:40:GLY:HA3	1:BR:111:GLY:HA2	1.95	0.48
1:BG:43:ASN:OD1	1:BG:46:THR:OG1	2.31	0.48
1:BP:20:TYR:CZ	1:BP:36:LYS:HD3	2.48	0.48
1:CN:20:TYR:CZ	1:CN:36:LYS:HD3	2.48	0.48
1:CW:38:SER:OG	2:RY:7:A:OP1	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DI:97:ASN:ND2	1:GU:94:SER:HA	2.29	0.48
1:DP:99:LEU:HB2	1:GW:8:ILE:HD11	1.95	0.48
1:EY:43:ASN:OD1	1:EY:46:THR:OG1	2.31	0.48
1:FB:20:TYR:CZ	1:FB:36:LYS:HD3	2.48	0.48
1:FS:37:ILE:HG12	1:FS:53:VAL:HG22	1.95	0.48
1:FS:53:VAL:HG12	1:GP:96:LEU:HD22	1.93	0.48
1:FW:43:ASN:OD1	1:FW:46:THR:OG1	2.31	0.48
1:GL:20:TYR:CZ	1:GL:36:LYS:HD3	2.48	0.48
1:HD:43:ASN:OD1	1:HD:46:THR:OG1	2.31	0.48
1:IP:37:ILE:HG12	1:IP:53:VAL:HG22	1.95	0.48
1:IZ:20:TYR:CZ	1:IZ:36:LYS:HD3	2.48	0.48
1:IZ:20:TYR:OH	2:SV:8:U:OP1	2.21	0.48
1:JK:111:GLY:HA2	1:KE:40:GLY:HA3	1.95	0.48
1:JN:37:ILE:HG12	1:JN:53:VAL:HG22	1.95	0.48
1:JR:94:SER:HA	1:ND:97:ASN:HD21	1.78	0.48
1:JY:43:ASN:OD1	1:JY:46:THR:OG1	2.24	0.48
1:LT:20:TYR:CZ	1:LT:36:LYS:HD3	2.48	0.48
1:MQ:37:ILE:HG12	1:MQ:53:VAL:HG22	1.95	0.48
1:MZ:37:ILE:HG12	1:MZ:53:VAL:HG22	1.95	0.48
1:NR:37:ILE:HG12	1:NR:53:VAL:HG22	1.95	0.48
1:AJ:35:ILE:HD13	1:BX:99:LEU:HD22	1.95	0.48
1:AJ:40:GLY:HA3	1:BX:111:GLY:HA2	1.96	0.48
1:AQ:105:LEU:HD23	1:AQ:105:LEU:HA	1.64	0.48
1:BI:37:ILE:HG12	1:BI:53:VAL:HG22	1.95	0.48
1:CE:20:TYR:OH	2:RS:8:U:OP1	2.21	0.48
1:CH:43:ASN:OD1	1:CH:46:THR:OG1	2.31	0.48
1:CQ:97:ASN:HD21	1:GC:94:SER:HA	1.78	0.48
1:CW:43:ASN:OD1	1:CW:46:THR:OG1	2.31	0.48
1:DC:43:ASN:OD1	1:DC:46:THR:OG1	2.31	0.48
1:DO:43:ASN:OD1	1:DO:46:THR:OG1	2.31	0.48
1:DP:94:SER:HA	1:GW:97:ASN:ND2	2.28	0.48
1:DX:43:ASN:OD1	1:DX:46:THR:OG1	2.31	0.48
1:EC:37:ILE:HG12	1:EC:53:VAL:HG22	1.95	0.48
1:EG:20:TYR:CZ	1:EG:36:LYS:HD3	2.48	0.48
1:FH:43:ASN:OD1	1:FH:46:THR:OG1	2.31	0.48
1:FU:43:ASN:OD1	1:FU:46:THR:OG1	2.24	0.48
1:FV:105:LEU:HD23	1:FV:105:LEU:HA	1.64	0.48
1:GT:37:ILE:HG12	1:GT:53:VAL:HG22	1.95	0.48
1:GU:43:ASN:OD1	1:GU:46:THR:OG1	2.31	0.48
1:HC:37:ILE:HG12	1:HC:53:VAL:HG22	1.95	0.48
1:HH:40:GLY:HA3	1:IV:111:GLY:HA2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HO:37:ILE:HG12	1:HO:53:VAL:HG22	1.95	0.48
1:HP:20:TYR:CZ	1:HP:36:LYS:HD3	2.48	0.48
1:HX:105:LEU:HD23	1:HX:105:LEU:HA	1.64	0.48
1:IC:92:LEU:HD22	1:IJ:55:ARG:HG3	1.94	0.48
1:IH:20:TYR:CZ	1:IH:36:LYS:HD3	2.48	0.48
1:IN:20:TYR:CZ	1:IN:36:LYS:HD3	2.48	0.48
1:IS:105:LEU:HD23	1:IS:105:LEU:HA	1.64	0.48
1:IT:43:ASN:OD1	1:IT:46:THR:OG1	2.31	0.48
1:JE:96:LEU:HD13	1:JJ:76:ILE:CD1	2.43	0.48
1:JF:43:ASN:OD1	1:JF:46:THR:OG1	2.31	0.48
1:JU:20:TYR:CZ	1:JU:36:LYS:HD3	2.48	0.48
1:KJ:20:TYR:CZ	1:KJ:36:LYS:HD3	2.48	0.48
1:KR:105:LEU:HD23	1:KR:105:LEU:HA	1.64	0.48
1:KY:43:ASN:OD1	1:KY:46:THR:OG1	2.31	0.48
1:LF:94:SER:HA	1:LM:97:ASN:ND2	2.28	0.48
1:LH:43:ASN:OD1	1:LH:46:THR:OG1	2.31	0.48
1:LK:43:ASN:OD1	1:LK:46:THR:OG1	2.31	0.48
1:LM:37:ILE:HG12	1:LM:53:VAL:HG22	1.95	0.48
1:LN:43:ASN:OD1	1:LN:46:THR:OG1	2.31	0.48
1:LZ:20:TYR:CZ	1:LZ:36:LYS:HD3	2.48	0.48
1:MK:37:ILE:HG12	1:MK:53:VAL:HG22	1.95	0.48
1:NI:37:ILE:HG12	1:NI:53:VAL:HG22	1.95	0.48
1:NM:43:ASN:OD1	1:NM:46:THR:OG1	2.31	0.48
1:AF:38:SER:OG	2:RB:7:A:OP1	2.26	0.48
1:AN:105:LEU:HD23	1:AN:105:LEU:HA	1.64	0.48
1:AO:20:TYR:CZ	1:AO:36:LYS:HD3	2.48	0.48
1:AS:96:LEU:HD22	1:EL:53:VAL:HG12	1.95	0.48
1:BL:37:ILE:HG12	1:BL:53:VAL:HG22	1.95	0.48
1:CW:53:VAL:HG12	1:GI:96:LEU:HD22	1.95	0.48
1:DI:53:VAL:HG12	1:GU:96:LEU:HD22	1.95	0.48
1:DN:37:ILE:HG12	1:DN:53:VAL:HG22	1.95	0.48
1:EO:105:LEU:HA	1:EO:105:LEU:HD23	1.64	0.48
1:FP:37:ILE:HG12	1:FP:53:VAL:HG22	1.95	0.48
1:FT:20:TYR:CZ	1:FT:36:LYS:HD3	2.48	0.48
1:GB:37:ILE:HG12	1:GB:53:VAL:HG22	1.95	0.48
1:GR:41:LYS:HD2	2:SB:26:A:OP1	2.12	0.48
1:HO:35:ILE:HD13	1:MS:99:LEU:HD22	1.95	0.48
1:IJ:37:ILE:HG12	1:IJ:53:VAL:HG22	1.95	0.48
1:JR:20:TYR:CZ	1:JR:36:LYS:HD3	2.48	0.48
1:JX:38:SER:OG	2:TD:7:A:OP1	2.26	0.48
1:LB:43:ASN:OD1	1:LB:46:THR:OG1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LD:37:ILE:HG12	1:LD:53:VAL:HG22	1.95	0.48
1:LG:37:ILE:HG12	1:LG:53:VAL:HG22	1.95	0.48
1:MR:43:ASN:OD1	1:MR:46:THR:OG1	2.31	0.48
1:AR:20:TYR:CZ	1:AR:36:LYS:HD3	2.48	0.48
1:BD:43:ASN:OD1	1:BD:46:THR:OG1	2.31	0.48
1:BM:43:ASN:OD1	1:BM:46:THR:OG1	2.31	0.48
1:CM:37:ILE:HG12	1:CM:53:VAL:HG22	1.95	0.48
1:CU:99:LEU:HD22	1:DH:35:ILE:HD13	1.95	0.48
1:CV:37:ILE:HG12	1:CV:53:VAL:HG22	1.95	0.48
1:CX:99:LEU:HB2	1:DK:8:ILE:HD11	1.95	0.48
1:DL:20:TYR:CZ	1:DL:36:LYS:HD3	2.48	0.48
1:DO:38:SER:OG	2:RA:27:U:OP1	2.29	0.48
1:DR:20:TYR:CZ	1:DR:36:LYS:HD3	2.48	0.48
1:EA:43:ASN:OD1	1:EA:46:THR:OG1	2.31	0.48
1:EJ:20:TYR:CZ	1:EJ:36:LYS:HD3	2.48	0.48
1:FH:20:TYR:CZ	1:FH:36:LYS:HD3	2.48	0.48
1:FM:37:ILE:HG12	1:FM:53:VAL:HG22	1.95	0.48
1:GC:20:TYR:OH	2:RW:28:A:OP1	2.26	0.48
1:GO:43:ASN:OD1	1:GO:46:THR:OG1	2.31	0.48
1:HD:20:TYR:OH	2:SF:8:U:OP1	2.21	0.48
1:HG:43:ASN:OD1	1:HG:46:THR:OG1	2.31	0.48
1:HJ:43:ASN:OD1	1:HJ:46:THR:OG1	2.31	0.48
1:IT:20:TYR:CZ	1:IT:36:LYS:HD3	2.48	0.48
1:JD:111:GLY:HA2	1:NL:40:GLY:HA3	1.95	0.48
1:JN:21:TYR:OH	1:KH:113:PHE:O	2.30	0.48
1:JO:43:ASN:OD1	1:JO:46:THR:OG1	2.31	0.48
1:KD:43:ASN:OD1	1:KD:46:THR:OG1	2.31	0.48
1:KJ:97:ASN:ND2	1:NV:94:SER:HA	2.28	0.48
1:KU:37:ILE:HG12	1:KU:53:VAL:HG22	1.95	0.48
1:LK:20:TYR:CZ	1:LK:36:LYS:HD3	2.48	0.48
1:LW:52:ALA:HB2	2:SQ:26:A:H4'	1.96	0.48
1:MF:43:ASN:OD1	1:MF:46:THR:OG1	2.31	0.48
1:MO:20:TYR:CZ	1:MO:36:LYS:HD3	2.48	0.48
1:NA:43:ASN:OD1	1:NA:46:THR:OG1	2.31	0.48
1:AL:43:ASN:OD1	1:AL:46:THR:OG1	2.31	0.48
1:BE:94:SER:HA	1:BL:97:ASN:HD21	1.78	0.48
1:BJ:20:TYR:CZ	1:BJ:36:LYS:HD3	2.48	0.48
1:BY:43:ASN:OD1	1:BY:46:THR:OG1	2.31	0.48
1:BY:109:LEU:O	1:FK:40:GLY:HA2	2.13	0.48
1:CQ:43:ASN:OD1	1:CQ:46:THR:OG1	2.31	0.48
1:CT:43:ASN:OD1	1:CT:46:THR:OG1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ED:43:ASN:OD1	1:ED:46:THR:OG1	2.31	0.48
1:GZ:37:ILE:HG12	1:GZ:53:VAL:HG22	1.95	0.48
1:HU:37:ILE:HG12	1:HU:53:VAL:HG22	1.95	0.48
1:HW:8:ILE:HD11	1:LG:99:LEU:HB2	1.94	0.48
1:IK:43:ASN:OD1	1:IK:46:THR:OG1	2.31	0.48
1:JB:37:ILE:HG12	1:JB:53:VAL:HG22	1.95	0.48
1:LE:20:TYR:CZ	1:LE:36:LYS:HD3	2.48	0.48
1:LO:94:SER:HA	1:MK:97:ASN:ND2	2.27	0.48
1:AB:37:ILE:HG12	1:AB:53:VAL:HG22	1.95	0.48
1:AL:38:SER:OG	2:RD:7:A:OP1	2.26	0.48
1:AU:20:TYR:CZ	1:AU:36:LYS:HD3	2.48	0.48
1:AZ:94:SER:HA	1:EW:97:ASN:ND2	2.28	0.48
1:BV:43:ASN:OD1	1:BV:46:THR:OG1	2.31	0.48
1:BV:111:GLY:HA2	1:FH:40:GLY:HA3	1.96	0.48
1:CC:43:ASN:OD1	1:CC:46:THR:OG1	2.24	0.48
1:CY:109:LEU:O	1:GG:40:GLY:HA2	2.13	0.48
1:EG:43:ASN:OD1	1:EG:46:THR:OG1	2.31	0.48
1:EN:99:LEU:HD22	1:FJ:35:ILE:HD13	1.94	0.48
1:GW:37:ILE:HG12	1:GW:53:VAL:HG22	1.95	0.48
1:HE:99:LEU:HB2	1:ID:8:ILE:HD11	1.94	0.48
1:HQ:8:ILE:HD11	1:LJ:99:LEU:HB2	1.95	0.48
1:IB:20:TYR:OH	2:SN:8:U:OP1	2.21	0.48
1:IB:97:ASN:ND2	1:LN:94:SER:HA	2.28	0.48
1:IT:96:LEU:HD21	1:MF:55:ARG:HB2	1.96	0.48
1:JK:97:ASN:ND2	1:KE:94:SER:HA	2.29	0.48
1:JT:37:ILE:HG12	1:JT:53:VAL:HG22	1.95	0.48
1:KE:43:ASN:OD1	1:KE:46:THR:OG1	2.24	0.48
1:LW:20:TYR:CZ	1:LW:36:LYS:HD3	2.48	0.48
1:LZ:43:ASN:OD1	1:LZ:46:THR:OG1	2.31	0.48
1:MA:43:ASN:OD1	1:MA:46:THR:OG1	2.24	0.48
1:NG:43:ASN:OD1	1:NG:46:THR:OG1	2.31	0.48
1:NQ:43:ASN:OD1	1:NQ:46:THR:OG1	2.24	0.48
1:BB:6:LEU:HD22	1:BR:99:LEU:HD11	1.96	0.48
1:BS:20:TYR:CZ	1:BS:36:LYS:HD3	2.48	0.48
1:CU:113:PHE:OXT	1:DH:21:TYR:OH	2.32	0.48
1:CZ:43:ASN:OD1	1:CZ:46:THR:OG1	2.31	0.48
1:DS:43:ASN:OD1	1:DS:46:THR:OG1	2.24	0.48
1:ED:41:LYS:HD2	2:RF:26:A:OP1	2.14	0.48
1:GE:37:ILE:HG12	1:GE:53:VAL:HG22	1.95	0.48
1:HO:111:GLY:HA2	1:MS:40:GLY:HA3	1.95	0.48
1:HY:20:TYR:OH	2:SM:8:U:OP1	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HY:38:SER:OG	2:SM:7:A:OP1	2.26	0.48
1:HY:43:ASN:OD1	1:HY:46:THR:OG1	2.31	0.48
1:JH:37:ILE:HG12	1:JH:53:VAL:HG22	1.95	0.48
1:JQ:35:ILE:HD13	1:KB:99:LEU:HD22	1.95	0.48
1:MC:43:ASN:OD1	1:MC:46:THR:OG1	2.31	0.48
1:MU:52:ALA:HB2	2:SY:26:A:H4'	1.95	0.48
1:AI:43:ASN:OD1	1:AI:46:THR:OG1	2.31	0.48
1:AZ:37:ILE:HG12	1:AZ:53:VAL:HG22	1.95	0.48
1:BS:97:ASN:HD21	1:FE:94:SER:HA	1.78	0.48
1:BU:105:LEU:HA	1:BU:105:LEU:HD23	1.64	0.48
1:CB:109:LEU:O	1:FN:40:GLY:HA2	2.14	0.48
1:CP:37:ILE:HG12	1:CP:53:VAL:HG22	1.95	0.48
1:DB:8:ILE:HD11	1:GJ:99:LEU:HB2	1.96	0.48
1:DE:37:ILE:HG12	1:DE:53:VAL:HG22	1.95	0.48
1:EF:37:ILE:HG12	1:EF:53:VAL:HG22	1.95	0.48
1:EU:37:ILE:HG12	1:EU:53:VAL:HG22	1.95	0.48
1:FX:43:ASN:OD1	1:FX:46:THR:OG1	2.24	0.48
1:FZ:43:ASN:OD1	1:FZ:46:THR:OG1	2.31	0.48
1:GF:43:ASN:OD1	1:GF:46:THR:OG1	2.31	0.48
1:GH:37:ILE:HG12	1:GH:53:VAL:HG22	1.95	0.48
1:GX:43:ASN:OD1	1:GX:46:THR:OG1	2.31	0.48
1:HL:37:ILE:HG12	1:HL:53:VAL:HG22	1.95	0.48
1:HR:37:ILE:HG12	1:HR:53:VAL:HG22	1.95	0.48
1:HU:40:GLY:HA3	1:MA:111:GLY:HA2	1.96	0.48
1:IC:99:LEU:HB2	1:IJ:8:ILE:HD11	1.96	0.48
1:IE:20:TYR:CZ	1:IE:36:LYS:HD3	2.48	0.48
1:IQ:92:LEU:HD22	1:MC:55:ARG:HG2	1.96	0.48
1:JC:20:TYR:CZ	1:JC:36:LYS:HD3	2.48	0.48
1:JU:20:TYR:OH	2:TC:8:U:OP1	2.21	0.48
1:JU:43:ASN:OD1	1:JU:46:THR:OG1	2.31	0.48
1:KA:38:SER:OG	2:TE:7:A:OP1	2.26	0.48
1:LJ:105:LEU:HA	1:LJ:105:LEU:HD23	1.64	0.48
1:LY:37:ILE:HG12	1:LY:53:VAL:HG22	1.95	0.48
1:NV:43:ASN:OD1	1:NV:46:THR:OG1	2.31	0.48
1:AN:37:ILE:HG12	1:AN:53:VAL:HG22	1.95	0.47
1:BQ:40:GLY:HA3	1:EC:111:GLY:HA2	1.96	0.47
1:BR:37:ILE:HG12	1:BR:53:VAL:HG22	1.95	0.47
1:BV:20:TYR:OH	2:RP:8:U:OP1	2.21	0.47
1:BV:38:SER:OG	2:RP:7:A:OP1	2.26	0.47
1:CN:96:LEU:HD22	1:FZ:53:VAL:HG12	1.96	0.47
1:CZ:97:ASN:ND2	1:GL:94:SER:HA	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EH:111:GLY:HA2	1:EO:40:GLY:HA3	1.96	0.47
1:EJ:43:ASN:OD1	1:EJ:46:THR:OG1	2.31	0.47
1:FG:37:ILE:HG12	1:FG:53:VAL:HG22	1.95	0.47
1:FK:43:ASN:OD1	1:FK:46:THR:OG1	2.31	0.47
1:FN:43:ASN:OD1	1:FN:46:THR:OG1	2.31	0.47
1:FV:37:ILE:HG12	1:FV:53:VAL:HG22	1.95	0.47
1:GX:20:TYR:CZ	1:GX:36:LYS:HD3	2.48	0.47
1:HI:37:ILE:HG12	1:HI:53:VAL:HG22	1.95	0.47
1:HM:43:ASN:OD1	1:HM:46:THR:OG1	2.31	0.47
1:JV:43:ASN:OD1	1:JV:46:THR:OG1	2.24	0.47
1:KJ:43:ASN:OD1	1:KJ:46:THR:OG1	2.31	0.47
1:KL:37:ILE:HG12	1:KL:53:VAL:HG22	1.95	0.47
1:KO:37:ILE:HG12	1:KO:53:VAL:HG22	1.95	0.47
1:KQ:35:ILE:HD13	1:NO:99:LEU:HD22	1.94	0.47
1:LE:41:LYS:HD2	2:SK:26:A:OP1	2.15	0.47
1:LT:43:ASN:OD1	1:LT:46:THR:OG1	2.31	0.47
1:AX:43:ASN:OD1	1:AX:46:THR:OG1	2.31	0.47
1:BG:94:SER:HA	1:ES:97:ASN:HD21	1.80	0.47
1:BN:96:LEU:CD2	1:DZ:53:VAL:HG12	2.43	0.47
1:BP:43:ASN:OD1	1:BP:46:THR:OG1	2.31	0.47
1:CA:37:ILE:HG12	1:CA:53:VAL:HG22	1.95	0.47
1:DL:43:ASN:OD1	1:DL:46:THR:OG1	2.31	0.47
1:EV:43:ASN:OD1	1:EV:46:THR:OG1	2.31	0.47
1:FB:43:ASN:OD1	1:FB:46:THR:OG1	2.31	0.47
1:FW:20:TYR:OH	2:RU:28:A:OP1	2.26	0.47
1:GL:43:ASN:OD1	1:GL:46:THR:OG1	2.31	0.47
1:HA:43:ASN:OD1	1:HA:46:THR:OG1	2.31	0.47
1:HZ:94:SER:HA	1:IP:97:ASN:HD21	1.79	0.47
1:ID:37:ILE:HG12	1:ID:53:VAL:HG22	1.95	0.47
1:IH:43:ASN:OD1	1:IH:46:THR:OG1	2.31	0.47
1:IH:97:ASN:HD21	1:LT:94:SER:HA	1.78	0.47
1:IP:105:LEU:HD23	1:IP:105:LEU:HA	1.64	0.47
1:IQ:43:ASN:OD1	1:IQ:46:THR:OG1	2.31	0.47
1:IZ:43:ASN:OD1	1:IZ:46:THR:OG1	2.31	0.47
1:JC:43:ASN:OD1	1:JC:46:THR:OG1	2.31	0.47
1:JD:40:GLY:HA3	1:NL:111:GLY:HA2	1.96	0.47
1:ML:43:ASN:OD1	1:ML:46:THR:OG1	2.31	0.47
1:MO:43:ASN:OD1	1:MO:46:THR:OG1	2.31	0.47
1:MR:20:TYR:HH	2:SX:28:A:P	2.36	0.47
1:AO:38:SER:OG	2:RE:7:A:OP1	2.26	0.47
1:AZ:55:ARG:CG	1:EW:92:LEU:HD22	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:43:ASN:OD1	1:BA:46:THR:OG1	2.31	0.47
1:BQ:107:GLN:CD	1:ED:14:ILE:HD13	2.39	0.47
1:CC:97:ASN:ND2	1:GK:94:SER:HA	2.29	0.47
1:CN:43:ASN:OD1	1:CN:46:THR:OG1	2.31	0.47
1:CY:105:LEU:HD23	1:CY:105:LEU:HA	1.64	0.47
1:DI:20:TYR:OH	2:SC:8:U:OP1	2.21	0.47
1:DU:43:ASN:OD1	1:DU:46:THR:OG1	2.31	0.47
1:FA:37:ILE:HG12	1:FA:53:VAL:HG22	1.95	0.47
1:FP:99:LEU:HD22	1:GV:35:ILE:HD13	1.96	0.47
1:HM:94:SER:HA	1:KY:97:ASN:ND2	2.28	0.47
1:IK:53:VAL:HG12	1:LW:96:LEU:HD22	1.95	0.47
1:IS:37:ILE:HG12	1:IS:53:VAL:HG22	1.95	0.47
1:KG:43:ASN:OD1	1:KG:46:THR:OG1	2.31	0.47
1:MH:37:ILE:HG12	1:MH:53:VAL:HG22	1.95	0.47
1:NS:43:ASN:OD1	1:NS:46:THR:OG1	2.31	0.47
1:AP:99:LEU:HB2	1:BU:8:ILE:HD11	1.96	0.47
1:AW:97:ASN:ND2	1:FC:94:SER:HA	2.28	0.47
1:BG:55:ARG:CG	1:ES:92:LEU:HD22	2.45	0.47
1:BJ:43:ASN:OD1	1:BJ:46:THR:OG1	2.31	0.47
1:BV:94:SER:HA	1:FH:97:ASN:HD21	1.79	0.47
1:CM:105:LEU:HD23	1:CM:105:LEU:HA	1.64	0.47
1:EL:37:ILE:HG12	1:EL:53:VAL:HG22	1.95	0.47
1:EP:43:ASN:OD1	1:EP:46:THR:OG1	2.31	0.47
1:FZ:52:ALA:HB2	2:RV:26:A:H4'	1.96	0.47
1:GZ:40:GLY:HA3	1:MV:111:GLY:HA2	1.96	0.47
1:HS:43:ASN:OD1	1:HS:46:THR:OG1	2.31	0.47
1:IG:37:ILE:HG12	1:IG:53:VAL:HG22	1.95	0.47
1:JC:94:SER:HA	1:MO:97:ASN:HD21	1.79	0.47
1:JK:53:VAL:HG12	1:KE:96:LEU:HD22	1.96	0.47
1:JQ:40:GLY:HA3	1:KB:111:GLY:HA2	1.97	0.47
1:JY:40:GLY:HA3	1:KC:111:GLY:HA2	1.96	0.47
1:KC:37:ILE:HG12	1:KC:53:VAL:HG22	1.95	0.47
1:KS:43:ASN:OD1	1:KS:46:THR:OG1	2.31	0.47
1:LF:8:ILE:HD11	1:LM:99:LEU:HB2	1.96	0.47
1:MN:99:LEU:HB2	1:NT:8:ILE:HD11	1.95	0.47
1:NP:43:ASN:OD1	1:NP:46:THR:OG1	2.31	0.47
1:AK:37:ILE:HG12	1:AK:53:VAL:HG22	1.95	0.47
1:AR:97:ASN:HD21	1:ED:94:SER:HA	1.79	0.47
1:BA:16:THR:HB	1:EW:111:GLY:HA3	1.97	0.47
1:BA:20:TYR:OH	2:RI:8:U:OP1	2.21	0.47
1:BA:38:SER:OG	2:RI:7:A:OP1	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:37:ILE:HG12	1:BX:53:VAL:HG22	1.95	0.47
1:CE:43:ASN:OD1	1:CE:46:THR:OG1	2.31	0.47
1:CH:38:SER:OG	2:RT:7:A:OP1	2.26	0.47
1:CJ:53:VAL:HG12	1:CO:96:LEU:HD22	1.95	0.47
1:CP:6:LEU:HD22	1:DJ:99:LEU:HD11	1.96	0.47
1:CX:94:SER:HA	1:DK:97:ASN:HD21	1.79	0.47
1:CZ:94:SER:HA	1:GL:97:ASN:ND2	2.29	0.47
1:DZ:37:ILE:HG12	1:DZ:53:VAL:HG22	1.95	0.47
1:ET:8:ILE:HD11	1:FG:99:LEU:HB2	1.96	0.47
1:FZ:38:SER:OG	2:RV:27:U:OP1	2.25	0.47
1:GH:105:LEU:HD23	1:GH:105:LEU:HA	1.64	0.47
1:GY:43:ASN:OD1	1:GY:46:THR:OG1	2.24	0.47
1:HY:109:LEU:O	1:LK:40:GLY:HA2	2.14	0.47
1:IB:43:ASN:OD1	1:IB:46:THR:OG1	2.31	0.47
1:IT:38:SER:OG	2:ST:7:A:OP1	2.26	0.47
1:JS:40:GLY:HA2	1:KF:109:LEU:O	2.14	0.47
1:JT:40:GLY:HA3	1:NK:111:GLY:HA2	1.96	0.47
1:KV:43:ASN:OD1	1:KV:46:THR:OG1	2.31	0.47
1:KW:113:PHE:OXT	1:MW:21:TYR:OH	2.29	0.47
1:LE:43:ASN:OD1	1:LE:46:THR:OG1	2.31	0.47
1:LJ:37:ILE:HG12	1:LJ:53:VAL:HG22	1.95	0.47
1:LW:43:ASN:OD1	1:LW:46:THR:OG1	2.31	0.47
1:ME:37:ILE:HG12	1:ME:53:VAL:HG22	1.95	0.47
1:MQ:109:LEU:O	1:NN:40:GLY:HA2	2.13	0.47
1:AA:40:GLY:HA3	1:BI:111:GLY:HA2	1.96	0.47
1:AE:37:ILE:HG12	1:AE:53:VAL:HG22	1.95	0.47
1:AH:8:ILE:HD11	1:GD:99:LEU:HB2	1.95	0.47
1:AR:43:ASN:OD1	1:AR:46:THR:OG1	2.31	0.47
1:CK:40:GLY:HA2	1:FW:109:LEU:O	2.14	0.47
1:DI:55:ARG:HG2	1:GU:92:LEU:HD22	1.97	0.47
1:DM:35:ILE:HD13	1:GT:99:LEU:HD22	1.96	0.47
1:DQ:37:ILE:HG12	1:DQ:53:VAL:HG22	1.95	0.47
1:DW:37:ILE:HG12	1:DW:53:VAL:HG22	1.95	0.47
1:EB:94:SER:HA	1:GB:97:ASN:ND2	2.30	0.47
1:FL:43:ASN:OD1	1:FL:46:THR:OG1	2.24	0.47
1:GC:43:ASN:OD1	1:GC:46:THR:OG1	2.31	0.47
1:IC:96:LEU:HD22	1:IJ:53:VAL:CG1	2.44	0.47
1:JA:94:SER:HA	1:NI:97:ASN:ND2	2.29	0.47
1:JQ:37:ILE:HG12	1:JQ:53:VAL:HG22	1.95	0.47
1:JX:43:ASN:OD1	1:JX:46:THR:OG1	2.31	0.47
1:JZ:37:ILE:HG12	1:JZ:53:VAL:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KX:37:ILE:HG12	1:KX:53:VAL:HG22	1.95	0.47
1:MQ:99:LEU:HD22	1:NN:35:ILE:HD13	1.95	0.47
1:NC:37:ILE:HG12	1:NC:53:VAL:HG22	1.95	0.47
1:AQ:37:ILE:HG12	1:AQ:53:VAL:HG22	1.95	0.47
1:AY:43:ASN:OD1	1:AY:46:THR:OG1	2.24	0.47
1:BF:37:ILE:HG12	1:BF:53:VAL:HG22	1.95	0.47
1:BK:8:ILE:HD11	1:DW:99:LEU:HB2	1.97	0.47
1:BP:97:ASN:ND2	1:FB:94:SER:HA	2.29	0.47
1:BQ:101:ASP:OD2	1:MM:10:SER:CB	2.61	0.47
1:BQ:109:LEU:O	1:EC:40:GLY:HA2	2.14	0.47
1:BY:20:TYR:OH	2:RQ:8:U:OP1	2.21	0.47
1:CB:43:ASN:OD1	1:CB:46:THR:OG1	2.31	0.47
1:DC:94:SER:HA	1:GO:97:ASN:HD21	1.80	0.47
1:DE:105:LEU:HD23	1:DE:105:LEU:HA	1.64	0.47
1:DI:43:ASN:OD1	1:DI:46:THR:OG1	2.31	0.47
1:DM:99:LEU:HB2	1:GT:8:ILE:HD11	1.97	0.47
1:FQ:43:ASN:OD1	1:FQ:46:THR:OG1	2.31	0.47
1:GQ:37:ILE:HG12	1:GQ:53:VAL:HG22	1.95	0.47
1:IK:20:TYR:OH	2:SQ:8:U:OP1	2.21	0.47
1:JA:35:ILE:HD13	1:NI:99:LEU:HD22	1.95	0.47
1:JI:94:SER:HA	1:MU:97:ASN:HD21	1.78	0.47
1:JK:35:ILE:HD13	1:KE:99:LEU:HD22	1.96	0.47
1:JQ:97:ASN:ND2	1:KB:94:SER:HA	2.29	0.47
1:JS:40:GLY:HA3	1:KF:111:GLY:HA2	1.97	0.47
1:KD:20:TYR:OH	2:TF:8:U:OP1	2.21	0.47
1:KM:43:ASN:OD1	1:KM:46:THR:OG1	2.31	0.47
1:LV:37:ILE:HG12	1:LV:53:VAL:HG22	1.95	0.47
1:MC:16:THR:HB	1:MD:111:GLY:HA3	1.97	0.47
1:MH:105:LEU:HD23	1:MH:105:LEU:HA	1.64	0.47
1:MQ:99:LEU:HB2	1:NN:8:ILE:HD11	1.97	0.47
1:MT:37:ILE:HG12	1:MT:53:VAL:HG22	1.95	0.47
1:MT:105:LEU:HA	1:MT:105:LEU:HD23	1.64	0.47
1:NJ:43:ASN:OD1	1:NJ:46:THR:OG1	2.31	0.47
1:NL:37:ILE:HG12	1:NL:53:VAL:HG22	1.95	0.47
1:NP:36:LYS:HE3	2:TF:27:U:OP1	2.15	0.47
1:NR:105:LEU:HD23	1:NR:105:LEU:HA	1.64	0.47
1:BA:94:SER:HA	1:EM:97:ASN:ND2	2.30	0.47
1:CH:96:LEU:HD22	1:FT:53:VAL:HG12	1.95	0.47
1:CJ:55:ARG:HG3	1:CO:92:LEU:HD22	1.97	0.47
1:CS:37:ILE:HG12	1:CS:53:VAL:HG22	1.95	0.47
1:HM:38:SER:OG	2:SI:7:A:OP1	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JK:37:ILE:HG12	1:JK:53:VAL:HG22	1.95	0.47
1:KO:105:LEU:HD23	1:KO:105:LEU:HA	1.64	0.47
1:KT:40:GLY:HA2	1:NC:109:LEU:O	2.15	0.47
1:KZ:35:ILE:HD13	1:MZ:99:LEU:HD22	1.96	0.47
1:NF:37:ILE:HG12	1:NF:53:VAL:HG22	1.95	0.47
1:NU:105:LEU:HD23	1:NU:105:LEU:HA	1.64	0.47
1:AG:40:GLY:HA3	1:BF:111:GLY:HA2	1.97	0.47
1:AM:40:GLY:HA3	1:CA:111:GLY:HA2	1.97	0.47
1:AS:40:GLY:HA3	1:EL:111:GLY:HA2	1.97	0.47
1:BL:105:LEU:HA	1:BL:105:LEU:HD23	1.64	0.47
1:BS:92:LEU:HD22	1:FE:55:ARG:CG	2.45	0.47
1:GU:38:SER:OG	2:SC:27:U:OP1	2.30	0.47
1:HU:99:LEU:HB2	1:MA:8:ILE:HD11	1.96	0.47
1:IQ:38:SER:OG	2:SS:7:A:OP1	2.26	0.47
1:JU:109:LEU:O	1:NG:40:GLY:HA2	2.14	0.47
1:KV:36:LYS:HE3	2:SH:27:U:OP1	2.15	0.47
1:MB:97:ASN:ND2	1:MD:94:SER:HA	2.30	0.47
1:MQ:96:LEU:HD22	1:NN:53:VAL:HG12	1.97	0.47
1:BZ:55:ARG:HG2	1:DT:92:LEU:HD22	1.97	0.47
1:CN:38:SER:OG	2:RV:7:A:OP1	2.26	0.47
1:CP:96:LEU:HD22	1:DJ:53:VAL:HG12	1.96	0.47
1:CT:38:SER:OG	2:RX:7:A:OP1	2.26	0.47
1:DT:105:LEU:HD23	1:DT:105:LEU:HA	1.64	0.47
1:EX:104:ARG:NH1	1:FI:3:PHE:CD1	2.83	0.47
1:HF:16:THR:HG21	1:ID:110:GLN:OE1	2.15	0.47
1:HN:99:LEU:HB2	1:IS:8:ILE:HD11	1.97	0.47
1:IC:104:ARG:HG2	1:IJ:3:PHE:CE1	2.49	0.47
1:IW:96:LEU:HD22	1:MI:53:VAL:HG12	1.97	0.47
1:JC:53:VAL:HG12	1:MO:96:LEU:HD22	1.97	0.47
1:JO:38:SER:OG	2:TA:7:A:OP1	2.26	0.47
1:JO:111:GLY:HA2	1:NA:40:GLY:HA3	1.96	0.47
1:JU:38:SER:OG	2:TC:7:A:OP1	2.26	0.47
1:LO:99:LEU:HB2	1:MK:8:ILE:HD11	1.97	0.47
1:MT:96:LEU:HD22	1:NQ:53:VAL:HG12	1.97	0.47
1:BC:28:PHE:HB3	1:BR:106:ASP:OD1	2.14	0.46
1:BW:40:GLY:HA3	1:DQ:111:GLY:HA2	1.97	0.46
1:CZ:94:SER:HA	1:GL:97:ASN:HD21	1.81	0.46
1:DI:94:SER:HA	1:GU:97:ASN:HD21	1.80	0.46
1:GQ:105:LEU:HA	1:GQ:105:LEU:HD23	1.64	0.46
1:HK:43:ASN:OD1	1:HK:46:THR:OG1	2.24	0.46
1:HM:20:TYR:OH	2:SI:8:U:OP1	2.21	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LR:40:GLY:HA3	1:ME:111:GLY:HA2	1.96	0.46
1:AN:111:GLY:HA2	1:FR:40:GLY:HA3	1.96	0.46
1:AR:20:TYR:OH	2:RF:8:U:OP1	2.21	0.46
1:CS:109:LEU:O	1:DD:40:GLY:HA2	2.16	0.46
1:GD:43:ASN:OD1	1:GD:46:THR:OG1	2.24	0.46
1:HK:21:TYR:HH	1:IY:113:PHE:C	2.23	0.46
1:HX:35:ILE:HD13	1:LU:99:LEU:HD22	1.97	0.46
1:IU:40:GLY:HA3	1:KO:111:GLY:HA2	1.97	0.46
1:JI:38:SER:OG	2:SY:7:A:OP1	2.26	0.46
1:JX:96:LEU:HD22	1:NJ:53:VAL:HG12	1.96	0.46
1:JZ:111:GLY:HA2	1:NH:40:GLY:HA3	1.96	0.46
1:AO:94:SER:HA	1:EA:97:ASN:ND2	2.30	0.46
1:BB:75:ALA:O	1:BR:76:ILE:HA	2.16	0.46
1:BC:105:LEU:HA	1:BC:105:LEU:HD23	1.64	0.46
1:BG:94:SER:HA	1:ES:97:ASN:ND2	2.30	0.46
1:BJ:20:TYR:OH	2:RL:8:U:OP1	2.21	0.46
1:BS:97:ASN:ND2	1:FE:94:SER:HA	2.30	0.46
1:DL:77:ILE:HD12	1:GX:77:ILE:HD12	1.98	0.46
1:FA:97:ASN:ND2	1:FL:94:SER:HA	2.31	0.46
1:FP:40:GLY:HA3	1:GV:111:GLY:HA2	1.97	0.46
1:HB:43:ASN:OD1	1:HB:46:THR:OG1	2.24	0.46
1:HI:96:LEU:CD2	1:MM:53:VAL:HG12	2.45	0.46
1:HI:105:LEU:HD23	1:HI:105:LEU:HA	1.64	0.46
1:HS:94:SER:HA	1:LE:97:ASN:HD21	1.81	0.46
1:IC:40:GLY:HA3	1:IJ:111:GLY:HA2	1.98	0.46
1:JT:109:LEU:O	1:NK:40:GLY:HA2	2.15	0.46
1:KA:40:GLY:HA2	1:NM:109:LEU:O	2.15	0.46
1:AF:16:THR:HB	1:GA:111:GLY:HA3	1.97	0.46
1:FA:105:LEU:HA	1:FA:105:LEU:HD23	1.64	0.46
1:FP:97:ASN:ND2	1:GV:94:SER:HA	2.29	0.46
1:IQ:53:VAL:HG12	1:MC:96:LEU:HD22	1.97	0.46
1:JY:35:ILE:HD13	1:KC:99:LEU:HD22	1.96	0.46
1:KQ:94:SER:HA	1:NO:97:ASN:ND2	2.29	0.46
1:AP:94:SER:HA	1:BU:97:ASN:HD21	1.80	0.46
1:BN:55:ARG:CG	1:DZ:92:LEU:HD22	2.46	0.46
1:BN:94:SER:HA	1:DZ:97:ASN:ND2	2.30	0.46
1:CG:105:LEU:HD23	1:CG:105:LEU:HA	1.64	0.46
1:CQ:20:TYR:OH	2:RW:8:U:OP1	2.21	0.46
1:CZ:92:LEU:HD22	1:GL:55:ARG:HG2	1.98	0.46
1:EN:94:SER:HA	1:FJ:97:ASN:ND2	2.30	0.46
1:IB:97:ASN:HD21	1:LN:94:SER:HA	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ID:105:LEU:HD23	1:ID:105:LEU:HA	1.64	0.46
1:IE:97:ASN:ND2	1:LQ:94:SER:HA	2.31	0.46
1:JE:106:ASP:OD2	1:JK:27:GLY:HA2	2.16	0.46
1:KN:109:LEU:O	1:NU:49:VAL:HG21	2.15	0.46
1:EB:40:GLY:HA3	1:GB:111:GLY:HA2	1.96	0.46
1:HF:105:LEU:HA	1:HF:105:LEU:HD23	1.64	0.46
1:IG:105:LEU:HA	1:IG:105:LEU:HD23	1.64	0.46
1:JS:43:ASN:OD1	1:JS:46:THR:OG1	2.24	0.46
1:KY:20:TYR:OH	2:SI:28:A:OP1	2.22	0.46
1:EE:8:ILE:HD11	1:EU:99:LEU:HB2	1.96	0.46
1:HX:99:LEU:HB2	1:LU:8:ILE:HD11	1.98	0.46
1:IW:53:VAL:HG12	1:MI:96:LEU:HD22	1.98	0.46
1:KK:43:ASN:OD1	1:KK:46:THR:OG1	2.24	0.46
1:LR:43:ASN:OD1	1:LR:46:THR:OG1	2.24	0.46
1:MN:105:LEU:HA	1:MN:105:LEU:HD23	1.64	0.46
1:AO:16:THR:HB	1:FR:111:GLY:HA3	1.97	0.46
1:BN:94:SER:HA	1:DZ:97:ASN:HD21	1.80	0.46
1:BQ:43:ASN:OD1	1:BQ:46:THR:OG1	2.24	0.46
1:CJ:105:LEU:HA	1:CJ:105:LEU:HD23	1.64	0.46
1:CU:43:ASN:OD1	1:CU:46:THR:OG1	2.23	0.46
1:CV:97:ASN:ND2	1:GM:94:SER:HA	2.31	0.46
1:DA:55:ARG:HG2	1:DE:92:LEU:HD22	1.97	0.46
1:DB:105:LEU:HA	1:DB:105:LEU:HD23	1.64	0.46
1:HI:70:SER:OG	1:MM:82:ARG:O	2.29	0.46
1:HS:20:TYR:OH	2:SK:8:U:OP1	2.21	0.46
1:IL:43:ASN:OD1	1:IL:46:THR:OG1	2.24	0.46
1:JE:105:LEU:HD13	1:JJ:89:ALA:HB3	1.97	0.46
1:JI:90:ASP:OD2	1:MU:102:PRO:HD3	2.16	0.46
1:NG:52:ALA:HB2	2:TC:26:A:H4'	1.98	0.46
1:AA:15:PRO:HB3	1:AA:21:TYR:CE1	2.51	0.46
1:AF:20:TYR:OH	2:RB:8:U:OP1	2.21	0.46
1:AG:15:PRO:HB3	1:AG:21:TYR:CE1	2.51	0.46
1:AK:105:LEU:HD23	1:AK:105:LEU:HA	1.64	0.46
1:AM:43:ASN:OD1	1:AM:46:THR:OG1	2.24	0.46
1:BN:15:PRO:HB3	1:BN:21:TYR:CE1	2.51	0.46
1:CF:99:LEU:HB2	1:GN:8:ILE:HD11	1.98	0.46
1:CX:15:PRO:HB3	1:CX:21:TYR:CE1	2.51	0.46
1:CY:40:GLY:HA3	1:GG:111:GLY:HA2	1.97	0.46
1:EQ:43:ASN:OD1	1:EQ:46:THR:OG1	2.24	0.46
1:ES:41:LYS:HD2	2:RK:26:A:OP1	2.16	0.46
1:FF:15:PRO:HB3	1:FF:21:TYR:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GJ:15:PRO:HB3	1:GJ:21:TYR:CE1	2.51	0.46
1:GP:15:PRO:HB3	1:GP:21:TYR:CE1	2.51	0.46
1:HZ:15:PRO:HB3	1:HZ:21:TYR:CE1	2.51	0.46
1:IC:43:ASN:OD1	1:IC:46:THR:OG1	2.24	0.46
1:JE:89:ALA:HB3	1:JJ:105:LEU:HD13	1.97	0.46
1:JG:43:ASN:OD1	1:JG:46:THR:OG1	2.24	0.46
1:KD:40:GLY:HA2	1:NP:109:LEU:O	2.16	0.46
1:KE:15:PRO:HB3	1:KE:21:TYR:CE1	2.51	0.46
1:KT:43:ASN:OD1	1:KT:46:THR:OG1	2.24	0.46
1:KW:111:GLY:HA3	1:MX:16:THR:HB	1.98	0.46
1:LI:15:PRO:HB3	1:LI:21:TYR:CE1	2.51	0.46
1:LR:96:LEU:HD22	1:ME:53:VAL:HG12	1.98	0.46
1:DG:15:PRO:HB3	1:DG:21:TYR:CE1	2.51	0.46
1:EL:105:LEU:HA	1:EL:105:LEU:HD23	1.64	0.46
1:EM:36:LYS:HG2	2:RI:27:U:H5"	1.98	0.46
1:FI:43:ASN:OD1	1:FI:46:THR:OG1	2.24	0.46
1:FO:15:PRO:HB3	1:FO:21:TYR:CE1	2.51	0.46
1:FX:15:PRO:HB3	1:FX:21:TYR:CE1	2.51	0.46
1:HP:110:GLN:OE1	1:KZ:16:THR:HG21	2.16	0.46
1:HT:15:PRO:HB3	1:HT:21:TYR:CE1	2.51	0.46
1:JC:38:SER:OG	2:SW:7:A:OP1	2.26	0.46
1:JH:105:LEU:HD23	1:JH:105:LEU:HA	1.64	0.46
1:JL:53:VAL:HG12	1:MX:96:LEU:HD22	1.97	0.46
1:JQ:53:VAL:HG12	1:KB:96:LEU:HD22	1.98	0.46
1:KH:15:PRO:HB3	1:KH:21:TYR:CE1	2.51	0.46
1:KX:105:LEU:HA	1:KX:105:LEU:HD23	1.64	0.46
1:MD:15:PRO:HB3	1:MD:21:TYR:CE1	2.51	0.46
1:MP:15:PRO:HB3	1:MP:21:TYR:CE1	2.51	0.46
1:MS:15:PRO:HB3	1:MS:21:TYR:CE1	2.51	0.46
1:NT:15:PRO:HB3	1:NT:21:TYR:CE1	2.51	0.46
1:AO:94:SER:HA	1:EA:97:ASN:HD21	1.81	0.45
1:BB:15:PRO:HB3	1:BB:21:TYR:CE1	2.51	0.45
1:BQ:3:PHE:CE1	1:EC:104:ARG:HG2	2.51	0.45
1:DJ:15:PRO:HB3	1:DJ:21:TYR:CE1	2.51	0.45
1:DY:15:PRO:HB3	1:DY:21:TYR:CE1	2.51	0.45
1:EK:111:GLY:HA2	1:ER:40:GLY:HA3	1.97	0.45
1:EW:15:PRO:HB3	1:EW:21:TYR:CE1	2.51	0.45
1:EX:106:ASP:OD2	1:FJ:27:GLY:HA2	2.15	0.45
1:GM:15:PRO:HB3	1:GM:21:TYR:CE1	2.51	0.45
1:HE:15:PRO:HB3	1:HE:21:TYR:CE1	2.51	0.45
1:HO:55:ARG:HG3	1:MS:92:LEU:HD22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IU:111:GLY:HA2	1:KO:40:GLY:HA3	1.97	0.45
1:JC:97:ASN:ND2	1:MO:94:SER:HA	2.31	0.45
1:JN:90:ASP:OD2	1:KH:102:PRO:HD3	2.15	0.45
1:JS:15:PRO:HB3	1:JS:21:TYR:CE1	2.51	0.45
1:JZ:105:LEU:HD23	1:JZ:105:LEU:HA	1.64	0.45
1:KB:15:PRO:HB3	1:KB:21:TYR:CE1	2.51	0.45
1:LE:38:SER:OG	2:SK:27:U:OP1	2.28	0.45
1:MM:15:PRO:HB3	1:MM:21:TYR:CE1	2.51	0.45
1:MY:15:PRO:HB3	1:MY:21:TYR:CE1	2.51	0.45
1:NH:15:PRO:HB3	1:NH:21:TYR:CE1	2.51	0.45
1:AW:8:ILE:HD11	1:FC:99:LEU:HB2	1.98	0.45
1:AW:35:ILE:HD13	1:FC:99:LEU:HD22	1.99	0.45
1:BE:15:PRO:HB3	1:BE:21:TYR:CE1	2.51	0.45
1:BR:105:LEU:HD23	1:BR:105:LEU:HA	1.64	0.45
1:BW:15:PRO:HB3	1:BW:21:TYR:CE1	2.52	0.45
1:CP:105:LEU:HD23	1:CP:105:LEU:HA	1.64	0.45
1:DJ:28:PHE:HA	1:GX:110:GLN:HG2	1.97	0.45
1:DP:43:ASN:OD1	1:DP:46:THR:OG1	2.24	0.45
1:DS:15:PRO:HB3	1:DS:21:TYR:CE1	2.51	0.45
1:EX:109:LEU:O	1:FI:40:GLY:HA2	2.16	0.45
1:FJ:105:LEU:HD23	1:FJ:105:LEU:HA	1.64	0.45
1:GA:43:ASN:OD1	1:GA:46:THR:OG1	2.24	0.45
1:IC:15:PRO:HB3	1:IC:21:TYR:CE1	2.51	0.45
1:JD:15:PRO:HB3	1:JD:21:TYR:CE1	2.51	0.45
1:JL:40:GLY:HA3	1:MX:111:GLY:HA2	1.98	0.45
1:JP:15:PRO:HB3	1:JP:21:TYR:CE1	2.51	0.45
1:JP:43:ASN:OD1	1:JP:46:THR:OG1	2.24	0.45
1:LL:15:PRO:HB3	1:LL:21:TYR:CE1	2.51	0.45
1:LR:15:PRO:HB3	1:LR:21:TYR:CE1	2.51	0.45
1:MA:15:PRO:HB3	1:MA:21:TYR:CE1	2.51	0.45
1:ML:104:ARG:O	1:ML:108:ILE:HG13	2.17	0.45
1:AF:97:ASN:ND2	1:DR:94:SER:HA	2.31	0.45
1:AI:108:ILE:HD13	1:DU:37:ILE:HG23	1.98	0.45
1:AQ:99:LEU:HB2	1:FU:8:ILE:HD11	1.97	0.45
1:AS:43:ASN:OD1	1:AS:46:THR:OG1	2.24	0.45
1:AX:104:ARG:O	1:AX:108:ILE:HG13	2.17	0.45
1:BK:15:PRO:HB3	1:BK:21:TYR:CE1	2.51	0.45
1:BN:43:ASN:OD1	1:BN:46:THR:OG1	2.24	0.45
1:BZ:43:ASN:OD1	1:BZ:46:THR:OG1	2.24	0.45
1:CF:94:SER:HA	1:GN:97:ASN:ND2	2.31	0.45
1:CQ:38:SER:OG	2:RW:7:A:OP1	2.26	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:40:GLY:HA2	1:GC:109:LEU:O	2.17	0.45
1:CQ:104:ARG:O	1:CQ:108:ILE:HG13	2.17	0.45
1:CT:20:TYR:OH	2:RX:8:U:OP1	2.21	0.45
1:DP:15:PRO:HB3	1:DP:21:TYR:CE1	2.51	0.45
1:EG:41:LYS:HD2	2:RG:26:A:OP1	2.16	0.45
1:EH:96:LEU:HD22	1:EO:53:VAL:HG12	1.98	0.45
1:EJ:104:ARG:O	1:EJ:108:ILE:HG13	2.17	0.45
1:EM:104:ARG:O	1:EM:108:ILE:HG13	2.17	0.45
1:EQ:15:PRO:HB3	1:EQ:21:TYR:CE1	2.51	0.45
1:GD:15:PRO:HB3	1:GD:21:TYR:CE1	2.51	0.45
1:HI:109:LEU:O	1:MM:40:GLY:HA2	2.16	0.45
1:HJ:104:ARG:O	1:HJ:108:ILE:HG13	2.17	0.45
1:HN:15:PRO:HB3	1:HN:21:TYR:CE1	2.51	0.45
1:IE:77:ILE:HD12	1:LQ:77:ILE:HD12	1.99	0.45
1:IK:38:SER:OG	2:SQ:7:A:OP1	2.26	0.45
1:IR:15:PRO:HB3	1:IR:21:TYR:CE1	2.51	0.45
1:IR:43:ASN:OD1	1:IR:46:THR:OG1	2.24	0.45
1:IT:104:ARG:O	1:IT:108:ILE:HG13	2.17	0.45
1:IW:40:GLY:HA2	1:MI:109:LEU:O	2.15	0.45
1:JJ:15:PRO:HB3	1:JJ:21:TYR:CE1	2.51	0.45
1:JX:109:LEU:O	1:NJ:40:GLY:HA2	2.17	0.45
1:JY:15:PRO:HB3	1:JY:21:TYR:CE1	2.51	0.45
1:KY:104:ARG:O	1:KY:108:ILE:HG13	2.17	0.45
1:NQ:15:PRO:HB3	1:NQ:21:TYR:CE1	2.51	0.45
1:NS:104:ARG:O	1:NS:108:ILE:HG13	2.17	0.45
1:AA:99:LEU:HB2	1:BI:8:ILE:HD11	1.98	0.45
1:AJ:15:PRO:HB3	1:AJ:21:TYR:CE1	2.51	0.45
1:AM:15:PRO:HB3	1:AM:21:TYR:CE1	2.51	0.45
1:AO:104:ARG:O	1:AO:108:ILE:HG13	2.17	0.45
1:BA:53:VAL:HG12	1:EM:96:LEU:HD22	1.98	0.45
1:CZ:104:ARG:O	1:CZ:108:ILE:HG13	2.17	0.45
1:DF:55:ARG:HG2	1:GR:92:LEU:HD22	1.98	0.45
1:DI:104:ARG:O	1:DI:108:ILE:HG13	2.17	0.45
1:EA:104:ARG:O	1:EA:108:ILE:HG13	2.17	0.45
1:EN:15:PRO:HB3	1:EN:21:TYR:CE1	2.51	0.45
1:EV:41:LYS:HD2	2:RL:26:A:OP1	2.16	0.45
1:FB:104:ARG:O	1:FB:108:ILE:HG13	2.17	0.45
1:FQ:104:ARG:O	1:FQ:108:ILE:HG13	2.17	0.45
1:FR:15:PRO:HB3	1:FR:21:TYR:CE1	2.51	0.45
1:GI:104:ARG:O	1:GI:108:ILE:HG13	2.17	0.45
1:GS:15:PRO:HB3	1:GS:21:TYR:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GU:104:ARG:O	1:GU:108:ILE:HG13	2.17	0.45
1:GV:16:THR:OG1	1:GV:17:ALA:N	2.50	0.45
1:HH:111:GLY:HA2	1:IV:40:GLY:HA3	1.98	0.45
1:HV:104:ARG:O	1:HV:108:ILE:HG13	2.17	0.45
1:IB:104:ARG:O	1:IB:108:ILE:HG13	2.17	0.45
1:IC:96:LEU:CD2	1:IJ:53:VAL:HG12	2.45	0.45
1:IO:16:THR:OG1	1:IO:17:ALA:N	2.50	0.45
1:IT:102:PRO:HD3	1:MF:90:ASP:OD2	2.16	0.45
1:IX:16:THR:OG1	1:IX:17:ALA:N	2.50	0.45
1:IZ:55:ARG:HB2	1:ML:96:LEU:HD21	1.99	0.45
1:IZ:104:ARG:O	1:IZ:108:ILE:HG13	2.17	0.45
1:JK:105:LEU:HA	1:JK:105:LEU:HD23	1.64	0.45
1:JV:15:PRO:HB3	1:JV:21:TYR:CE1	2.51	0.45
1:KD:21:TYR:HH	1:NP:113:PHE:C	2.24	0.45
1:KN:8:ILE:HD11	1:NU:99:LEU:HB2	1.97	0.45
1:KQ:15:PRO:HB3	1:KQ:21:TYR:CE1	2.51	0.45
1:KV:52:ALA:HB2	2:SH:26:A:H4'	1.98	0.45
1:MG:15:PRO:HB3	1:MG:21:TYR:CE1	2.51	0.45
1:MV:15:PRO:HB3	1:MV:21:TYR:CE1	2.51	0.45
1:MV:43:ASN:OD1	1:MV:46:THR:OG1	2.24	0.45
1:MX:104:ARG:O	1:MX:108:ILE:HG13	2.17	0.45
1:NJ:104:ARG:O	1:NJ:108:ILE:HG13	2.17	0.45
1:AC:104:ARG:O	1:AC:108:ILE:HG13	2.17	0.45
1:AJ:40:GLY:HA2	1:BX:109:LEU:O	2.16	0.45
1:AV:15:PRO:HB3	1:AV:21:TYR:CE1	2.51	0.45
1:AV:16:THR:OG1	1:AV:17:ALA:N	2.50	0.45
1:BF:105:LEU:HA	1:BF:105:LEU:HD23	1.64	0.45
1:BK:43:ASN:OD1	1:BK:46:THR:OG1	2.24	0.45
1:BQ:15:PRO:HB3	1:BQ:21:TYR:CE1	2.52	0.45
1:BQ:16:THR:OG1	1:BQ:17:ALA:N	2.50	0.45
1:BT:15:PRO:HB3	1:BT:21:TYR:CE1	2.51	0.45
1:BT:16:THR:OG1	1:BT:17:ALA:N	2.50	0.45
1:BZ:15:PRO:HB3	1:BZ:21:TYR:CE1	2.51	0.45
1:CF:15:PRO:HB3	1:CF:21:TYR:CE1	2.51	0.45
1:CL:16:THR:OG1	1:CL:17:ALA:N	2.50	0.45
1:CP:40:GLY:HA3	1:DJ:111:GLY:HA2	1.99	0.45
1:CR:16:THR:OG1	1:CR:17:ALA:N	2.50	0.45
1:CX:53:VAL:HG21	1:DK:100:LEU:HD21	1.98	0.45
1:DA:15:PRO:HB3	1:DA:21:TYR:CE1	2.52	0.45
1:DU:104:ARG:O	1:DU:108:ILE:HG13	2.17	0.45
1:DW:105:LEU:HA	1:DW:105:LEU:HD23	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EE:16:THR:OG1	1:EE:17:ALA:N	2.50	0.45
1:EH:16:THR:OG1	1:EH:17:ALA:N	2.50	0.45
1:EH:99:LEU:HB2	1:EO:8:ILE:HD11	1.97	0.45
1:EN:16:THR:OG1	1:EN:17:ALA:N	2.50	0.45
1:ES:104:ARG:O	1:ES:108:ILE:HG13	2.17	0.45
1:FC:16:THR:OG1	1:FC:17:ALA:N	2.50	0.45
1:FZ:104:ARG:O	1:FZ:108:ILE:HG13	2.17	0.45
1:GF:104:ARG:O	1:GF:108:ILE:HG13	2.17	0.45
1:GY:15:PRO:HB3	1:GY:21:TYR:CE1	2.51	0.45
1:HW:15:PRO:HB3	1:HW:21:TYR:CE1	2.51	0.45
1:HW:16:THR:OG1	1:HW:17:ALA:N	2.50	0.45
1:IC:16:THR:OG1	1:IC:17:ALA:N	2.50	0.45
1:IH:104:ARG:O	1:IH:108:ILE:HG13	2.17	0.45
1:II:55:ARG:HG2	1:KU:92:LEU:HD22	1.99	0.45
1:IO:97:ASN:ND2	1:LA:94:SER:HA	2.31	0.45
1:JA:16:THR:OG1	1:JA:17:ALA:N	2.50	0.45
1:JG:15:PRO:HB3	1:JG:21:TYR:CE1	2.51	0.45
1:JM:15:PRO:HB3	1:JM:21:TYR:CE1	2.51	0.45
1:JN:105:LEU:HD23	1:JN:105:LEU:HA	1.64	0.45
1:JR:94:SER:HA	1:ND:97:ASN:ND2	2.32	0.45
1:JU:104:ARG:O	1:JU:108:ILE:HG13	2.17	0.45
1:KP:104:ARG:O	1:KP:108:ILE:HG13	2.17	0.45
1:KZ:15:PRO:HB3	1:KZ:21:TYR:CE1	2.51	0.45
1:LO:16:THR:OG1	1:LO:17:ALA:N	2.50	0.45
1:LO:43:ASN:OD1	1:LO:46:THR:OG1	2.24	0.45
1:LX:16:THR:OG1	1:LX:17:ALA:N	2.50	0.45
1:MC:104:ARG:O	1:MC:108:ILE:HG13	2.17	0.45
1:MJ:16:THR:OG1	1:MJ:17:ALA:N	2.50	0.45
1:NV:104:ARG:O	1:NV:108:ILE:HG13	2.17	0.45
1:AJ:16:THR:OG1	1:AJ:17:ALA:N	2.50	0.45
1:AM:99:LEU:HB2	1:CA:8:ILE:HD11	1.99	0.45
1:BK:16:THR:OG1	1:BK:17:ALA:N	2.50	0.45
1:BY:104:ARG:O	1:BY:108:ILE:HG13	2.17	0.45
1:CC:15:PRO:HB3	1:CC:21:TYR:CE1	2.51	0.45
1:CH:41:LYS:HD2	2:RT:6:U:OP1	2.17	0.45
1:CI:15:PRO:HB3	1:CI:21:TYR:CE1	2.51	0.45
1:DB:27:GLY:HA2	1:DE:106:ASP:OD2	2.16	0.45
1:DC:104:ARG:O	1:DC:108:ILE:HG13	2.17	0.45
1:DG:16:THR:OG1	1:DG:17:ALA:N	2.50	0.45
1:DM:16:THR:OG1	1:DM:17:ALA:N	2.50	0.45
1:DV:15:PRO:HB3	1:DV:21:TYR:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EZ:15:PRO:HB3	1:EZ:21:TYR:CE1	2.51	0.45
1:FC:15:PRO:HB3	1:FC:21:TYR:CE1	2.51	0.45
1:FC:43:ASN:OD1	1:FC:46:THR:OG1	2.24	0.45
1:FF:16:THR:OG1	1:FF:17:ALA:N	2.50	0.45
1:FL:15:PRO:HB3	1:FL:21:TYR:CE1	2.51	0.45
1:GA:15:PRO:HB3	1:GA:21:TYR:CE1	2.51	0.45
1:GJ:16:THR:OG1	1:GJ:17:ALA:N	2.50	0.45
1:GV:15:PRO:HB3	1:GV:21:TYR:CE1	2.51	0.45
1:HO:99:LEU:HD22	1:MS:35:ILE:HD13	1.97	0.45
1:HZ:16:THR:OG1	1:HZ:17:ALA:N	2.50	0.45
1:IE:92:LEU:HD22	1:LQ:55:ARG:CG	2.47	0.45
1:IF:15:PRO:HB3	1:IF:21:TYR:CE1	2.51	0.45
1:IH:40:GLY:HA3	1:LT:111:GLY:HA2	1.99	0.45
1:IX:15:PRO:HB3	1:IX:21:TYR:CE1	2.51	0.45
1:JA:15:PRO:HB3	1:JA:21:TYR:CE1	2.51	0.45
1:JA:40:GLY:HA3	1:NI:111:GLY:HA2	1.98	0.45
1:JD:16:THR:OG1	1:JD:17:ALA:N	2.50	0.45
1:JM:16:THR:OG1	1:JM:17:ALA:N	2.50	0.45
1:JO:104:ARG:O	1:JO:108:ILE:HG13	2.17	0.45
1:JY:16:THR:OG1	1:JY:17:ALA:N	2.50	0.45
1:KD:104:ARG:O	1:KD:108:ILE:HG13	2.17	0.45
1:KG:41:LYS:HD2	2:TG:6:U:OP1	2.17	0.45
1:KI:105:LEU:HA	1:KI:105:LEU:HD23	1.64	0.45
1:KQ:16:THR:OG1	1:KQ:17:ALA:N	2.50	0.45
1:KW:99:LEU:HD22	1:MW:35:ILE:HD13	1.99	0.45
1:LD:105:LEU:HA	1:LD:105:LEU:HD23	1.64	0.45
1:LI:16:THR:OG1	1:LI:17:ALA:N	2.50	0.45
1:LN:104:ARG:O	1:LN:108:ILE:HG13	2.17	0.45
1:LO:15:PRO:HB3	1:LO:21:TYR:CE1	2.51	0.45
1:LU:15:PRO:HB3	1:LU:21:TYR:CE1	2.51	0.45
1:MF:104:ARG:O	1:MF:108:ILE:HG13	2.17	0.45
1:MJ:15:PRO:HB3	1:MJ:21:TYR:CE1	2.51	0.45
1:NA:104:ARG:O	1:NA:108:ILE:HG13	2.17	0.45
1:ND:104:ARG:O	1:ND:108:ILE:HG13	2.17	0.45
1:NE:16:THR:OG1	1:NE:17:ALA:N	2.50	0.45
1:NK:15:PRO:HB3	1:NK:21:TYR:CE1	2.51	0.45
1:NP:104:ARG:O	1:NP:108:ILE:HG13	2.17	0.45
1:AD:16:THR:OG1	1:AD:17:ALA:N	2.50	0.45
1:AF:104:ARG:O	1:AF:108:ILE:HG13	2.17	0.45
1:AI:41:LYS:HD2	2:RC:6:U:OP1	2.17	0.45
1:AP:15:PRO:HB3	1:AP:21:TYR:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:110:GLN:HE21	1:FA:28:PHE:HA	1.81	0.45
1:AU:104:ARG:O	1:AU:108:ILE:HG13	2.17	0.45
1:AV:35:ILE:HD13	1:EF:99:LEU:HD22	1.98	0.45
1:BE:16:THR:OG1	1:BE:17:ALA:N	2.50	0.45
1:CM:94:SER:HA	1:DG:97:ASN:ND2	2.32	0.45
1:CP:8:ILE:HD11	1:DJ:99:LEU:HB2	1.98	0.45
1:CR:15:PRO:HB3	1:CR:21:TYR:CE1	2.51	0.45
1:CT:41:LYS:HD2	2:RX:6:U:OP1	2.17	0.45
1:CU:16:THR:OG1	1:CU:17:ALA:N	2.50	0.45
1:DA:16:THR:OG1	1:DA:17:ALA:N	2.50	0.45
1:DD:15:PRO:HB3	1:DD:21:TYR:CE1	2.51	0.45
1:DI:97:ASN:HD21	1:GU:94:SER:HA	1.82	0.45
1:EH:15:PRO:HB3	1:EH:21:TYR:CE1	2.51	0.45
1:FK:104:ARG:O	1:FK:108:ILE:HG13	2.17	0.45
1:FU:15:PRO:HB3	1:FU:21:TYR:CE1	2.51	0.45
1:GO:104:ARG:O	1:GO:108:ILE:HG13	2.17	0.45
1:GX:104:ARG:O	1:GX:108:ILE:HG13	2.17	0.45
1:HD:41:LYS:HD2	2:SF:6:U:OP1	2.17	0.45
1:HO:55:ARG:CG	1:MS:92:LEU:HD22	2.47	0.45
1:IE:41:LYS:HD2	2:SO:6:U:OP1	2.17	0.45
1:IH:38:SER:OG	2:SP:7:A:OP1	2.26	0.45
1:IU:15:PRO:HB3	1:IU:21:TYR:CE1	2.51	0.45
1:IZ:41:LYS:HD2	2:SV:6:U:OP1	2.17	0.45
1:JJ:16:THR:OG1	1:JJ:17:ALA:N	2.50	0.45
1:JQ:113:PHE:C	1:KB:21:TYR:HH	2.24	0.45
1:JU:41:LYS:HD2	2:TC:6:U:OP1	2.17	0.45
1:KH:16:THR:OG1	1:KH:17:ALA:N	2.50	0.45
1:KT:35:ILE:HD13	1:NC:99:LEU:HD22	1.98	0.45
1:LC:15:PRO:HB3	1:LC:21:TYR:CE1	2.51	0.45
1:LC:16:THR:OG1	1:LC:17:ALA:N	2.50	0.45
1:LF:16:THR:OG1	1:LF:17:ALA:N	2.50	0.45
1:NE:15:PRO:HB3	1:NE:21:TYR:CE1	2.51	0.45
1:AD:15:PRO:HB3	1:AD:21:TYR:CE1	2.51	0.45
1:AW:111:GLY:HA2	1:FC:40:GLY:HA3	1.97	0.45
1:BB:83:GLY:HA3	1:BR:61:VAL:HG11	1.99	0.45
1:BH:15:PRO:HB3	1:BH:21:TYR:CE1	2.51	0.45
1:BH:16:THR:OG1	1:BH:17:ALA:N	2.50	0.45
1:BS:41:LYS:HD2	2:RO:6:U:OP1	2.17	0.45
1:BS:104:ARG:O	1:BS:108:ILE:HG13	2.17	0.45
1:CC:16:THR:OG1	1:CC:17:ALA:N	2.50	0.45
1:CW:41:LYS:HD2	2:RY:6:U:OP1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:55:ARG:HB2	1:DK:96:LEU:HG	1.99	0.45
1:DV:16:THR:OG1	1:DV:17:ALA:N	2.50	0.45
1:DX:104:ARG:O	1:DX:108:ILE:HG13	2.17	0.45
1:EK:99:LEU:HB2	1:ER:8:ILE:HD11	1.98	0.45
1:ET:40:GLY:HA3	1:FG:111:GLY:HA2	1.98	0.45
1:EW:16:THR:OG1	1:EW:17:ALA:N	2.50	0.45
1:FL:16:THR:OG1	1:FL:17:ALA:N	2.50	0.45
1:GK:105:LEU:HD23	1:GK:105:LEU:HA	1.64	0.45
1:GY:16:THR:OG1	1:GY:17:ALA:N	2.50	0.45
1:HI:53:VAL:CG1	1:MM:96:LEU:HD22	2.47	0.45
1:IL:111:GLY:HA2	1:KX:40:GLY:HA3	1.98	0.45
1:JC:104:ARG:O	1:JC:108:ILE:HG13	2.17	0.45
1:JE:86:ALA:HB1	1:JJ:105:LEU:HB2	1.98	0.45
1:JX:40:GLY:HA2	1:NJ:109:LEU:O	2.17	0.45
1:JX:104:ARG:O	1:JX:108:ILE:HG13	2.17	0.45
1:KG:104:ARG:O	1:KG:108:ILE:HG13	2.17	0.45
1:KK:15:PRO:HB3	1:KK:21:TYR:CE1	2.51	0.45
1:KT:15:PRO:HB3	1:KT:21:TYR:CE1	2.51	0.45
1:KT:16:THR:OG1	1:KT:17:ALA:N	2.50	0.45
1:LF:15:PRO:HB3	1:LF:21:TYR:CE1	2.51	0.45
1:LI:8:ILE:HD11	1:LP:99:LEU:HB2	1.98	0.45
1:LS:27:GLY:HA2	1:ME:106:ASP:OD2	2.17	0.45
1:LT:38:SER:OG	2:SP:27:U:OP1	2.27	0.45
1:MP:16:THR:OG1	1:MP:17:ALA:N	2.50	0.45
1:NB:15:PRO:HB3	1:NB:21:TYR:CE1	2.51	0.45
1:NB:16:THR:OG1	1:NB:17:ALA:N	2.50	0.45
1:NM:104:ARG:O	1:NM:108:ILE:HG13	2.17	0.45
1:AF:97:ASN:HD21	1:DR:94:SER:HA	1.81	0.45
1:AQ:111:GLY:HA2	1:FU:40:GLY:HA3	1.99	0.45
1:AS:15:PRO:HB3	1:AS:21:TYR:CE1	2.51	0.45
1:BG:104:ARG:O	1:BG:108:ILE:HG13	2.17	0.45
1:BH:53:VAL:HG12	1:BO:96:LEU:CD2	2.47	0.45
1:BI:105:LEU:HA	1:BI:105:LEU:HD23	1.64	0.45
1:BP:97:ASN:HD21	1:FB:94:SER:HA	1.81	0.45
1:BZ:16:THR:OG1	1:BZ:17:ALA:N	2.50	0.45
1:CB:38:SER:OG	2:RR:7:A:OP1	2.26	0.45
1:CE:104:ARG:O	1:CE:108:ILE:HG13	2.17	0.45
1:CH:104:ARG:O	1:CH:108:ILE:HG13	2.17	0.45
1:DC:94:SER:HA	1:GO:97:ASN:ND2	2.32	0.45
1:DD:16:THR:OG1	1:DD:17:ALA:N	2.50	0.45
1:DL:38:SER:OG	2:SD:7:A:OP1	2.26	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:16:THR:OG1	1:DP:17:ALA:N	2.50	0.45
1:DV:43:ASN:OD1	1:DV:46:THR:OG1	2.24	0.45
1:EE:15:PRO:HB3	1:EE:21:TYR:CE1	2.51	0.45
1:EG:104:ARG:O	1:EG:108:ILE:HG13	2.17	0.45
1:EI:105:LEU:HA	1:EI:105:LEU:HD23	1.64	0.45
1:FS:55:ARG:CG	1:GP:92:LEU:HD22	2.47	0.45
1:FS:99:LEU:HB2	1:GP:8:ILE:HD11	1.99	0.45
1:GA:16:THR:OG1	1:GA:17:ALA:N	2.50	0.45
1:GS:16:THR:OG1	1:GS:17:ALA:N	2.50	0.45
1:HA:41:LYS:HD2	2:SE:6:U:OP1	2.17	0.45
1:HA:55:ARG:CG	1:KM:92:LEU:HD22	2.47	0.45
1:HB:16:THR:OG1	1:HB:17:ALA:N	2.50	0.45
1:HO:105:LEU:HD23	1:HO:105:LEU:HA	1.64	0.45
1:HT:111:GLY:HA2	1:LD:40:GLY:HA3	1.99	0.45
1:IE:104:ARG:O	1:IE:108:ILE:HG13	2.17	0.45
1:IT:90:ASP:OD2	1:MF:102:PRO:HD3	2.15	0.45
1:JA:99:LEU:HD22	1:NI:35:ILE:HD13	1.98	0.45
1:JP:16:THR:OG1	1:JP:17:ALA:N	2.50	0.45
1:JV:16:THR:OG1	1:JV:17:ALA:N	2.50	0.45
1:KE:16:THR:OG1	1:KE:17:ALA:N	2.50	0.45
1:KK:16:THR:OG1	1:KK:17:ALA:N	2.50	0.45
1:KS:104:ARG:O	1:KS:108:ILE:HG13	2.17	0.45
1:LL:16:THR:OG1	1:LL:17:ALA:N	2.50	0.45
1:LZ:104:ARG:O	1:LZ:108:ILE:HG13	2.17	0.45
1:MA:16:THR:OG1	1:MA:17:ALA:N	2.50	0.45
1:NG:104:ARG:O	1:NG:108:ILE:HG13	2.17	0.45
1:NK:16:THR:OG1	1:NK:17:ALA:N	2.50	0.45
1:AA:16:THR:OG1	1:AA:17:ALA:N	2.50	0.45
1:AG:16:THR:OG1	1:AG:17:ALA:N	2.50	0.45
1:AI:96:LEU:HD21	1:DU:55:ARG:HB2	1.98	0.45
1:AI:104:ARG:O	1:AI:108:ILE:HG13	2.17	0.45
1:AN:99:LEU:HB2	1:FR:8:ILE:HD11	1.98	0.45
1:AP:109:LEU:O	1:BU:40:GLY:HA2	2.16	0.45
1:AY:53:VAL:HG12	1:EI:96:LEU:HD22	1.99	0.45
1:BD:38:SER:OG	2:RJ:7:A:OP1	2.26	0.45
1:BD:92:LEU:HD22	1:EP:55:ARG:HG2	1.99	0.45
1:BJ:97:ASN:HD21	1:EV:94:SER:HA	1.82	0.45
1:CO:16:THR:OG1	1:CO:17:ALA:N	2.50	0.45
1:CW:20:TYR:OH	2:RY:8:U:OP1	2.21	0.45
1:FO:16:THR:OG1	1:FO:17:ALA:N	2.50	0.45
1:FX:16:THR:OG1	1:FX:17:ALA:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GG:15:PRO:HB3	1:GG:21:TYR:CE1	2.51	0.45
1:HE:83:GLY:HA3	1:ID:61:VAL:HG11	1.99	0.45
1:HH:16:THR:OG1	1:HH:17:ALA:N	2.50	0.45
1:HP:41:LYS:HD2	2:SJ:6:U:OP1	2.17	0.45
1:HT:16:THR:OG1	1:HT:17:ALA:N	2.50	0.45
1:HY:104:ARG:O	1:HY:108:ILE:HG13	2.17	0.45
1:IH:40:GLY:HA2	1:LT:109:LEU:O	2.17	0.45
1:IL:15:PRO:HB3	1:IL:21:TYR:CE1	2.51	0.45
1:IN:104:ARG:O	1:IN:108:ILE:HG13	2.17	0.45
1:JF:41:LYS:HD2	2:SX:6:U:OP1	2.17	0.45
1:JG:16:THR:OG1	1:JG:17:ALA:N	2.50	0.45
1:JL:104:ARG:O	1:JL:108:ILE:HG13	2.17	0.45
1:KN:15:PRO:HB3	1:KN:21:TYR:CE1	2.51	0.45
1:LK:104:ARG:O	1:LK:108:ILE:HG13	2.17	0.45
1:LX:15:PRO:HB3	1:LX:21:TYR:CE1	2.51	0.45
1:MB:99:LEU:HD22	1:MD:35:ILE:HD13	1.99	0.45
1:MB:111:GLY:HA2	1:MD:40:GLY:HA3	1.99	0.45
1:NH:16:THR:OG1	1:NH:17:ALA:N	2.50	0.45
1:NL:105:LEU:HD23	1:NL:105:LEU:HA	1.64	0.45
1:NM:20:TYR:OH	2:TE:28:A:OP1	2.27	0.45
1:AA:94:SER:HA	1:BI:97:ASN:ND2	2.32	0.44
1:AM:16:THR:OG1	1:AM:17:ALA:N	2.50	0.44
1:AR:41:LYS:HD2	2:RF:6:U:OP1	2.17	0.44
1:BM:41:LYS:HD2	2:RM:6:U:OP1	2.17	0.44
1:BV:104:ARG:O	1:BV:108:ILE:HG13	2.17	0.44
1:CH:53:VAL:HG12	1:FT:96:LEU:HD22	1.98	0.44
1:CT:104:ARG:O	1:CT:108:ILE:HG13	2.17	0.44
1:CU:15:PRO:HB3	1:CU:21:TYR:CE1	2.51	0.44
1:DC:41:LYS:HD2	2:SA:6:U:OP1	2.17	0.44
1:DJ:16:THR:OG1	1:DJ:17:ALA:N	2.50	0.44
1:DL:41:LYS:HD2	2:SD:6:U:OP1	2.17	0.44
1:DM:15:PRO:HB3	1:DM:21:TYR:CE1	2.51	0.44
1:DM:94:SER:HA	1:GT:97:ASN:ND2	2.31	0.44
1:EB:16:THR:OG1	1:EB:17:ALA:N	2.50	0.44
1:EG:52:ALA:HB2	2:RG:26:A:H4'	1.99	0.44
1:EP:104:ARG:O	1:EP:108:ILE:HG13	2.17	0.44
1:EQ:16:THR:OG1	1:EQ:17:ALA:N	2.50	0.44
1:ET:43:ASN:OD1	1:ET:46:THR:OG1	2.24	0.44
1:ET:111:GLY:HA3	1:FH:16:THR:HB	1.99	0.44
1:FI:16:THR:OG1	1:FI:17:ALA:N	2.50	0.44
1:FS:49:VAL:HG21	1:GP:109:LEU:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HC:92:LEU:HD22	1:MY:55:ARG:HG2	1.99	0.44
1:HG:104:ARG:O	1:HG:108:ILE:HG13	2.17	0.44
1:HH:15:PRO:HB3	1:HH:21:TYR:CE1	2.51	0.44
1:HX:111:GLY:HA2	1:LU:40:GLY:HA3	1.98	0.44
1:IA:105:LEU:HA	1:IA:105:LEU:HD23	1.64	0.44
1:IB:109:LEU:O	1:LN:40:GLY:HA2	2.16	0.44
1:II:16:THR:OG1	1:II:17:ALA:N	2.50	0.44
1:IR:16:THR:OG1	1:IR:17:ALA:N	2.50	0.44
1:JH:92:LEU:HD22	1:JM:55:ARG:HG2	1.99	0.44
1:KA:96:LEU:HD22	1:NM:53:VAL:HG12	1.99	0.44
1:KG:109:LEU:O	1:NS:40:GLY:HA2	2.18	0.44
1:KJ:41:LYS:HD2	2:TH:6:U:OP1	2.17	0.44
1:LB:52:ALA:HB2	2:SJ:26:A:H4'	1.99	0.44
1:LB:104:ARG:O	1:LB:108:ILE:HG13	2.17	0.44
1:LH:104:ARG:O	1:LH:108:ILE:HG13	2.17	0.44
1:LU:16:THR:OG1	1:LU:17:ALA:N	2.50	0.44
1:LW:36:LYS:HE3	2:SQ:27:U:OP1	2.17	0.44
1:MM:16:THR:OG1	1:MM:17:ALA:N	2.50	0.44
1:MR:36:LYS:HG2	2:SX:27:U:H5''	1.97	0.44
1:MV:16:THR:OG1	1:MV:17:ALA:N	2.50	0.44
1:NQ:16:THR:OG1	1:NQ:17:ALA:N	2.50	0.44
1:AP:16:THR:OG1	1:AP:17:ALA:N	2.50	0.44
1:BA:41:LYS:HD2	2:RI:6:U:OP1	2.17	0.44
1:BD:104:ARG:O	1:BD:108:ILE:HG13	2.17	0.44
1:BP:20:TYR:OH	2:RN:8:U:OP1	2.21	0.44
1:CC:109:LEU:O	1:GK:49:VAL:HG21	2.17	0.44
1:CK:97:ASN:HD21	1:FW:94:SER:HA	1.82	0.44
1:CL:15:PRO:HB3	1:CL:21:TYR:CE1	2.51	0.44
1:CN:104:ARG:O	1:CN:108:ILE:HG13	2.17	0.44
1:CO:15:PRO:HB3	1:CO:21:TYR:CE1	2.51	0.44
1:CX:16:THR:OG1	1:CX:17:ALA:N	2.50	0.44
1:DH:105:LEU:HA	1:DH:105:LEU:HD23	1.64	0.44
1:DI:96:LEU:HD22	1:GU:53:VAL:HG12	1.99	0.44
1:DO:104:ARG:O	1:DO:108:ILE:HG13	2.17	0.44
1:DS:16:THR:OG1	1:DS:17:ALA:N	2.50	0.44
1:EB:15:PRO:HB3	1:EB:21:TYR:CE1	2.51	0.44
1:EK:15:PRO:HB3	1:EK:21:TYR:CE1	2.51	0.44
1:ET:16:THR:OG1	1:ET:17:ALA:N	2.50	0.44
1:FH:104:ARG:O	1:FH:108:ILE:HG13	2.17	0.44
1:FP:35:ILE:HD13	1:GV:99:LEU:HD22	1.98	0.44
1:FP:105:LEU:HD23	1:FP:105:LEU:HA	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FR:16:THR:OG1	1:FR:17:ALA:N	2.50	0.44
1:GB:105:LEU:HA	1:GB:105:LEU:HD23	1.64	0.44
1:GY:99:LEU:HB2	1:IG:8:ILE:HD11	1.98	0.44
1:HA:92:LEU:HD22	1:KM:55:ARG:CG	2.47	0.44
1:HM:41:LYS:HD2	2:SI:6:U:OP1	2.17	0.44
1:HN:94:SER:HA	1:IS:97:ASN:ND2	2.32	0.44
1:HQ:16:THR:OG1	1:HQ:17:ALA:N	2.50	0.44
1:HV:97:ASN:HD21	1:LH:94:SER:HA	1.82	0.44
1:II:15:PRO:HB3	1:II:21:TYR:CE1	2.51	0.44
1:IL:16:THR:OG1	1:IL:17:ALA:N	2.50	0.44
1:IO:15:PRO:HB3	1:IO:21:TYR:CE1	2.51	0.44
1:IT:97:ASN:HD21	1:MF:94:SER:HA	1.81	0.44
1:JB:99:LEU:HB2	1:JP:8:ILE:HD11	1.98	0.44
1:JD:43:ASN:OD1	1:JD:46:THR:OG1	2.24	0.44
1:JO:41:LYS:HD2	2:TA:6:U:OP1	2.17	0.44
1:JR:104:ARG:O	1:JR:108:ILE:HG13	2.17	0.44
1:JT:105:LEU:HA	1:JT:105:LEU:HD23	1.64	0.44
1:KA:104:ARG:O	1:KA:108:ILE:HG13	2.17	0.44
1:KJ:20:TYR:OH	2:TH:8:U:OP1	2.21	0.44
1:KT:99:LEU:HB2	1:NC:8:ILE:HD11	1.99	0.44
1:KW:15:PRO:HB3	1:KW:21:TYR:CE1	2.51	0.44
1:MY:16:THR:OG1	1:MY:17:ALA:N	2.50	0.44
1:AG:43:ASN:OD1	1:AG:46:THR:OG1	2.24	0.44
1:AL:104:ARG:O	1:AL:108:ILE:HG13	2.17	0.44
1:AS:16:THR:OG1	1:AS:17:ALA:N	2.50	0.44
1:AZ:40:GLY:HA3	1:EW:111:GLY:HA2	2.00	0.44
1:BA:102:PRO:HD3	1:EM:90:ASP:OD2	2.18	0.44
1:BJ:38:SER:OG	2:RL:7:A:OP1	2.26	0.44
1:BJ:41:LYS:HD2	2:RL:6:U:OP1	2.17	0.44
1:CB:104:ARG:O	1:CB:108:ILE:HG13	2.17	0.44
1:CK:104:ARG:O	1:CK:108:ILE:HG13	2.17	0.44
1:GC:104:ARG:O	1:GC:108:ILE:HG13	2.17	0.44
1:GM:16:THR:OG1	1:GM:17:ALA:N	2.50	0.44
1:GR:104:ARG:O	1:GR:108:ILE:HG13	2.17	0.44
1:HA:40:GLY:HA2	1:KM:109:LEU:O	2.18	0.44
1:HB:15:PRO:HB3	1:HB:21:TYR:CE1	2.51	0.44
1:HN:16:THR:OG1	1:HN:17:ALA:N	2.50	0.44
1:IB:41:LYS:HD2	2:SN:6:U:OP1	2.17	0.44
1:IE:97:ASN:HD21	1:LQ:94:SER:HA	1.81	0.44
1:IQ:104:ARG:O	1:IQ:108:ILE:HG13	2.17	0.44
1:IW:104:ARG:O	1:IW:108:ILE:HG13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IY:105:LEU:HA	1:IY:105:LEU:HD23	1.64	0.44
1:JS:113:PHE:OXT	1:KF:21:TYR:OH	2.36	0.44
1:KV:104:ARG:O	1:KV:108:ILE:HG13	2.17	0.44
1:KW:53:VAL:HG12	1:MW:96:LEU:HD22	2.00	0.44
1:LW:104:ARG:O	1:LW:108:ILE:HG13	2.17	0.44
1:LY:106:ASP:OD2	1:MK:27:GLY:HA2	2.16	0.44
1:MG:16:THR:OG1	1:MG:17:ALA:N	2.50	0.44
1:MU:104:ARG:O	1:MU:108:ILE:HG13	2.17	0.44
1:NT:16:THR:OG1	1:NT:17:ALA:N	2.50	0.44
1:AC:41:LYS:HD2	2:RA:6:U:OP1	2.17	0.44
1:AY:15:PRO:HB3	1:AY:21:TYR:CE1	2.51	0.44
1:AY:16:THR:OG1	1:AY:17:ALA:N	2.50	0.44
1:BP:41:LYS:HD2	2:RN:6:U:OP1	2.17	0.44
1:BS:20:TYR:OH	2:RO:8:U:OP1	2.21	0.44
1:CA:27:GLY:HA2	1:DT:106:ASP:OD2	2.17	0.44
1:CF:35:ILE:HD13	1:GN:99:LEU:HD22	2.00	0.44
1:CQ:97:ASN:ND2	1:GC:94:SER:HA	2.32	0.44
1:CV:8:ILE:HD11	1:GM:99:LEU:HB2	1.98	0.44
1:CZ:41:LYS:HD2	2:RZ:6:U:OP1	2.17	0.44
1:DI:41:LYS:HD2	2:SC:6:U:OP1	2.17	0.44
1:DR:104:ARG:O	1:DR:108:ILE:HG13	2.17	0.44
1:EK:16:THR:OG1	1:EK:17:ALA:N	2.50	0.44
1:FU:16:THR:OG1	1:FU:17:ALA:N	2.50	0.44
1:HP:104:ARG:O	1:HP:108:ILE:HG13	2.17	0.44
1:HV:109:LEU:O	1:LH:40:GLY:HA2	2.17	0.44
1:IH:41:LYS:HD2	2:SP:6:U:OP1	2.17	0.44
1:JZ:92:LEU:HD22	1:NH:55:ARG:HG2	1.99	0.44
1:KM:104:ARG:O	1:KM:108:ILE:HG13	2.17	0.44
1:LB:36:LYS:HE3	2:SJ:27:U:OP1	2.17	0.44
1:NN:16:THR:OG1	1:NN:17:ALA:N	2.50	0.44
1:AF:41:LYS:HD2	2:RB:6:U:OP1	2.17	0.44
1:AR:104:ARG:O	1:AR:108:ILE:HG13	2.17	0.44
1:AT:99:LEU:HB2	1:EZ:8:ILE:HD11	2.00	0.44
1:CX:83:GLY:HA3	1:DK:61:VAL:HG11	2.00	0.44
1:DY:16:THR:OG1	1:DY:17:ALA:N	2.50	0.44
1:FA:99:LEU:HB2	1:FL:8:ILE:HD11	1.99	0.44
1:FI:15:PRO:HB3	1:FI:21:TYR:CE1	2.51	0.44
1:FT:104:ARG:O	1:FT:108:ILE:HG13	2.17	0.44
1:GC:36:LYS:HE3	2:RW:27:U:OP1	2.17	0.44
1:GY:94:SER:HA	1:IG:97:ASN:ND2	2.32	0.44
1:HA:104:ARG:O	1:HA:108:ILE:HG13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HK:15:PRO:HB3	1:HK:21:TYR:CE1	2.51	0.44
1:HK:16:THR:OG1	1:HK:17:ALA:N	2.50	0.44
1:HS:104:ARG:O	1:HS:108:ILE:HG13	2.17	0.44
1:HU:111:GLY:HA2	1:MA:40:GLY:HA3	2.00	0.44
1:HV:41:LYS:HD2	2:SL:6:U:OP1	2.17	0.44
1:IE:20:TYR:OH	2:SO:8:U:OP1	2.21	0.44
1:IQ:55:ARG:HG2	1:MC:92:LEU:HD22	1.99	0.44
1:JF:104:ARG:O	1:JF:108:ILE:HG13	2.17	0.44
1:JI:40:GLY:HA3	1:MU:111:GLY:HA2	2.00	0.44
1:KJ:104:ARG:O	1:KJ:108:ILE:HG13	2.17	0.44
1:KW:16:THR:OG1	1:KW:17:ALA:N	2.50	0.44
1:LC:3:PHE:CE1	1:LS:104:ARG:HG2	2.53	0.44
1:LC:43:ASN:OD1	1:LC:46:THR:OG1	2.24	0.44
1:LM:6:LEU:HB2	1:LM:13:PHE:HB2	2.00	0.44
1:LR:16:THR:OG1	1:LR:17:ALA:N	2.50	0.44
1:NI:105:LEU:HD23	1:NI:105:LEU:HA	1.64	0.44
1:AC:20:TYR:OH	2:RA:8:U:OP1	2.21	0.44
1:AH:6:LEU:HB2	1:AH:13:PHE:HB2	2.00	0.44
1:BF:6:LEU:HB2	1:BF:13:PHE:HB2	2.00	0.44
1:BJ:104:ARG:O	1:BJ:108:ILE:HG13	2.17	0.44
1:BN:53:VAL:HG12	1:DZ:96:LEU:HD22	1.99	0.44
1:BY:41:LYS:HD2	2:RQ:6:U:OP1	2.17	0.44
1:CA:6:LEU:HB2	1:CA:13:PHE:HB2	2.00	0.44
1:DF:104:ARG:O	1:DF:108:ILE:HG13	2.17	0.44
1:DN:6:LEU:HB2	1:DN:13:PHE:HB2	2.00	0.44
1:EB:43:ASN:OD1	1:EB:46:THR:OG1	2.24	0.44
1:ED:104:ARG:O	1:ED:108:ILE:HG13	2.17	0.44
1:EX:6:LEU:HB2	1:EX:13:PHE:HB2	2.00	0.44
1:EY:104:ARG:O	1:EY:108:ILE:HG13	2.17	0.44
1:FB:52:ALA:HB2	2:RN:26:A:H4'	2.00	0.44
1:FN:104:ARG:O	1:FN:108:ILE:HG13	2.17	0.44
1:GT:6:LEU:HB2	1:GT:13:PHE:HB2	2.00	0.44
1:GW:6:LEU:HB2	1:GW:13:PHE:HB2	2.00	0.44
1:GZ:92:LEU:HD22	1:MV:55:ARG:HG2	2.00	0.44
1:HG:41:LYS:HD2	2:SG:6:U:OP1	2.17	0.44
1:HM:104:ARG:O	1:HM:108:ILE:HG13	2.17	0.44
1:HV:20:TYR:OH	2:SL:8:U:OP1	2.21	0.44
1:HW:99:LEU:HD22	1:LG:35:ILE:HD13	2.00	0.44
1:IK:41:LYS:HD2	2:SQ:6:U:OP1	2.17	0.44
1:IK:104:ARG:O	1:IK:108:ILE:HG13	2.17	0.44
1:JB:6:LEU:HB2	1:JB:13:PHE:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JC:41:LYS:HD2	2:SW:6:U:OP1	2.17	0.44
1:JG:111:GLY:HA3	1:NG:16:THR:HB	1.99	0.44
1:JI:104:ARG:O	1:JI:108:ILE:HG13	2.17	0.44
1:JK:6:LEU:HB2	1:JK:13:PHE:HB2	2.00	0.44
1:JN:97:ASN:HD22	1:KH:97:ASN:HB3	1.82	0.44
1:JN:102:PRO:HD3	1:KH:90:ASP:OD2	2.18	0.44
1:JO:102:PRO:HD3	1:NA:90:ASP:OD2	2.17	0.44
1:KF:6:LEU:HB2	1:KF:13:PHE:HB2	2.00	0.44
1:KL:6:LEU:HB2	1:KL:13:PHE:HB2	2.00	0.44
1:KZ:16:THR:OG1	1:KZ:17:ALA:N	2.50	0.44
1:LG:6:LEU:HB2	1:LG:13:PHE:HB2	2.00	0.44
1:MD:16:THR:OG1	1:MD:17:ALA:N	2.50	0.44
1:MF:36:LYS:HE3	2:ST:27:U:OP1	2.18	0.44
1:AE:6:LEU:HB2	1:AE:13:PHE:HB2	2.00	0.44
1:BM:104:ARG:O	1:BM:108:ILE:HG13	2.17	0.44
1:BN:16:THR:OG1	1:BN:17:ALA:N	2.50	0.44
1:CB:41:LYS:HD2	2:RR:6:U:OP1	2.17	0.44
1:CF:16:THR:OG1	1:CF:17:ALA:N	2.50	0.44
1:CF:99:LEU:HD22	1:GN:35:ILE:HD13	1.98	0.44
1:CK:96:LEU:HD22	1:FW:53:VAL:HG12	2.00	0.44
1:CM:6:LEU:HB2	1:CM:13:PHE:HB2	2.00	0.44
1:EO:6:LEU:HB2	1:EO:13:PHE:HB2	2.00	0.44
1:ER:6:LEU:HB2	1:ER:13:PHE:HB2	2.00	0.44
1:ET:15:PRO:HB3	1:ET:21:TYR:CE1	2.51	0.44
1:EX:105:LEU:HA	1:EX:105:LEU:HD23	1.64	0.44
1:FE:104:ARG:O	1:FE:108:ILE:HG13	2.17	0.44
1:GD:16:THR:OG1	1:GD:17:ALA:N	2.50	0.44
1:GL:104:ARG:O	1:GL:108:ILE:HG13	2.17	0.44
1:GP:16:THR:OG1	1:GP:17:ALA:N	2.50	0.44
1:IP:6:LEU:HB2	1:IP:13:PHE:HB2	2.00	0.44
1:JH:40:GLY:HA3	1:JM:111:GLY:HA2	2.00	0.44
1:JL:16:THR:HB	1:KE:111:GLY:HA3	1.99	0.44
1:JL:41:LYS:HD2	2:SZ:6:U:OP1	2.17	0.44
1:NC:6:LEU:HB2	1:NC:13:PHE:HB2	2.00	0.44
1:AR:97:ASN:ND2	1:ED:94:SER:HA	2.33	0.44
1:AX:41:LYS:HD2	2:RH:6:U:OP1	2.17	0.44
1:AZ:27:GLY:HA2	1:EI:106:ASP:OD2	2.18	0.44
1:BD:41:LYS:HD2	2:RJ:6:U:OP1	2.17	0.44
1:BO:6:LEU:HB2	1:BO:13:PHE:HB2	2.00	0.44
1:CQ:41:LYS:HD2	2:RW:6:U:OP1	2.17	0.44
1:CX:99:LEU:HD22	1:DK:35:ILE:HD13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:38:SER:OG	2:RZ:7:A:OP1	2.26	0.44
1:CZ:53:VAL:HG12	1:GL:96:LEU:HD22	1.98	0.44
1:CZ:97:ASN:HD21	1:GL:94:SER:HA	1.82	0.44
1:DB:21:TYR:HH	1:GJ:113:PHE:C	2.22	0.44
1:DF:41:LYS:HD2	2:SB:6:U:OP1	2.17	0.44
1:DI:92:LEU:HD22	1:GU:55:ARG:HG2	1.99	0.44
1:GN:6:LEU:HB2	1:GN:13:PHE:HB2	2.00	0.44
1:HJ:41:LYS:HD2	2:SH:6:U:OP1	2.17	0.44
1:HS:41:LYS:HD2	2:SK:6:U:OP1	2.17	0.44
1:HT:40:GLY:HA3	1:LD:111:GLY:HA2	2.00	0.44
1:IN:41:LYS:HD2	2:SR:6:U:OP1	2.17	0.44
1:IQ:97:ASN:ND2	1:MC:94:SER:HA	2.33	0.44
1:IU:16:THR:OG1	1:IU:17:ALA:N	2.50	0.44
1:IU:97:ASN:ND2	1:KO:94:SER:HA	2.33	0.44
1:JX:41:LYS:HD2	2:TD:6:U:OP1	2.17	0.44
1:KD:41:LYS:HD2	2:TF:6:U:OP1	2.17	0.44
1:KR:6:LEU:HB2	1:KR:13:PHE:HB2	2.00	0.44
1:LA:105:LEU:HA	1:LA:105:LEU:HD23	1.64	0.44
1:LE:104:ARG:O	1:LE:108:ILE:HG13	2.17	0.44
1:LQ:104:ARG:O	1:LQ:108:ILE:HG13	2.17	0.44
1:LR:55:ARG:CG	1:ME:92:LEU:HD22	2.48	0.44
1:LT:104:ARG:O	1:LT:108:ILE:HG13	2.17	0.44
1:MO:104:ARG:O	1:MO:108:ILE:HG13	2.17	0.44
1:MQ:6:LEU:HB2	1:MQ:13:PHE:HB2	2.00	0.44
1:MS:16:THR:OG1	1:MS:17:ALA:N	2.50	0.44
1:MZ:6:LEU:HB2	1:MZ:13:PHE:HB2	2.00	0.44
1:NN:15:PRO:HB3	1:NN:21:TYR:CE1	2.51	0.44
1:NS:52:ALA:HB2	2:TG:26:A:H4'	2.00	0.44
1:AB:105:LEU:HD23	1:AB:105:LEU:HA	1.64	0.44
1:AF:92:LEU:HD22	1:DR:55:ARG:CG	2.48	0.44
1:AL:41:LYS:HD2	2:RD:6:U:OP1	2.17	0.44
1:AO:50:THR:HA	1:AO:78:MET:O	2.18	0.44
1:AP:35:ILE:HD13	1:BU:99:LEU:HD22	2.00	0.44
1:BB:16:THR:OG1	1:BB:17:ALA:N	2.50	0.44
1:BH:3:PHE:CD1	1:BO:104:ARG:NH1	2.86	0.44
1:CE:41:LYS:HD2	2:RS:6:U:OP1	2.17	0.44
1:CI:16:THR:OG1	1:CI:17:ALA:N	2.50	0.44
1:CZ:20:TYR:OH	2:RZ:8:U:OP1	2.21	0.44
1:DK:105:LEU:HD23	1:DK:105:LEU:HA	1.64	0.44
1:DL:104:ARG:O	1:DL:108:ILE:HG13	2.17	0.44
1:DM:99:LEU:HD22	1:GT:35:ILE:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DZ:6:LEU:HB2	1:DZ:13:PHE:HB2	2.00	0.44
1:EQ:102:PRO:HD3	1:FM:90:ASP:OD2	2.18	0.44
1:EV:104:ARG:O	1:EV:108:ILE:HG13	2.17	0.44
1:FM:6:LEU:HB2	1:FM:13:PHE:HB2	2.00	0.44
1:FW:50:THR:HA	1:FW:78:MET:O	2.18	0.44
1:GG:16:THR:OG1	1:GG:17:ALA:N	2.50	0.44
1:GX:50:THR:HA	1:GX:78:MET:O	2.18	0.44
1:HE:16:THR:OG1	1:HE:17:ALA:N	2.50	0.44
1:HL:6:LEU:HB2	1:HL:13:PHE:HB2	2.00	0.44
1:HN:40:GLY:HA3	1:IS:111:GLY:HA2	1.99	0.44
1:HQ:15:PRO:HB3	1:HQ:21:TYR:CE1	2.51	0.44
1:HQ:43:ASN:OD1	1:HQ:46:THR:OG1	2.24	0.44
1:II:43:ASN:OD1	1:II:46:THR:OG1	2.24	0.44
1:JC:97:ASN:HD21	1:MO:94:SER:HA	1.83	0.44
1:JE:6:LEU:HB2	1:JE:13:PHE:HB2	2.00	0.44
1:JR:40:GLY:HA2	1:ND:109:LEU:O	2.18	0.44
1:JR:41:LYS:HD2	2:TB:6:U:OP1	2.17	0.44
1:JS:16:THR:OG1	1:JS:17:ALA:N	2.50	0.44
1:KN:16:THR:OG1	1:KN:17:ALA:N	2.50	0.44
1:KO:6:LEU:HB2	1:KO:13:PHE:HB2	2.00	0.44
1:LT:77:ILE:HD11	2:SP:26:A:H1'	2.00	0.44
1:ME:6:LEU:HB2	1:ME:13:PHE:HB2	2.00	0.44
1:MI:50:THR:HA	1:MI:78:MET:O	2.18	0.44
1:MI:104:ARG:O	1:MI:108:ILE:HG13	2.17	0.44
1:MW:6:LEU:HB2	1:MW:13:PHE:HB2	2.00	0.44
1:NF:6:LEU:HB2	1:NF:13:PHE:HB2	2.00	0.44
1:NK:43:ASN:OD1	1:NK:46:THR:OG1	2.24	0.44
1:AO:41:LYS:HD2	2:RE:6:U:OP1	2.17	0.43
1:AU:41:LYS:HD2	2:RG:6:U:OP1	2.17	0.43
1:AZ:6:LEU:HB2	1:AZ:13:PHE:HB2	2.00	0.43
1:BA:104:ARG:O	1:BA:108:ILE:HG13	2.17	0.43
1:BG:41:LYS:HD2	2:RK:6:U:OP1	2.17	0.43
1:BG:53:VAL:CG1	1:ES:96:LEU:HD22	2.45	0.43
1:BI:6:LEU:HB2	1:BI:13:PHE:HB2	2.00	0.43
1:BM:20:TYR:OH	2:RM:8:U:OP1	2.21	0.43
1:BQ:104:ARG:HG2	1:EC:3:PHE:CE1	2.52	0.43
1:BY:50:THR:HA	1:BY:78:MET:O	2.18	0.43
1:CB:50:THR:HA	1:CB:78:MET:O	2.18	0.43
1:CE:109:LEU:O	1:FQ:40:GLY:HA2	2.18	0.43
1:CS:6:LEU:HB2	1:CS:13:PHE:HB2	2.00	0.43
1:DI:50:THR:HA	1:DI:78:MET:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DK:6:LEU:HB2	1:DK:13:PHE:HB2	2.00	0.43
1:DR:50:THR:HA	1:DR:78:MET:O	2.18	0.43
1:DS:40:GLY:HA3	1:GQ:111:GLY:HA2	2.00	0.43
1:DX:50:THR:HA	1:DX:78:MET:O	2.18	0.43
1:EM:52:ALA:CB	2:RI:26:A:H4'	2.45	0.43
1:FS:3:PHE:CD1	1:GP:104:ARG:NH1	2.86	0.43
1:GE:6:LEU:HB2	1:GE:13:PHE:HB2	2.00	0.43
1:GH:6:LEU:HB2	1:GH:13:PHE:HB2	2.00	0.43
1:GI:50:THR:HA	1:GI:78:MET:O	2.18	0.43
1:GK:6:LEU:HB2	1:GK:13:PHE:HB2	2.00	0.43
1:IB:50:THR:HA	1:IB:78:MET:O	2.18	0.43
1:IC:109:LEU:O	1:IJ:40:GLY:HA2	2.18	0.43
1:IH:105:LEU:HD23	1:IH:105:LEU:HA	1.93	0.43
1:IT:50:THR:HA	1:IT:78:MET:O	2.18	0.43
1:JC:55:ARG:HG2	1:MO:92:LEU:HD22	1.99	0.43
1:JI:41:LYS:HD2	2:SY:6:U:OP1	2.17	0.43
1:JR:50:THR:HA	1:JR:78:MET:O	2.18	0.43
1:KA:41:LYS:HD2	2:TE:6:U:OP1	2.17	0.43
1:KD:50:THR:HA	1:KD:78:MET:O	2.18	0.43
1:LP:6:LEU:HB2	1:LP:13:PHE:HB2	2.00	0.43
1:LS:6:LEU:HB2	1:LS:13:PHE:HB2	2.00	0.43
1:LY:105:LEU:HD23	1:LY:105:LEU:HA	1.64	0.43
1:MN:6:LEU:HB2	1:MN:13:PHE:HB2	2.00	0.43
1:MR:104:ARG:O	1:MR:108:ILE:HG13	2.17	0.43
1:MT:106:ASP:OD2	1:NR:27:GLY:HA2	2.18	0.43
1:NP:50:THR:HA	1:NP:78:MET:O	2.18	0.43
1:NT:43:ASN:OD1	1:NT:46:THR:OG1	2.24	0.43
1:AA:109:LEU:O	1:BI:40:GLY:HA2	2.17	0.43
1:AI:16:THR:HB	1:GD:111:GLY:HA3	1.99	0.43
1:AN:6:LEU:HB2	1:AN:13:PHE:HB2	2.00	0.43
1:AX:97:ASN:ND2	1:EJ:94:SER:HA	2.32	0.43
1:BH:43:ASN:OD1	1:BH:46:THR:OG1	2.24	0.43
1:BL:6:LEU:HB2	1:BL:13:PHE:HB2	2.00	0.43
1:BV:40:GLY:HA3	1:FH:111:GLY:HA2	2.00	0.43
1:CK:41:LYS:HD2	2:RU:6:U:OP1	2.17	0.43
1:CW:104:ARG:O	1:CW:108:ILE:HG13	2.17	0.43
1:CZ:96:LEU:HD22	1:GL:53:VAL:HG12	2.00	0.43
1:DQ:6:LEU:HB2	1:DQ:13:PHE:HB2	2.00	0.43
1:FD:6:LEU:HB2	1:FD:13:PHE:HB2	2.00	0.43
1:FK:50:THR:HA	1:FK:78:MET:O	2.18	0.43
1:FW:104:ARG:O	1:FW:108:ILE:HG13	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GZ:6:LEU:HB2	1:GZ:13:PHE:HB2	2.00	0.43
1:HN:99:LEU:HD22	1:IS:35:ILE:HD13	1.99	0.43
1:IF:16:THR:OG1	1:IF:17:ALA:N	2.50	0.43
1:IT:21:TYR:HH	1:MF:113:PHE:C	2.26	0.43
1:JC:50:THR:HA	1:JC:78:MET:O	2.18	0.43
1:KI:6:LEU:HB2	1:KI:13:PHE:HB2	2.00	0.43
1:KM:50:THR:HA	1:KM:78:MET:O	2.18	0.43
1:KP:50:THR:HA	1:KP:78:MET:O	2.18	0.43
1:LB:105:LEU:HD23	1:LB:105:LEU:HA	1.93	0.43
1:MK:6:LEU:HB2	1:MK:13:PHE:HB2	2.00	0.43
1:MR:50:THR:HA	1:MR:78:MET:O	2.18	0.43
1:NA:50:THR:HA	1:NA:78:MET:O	2.18	0.43
1:AF:50:THR:HA	1:AF:78:MET:O	2.18	0.43
1:AR:21:TYR:OH	1:ED:113:PHE:OXT	2.35	0.43
1:BG:50:THR:HA	1:BG:78:MET:O	2.18	0.43
1:CD:6:LEU:HB2	1:CD:13:PHE:HB2	2.00	0.43
1:CD:99:LEU:HB2	1:CR:8:ILE:HD11	2.00	0.43
1:CN:41:LYS:HD2	2:RV:6:U:OP1	2.17	0.43
1:DA:111:GLY:HA2	1:DE:40:GLY:HA3	2.00	0.43
1:DC:50:THR:HA	1:DC:78:MET:O	2.18	0.43
1:DF:94:SER:HA	1:GR:97:ASN:HD21	1.83	0.43
1:EA:50:THR:HA	1:EA:78:MET:O	2.18	0.43
1:EF:6:LEU:HB2	1:EF:13:PHE:HB2	2.00	0.43
1:ES:50:THR:HA	1:ES:78:MET:O	2.19	0.43
1:EY:50:THR:HA	1:EY:78:MET:O	2.18	0.43
1:GO:50:THR:HA	1:GO:78:MET:O	2.18	0.43
1:HK:94:SER:HA	1:IY:97:ASN:ND2	2.32	0.43
1:HP:50:THR:HA	1:HP:78:MET:O	2.18	0.43
1:HP:96:LEU:HD22	1:LB:53:VAL:HG12	1.99	0.43
1:HS:94:SER:HA	1:LE:97:ASN:ND2	2.33	0.43
1:IS:6:LEU:HB2	1:IS:13:PHE:HB2	2.00	0.43
1:IT:41:LYS:HD2	2:ST:6:U:OP1	2.17	0.43
1:IW:41:LYS:HD2	2:SU:6:U:OP1	2.17	0.43
1:JF:20:TYR:OH	2:SX:8:U:OP1	2.21	0.43
1:JO:50:THR:HA	1:JO:78:MET:O	2.18	0.43
1:JT:6:LEU:HB2	1:JT:13:PHE:HB2	2.00	0.43
1:JW:6:LEU:HB2	1:JW:13:PHE:HB2	2.00	0.43
1:KA:50:THR:HA	1:KA:78:MET:O	2.18	0.43
1:KW:40:GLY:HA2	1:MW:109:LEU:O	2.18	0.43
1:LD:6:LEU:HB2	1:LD:13:PHE:HB2	2.00	0.43
1:LY:6:LEU:HB2	1:LY:13:PHE:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MT:109:LEU:O	1:NQ:40:GLY:HA2	2.18	0.43
1:MX:50:THR:HA	1:MX:78:MET:O	2.18	0.43
1:ND:50:THR:HA	1:ND:78:MET:O	2.18	0.43
1:NM:50:THR:HA	1:NM:78:MET:O	2.19	0.43
1:AL:50:THR:HA	1:AL:78:MET:O	2.18	0.43
1:AT:109:LEU:O	1:EZ:40:GLY:HA2	2.18	0.43
1:AW:6:LEU:HB2	1:AW:13:PHE:HB2	2.00	0.43
1:AX:38:SER:OG	2:RH:7:A:OP1	2.26	0.43
1:AX:50:THR:HA	1:AX:78:MET:O	2.18	0.43
1:BE:27:GLY:HA2	1:ES:106:ASP:OD2	2.19	0.43
1:BP:104:ARG:O	1:BP:108:ILE:HG13	2.17	0.43
1:CE:50:THR:HA	1:CE:78:MET:O	2.18	0.43
1:CQ:21:TYR:HH	1:GC:113:PHE:C	2.26	0.43
1:CS:97:ASN:ND2	1:DD:94:SER:HA	2.34	0.43
1:DF:50:THR:HA	1:DF:78:MET:O	2.18	0.43
1:EZ:16:THR:OG1	1:EZ:17:ALA:N	2.50	0.43
1:FA:53:VAL:HG12	1:FL:96:LEU:HD22	1.98	0.43
1:FH:50:THR:HA	1:FH:78:MET:O	2.18	0.43
1:FH:105:LEU:HD23	1:FH:105:LEU:HA	1.93	0.43
1:FV:6:LEU:HB2	1:FV:13:PHE:HB2	2.00	0.43
1:GO:105:LEU:HD23	1:GO:105:LEU:HA	1.93	0.43
1:HD:96:LEU:HD22	1:KP:53:VAL:HG12	1.99	0.43
1:HM:50:THR:HA	1:HM:78:MET:O	2.18	0.43
1:HO:6:LEU:HB2	1:HO:13:PHE:HB2	2.00	0.43
1:IQ:50:THR:HA	1:IQ:78:MET:O	2.18	0.43
1:IR:99:LEU:HD22	1:KL:35:ILE:HD13	2.00	0.43
1:JL:50:THR:HA	1:JL:78:MET:O	2.18	0.43
1:JN:99:LEU:HD22	1:KH:35:ILE:HD13	1.99	0.43
1:JQ:6:LEU:HB2	1:JQ:13:PHE:HB2	2.00	0.43
1:JX:50:THR:HA	1:JX:78:MET:O	2.18	0.43
1:KG:50:THR:HA	1:KG:78:MET:O	2.18	0.43
1:LF:53:VAL:HG12	1:LM:96:LEU:CD2	2.48	0.43
1:LO:40:GLY:HA3	1:MK:111:GLY:HA2	1.99	0.43
1:LR:53:VAL:HG12	1:ME:96:LEU:HD22	2.00	0.43
1:MF:50:THR:HA	1:MF:78:MET:O	2.18	0.43
1:NM:38:SER:OG	2:TE:27:U:OP1	2.34	0.43
1:AS:92:LEU:HD22	1:EL:55:ARG:CG	2.48	0.43
1:AU:50:THR:HA	1:AU:78:MET:O	2.18	0.43
1:BH:94:SER:HA	1:BO:97:ASN:ND2	2.32	0.43
1:BM:50:THR:HA	1:BM:78:MET:O	2.18	0.43
1:BN:92:LEU:HD22	1:DZ:55:ARG:HG2	1.97	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:50:THR:HA	1:BP:78:MET:O	2.18	0.43
1:CK:50:THR:HA	1:CK:78:MET:O	2.18	0.43
1:CN:50:THR:HA	1:CN:78:MET:O	2.18	0.43
1:DB:6:LEU:HB2	1:DB:13:PHE:HB2	2.00	0.43
1:DP:109:LEU:O	1:GW:40:GLY:HA2	2.18	0.43
1:DT:6:LEU:HB2	1:DT:13:PHE:HB2	2.00	0.43
1:DY:35:ILE:HD13	1:FY:99:LEU:HD22	1.99	0.43
1:EJ:50:THR:HA	1:EJ:78:MET:O	2.18	0.43
1:EV:50:THR:HA	1:EV:78:MET:O	2.18	0.43
1:FD:105:LEU:HD23	1:FD:105:LEU:HA	1.64	0.43
1:FS:6:LEU:HB2	1:FS:13:PHE:HB2	2.00	0.43
1:FT:50:THR:HA	1:FT:78:MET:O	2.18	0.43
1:FZ:50:THR:HA	1:FZ:78:MET:O	2.18	0.43
1:HC:6:LEU:HB2	1:HC:13:PHE:HB2	2.00	0.43
1:HO:53:VAL:CG1	1:MS:96:LEU:HD22	2.48	0.43
1:HS:50:THR:HA	1:HS:78:MET:O	2.18	0.43
1:IZ:50:THR:HA	1:IZ:78:MET:O	2.18	0.43
1:IZ:53:VAL:HG12	1:ML:96:LEU:HD22	2.00	0.43
1:JA:113:PHE:OXT	1:NI:21:TYR:OH	2.36	0.43
1:JC:105:LEU:HD23	1:JC:105:LEU:HA	1.93	0.43
1:JE:92:LEU:HD22	1:JJ:55:ARG:HG2	2.01	0.43
1:JE:105:LEU:HD23	1:JE:105:LEU:HA	1.64	0.43
1:JI:50:THR:HA	1:JI:78:MET:O	2.18	0.43
1:JT:99:LEU:HB2	1:NK:8:ILE:HD11	2.01	0.43
1:KC:6:LEU:HB2	1:KC:13:PHE:HB2	2.00	0.43
1:KU:105:LEU:HD23	1:KU:105:LEU:HA	1.64	0.43
1:KX:6:LEU:HB2	1:KX:13:PHE:HB2	2.00	0.43
1:LB:41:LYS:HD2	2:SJ:26:A:OP1	2.18	0.43
1:LB:50:THR:HA	1:LB:78:MET:O	2.18	0.43
1:LC:94:SER:HA	1:LS:97:ASN:HD21	1.83	0.43
1:MC:50:THR:HA	1:MC:78:MET:O	2.18	0.43
1:ME:105:LEU:HD23	1:ME:105:LEU:HA	1.64	0.43
1:MH:6:LEU:HB2	1:MH:13:PHE:HB2	2.00	0.43
1:ML:50:THR:HA	1:ML:78:MET:O	2.18	0.43
1:MT:6:LEU:HB2	1:MT:13:PHE:HB2	2.00	0.43
1:NE:43:ASN:OD1	1:NE:46:THR:OG1	2.24	0.43
1:NR:6:LEU:HB2	1:NR:13:PHE:HB2	2.00	0.43
1:NV:50:THR:HA	1:NV:78:MET:O	2.18	0.43
1:AB:6:LEU:HB2	1:AB:13:PHE:HB2	2.00	0.43
1:AS:109:LEU:O	1:EL:49:VAL:HG21	2.19	0.43
1:AU:96:LEU:HD22	1:EG:53:VAL:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:55:ARG:HG3	1:EW:92:LEU:HD22	2.00	0.43
1:BA:50:THR:HA	1:BA:78:MET:O	2.18	0.43
1:BD:50:THR:HA	1:BD:78:MET:O	2.18	0.43
1:BJ:96:LEU:HD22	1:EV:53:VAL:HG12	2.01	0.43
1:BN:53:VAL:HG12	1:DZ:96:LEU:CD2	2.49	0.43
1:BV:41:LYS:HD2	2:RP:6:U:OP1	2.17	0.43
1:BZ:111:GLY:HA3	1:DU:16:THR:HB	2.01	0.43
1:CE:37:ILE:HG23	1:FQ:108:ILE:HD13	2.01	0.43
1:CJ:92:LEU:HD22	1:CO:55:ARG:HG2	1.99	0.43
1:CT:111:GLY:HA2	1:GF:40:GLY:HA3	2.01	0.43
1:CV:6:LEU:HB2	1:CV:13:PHE:HB2	2.00	0.43
1:CW:94:SER:HA	1:GI:97:ASN:HD21	1.83	0.43
1:DA:53:VAL:HG12	1:DE:96:LEU:HD22	2.00	0.43
1:EB:111:GLY:HA3	1:GC:16:THR:HB	1.99	0.43
1:EF:105:LEU:HD23	1:EF:105:LEU:HA	1.64	0.43
1:EP:50:THR:HA	1:EP:78:MET:O	2.18	0.43
1:EQ:97:ASN:HB3	1:FM:97:ASN:HD22	1.83	0.43
1:EQ:99:LEU:HB2	1:FM:8:ILE:HD11	2.00	0.43
1:EX:99:LEU:HD22	1:FI:35:ILE:HD13	1.99	0.43
1:GL:50:THR:HA	1:GL:78:MET:O	2.18	0.43
1:GQ:6:LEU:HB2	1:GQ:13:PHE:HB2	2.00	0.43
1:HA:106:ASP:OD2	1:KK:27:GLY:HA2	2.18	0.43
1:HD:104:ARG:O	1:HD:108:ILE:HG13	2.17	0.43
1:HG:50:THR:HA	1:HG:78:MET:O	2.18	0.43
1:HM:97:ASN:HD21	1:KY:94:SER:HA	1.81	0.43
1:HU:6:LEU:HB2	1:HU:13:PHE:HB2	2.00	0.43
1:HX:6:LEU:HB2	1:HX:13:PHE:HB2	2.00	0.43
1:HY:50:THR:HA	1:HY:78:MET:O	2.18	0.43
1:IH:50:THR:HA	1:IH:78:MET:O	2.18	0.43
1:IL:97:ASN:ND2	1:KX:94:SER:HA	2.33	0.43
1:IN:50:THR:HA	1:IN:78:MET:O	2.18	0.43
1:IQ:41:LYS:HD2	2:SS:6:U:OP1	2.17	0.43
1:JF:50:THR:HA	1:JF:78:MET:O	2.19	0.43
1:JF:90:ASP:OD2	1:MR:102:PRO:HD3	2.19	0.43
1:JI:53:VAL:HG12	1:MU:96:LEU:HD22	2.01	0.43
1:JO:90:ASP:OD2	1:NA:102:PRO:HD3	2.19	0.43
1:KS:50:THR:HA	1:KS:78:MET:O	2.18	0.43
1:LK:50:THR:HA	1:LK:78:MET:O	2.18	0.43
1:LT:50:THR:HA	1:LT:78:MET:O	2.18	0.43
1:LU:43:ASN:OD1	1:LU:46:THR:OG1	2.24	0.43
1:LW:50:THR:HA	1:LW:78:MET:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MQ:105:LEU:HA	1:MQ:105:LEU:HD23	1.64	0.43
1:NA:105:LEU:HD23	1:NA:105:LEU:HA	1.93	0.43
1:NG:105:LEU:HD23	1:NG:105:LEU:HA	1.93	0.43
1:AI:50:THR:HA	1:AI:78:MET:O	2.18	0.43
1:AY:55:ARG:HG2	1:EI:92:LEU:HD22	2.00	0.43
1:AZ:96:LEU:HD13	1:EW:76:ILE:CD1	2.49	0.43
1:BH:99:LEU:HB2	1:BO:8:ILE:HD11	2.00	0.43
1:BS:50:THR:HA	1:BS:78:MET:O	2.18	0.43
1:BU:6:LEU:HB2	1:BU:13:PHE:HB2	2.00	0.43
1:BX:6:LEU:HB2	1:BX:13:PHE:HB2	2.00	0.43
1:CP:70:SER:OG	1:DJ:82:ARG:O	2.34	0.43
1:CW:94:SER:HA	1:GI:97:ASN:ND2	2.33	0.43
1:CY:6:LEU:HB2	1:CY:13:PHE:HB2	2.00	0.43
1:CZ:50:THR:HA	1:CZ:78:MET:O	2.18	0.43
1:DE:6:LEU:HB2	1:DE:13:PHE:HB2	2.00	0.43
1:DY:111:GLY:HA2	1:FY:40:GLY:HA3	2.00	0.43
1:DZ:105:LEU:HA	1:DZ:105:LEU:HD23	1.64	0.43
1:EL:6:LEU:HB2	1:EL:13:PHE:HB2	2.00	0.43
1:FB:50:THR:HA	1:FB:78:MET:O	2.18	0.43
1:FD:99:LEU:HB2	1:FF:8:ILE:HD11	2.00	0.43
1:FE:50:THR:HA	1:FE:78:MET:O	2.18	0.43
1:FG:105:LEU:HA	1:FG:105:LEU:HD23	1.64	0.43
1:FN:50:THR:HA	1:FN:78:MET:O	2.18	0.43
1:FP:8:ILE:HD11	1:GV:99:LEU:HB2	1.99	0.43
1:FQ:50:THR:HA	1:FQ:78:MET:O	2.18	0.43
1:FV:40:GLY:HA3	1:GS:111:GLY:HA2	2.00	0.43
1:GX:105:LEU:HD23	1:GX:105:LEU:HA	1.93	0.43
1:GZ:94:SER:HA	1:MV:97:ASN:ND2	2.32	0.43
1:HA:50:THR:HA	1:HA:78:MET:O	2.18	0.43
1:HA:99:LEU:HD11	1:KM:6:LEU:HD22	2.01	0.43
1:HD:50:THR:HA	1:HD:78:MET:O	2.18	0.43
1:HJ:50:THR:HA	1:HJ:78:MET:O	2.18	0.43
1:HR:94:SER:HA	1:LX:97:ASN:ND2	2.34	0.43
1:HY:41:LYS:HD2	2:SM:6:U:OP1	2.17	0.43
1:IE:50:THR:HA	1:IE:78:MET:O	2.18	0.43
1:IM:6:LEU:HB2	1:IM:13:PHE:HB2	2.00	0.43
1:IN:96:LEU:HD22	1:LZ:53:VAL:HG12	2.01	0.43
1:IW:50:THR:HA	1:IW:78:MET:O	2.18	0.43
1:JN:6:LEU:HB2	1:JN:13:PHE:HB2	2.00	0.43
1:KJ:50:THR:HA	1:KJ:78:MET:O	2.18	0.43
1:LQ:50:THR:HA	1:LQ:78:MET:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MN:74:VAL:HG22	1:NT:78:MET:HG2	2.01	0.43
1:NI:6:LEU:HB2	1:NI:13:PHE:HB2	2.00	0.43
1:NJ:50:THR:HA	1:NJ:78:MET:O	2.18	0.43
1:AD:111:GLY:HA2	1:BC:40:GLY:HA3	2.00	0.43
1:AM:35:ILE:HD13	1:CA:99:LEU:HD22	2.00	0.43
1:AR:50:THR:HA	1:AR:78:MET:O	2.18	0.43
1:AZ:92:LEU:HD22	1:EW:55:ARG:HG2	2.01	0.43
1:BB:43:ASN:OD1	1:BB:46:THR:OG1	2.24	0.43
1:BV:50:THR:HA	1:BV:78:MET:O	2.18	0.43
1:CH:50:THR:HA	1:CH:78:MET:O	2.19	0.43
1:CS:105:LEU:HA	1:CS:105:LEU:HD23	1.64	0.43
1:CW:50:THR:HA	1:CW:78:MET:O	2.18	0.43
1:DV:40:GLY:HA3	1:GE:111:GLY:HA2	2.01	0.43
1:FN:41:LYS:HD2	2:RR:26:A:OP1	2.19	0.43
1:FP:6:LEU:HB2	1:FP:13:PHE:HB2	2.00	0.43
1:GR:50:THR:HA	1:GR:78:MET:O	2.18	0.43
1:HE:43:ASN:OD1	1:HE:46:THR:OG1	2.24	0.43
1:HU:105:LEU:HD23	1:HU:105:LEU:HA	1.64	0.43
1:ID:6:LEU:HB2	1:ID:13:PHE:HB2	2.00	0.43
1:JH:6:LEU:HB2	1:JH:13:PHE:HB2	2.00	0.43
1:KQ:40:GLY:HA2	1:NO:109:LEU:O	2.18	0.43
1:KV:50:THR:HA	1:KV:78:MET:O	2.18	0.43
1:LR:77:ILE:HD12	1:ME:77:ILE:HD12	2.00	0.43
1:MR:20:TYR:OH	2:SX:28:A:P	2.77	0.43
1:AJ:99:LEU:HD22	1:BX:35:ILE:HD13	2.01	0.43
1:BH:3:PHE:CE1	1:BO:104:ARG:HG2	2.54	0.43
1:BQ:109:LEU:O	1:EC:49:VAL:HG21	2.18	0.43
1:BR:6:LEU:HB2	1:BR:13:PHE:HB2	2.00	0.43
1:CH:16:THR:HB	1:CL:111:GLY:HA3	1.99	0.43
1:CQ:50:THR:HA	1:CQ:78:MET:O	2.18	0.43
1:CS:35:ILE:HD13	1:DD:99:LEU:HD22	1.99	0.43
1:CU:40:GLY:HA3	1:DH:111:GLY:HA2	2.01	0.43
1:CX:43:ASN:OD1	1:CX:46:THR:OG1	2.24	0.43
1:DB:99:LEU:HD22	1:GJ:35:ILE:HD13	2.00	0.43
1:DC:97:ASN:HD21	1:GO:94:SER:HA	1.83	0.43
1:DH:6:LEU:HB2	1:DH:13:PHE:HB2	2.00	0.43
1:DN:105:LEU:HD23	1:DN:105:LEU:HA	1.64	0.43
1:DU:50:THR:HA	1:DU:78:MET:O	2.18	0.43
1:EX:110:GLN:HE21	1:FJ:28:PHE:HA	1.83	0.43
1:FJ:6:LEU:HB2	1:FJ:13:PHE:HB2	2.00	0.43
1:GC:50:THR:HA	1:GC:78:MET:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HF:28:PHE:HB3	1:ID:106:ASP:OD1	2.18	0.43
1:HO:49:VAL:HG21	1:MS:109:LEU:O	2.19	0.43
1:HX:53:VAL:HG12	1:LU:96:LEU:HD22	2.01	0.43
1:IB:53:VAL:HG12	1:LN:96:LEU:HD22	2.01	0.43
1:II:92:LEU:HD22	1:KU:55:ARG:CG	2.49	0.43
1:IR:40:GLY:HA3	1:KL:111:GLY:HA2	2.00	0.43
1:IY:6:LEU:HB2	1:IY:13:PHE:HB2	2.00	0.43
1:JU:50:THR:HA	1:JU:78:MET:O	2.18	0.43
1:JX:53:VAL:HG12	1:NJ:96:LEU:HD22	2.01	0.43
1:KJ:55:ARG:CG	1:NV:92:LEU:HD22	2.48	0.43
1:KK:99:LEU:HB2	1:NR:8:ILE:HD11	2.01	0.43
1:KU:6:LEU:HB2	1:KU:13:PHE:HB2	2.00	0.43
1:LW:16:THR:HB	1:MG:111:GLY:HA3	2.00	0.43
1:MU:50:THR:HA	1:MU:78:MET:O	2.18	0.43
1:NL:6:LEU:HB2	1:NL:13:PHE:HB2	2.00	0.43
1:NO:6:LEU:HB2	1:NO:13:PHE:HB2	2.00	0.43
1:NU:6:LEU:HB2	1:NU:13:PHE:HB2	2.00	0.43
1:AB:94:SER:HA	1:FX:97:ASN:ND2	2.34	0.43
1:AJ:99:LEU:HB2	1:BX:8:ILE:HD11	1.99	0.43
1:AO:40:GLY:HA2	1:EA:109:LEU:O	2.19	0.43
1:AT:6:LEU:HB2	1:AT:13:PHE:HB2	2.00	0.43
1:BN:107:GLN:CD	1:EA:14:ILE:HD13	2.44	0.43
1:CY:99:LEU:HD22	1:GG:35:ILE:HD13	2.01	0.43
1:DC:97:ASN:ND2	1:GO:94:SER:HA	2.34	0.43
1:DL:50:THR:HA	1:DL:78:MET:O	2.18	0.43
1:DO:50:THR:HA	1:DO:78:MET:O	2.18	0.43
1:DW:6:LEU:HB2	1:DW:13:PHE:HB2	2.00	0.43
1:EI:6:LEU:HB2	1:EI:13:PHE:HB2	2.00	0.43
1:ER:105:LEU:HA	1:ER:105:LEU:HD23	1.64	0.43
1:IA:6:LEU:HB2	1:IA:13:PHE:HB2	2.00	0.43
1:II:8:ILE:HD11	1:KU:99:LEU:HB2	2.01	0.43
1:IZ:37:ILE:HG23	1:ML:108:ILE:HD13	2.01	0.43
1:KD:21:TYR:OH	1:NP:113:PHE:OXT	2.37	0.43
1:LO:111:GLY:HA3	1:ML:16:THR:HB	2.01	0.43
1:ML:52:ALA:HB2	2:SV:26:A:H4'	2.01	0.43
1:MO:50:THR:HA	1:MO:78:MET:O	2.18	0.43
1:NS:50:THR:HA	1:NS:78:MET:O	2.18	0.43
1:CG:99:LEU:HB2	1:CL:8:ILE:HD11	2.01	0.42
1:CR:43:ASN:OD1	1:CR:46:THR:OG1	2.24	0.42
1:CT:105:LEU:HD23	1:CT:105:LEU:HA	1.93	0.42
1:EV:20:TYR:OH	2:RL:28:A:OP1	2.24	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EY:105:LEU:HD23	1:EY:105:LEU:HA	1.93	0.42
1:FA:6:LEU:HB2	1:FA:13:PHE:HB2	2.00	0.42
1:GB:6:LEU:HB2	1:GB:13:PHE:HB2	2.00	0.42
1:GF:50:THR:HA	1:GF:78:MET:O	2.18	0.42
1:HB:8:ILE:HD11	1:IA:99:LEU:HB2	2.00	0.42
1:HF:6:LEU:HB2	1:HF:13:PHE:HB2	2.00	0.42
1:HM:94:SER:HA	1:KY:97:ASN:HD21	1.84	0.42
1:HR:105:LEU:HD23	1:HR:105:LEU:HA	1.64	0.42
1:IO:89:ALA:HB3	1:LA:105:LEU:HD13	2.01	0.42
1:IR:35:ILE:HD13	1:KL:99:LEU:HD22	2.01	0.42
1:IR:99:LEU:HB2	1:KL:8:ILE:HD11	2.00	0.42
1:JI:94:SER:HA	1:MU:97:ASN:ND2	2.34	0.42
1:KD:96:LEU:HD21	1:NP:55:ARG:HB2	2.00	0.42
1:KJ:77:ILE:HD12	1:NV:77:ILE:HD12	2.01	0.42
1:AT:40:GLY:HA3	1:EZ:111:GLY:HA2	2.00	0.42
1:AU:40:GLY:HA2	1:EG:109:LEU:O	2.20	0.42
1:BC:6:LEU:HB2	1:BC:13:PHE:HB2	2.00	0.42
1:BN:99:LEU:HD11	1:DZ:6:LEU:HD22	2.00	0.42
1:CZ:55:ARG:HG2	1:GL:92:LEU:HD22	2.01	0.42
1:EU:105:LEU:HD23	1:EU:105:LEU:HA	1.64	0.42
1:HM:92:LEU:HD22	1:KY:55:ARG:CG	2.49	0.42
1:HO:6:LEU:HD22	1:MS:99:LEU:HD11	2.00	0.42
1:JK:99:LEU:HB2	1:KE:8:ILE:HD11	2.02	0.42
1:JQ:105:LEU:HD23	1:JQ:105:LEU:HA	1.64	0.42
1:KJ:97:ASN:HD21	1:NV:94:SER:HA	1.84	0.42
1:KY:50:THR:HA	1:KY:78:MET:O	2.18	0.42
1:LA:6:LEU:HB2	1:LA:13:PHE:HB2	2.00	0.42
1:LH:50:THR:HA	1:LH:78:MET:O	2.18	0.42
1:LO:99:LEU:HD22	1:MK:35:ILE:HD13	2.01	0.42
1:LZ:50:THR:HA	1:LZ:78:MET:O	2.18	0.42
1:MQ:40:GLY:HA3	1:NN:111:GLY:HA2	2.01	0.42
1:AH:35:ILE:HD13	1:GD:99:LEU:HD22	2.00	0.42
1:AP:96:LEU:HD22	1:BU:53:VAL:HG12	2.01	0.42
1:AS:8:ILE:HD11	1:EL:99:LEU:HB2	2.00	0.42
1:BE:109:LEU:O	1:BL:40:GLY:HA2	2.19	0.42
1:CD:94:SER:HA	1:CR:97:ASN:ND2	2.34	0.42
1:CG:6:LEU:HB2	1:CG:13:PHE:HB2	2.00	0.42
1:CI:96:LEU:HD22	1:GH:53:VAL:HG12	2.01	0.42
1:CP:6:LEU:HB2	1:CP:13:PHE:HB2	2.00	0.42
1:DQ:105:LEU:HD23	1:DQ:105:LEU:HA	1.64	0.42
1:EC:6:LEU:HB2	1:EC:13:PHE:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ED:50:THR:HA	1:ED:78:MET:O	2.18	0.42
1:FG:6:LEU:HB2	1:FG:13:PHE:HB2	2.00	0.42
1:GU:50:THR:HA	1:GU:78:MET:O	2.18	0.42
1:HQ:40:GLY:HA3	1:LJ:111:GLY:HA2	2.00	0.42
1:HW:40:GLY:HA3	1:LG:111:GLY:HA2	2.01	0.42
1:IG:6:LEU:HB2	1:IG:13:PHE:HB2	2.00	0.42
1:IJ:6:LEU:HB2	1:IJ:13:PHE:HB2	2.00	0.42
1:IV:6:LEU:HB2	1:IV:13:PHE:HB2	2.00	0.42
1:LI:111:GLY:HA3	1:LQ:16:THR:HB	2.01	0.42
1:MJ:43:ASN:OD1	1:MJ:46:THR:OG1	2.24	0.42
1:MW:105:LEU:HA	1:MW:105:LEU:HD23	1.64	0.42
1:NG:50:THR:HA	1:NG:78:MET:O	2.18	0.42
1:AC:50:THR:HA	1:AC:78:MET:O	2.18	0.42
1:AL:37:ILE:HG23	1:DX:108:ILE:HD13	2.02	0.42
1:BS:77:ILE:HD12	1:FE:77:ILE:HD12	2.01	0.42
1:CJ:6:LEU:HB2	1:CJ:13:PHE:HB2	2.00	0.42
1:CT:50:THR:HA	1:CT:78:MET:O	2.18	0.42
1:DM:40:GLY:HA3	1:GT:111:GLY:HA2	2.01	0.42
1:EG:50:THR:HA	1:EG:78:MET:O	2.19	0.42
1:FD:111:GLY:HA2	1:FF:40:GLY:HA3	2.01	0.42
1:FT:20:TYR:OH	2:RT:28:A:OP1	2.27	0.42
1:HI:6:LEU:HB2	1:HI:13:PHE:HB2	2.00	0.42
1:II:40:GLY:HA3	1:KU:111:GLY:HA2	2.00	0.42
1:IY:27:GLY:HA2	1:KR:106:ASP:OD2	2.20	0.42
1:JI:105:LEU:HD23	1:JI:105:LEU:HA	1.93	0.42
1:KM:105:LEU:HD23	1:KM:105:LEU:HA	1.93	0.42
1:KW:75:ALA:O	1:MW:76:ILE:HA	2.19	0.42
1:LE:50:THR:HA	1:LE:78:MET:O	2.18	0.42
1:LG:105:LEU:HA	1:LG:105:LEU:HD23	1.64	0.42
1:LJ:6:LEU:HB2	1:LJ:13:PHE:HB2	2.00	0.42
1:LL:99:LEU:HB2	1:MH:8:ILE:HD11	2.02	0.42
1:LN:50:THR:HA	1:LN:78:MET:O	2.18	0.42
1:AY:111:GLY:HA3	1:EJ:16:THR:HB	2.01	0.42
1:BG:53:VAL:HG12	1:ES:96:LEU:CD2	2.46	0.42
1:BJ:50:THR:HA	1:BJ:78:MET:O	2.18	0.42
1:BT:111:GLY:HA2	1:DN:40:GLY:HA3	2.01	0.42
1:CP:55:ARG:HG3	1:DJ:92:LEU:HD22	2.01	0.42
1:DA:111:GLY:HA3	1:DF:16:THR:HB	2.00	0.42
1:DB:111:GLY:HA2	1:GJ:40:GLY:HA3	2.00	0.42
1:DJ:14:ILE:HD12	1:GX:107:GLN:HG2	2.00	0.42
1:EK:53:VAL:HG12	1:ER:96:LEU:HD22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EU:6:LEU:HB2	1:EU:13:PHE:HB2	2.00	0.42
1:FY:6:LEU:HB2	1:FY:13:PHE:HB2	2.00	0.42
1:IK:50:THR:HA	1:IK:78:MET:O	2.18	0.42
1:IM:105:LEU:HA	1:IM:105:LEU:HD23	1.64	0.42
1:IX:55:ARG:HG2	1:KR:92:LEU:HD22	2.00	0.42
1:JB:8:ILE:HD11	1:JP:99:LEU:HB2	2.02	0.42
1:JO:40:GLY:HA2	1:NA:109:LEU:O	2.19	0.42
1:JV:55:ARG:HG2	1:KI:92:LEU:HD22	2.01	0.42
1:JZ:6:LEU:HB2	1:JZ:13:PHE:HB2	2.00	0.42
1:NF:105:LEU:HD23	1:NF:105:LEU:HA	1.64	0.42
1:AK:6:LEU:HB2	1:AK:13:PHE:HB2	2.00	0.42
1:AV:40:GLY:HA3	1:EF:111:GLY:HA2	2.00	0.42
1:BJ:97:ASN:ND2	1:EV:94:SER:HA	2.34	0.42
1:CC:76:ILE:CD1	1:GK:96:LEU:HD13	2.50	0.42
1:CX:53:VAL:HG12	1:DK:96:LEU:CD2	2.49	0.42
1:CZ:77:ILE:HD12	1:GL:77:ILE:HD12	2.02	0.42
1:EM:50:THR:HA	1:EM:78:MET:O	2.18	0.42
1:HV:50:THR:HA	1:HV:78:MET:O	2.18	0.42
1:IE:55:ARG:HG2	1:LQ:92:LEU:HD22	2.00	0.42
1:IX:97:ASN:ND2	1:KR:94:SER:HA	2.34	0.42
1:IZ:40:GLY:HA3	1:ML:111:GLY:HA2	2.00	0.42
1:KF:105:LEU:HD23	1:KF:105:LEU:HA	1.64	0.42
1:KM:52:ALA:HB2	2:SE:26:A:H4'	2.01	0.42
1:LP:105:LEU:HD23	1:LP:105:LEU:HA	1.64	0.42
1:LY:92:LEU:HD22	1:MJ:55:ARG:CG	2.50	0.42
1:BW:16:THR:OG1	1:BW:17:ALA:N	2.50	0.42
1:BW:99:LEU:HB2	1:DQ:8:ILE:HD11	2.01	0.42
1:BY:53:VAL:HG12	1:FK:96:LEU:HD22	2.02	0.42
1:CC:105:LEU:HD13	1:GK:89:ALA:HB3	2.02	0.42
1:CK:97:ASN:ND2	1:FW:94:SER:HA	2.35	0.42
1:CP:55:ARG:CG	1:DJ:92:LEU:HD22	2.50	0.42
1:CX:6:LEU:HD23	1:DK:104:ARG:NH1	2.35	0.42
1:DF:105:LEU:HD23	1:DF:105:LEU:HA	1.93	0.42
1:DL:55:ARG:HG2	1:GX:92:LEU:HD22	2.02	0.42
1:EC:105:LEU:HD23	1:EC:105:LEU:HA	1.64	0.42
1:FP:109:LEU:O	1:GV:40:GLY:HA2	2.19	0.42
1:HE:99:LEU:HD22	1:ID:35:ILE:HD13	2.02	0.42
1:HM:77:ILE:HD12	1:KY:77:ILE:HD12	2.01	0.42
1:IC:92:LEU:HD22	1:IJ:55:ARG:CG	2.50	0.42
1:LL:111:GLY:HA3	1:MI:16:THR:HB	2.02	0.42
1:LR:92:LEU:HD22	1:ME:55:ARG:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LY:96:LEU:HD13	1:MJ:76:ILE:CD1	2.50	0.42
1:MB:6:LEU:HB2	1:MB:13:PHE:HB2	2.00	0.42
1:AH:105:LEU:HD23	1:AH:105:LEU:HA	1.64	0.42
1:AV:43:ASN:OD1	1:AV:46:THR:OG1	2.24	0.42
1:DP:21:TYR:HH	1:GW:113:PHE:C	2.26	0.42
1:EH:94:SER:HA	1:EO:97:ASN:HD21	1.85	0.42
1:GM:43:ASN:OD1	1:GM:46:THR:OG1	2.24	0.42
1:HW:96:LEU:HD22	1:LG:53:VAL:HG12	2.02	0.42
1:HX:40:GLY:HA2	1:LU:109:LEU:O	2.19	0.42
1:IC:3:PHE:CE1	1:IJ:104:ARG:HG2	2.55	0.42
1:JI:16:THR:HB	1:JM:111:GLY:HA3	2.01	0.42
1:JW:111:GLY:HA2	1:NE:40:GLY:HA3	2.02	0.42
1:KB:16:THR:OG1	1:KB:17:ALA:N	2.50	0.42
1:KT:40:GLY:HA3	1:NC:111:GLY:HA2	2.00	0.42
1:MR:105:LEU:HD23	1:MR:105:LEU:HA	1.93	0.42
1:MY:43:ASN:OD1	1:MY:46:THR:OG1	2.24	0.42
1:BN:3:PHE:CD1	1:DZ:104:ARG:NH1	2.88	0.42
1:BP:53:VAL:HG12	1:FB:96:LEU:HD22	2.01	0.42
1:BW:43:ASN:OD1	1:BW:46:THR:OG1	2.24	0.42
1:CP:99:LEU:HD11	1:DJ:6:LEU:HD22	2.02	0.42
1:EM:77:ILE:HD11	2:RI:26:A:H1'	2.02	0.42
1:FQ:52:ALA:HB2	2:RS:26:A:H4'	2.01	0.42
1:HR:6:LEU:HB2	1:HR:13:PHE:HB2	2.00	0.42
1:IB:38:SER:OG	2:SN:7:A:OP1	2.26	0.42
1:IJ:105:LEU:HD23	1:IJ:105:LEU:HA	1.64	0.42
1:AH:96:LEU:CD2	1:GD:53:VAL:HG12	2.50	0.42
1:AQ:6:LEU:HB2	1:AQ:13:PHE:HB2	2.00	0.42
1:AQ:21:TYR:OH	1:FU:113:PHE:OXT	2.33	0.42
1:AR:16:THR:HB	1:FU:111:GLY:HA3	2.02	0.42
1:BG:92:LEU:HD22	1:ES:55:ARG:HG2	2.02	0.42
1:CB:105:LEU:HD23	1:CB:105:LEU:HA	1.93	0.42
1:CK:16:THR:HB	1:CO:111:GLY:HA3	2.01	0.42
1:HC:77:ILE:HD12	1:MY:77:ILE:HD12	2.02	0.42
1:HE:75:ALA:O	1:ID:76:ILE:HA	2.20	0.42
1:IN:105:LEU:HD23	1:IN:105:LEU:HA	1.93	0.42
1:JG:55:ARG:HG2	1:NF:92:LEU:HD22	2.02	0.42
1:KB:43:ASN:OD1	1:KB:46:THR:OG1	2.24	0.42
1:KQ:99:LEU:HB2	1:NO:8:ILE:HD11	2.02	0.42
1:AD:109:LEU:O	1:BC:40:GLY:HA2	2.20	0.41
1:AV:99:LEU:HB2	1:EF:8:ILE:HD11	2.02	0.41
1:BM:111:GLY:HA2	1:EY:40:GLY:HA3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:35:ILE:HD13	1:DQ:99:LEU:HD22	2.02	0.41
1:CP:3:PHE:CD1	1:DJ:104:ARG:NH1	2.88	0.41
1:EX:92:LEU:HD22	1:FI:55:ARG:HG2	2.01	0.41
1:FR:43:ASN:OD1	1:FR:46:THR:OG1	2.24	0.41
1:GZ:96:LEU:HD13	1:MV:76:ILE:CD1	2.50	0.41
1:HA:6:LEU:HD22	1:KM:99:LEU:HD11	2.01	0.41
1:HM:55:ARG:CG	1:KY:92:LEU:HD22	2.50	0.41
1:HV:21:TYR:OH	1:LH:113:PHE:OXT	2.37	0.41
1:IR:94:SER:HA	1:KL:97:ASN:ND2	2.34	0.41
1:JH:53:VAL:HG12	1:JM:96:LEU:HD22	2.02	0.41
1:JI:102:PRO:HD3	1:MU:90:ASP:OD2	2.20	0.41
1:JN:35:ILE:HD13	1:KH:99:LEU:HD22	2.01	0.41
1:AE:92:LEU:HD22	1:GA:55:ARG:HG2	2.02	0.41
1:AT:105:LEU:HA	1:AT:105:LEU:HD23	1.64	0.41
1:AY:111:GLY:HA2	1:EI:40:GLY:HA3	2.02	0.41
1:BO:105:LEU:HA	1:BO:105:LEU:HD23	1.64	0.41
1:CI:8:ILE:HD11	1:GH:99:LEU:HB2	2.01	0.41
1:DS:97:ASN:ND2	1:GQ:94:SER:HA	2.35	0.41
1:FS:55:ARG:HG3	1:GP:92:LEU:HD22	2.02	0.41
1:GF:105:LEU:HD23	1:GF:105:LEU:HA	1.93	0.41
1:GY:27:GLY:HA2	1:KM:106:ASP:OD2	2.20	0.41
1:HA:105:LEU:HD23	1:HA:105:LEU:HA	1.93	0.41
1:IF:111:GLY:HA2	1:IM:40:GLY:HA3	2.03	0.41
1:JD:35:ILE:HD13	1:NL:99:LEU:HD22	2.01	0.41
1:LV:6:LEU:HB2	1:LV:13:PHE:HB2	2.00	0.41
1:AO:96:LEU:HD22	1:EA:53:VAL:HG12	2.02	0.41
1:BQ:92:LEU:HD22	1:EC:55:ARG:HG3	2.01	0.41
1:EB:111:GLY:HA2	1:GB:40:GLY:HA3	2.02	0.41
1:GT:105:LEU:HD23	1:GT:105:LEU:HA	1.64	0.41
1:HF:99:LEU:HD22	1:NB:35:ILE:HD13	2.02	0.41
1:HN:43:ASN:OD1	1:HN:46:THR:OG1	2.24	0.41
1:HY:40:GLY:HA2	1:LK:109:LEU:O	2.19	0.41
1:IN:55:ARG:HB2	1:LZ:96:LEU:HD21	2.00	0.41
1:LL:43:ASN:OD1	1:LL:46:THR:OG1	2.24	0.41
1:LW:105:LEU:HD23	1:LW:105:LEU:HA	1.93	0.41
1:MN:96:LEU:CD2	1:NT:53:VAL:HG12	2.49	0.41
1:NA:52:ALA:HB2	2:TA:26:A:H4'	2.02	0.41
1:NO:105:LEU:HA	1:NO:105:LEU:HD23	1.64	0.41
1:AZ:94:SER:HA	1:EW:97:ASN:HD21	1.86	0.41
1:BK:109:LEU:O	1:DW:49:VAL:HG21	2.20	0.41
1:CF:111:GLY:HA3	1:GO:16:THR:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:40:GLY:HA2	1:DK:109:LEU:C	2.42	0.41
1:DV:99:LEU:HB2	1:GE:8:ILE:HD11	2.02	0.41
1:FA:55:ARG:CG	1:FL:92:LEU:HD22	2.50	0.41
1:FN:105:LEU:HD23	1:FN:105:LEU:HA	1.93	0.41
1:GU:41:LYS:HD2	2:SC:26:A:OP1	2.19	0.41
1:HA:53:VAL:CG1	1:KM:96:LEU:HD22	2.47	0.41
1:HA:96:LEU:HD22	1:KM:53:VAL:CG1	2.49	0.41
1:HI:53:VAL:HG12	1:MM:96:LEU:CD2	2.50	0.41
1:HZ:40:GLY:HA3	1:IP:111:GLY:HA2	2.03	0.41
1:IE:53:VAL:HG12	1:LQ:96:LEU:HD22	2.03	0.41
1:IK:94:SER:HA	1:LW:97:ASN:HD21	1.84	0.41
1:JA:43:ASN:OD1	1:JA:46:THR:OG1	2.24	0.41
1:JS:99:LEU:HD22	1:KF:35:ILE:HD13	2.02	0.41
1:KD:105:LEU:HD23	1:KD:105:LEU:HA	1.93	0.41
1:LS:105:LEU:HA	1:LS:105:LEU:HD23	1.64	0.41
1:LV:111:GLY:HA2	1:MG:40:GLY:HA3	2.02	0.41
1:MT:99:LEU:HB2	1:NQ:8:ILE:HD11	2.03	0.41
1:MU:77:ILE:HD11	2:SY:26:A:H1'	2.02	0.41
1:AG:8:ILE:HD11	1:BF:99:LEU:HB2	2.02	0.41
1:CJ:99:LEU:HB2	1:CO:8:ILE:HD11	2.01	0.41
1:CX:51:ALA:HB2	1:DK:109:LEU:HD23	2.03	0.41
1:DL:105:LEU:HD23	1:DL:105:LEU:HA	1.93	0.41
1:FZ:105:LEU:HD23	1:FZ:105:LEU:HA	1.93	0.41
1:HK:109:LEU:O	1:IY:40:GLY:HA2	2.20	0.41
1:IQ:94:SER:HA	1:MC:97:ASN:ND2	2.35	0.41
1:JH:106:ASP:OD2	1:JN:27:GLY:HA2	2.20	0.41
1:JU:105:LEU:HD23	1:JU:105:LEU:HA	1.93	0.41
1:KV:41:LYS:HD2	2:SH:26:A:OP1	2.21	0.41
1:AH:97:ASN:ND2	1:GD:94:SER:HA	2.36	0.41
1:BQ:96:LEU:HD22	1:EC:53:VAL:CG1	2.50	0.41
1:BY:105:LEU:HD23	1:BY:105:LEU:HA	1.93	0.41
1:CV:35:ILE:HD13	1:GM:99:LEU:HD22	2.03	0.41
1:DA:92:LEU:HD22	1:DE:55:ARG:CG	2.50	0.41
1:DO:52:ALA:HB2	2:RA:26:A:H4'	2.03	0.41
1:GS:43:ASN:OD1	1:GS:46:THR:OG1	2.24	0.41
1:GU:52:ALA:HB2	2:SC:26:A:H4'	2.02	0.41
1:HD:97:ASN:HD21	1:KP:94:SER:HA	1.85	0.41
1:HH:96:LEU:HD22	1:IV:53:VAL:HG12	2.02	0.41
1:IV:105:LEU:HA	1:IV:105:LEU:HD23	1.64	0.41
1:JE:55:ARG:CG	1:JJ:92:LEU:HD22	2.49	0.41
1:JK:8:ILE:HD11	1:KE:99:LEU:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JS:94:SER:HA	1:KF:97:ASN:ND2	2.33	0.41
1:MR:38:SER:OG	2:SX:27:U:OP1	2.26	0.41
1:AU:105:LEU:HD23	1:AU:105:LEU:HA	1.93	0.41
1:BT:8:ILE:HD11	1:DN:99:LEU:HB2	2.02	0.41
1:DA:53:VAL:HG12	1:DE:96:LEU:CD2	2.51	0.41
1:EK:99:LEU:HD22	1:ER:35:ILE:HD13	2.01	0.41
1:HA:84:ILE:HG13	1:KM:72:ALA:HB2	2.02	0.41
1:ML:77:ILE:HD11	2:SV:26:A:HI'	2.03	0.41
1:AR:105:LEU:HD23	1:AR:105:LEU:HA	1.93	0.41
1:DF:113:PHE:OXT	1:GR:21:TYR:OH	2.38	0.41
1:HM:105:LEU:HD23	1:HM:105:LEU:HA	1.93	0.41
1:HO:53:VAL:HG12	1:MS:96:LEU:CD2	2.48	0.41
1:IQ:97:ASN:HD21	1:MC:94:SER:HA	1.85	0.41
1:IZ:109:LEU:O	1:ML:40:GLY:HA2	2.21	0.41
1:JF:21:TYR:OH	1:MR:113:PHE:OXT	2.36	0.41
1:KJ:92:LEU:HD22	1:NV:55:ARG:HG2	2.01	0.41
1:KY:105:LEU:HD23	1:KY:105:LEU:HA	1.93	0.41
1:LF:99:LEU:HB2	1:LM:8:ILE:HD11	2.03	0.41
1:LR:53:VAL:HG12	1:ME:96:LEU:CD2	2.51	0.41
1:AD:99:LEU:HD22	1:BC:35:ILE:HD13	2.03	0.41
1:AI:55:ARG:HB2	1:DU:96:LEU:HD21	2.03	0.41
1:AI:105:LEU:HD23	1:AI:105:LEU:HA	1.93	0.41
1:AL:3:PHE:CE1	1:DX:104:ARG:HG2	2.56	0.41
1:AZ:105:LEU:HD23	1:AZ:105:LEU:HA	1.64	0.41
1:BA:55:ARG:HB2	1:EM:96:LEU:HD21	2.03	0.41
1:BB:94:SER:HA	1:BR:97:ASN:ND2	2.36	0.41
1:BB:111:GLY:HA3	1:BS:16:THR:HB	2.03	0.41
1:BD:92:LEU:HD22	1:EP:55:ARG:CG	2.51	0.41
1:BS:96:LEU:CD2	1:FE:53:VAL:HG12	2.50	0.41
1:BV:102:PRO:HD3	1:FH:90:ASP:OD2	2.21	0.41
1:CV:96:LEU:HD22	1:GM:53:VAL:HG12	2.03	0.41
1:DF:55:ARG:CG	1:GR:92:LEU:HD22	2.51	0.41
1:EB:99:LEU:HB2	1:GB:8:ILE:HD11	2.03	0.41
1:EB:99:LEU:HD22	1:GB:35:ILE:HD13	2.03	0.41
1:EK:94:SER:HA	1:ER:97:ASN:ND2	2.35	0.41
1:GY:96:LEU:HD22	1:IG:53:VAL:HG12	2.02	0.41
1:HH:53:VAL:HG12	1:IV:96:LEU:HD22	2.03	0.41
1:HJ:94:SER:HA	1:KV:97:ASN:HD21	1.85	0.41
1:HL:105:LEU:HD23	1:HL:105:LEU:HA	1.64	0.41
1:HL:109:LEU:O	1:MP:40:GLY:HA2	2.20	0.41
1:HM:93:LEU:HD12	1:HM:93:LEU:HA	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HS:16:THR:HB	1:LX:111:GLY:HA3	2.03	0.41
1:IE:94:SER:HA	1:LQ:97:ASN:ND2	2.36	0.41
1:IX:76:ILE:CD1	1:KR:96:LEU:HD13	2.50	0.41
1:JE:55:ARG:HG2	1:JJ:92:LEU:HD22	2.03	0.41
1:JH:55:ARG:CG	1:JM:92:LEU:HD22	2.51	0.41
1:KK:35:ILE:HD13	1:NR:99:LEU:HD22	2.02	0.41
1:KQ:111:GLY:HA2	1:NO:40:GLY:HA3	2.02	0.41
1:LM:105:LEU:HD23	1:LM:105:LEU:HA	1.64	0.41
1:LR:92:LEU:HD22	1:ME:55:ARG:HG2	2.03	0.41
1:MC:105:LEU:HD23	1:MC:105:LEU:HA	1.93	0.41
1:ML:105:LEU:HD23	1:ML:105:LEU:HA	1.93	0.41
1:MO:105:LEU:HD23	1:MO:105:LEU:HA	1.93	0.41
1:NJ:41:LYS:HD2	2:TD:26:A:OP1	2.20	0.41
1:AM:99:LEU:HD22	1:CA:35:ILE:HD13	2.03	0.41
1:AW:105:LEU:HD23	1:AW:105:LEU:HA	1.64	0.41
1:BJ:94:SER:HA	1:EV:97:ASN:ND2	2.36	0.41
1:DI:105:LEU:HD23	1:DI:105:LEU:HA	1.93	0.41
1:EB:77:ILE:HD12	1:GB:77:ILE:HD12	2.03	0.41
1:IJ:27:GLY:C	1:KU:110:GLN:HE21	2.29	0.41
1:IT:21:TYR:OH	1:MF:113:PHE:OXT	2.37	0.41
1:LN:52:ALA:HB2	2:SN:26:A:H4'	2.02	0.41
1:MT:76:ILE:HA	1:NQ:75:ALA:O	2.21	0.41
1:BN:76:ILE:CD1	1:DZ:96:LEU:HD13	2.51	0.40
1:BN:107:GLN:NE2	1:EA:24:SER:HB2	2.36	0.40
1:BW:111:GLY:HA3	1:DR:16:THR:HB	2.02	0.40
1:CP:104:ARG:HG2	1:DJ:3:PHE:CE1	2.56	0.40
1:EE:99:LEU:HD22	1:EU:35:ILE:HD13	2.03	0.40
1:FA:35:ILE:HD13	1:FL:99:LEU:HD22	2.03	0.40
1:HC:55:ARG:CG	1:MY:92:LEU:HD22	2.52	0.40
1:HF:40:GLY:HA3	1:NB:111:GLY:HA2	2.02	0.40
1:HY:96:LEU:HD22	1:LK:53:VAL:HG12	2.03	0.40
1:KN:97:ASN:ND2	1:NU:94:SER:HA	2.36	0.40
1:KP:41:LYS:HD2	2:SF:26:A:OP1	2.20	0.40
1:KW:78:MET:HG2	1:MW:74:VAL:HG22	2.03	0.40
1:NM:52:ALA:HB2	2:TE:26:A:H4'	2.01	0.40
1:CQ:94:SER:HA	1:GC:97:ASN:HD21	1.86	0.40
1:CV:105:LEU:HD23	1:CV:105:LEU:HA	1.64	0.40
1:DC:93:LEU:HD12	1:DC:93:LEU:HA	1.91	0.40
1:DS:8:ILE:HD11	1:GQ:99:LEU:HB2	2.03	0.40
1:EQ:90:ASP:OD2	1:FM:102:PRO:HD3	2.21	0.40
1:GW:105:LEU:HA	1:GW:105:LEU:HD23	1.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HE:53:VAL:HG12	1:ID:96:LEU:CD2	2.52	0.40
1:IB:40:GLY:HA3	1:LN:111:GLY:HA2	2.03	0.40
1:IC:109:LEU:O	1:IJ:49:VAL:HG21	2.21	0.40
1:IN:108:ILE:HD13	1:LZ:37:ILE:HG23	2.03	0.40
1:AL:6:LEU:HD22	1:DX:99:LEU:HD11	2.04	0.40
1:AW:99:LEU:HD22	1:FC:35:ILE:HD13	2.02	0.40
1:AY:53:VAL:HG12	1:EI:96:LEU:CD2	2.51	0.40
1:BA:105:LEU:HD23	1:BA:105:LEU:HA	1.93	0.40
1:BC:16:THR:HG21	1:BR:110:GLN:OE1	2.21	0.40
1:BN:77:ILE:HD12	1:DZ:77:ILE:HD12	2.03	0.40
1:BV:40:GLY:HA2	1:FH:109:LEU:O	2.22	0.40
1:CQ:21:TYR:OH	1:GC:113:PHE:OXT	2.36	0.40
1:CQ:94:SER:HA	1:GC:97:ASN:ND2	2.36	0.40
1:CT:40:GLY:HA2	1:GF:109:LEU:O	2.20	0.40
1:CT:53:VAL:HG12	1:GF:96:LEU:HD22	2.03	0.40
1:CU:94:SER:HA	1:DH:97:ASN:ND2	2.36	0.40
1:DP:40:GLY:HA3	1:GW:111:GLY:HA2	2.02	0.40
1:HB:111:GLY:HA3	1:IB:16:THR:HB	2.03	0.40
1:IQ:109:LEU:O	1:MC:40:GLY:HA2	2.21	0.40
1:JO:40:GLY:HA3	1:NA:111:GLY:HA2	2.04	0.40
1:KG:105:LEU:HD23	1:KG:105:LEU:HA	1.93	0.40
1:LF:111:GLY:HA2	1:LM:40:GLY:HA3	2.04	0.40
1:LI:99:LEU:HB2	1:LP:8:ILE:HD11	2.03	0.40
1:LY:55:ARG:CG	1:MJ:92:LEU:HD22	2.51	0.40
1:MB:96:LEU:HD22	1:MD:53:VAL:HG12	2.02	0.40
1:MK:105:LEU:HA	1:MK:105:LEU:HD23	1.64	0.40
1:MT:74:VAL:HG22	1:NQ:78:MET:HG2	2.03	0.40
1:AD:40:GLY:HA2	1:BC:109:LEU:O	2.22	0.40
1:BB:99:LEU:HB2	1:BR:8:ILE:HD11	2.03	0.40
1:BH:111:GLY:HA3	1:BP:16:THR:HB	2.04	0.40
1:CW:55:ARG:HG2	1:GI:92:LEU:HD22	2.03	0.40
1:HK:35:ILE:HD13	1:IY:99:LEU:HD22	2.02	0.40
1:HR:40:GLY:HA3	1:LX:111:GLY:HA2	2.02	0.40
1:JB:105:LEU:HA	1:JB:105:LEU:HD23	1.64	0.40
1:JN:8:ILE:CD1	1:KH:99:LEU:HB2	2.52	0.40
1:JY:53:VAL:HG12	1:KC:96:LEU:HD22	2.03	0.40
1:LL:40:GLY:HA3	1:MH:111:GLY:HA2	2.02	0.40
1:LN:105:LEU:HD23	1:LN:105:LEU:HA	1.93	0.40
1:LV:8:ILE:HD11	1:MG:99:LEU:HB2	2.03	0.40
1:MI:41:LYS:HD2	2:SU:26:A:OP1	2.21	0.40
1:AG:97:ASN:ND2	1:BF:94:SER:HA	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:99:LEU:HD11	1:DX:6:LEU:HD22	2.03	0.40
1:AX:105:LEU:HD23	1:AX:105:LEU:HA	1.93	0.40
1:BC:27:GLY:HA2	1:BR:106:ASP:OD2	2.22	0.40
1:BS:96:LEU:HD22	1:FE:53:VAL:CG1	2.49	0.40
1:BW:99:LEU:HD22	1:DQ:35:ILE:HD13	2.03	0.40
1:DV:99:LEU:HD22	1:GE:35:ILE:HD13	2.03	0.40
1:DY:111:GLY:HA3	1:FZ:16:THR:HB	2.04	0.40
1:HC:105:LEU:HD23	1:HC:105:LEU:HA	1.64	0.40
1:HJ:105:LEU:HD23	1:HJ:105:LEU:HA	1.93	0.40
1:HN:40:GLY:HA2	1:IS:109:LEU:O	2.22	0.40
1:IB:105:LEU:HD23	1:IB:105:LEU:HA	1.93	0.40
1:IR:96:LEU:HD22	1:KL:53:VAL:HG12	2.03	0.40
1:JW:8:ILE:HD11	1:NE:99:LEU:HB2	2.04	0.40
1:KQ:99:LEU:HD22	1:NO:35:ILE:HD13	2.03	0.40
1:KV:105:LEU:HD23	1:KV:105:LEU:HA	1.93	0.40
1:LC:78:MET:HG2	1:LS:74:VAL:HG22	2.02	0.40
1:LT:105:LEU:HD23	1:LT:105:LEU:HA	1.93	0.40
1:LY:77:ILE:HD12	1:MJ:77:ILE:HD12	2.02	0.40
1:MN:65:GLY:HA3	1:NU:67:PRO:CB	2.52	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HR:10:SER:OG	1:KI:24:SER:CB[1_655]	1.58	0.62
1:AZ:101:ASP:OD2	1:NL:10:SER:N[1_545]	2.02	0.18
1:AZ:101:ASP:OD2	1:NL:10:SER:OG[1_545]	2.11	0.09
1:EU:10:SER:OG	1:GK:24:SER:CB[1_655]	2.13	0.07
1:FS:9:GLY:O	1:ME:104:ARG:NH2[1_446]	2.13	0.07

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AC	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	AD	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AF	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	AG	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AI	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	AJ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AL	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	AM	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AO	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	AP	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AR	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	AS	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AT	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AU	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	AV	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AW	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AX	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	AY	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	AZ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BA	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	BB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BC	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BD	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	BE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BG	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	BH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BI	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BJ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	BK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BL	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BM	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	BN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BO	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BP	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	BQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BR	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BS	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	BT	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BU	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BV	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	BW	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BX	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	BY	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	BZ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CA	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CB	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	CC	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CD	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CE	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	CF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CG	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CH	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	CI	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CJ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CK	111/113 (98%)	110 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CL	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CM	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CN	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	CO	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CP	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CQ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	CR	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CS	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CT	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	CU	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CV	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CW	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	CX	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CY	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	CZ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	DA	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DC	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	DD	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DF	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	DG	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DI	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	DJ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DL	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	DM	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DO	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	DP	111/113 (98%)	109 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DR	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	DS	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DT	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DU	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	DV	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DW	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DX	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	DY	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	DZ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EA	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	EB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EC	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	ED	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	EE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EG	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	EH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EI	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EJ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	EK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EL	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EM	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	EN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EO	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EP	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	EQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	ER	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	ES	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	ET	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EU	111/113 (98%)	109 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EV	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	EW	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EX	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	EY	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	EZ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FA	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FB	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	FC	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FD	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FE	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	FF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FG	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FH	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	FI	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FJ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FK	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	FL	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FM	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FN	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	FO	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FP	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FQ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	FR	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FS	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FT	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	FU	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FV	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FW	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	FX	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FY	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	FZ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GA	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GC	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	GD	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GF	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	GG	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GI	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	GJ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GL	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	GM	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GO	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	GP	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GR	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	GS	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GT	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GU	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	GV	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GW	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GX	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	GY	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	GZ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HA	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	HB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HC	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HD	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	HE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	HF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HG	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	HH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HI	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HJ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	HK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HL	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HM	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	HN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HO	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HP	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	HQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HR	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HS	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	HT	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HU	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HV	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	HW	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HX	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	HY	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	HZ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IA	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IB	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	IC	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	ID	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IE	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	IF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IG	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IH	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	II	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IJ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	IK	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	IL	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IM	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IN	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	IO	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IP	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IQ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	IR	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IS	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IT	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	IU	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IV	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IW	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	IX	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IY	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	IZ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	JA	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JC	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	JD	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JF	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	JG	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JI	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	JJ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JL	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	JM	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JO	111/113 (98%)	110 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	JP	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JR	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	JS	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JT	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JU	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	JV	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JW	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JX	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	JY	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	JZ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KA	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	KB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KC	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KD	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	KE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KG	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	KH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KI	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KJ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	KK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KL	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KM	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	KN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KO	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KP	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	KQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KR	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KS	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	KT	111/113 (98%)	109 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	KU	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KV	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	KW	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KX	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	KY	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	KZ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LA	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LB	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	LC	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LD	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LE	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	LF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LG	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LH	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	LI	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LJ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LK	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	LL	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LM	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LN	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	LO	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LP	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LQ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	LR	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LS	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LT	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	LU	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LV	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LW	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	LX	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	LY	111/113 (98%)	109 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LZ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	MA	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MC	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	MD	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	ME	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MF	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	MG	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MI	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	MJ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	ML	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	MM	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MO	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	MP	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MR	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	MS	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MT	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MU	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	MV	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MW	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MX	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	MY	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	MZ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NA	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	NB	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NC	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	ND	111/113 (98%)	110 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	NE	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NF	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NG	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	NH	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NI	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NJ	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	NK	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NL	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NM	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	NN	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NO	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NP	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	NQ	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NR	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NS	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
1	NT	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NU	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
1	NV	111/113 (98%)	110 (99%)	1 (1%)	0	100	100
All	All	39960/40680 (98%)	39360 (98%)	600 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	91/91 (100%)	91 (100%)	0	100	100
1	AB	91/91 (100%)	91 (100%)	0	100	100
1	AC	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AD	91/91 (100%)	91 (100%)	0	100	100
1	AE	91/91 (100%)	91 (100%)	0	100	100
1	AF	91/91 (100%)	91 (100%)	0	100	100
1	AG	91/91 (100%)	91 (100%)	0	100	100
1	AH	91/91 (100%)	91 (100%)	0	100	100
1	AI	91/91 (100%)	91 (100%)	0	100	100
1	AJ	91/91 (100%)	91 (100%)	0	100	100
1	AK	91/91 (100%)	91 (100%)	0	100	100
1	AL	91/91 (100%)	91 (100%)	0	100	100
1	AM	91/91 (100%)	91 (100%)	0	100	100
1	AN	91/91 (100%)	91 (100%)	0	100	100
1	AO	91/91 (100%)	91 (100%)	0	100	100
1	AP	91/91 (100%)	91 (100%)	0	100	100
1	AQ	91/91 (100%)	91 (100%)	0	100	100
1	AR	91/91 (100%)	91 (100%)	0	100	100
1	AS	91/91 (100%)	91 (100%)	0	100	100
1	AT	91/91 (100%)	91 (100%)	0	100	100
1	AU	91/91 (100%)	91 (100%)	0	100	100
1	AV	91/91 (100%)	91 (100%)	0	100	100
1	AW	91/91 (100%)	91 (100%)	0	100	100
1	AX	91/91 (100%)	91 (100%)	0	100	100
1	AY	91/91 (100%)	91 (100%)	0	100	100
1	AZ	91/91 (100%)	91 (100%)	0	100	100
1	BA	91/91 (100%)	91 (100%)	0	100	100
1	BB	91/91 (100%)	91 (100%)	0	100	100
1	BC	91/91 (100%)	91 (100%)	0	100	100
1	BD	91/91 (100%)	91 (100%)	0	100	100
1	BE	91/91 (100%)	91 (100%)	0	100	100
1	BF	91/91 (100%)	91 (100%)	0	100	100
1	BG	91/91 (100%)	91 (100%)	0	100	100
1	BH	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BI	91/91 (100%)	91 (100%)	0	100	100
1	BJ	91/91 (100%)	91 (100%)	0	100	100
1	BK	91/91 (100%)	91 (100%)	0	100	100
1	BL	91/91 (100%)	91 (100%)	0	100	100
1	BM	91/91 (100%)	91 (100%)	0	100	100
1	BN	91/91 (100%)	91 (100%)	0	100	100
1	BO	91/91 (100%)	91 (100%)	0	100	100
1	BP	91/91 (100%)	91 (100%)	0	100	100
1	BQ	91/91 (100%)	91 (100%)	0	100	100
1	BR	91/91 (100%)	91 (100%)	0	100	100
1	BS	91/91 (100%)	91 (100%)	0	100	100
1	BT	91/91 (100%)	91 (100%)	0	100	100
1	BU	91/91 (100%)	91 (100%)	0	100	100
1	BV	91/91 (100%)	91 (100%)	0	100	100
1	BW	91/91 (100%)	91 (100%)	0	100	100
1	BX	91/91 (100%)	91 (100%)	0	100	100
1	BY	91/91 (100%)	91 (100%)	0	100	100
1	BZ	91/91 (100%)	91 (100%)	0	100	100
1	CA	91/91 (100%)	91 (100%)	0	100	100
1	CB	91/91 (100%)	91 (100%)	0	100	100
1	CC	91/91 (100%)	91 (100%)	0	100	100
1	CD	91/91 (100%)	91 (100%)	0	100	100
1	CE	91/91 (100%)	91 (100%)	0	100	100
1	CF	91/91 (100%)	91 (100%)	0	100	100
1	CG	91/91 (100%)	91 (100%)	0	100	100
1	CH	91/91 (100%)	91 (100%)	0	100	100
1	CI	91/91 (100%)	91 (100%)	0	100	100
1	CJ	91/91 (100%)	91 (100%)	0	100	100
1	CK	91/91 (100%)	91 (100%)	0	100	100
1	CL	91/91 (100%)	91 (100%)	0	100	100
1	CM	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CN	91/91 (100%)	91 (100%)	0	100	100
1	CO	91/91 (100%)	91 (100%)	0	100	100
1	CP	91/91 (100%)	91 (100%)	0	100	100
1	CQ	91/91 (100%)	91 (100%)	0	100	100
1	CR	91/91 (100%)	91 (100%)	0	100	100
1	CS	91/91 (100%)	91 (100%)	0	100	100
1	CT	91/91 (100%)	91 (100%)	0	100	100
1	CU	91/91 (100%)	91 (100%)	0	100	100
1	CV	91/91 (100%)	91 (100%)	0	100	100
1	CW	91/91 (100%)	91 (100%)	0	100	100
1	CX	91/91 (100%)	91 (100%)	0	100	100
1	CY	91/91 (100%)	91 (100%)	0	100	100
1	CZ	91/91 (100%)	91 (100%)	0	100	100
1	DA	91/91 (100%)	91 (100%)	0	100	100
1	DB	91/91 (100%)	91 (100%)	0	100	100
1	DC	91/91 (100%)	91 (100%)	0	100	100
1	DD	91/91 (100%)	91 (100%)	0	100	100
1	DE	91/91 (100%)	91 (100%)	0	100	100
1	DF	91/91 (100%)	91 (100%)	0	100	100
1	DG	91/91 (100%)	91 (100%)	0	100	100
1	DH	91/91 (100%)	91 (100%)	0	100	100
1	DI	91/91 (100%)	91 (100%)	0	100	100
1	DJ	91/91 (100%)	91 (100%)	0	100	100
1	DK	91/91 (100%)	91 (100%)	0	100	100
1	DL	91/91 (100%)	91 (100%)	0	100	100
1	DM	91/91 (100%)	91 (100%)	0	100	100
1	DN	91/91 (100%)	91 (100%)	0	100	100
1	DO	91/91 (100%)	91 (100%)	0	100	100
1	DP	91/91 (100%)	91 (100%)	0	100	100
1	DQ	91/91 (100%)	91 (100%)	0	100	100
1	DR	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DS	91/91 (100%)	91 (100%)	0	100	100
1	DT	91/91 (100%)	91 (100%)	0	100	100
1	DU	91/91 (100%)	91 (100%)	0	100	100
1	DV	91/91 (100%)	91 (100%)	0	100	100
1	DW	91/91 (100%)	91 (100%)	0	100	100
1	DX	91/91 (100%)	91 (100%)	0	100	100
1	DY	91/91 (100%)	91 (100%)	0	100	100
1	DZ	91/91 (100%)	91 (100%)	0	100	100
1	EA	91/91 (100%)	91 (100%)	0	100	100
1	EB	91/91 (100%)	91 (100%)	0	100	100
1	EC	91/91 (100%)	91 (100%)	0	100	100
1	ED	91/91 (100%)	91 (100%)	0	100	100
1	EE	91/91 (100%)	91 (100%)	0	100	100
1	EF	91/91 (100%)	91 (100%)	0	100	100
1	EG	91/91 (100%)	91 (100%)	0	100	100
1	EH	91/91 (100%)	91 (100%)	0	100	100
1	EI	91/91 (100%)	91 (100%)	0	100	100
1	EJ	91/91 (100%)	91 (100%)	0	100	100
1	EK	91/91 (100%)	91 (100%)	0	100	100
1	EL	91/91 (100%)	91 (100%)	0	100	100
1	EM	91/91 (100%)	91 (100%)	0	100	100
1	EN	91/91 (100%)	91 (100%)	0	100	100
1	EO	91/91 (100%)	91 (100%)	0	100	100
1	EP	91/91 (100%)	91 (100%)	0	100	100
1	EQ	91/91 (100%)	91 (100%)	0	100	100
1	ER	91/91 (100%)	91 (100%)	0	100	100
1	ES	91/91 (100%)	91 (100%)	0	100	100
1	ET	91/91 (100%)	91 (100%)	0	100	100
1	EU	91/91 (100%)	91 (100%)	0	100	100
1	EV	91/91 (100%)	91 (100%)	0	100	100
1	EW	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	EX	91/91 (100%)	91 (100%)	0	100	100
1	EY	91/91 (100%)	91 (100%)	0	100	100
1	EZ	91/91 (100%)	91 (100%)	0	100	100
1	FA	91/91 (100%)	91 (100%)	0	100	100
1	FB	91/91 (100%)	91 (100%)	0	100	100
1	FC	91/91 (100%)	91 (100%)	0	100	100
1	FD	91/91 (100%)	91 (100%)	0	100	100
1	FE	91/91 (100%)	91 (100%)	0	100	100
1	FF	91/91 (100%)	91 (100%)	0	100	100
1	FG	91/91 (100%)	91 (100%)	0	100	100
1	FH	91/91 (100%)	91 (100%)	0	100	100
1	FI	91/91 (100%)	91 (100%)	0	100	100
1	FJ	91/91 (100%)	91 (100%)	0	100	100
1	FK	91/91 (100%)	91 (100%)	0	100	100
1	FL	91/91 (100%)	91 (100%)	0	100	100
1	FM	91/91 (100%)	91 (100%)	0	100	100
1	FN	91/91 (100%)	91 (100%)	0	100	100
1	FO	91/91 (100%)	91 (100%)	0	100	100
1	FP	91/91 (100%)	91 (100%)	0	100	100
1	FQ	91/91 (100%)	91 (100%)	0	100	100
1	FR	91/91 (100%)	91 (100%)	0	100	100
1	FS	91/91 (100%)	91 (100%)	0	100	100
1	FT	91/91 (100%)	91 (100%)	0	100	100
1	FU	91/91 (100%)	91 (100%)	0	100	100
1	FV	91/91 (100%)	91 (100%)	0	100	100
1	FW	91/91 (100%)	91 (100%)	0	100	100
1	FX	91/91 (100%)	91 (100%)	0	100	100
1	FY	91/91 (100%)	91 (100%)	0	100	100
1	FZ	91/91 (100%)	91 (100%)	0	100	100
1	GA	91/91 (100%)	91 (100%)	0	100	100
1	GB	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	GC	91/91 (100%)	91 (100%)	0	100	100
1	GD	91/91 (100%)	91 (100%)	0	100	100
1	GE	91/91 (100%)	91 (100%)	0	100	100
1	GF	91/91 (100%)	91 (100%)	0	100	100
1	GG	91/91 (100%)	91 (100%)	0	100	100
1	GH	91/91 (100%)	91 (100%)	0	100	100
1	GI	91/91 (100%)	91 (100%)	0	100	100
1	GJ	91/91 (100%)	91 (100%)	0	100	100
1	GK	91/91 (100%)	91 (100%)	0	100	100
1	GL	91/91 (100%)	91 (100%)	0	100	100
1	GM	91/91 (100%)	91 (100%)	0	100	100
1	GN	91/91 (100%)	91 (100%)	0	100	100
1	GO	91/91 (100%)	91 (100%)	0	100	100
1	GP	91/91 (100%)	91 (100%)	0	100	100
1	GQ	91/91 (100%)	91 (100%)	0	100	100
1	GR	91/91 (100%)	91 (100%)	0	100	100
1	GS	91/91 (100%)	91 (100%)	0	100	100
1	GT	91/91 (100%)	91 (100%)	0	100	100
1	GU	91/91 (100%)	91 (100%)	0	100	100
1	GV	91/91 (100%)	91 (100%)	0	100	100
1	GW	91/91 (100%)	91 (100%)	0	100	100
1	GX	91/91 (100%)	91 (100%)	0	100	100
1	GY	91/91 (100%)	91 (100%)	0	100	100
1	GZ	91/91 (100%)	91 (100%)	0	100	100
1	HA	91/91 (100%)	91 (100%)	0	100	100
1	HB	91/91 (100%)	91 (100%)	0	100	100
1	HC	91/91 (100%)	91 (100%)	0	100	100
1	HD	91/91 (100%)	91 (100%)	0	100	100
1	HE	91/91 (100%)	91 (100%)	0	100	100
1	HF	91/91 (100%)	91 (100%)	0	100	100
1	HG	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	HH	91/91 (100%)	91 (100%)	0	100	100
1	HI	91/91 (100%)	91 (100%)	0	100	100
1	HJ	91/91 (100%)	91 (100%)	0	100	100
1	HK	91/91 (100%)	91 (100%)	0	100	100
1	HL	91/91 (100%)	91 (100%)	0	100	100
1	HM	91/91 (100%)	91 (100%)	0	100	100
1	HN	91/91 (100%)	91 (100%)	0	100	100
1	HO	91/91 (100%)	91 (100%)	0	100	100
1	HP	91/91 (100%)	91 (100%)	0	100	100
1	HQ	91/91 (100%)	91 (100%)	0	100	100
1	HR	91/91 (100%)	91 (100%)	0	100	100
1	HS	91/91 (100%)	91 (100%)	0	100	100
1	HT	91/91 (100%)	91 (100%)	0	100	100
1	HU	91/91 (100%)	91 (100%)	0	100	100
1	HV	91/91 (100%)	91 (100%)	0	100	100
1	HW	91/91 (100%)	91 (100%)	0	100	100
1	HX	91/91 (100%)	91 (100%)	0	100	100
1	HY	91/91 (100%)	91 (100%)	0	100	100
1	HZ	91/91 (100%)	91 (100%)	0	100	100
1	IA	91/91 (100%)	91 (100%)	0	100	100
1	IB	91/91 (100%)	91 (100%)	0	100	100
1	IC	91/91 (100%)	91 (100%)	0	100	100
1	ID	91/91 (100%)	91 (100%)	0	100	100
1	IE	91/91 (100%)	91 (100%)	0	100	100
1	IF	91/91 (100%)	91 (100%)	0	100	100
1	IG	91/91 (100%)	91 (100%)	0	100	100
1	IH	91/91 (100%)	91 (100%)	0	100	100
1	II	91/91 (100%)	91 (100%)	0	100	100
1	IJ	91/91 (100%)	91 (100%)	0	100	100
1	IK	91/91 (100%)	91 (100%)	0	100	100
1	IL	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	IM	91/91 (100%)	91 (100%)	0	100	100
1	IN	91/91 (100%)	91 (100%)	0	100	100
1	IO	91/91 (100%)	91 (100%)	0	100	100
1	IP	91/91 (100%)	91 (100%)	0	100	100
1	IQ	91/91 (100%)	91 (100%)	0	100	100
1	IR	91/91 (100%)	91 (100%)	0	100	100
1	IS	91/91 (100%)	91 (100%)	0	100	100
1	IT	91/91 (100%)	91 (100%)	0	100	100
1	IU	91/91 (100%)	91 (100%)	0	100	100
1	IV	91/91 (100%)	91 (100%)	0	100	100
1	IW	91/91 (100%)	91 (100%)	0	100	100
1	IX	91/91 (100%)	91 (100%)	0	100	100
1	IY	91/91 (100%)	91 (100%)	0	100	100
1	IZ	91/91 (100%)	91 (100%)	0	100	100
1	JA	91/91 (100%)	91 (100%)	0	100	100
1	JB	91/91 (100%)	91 (100%)	0	100	100
1	JC	91/91 (100%)	91 (100%)	0	100	100
1	JD	91/91 (100%)	91 (100%)	0	100	100
1	JE	91/91 (100%)	91 (100%)	0	100	100
1	JF	91/91 (100%)	91 (100%)	0	100	100
1	JG	91/91 (100%)	91 (100%)	0	100	100
1	JH	91/91 (100%)	91 (100%)	0	100	100
1	JI	91/91 (100%)	91 (100%)	0	100	100
1	JJ	91/91 (100%)	91 (100%)	0	100	100
1	JK	91/91 (100%)	91 (100%)	0	100	100
1	JL	91/91 (100%)	91 (100%)	0	100	100
1	JM	91/91 (100%)	91 (100%)	0	100	100
1	JN	91/91 (100%)	91 (100%)	0	100	100
1	JO	91/91 (100%)	91 (100%)	0	100	100
1	JP	91/91 (100%)	91 (100%)	0	100	100
1	JQ	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	JR	91/91 (100%)	91 (100%)	0	100	100
1	JS	91/91 (100%)	91 (100%)	0	100	100
1	JT	91/91 (100%)	91 (100%)	0	100	100
1	JU	91/91 (100%)	91 (100%)	0	100	100
1	JV	91/91 (100%)	91 (100%)	0	100	100
1	JW	91/91 (100%)	91 (100%)	0	100	100
1	JX	91/91 (100%)	91 (100%)	0	100	100
1	JY	91/91 (100%)	91 (100%)	0	100	100
1	JZ	91/91 (100%)	91 (100%)	0	100	100
1	KA	91/91 (100%)	91 (100%)	0	100	100
1	KB	91/91 (100%)	91 (100%)	0	100	100
1	KC	91/91 (100%)	91 (100%)	0	100	100
1	KD	91/91 (100%)	91 (100%)	0	100	100
1	KE	91/91 (100%)	91 (100%)	0	100	100
1	KF	91/91 (100%)	91 (100%)	0	100	100
1	KG	91/91 (100%)	91 (100%)	0	100	100
1	KH	91/91 (100%)	91 (100%)	0	100	100
1	KI	91/91 (100%)	91 (100%)	0	100	100
1	KJ	91/91 (100%)	91 (100%)	0	100	100
1	KK	91/91 (100%)	91 (100%)	0	100	100
1	KL	91/91 (100%)	91 (100%)	0	100	100
1	KM	91/91 (100%)	91 (100%)	0	100	100
1	KN	91/91 (100%)	91 (100%)	0	100	100
1	KO	91/91 (100%)	91 (100%)	0	100	100
1	KP	91/91 (100%)	91 (100%)	0	100	100
1	KQ	91/91 (100%)	91 (100%)	0	100	100
1	KR	91/91 (100%)	91 (100%)	0	100	100
1	KS	91/91 (100%)	91 (100%)	0	100	100
1	KT	91/91 (100%)	91 (100%)	0	100	100
1	KU	91/91 (100%)	91 (100%)	0	100	100
1	KV	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	KW	91/91 (100%)	91 (100%)	0	100	100
1	KX	91/91 (100%)	91 (100%)	0	100	100
1	KY	91/91 (100%)	91 (100%)	0	100	100
1	KZ	91/91 (100%)	91 (100%)	0	100	100
1	LA	91/91 (100%)	91 (100%)	0	100	100
1	LB	91/91 (100%)	91 (100%)	0	100	100
1	LC	91/91 (100%)	91 (100%)	0	100	100
1	LD	91/91 (100%)	91 (100%)	0	100	100
1	LE	91/91 (100%)	91 (100%)	0	100	100
1	LF	91/91 (100%)	91 (100%)	0	100	100
1	LG	91/91 (100%)	91 (100%)	0	100	100
1	LH	91/91 (100%)	91 (100%)	0	100	100
1	LI	91/91 (100%)	91 (100%)	0	100	100
1	LJ	91/91 (100%)	91 (100%)	0	100	100
1	LK	91/91 (100%)	91 (100%)	0	100	100
1	LL	91/91 (100%)	91 (100%)	0	100	100
1	LM	91/91 (100%)	91 (100%)	0	100	100
1	LN	91/91 (100%)	91 (100%)	0	100	100
1	LO	91/91 (100%)	91 (100%)	0	100	100
1	LP	91/91 (100%)	91 (100%)	0	100	100
1	LQ	91/91 (100%)	91 (100%)	0	100	100
1	LR	91/91 (100%)	91 (100%)	0	100	100
1	LS	91/91 (100%)	91 (100%)	0	100	100
1	LT	91/91 (100%)	91 (100%)	0	100	100
1	LU	91/91 (100%)	91 (100%)	0	100	100
1	LV	91/91 (100%)	91 (100%)	0	100	100
1	LW	91/91 (100%)	91 (100%)	0	100	100
1	LX	91/91 (100%)	91 (100%)	0	100	100
1	LY	91/91 (100%)	91 (100%)	0	100	100
1	LZ	91/91 (100%)	91 (100%)	0	100	100
1	MA	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	MB	91/91 (100%)	91 (100%)	0	100	100
1	MC	91/91 (100%)	91 (100%)	0	100	100
1	MD	91/91 (100%)	91 (100%)	0	100	100
1	ME	91/91 (100%)	91 (100%)	0	100	100
1	MF	91/91 (100%)	91 (100%)	0	100	100
1	MG	91/91 (100%)	91 (100%)	0	100	100
1	MH	91/91 (100%)	91 (100%)	0	100	100
1	MI	91/91 (100%)	91 (100%)	0	100	100
1	MJ	91/91 (100%)	91 (100%)	0	100	100
1	MK	91/91 (100%)	91 (100%)	0	100	100
1	ML	91/91 (100%)	91 (100%)	0	100	100
1	MM	91/91 (100%)	91 (100%)	0	100	100
1	MN	91/91 (100%)	91 (100%)	0	100	100
1	MO	91/91 (100%)	91 (100%)	0	100	100
1	MP	91/91 (100%)	91 (100%)	0	100	100
1	MQ	91/91 (100%)	91 (100%)	0	100	100
1	MR	91/91 (100%)	91 (100%)	0	100	100
1	MS	91/91 (100%)	91 (100%)	0	100	100
1	MT	91/91 (100%)	91 (100%)	0	100	100
1	MU	91/91 (100%)	91 (100%)	0	100	100
1	MV	91/91 (100%)	91 (100%)	0	100	100
1	MW	91/91 (100%)	91 (100%)	0	100	100
1	MX	91/91 (100%)	91 (100%)	0	100	100
1	MY	91/91 (100%)	91 (100%)	0	100	100
1	MZ	91/91 (100%)	91 (100%)	0	100	100
1	NA	91/91 (100%)	91 (100%)	0	100	100
1	NB	91/91 (100%)	91 (100%)	0	100	100
1	NC	91/91 (100%)	91 (100%)	0	100	100
1	ND	91/91 (100%)	91 (100%)	0	100	100
1	NE	91/91 (100%)	91 (100%)	0	100	100
1	NF	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	NG	91/91 (100%)	91 (100%)	0	100	100
1	NH	91/91 (100%)	91 (100%)	0	100	100
1	NI	91/91 (100%)	91 (100%)	0	100	100
1	NJ	91/91 (100%)	91 (100%)	0	100	100
1	NK	91/91 (100%)	91 (100%)	0	100	100
1	NL	91/91 (100%)	91 (100%)	0	100	100
1	NM	91/91 (100%)	91 (100%)	0	100	100
1	NN	91/91 (100%)	91 (100%)	0	100	100
1	NO	91/91 (100%)	91 (100%)	0	100	100
1	NP	91/91 (100%)	91 (100%)	0	100	100
1	NQ	91/91 (100%)	91 (100%)	0	100	100
1	NR	91/91 (100%)	91 (100%)	0	100	100
1	NS	91/91 (100%)	91 (100%)	0	100	100
1	NT	91/91 (100%)	91 (100%)	0	100	100
1	NU	91/91 (100%)	91 (100%)	0	100	100
1	NV	91/91 (100%)	91 (100%)	0	100	100
All	All	32760/32760 (100%)	32760 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (346) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	107	GLN
1	AB	97	ASN
1	AC	97	ASN
1	AC	107	GLN
1	AD	97	ASN
1	AE	97	ASN
1	AF	97	ASN
1	AH	97	ASN
1	AI	107	GLN
1	AK	97	ASN
1	AN	97	ASN
1	AO	107	GLN
1	AP	107	GLN

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Mol	Chain	Res	Type
1	AQ	97	ASN
1	AR	97	ASN
1	AS	97	ASN
1	AS	107	GLN
1	AT	97	ASN
1	AW	97	ASN
1	AX	97	ASN
1	AX	107	GLN
1	AZ	97	ASN
1	BB	107	GLN
1	BC	97	ASN
1	BE	107	GLN
1	BF	97	ASN
1	BF	107	GLN
1	BG	97	ASN
1	BH	107	GLN
1	BI	97	ASN
1	BJ	97	ASN
1	BJ	107	GLN
1	BL	97	ASN
1	BM	97	ASN
1	BO	97	ASN
1	BP	97	ASN
1	BQ	107	GLN
1	BR	97	ASN
1	BT	97	ASN
1	BT	107	GLN
1	BU	97	ASN
1	BV	97	ASN
1	BV	107	GLN
1	BX	97	ASN
1	BZ	97	ASN
1	BZ	107	GLN
1	CA	97	ASN
1	CB	107	GLN
1	CC	97	ASN
1	CD	97	ASN
1	CE	107	GLN
1	CF	107	GLN
1	CG	97	ASN
1	CH	97	ASN
1	CH	107	GLN

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Mol	Chain	Res	Type
1	CI	97	ASN
1	CI	107	GLN
1	CJ	97	ASN
1	CK	97	ASN
1	CL	97	ASN
1	CL	107	GLN
1	CM	97	ASN
1	CN	97	ASN
1	CO	97	ASN
1	CP	97	ASN
1	CQ	97	ASN
1	CQ	107	GLN
1	CS	97	ASN
1	CV	97	ASN
1	CW	107	GLN
1	CX	107	GLN
1	CY	97	ASN
1	DA	97	ASN
1	DA	107	GLN
1	DB	97	ASN
1	DC	97	ASN
1	DE	97	ASN
1	DG	97	ASN
1	DH	97	ASN
1	DJ	107	GLN
1	DK	97	ASN
1	DL	97	ASN
1	DN	97	ASN
1	DO	97	ASN
1	DQ	97	ASN
1	DR	97	ASN
1	DR	107	GLN
1	DS	97	ASN
1	DS	107	GLN
1	DT	97	ASN
1	DU	107	GLN
1	DW	97	ASN
1	EC	97	ASN
1	ED	97	ASN
1	EF	97	ASN
1	EG	107	GLN
1	EH	107	GLN

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Mol	Chain	Res	Type
1	EI	97	ASN
1	EL	97	ASN
1	EM	97	ASN
1	EO	97	ASN
1	ER	97	ASN
1	ES	97	ASN
1	ET	97	ASN
1	ET	107	GLN
1	EU	97	ASN
1	EV	97	ASN
1	EW	97	ASN
1	EW	107	GLN
1	EX	97	ASN
1	EY	97	ASN
1	FA	97	ASN
1	FB	97	ASN
1	FB	107	GLN
1	FD	97	ASN
1	FF	97	ASN
1	FF	107	GLN
1	FG	97	ASN
1	FH	97	ASN
1	FI	97	ASN
1	FI	107	GLN
1	FJ	97	ASN
1	FK	97	ASN
1	FK	107	GLN
1	FL	97	ASN
1	FL	107	GLN
1	FM	97	ASN
1	FP	97	ASN
1	FQ	107	GLN
1	FR	97	ASN
1	FR	107	GLN
1	FS	97	ASN
1	FT	97	ASN
1	FT	107	GLN
1	FV	97	ASN
1	FV	107	GLN
1	FW	97	ASN
1	FX	97	ASN
1	FY	97	ASN

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Mol	Chain	Res	Type
1	FZ	97	ASN
1	FZ	107	GLN
1	GA	97	ASN
1	GA	107	GLN
1	GB	97	ASN
1	GC	97	ASN
1	GD	107	GLN
1	GE	97	ASN
1	GG	97	ASN
1	GH	97	ASN
1	GK	97	ASN
1	GM	107	GLN
1	GN	97	ASN
1	GO	97	ASN
1	GO	107	GLN
1	GP	97	ASN
1	GP	107	GLN
1	GQ	97	ASN
1	GR	97	ASN
1	GS	97	ASN
1	GS	107	GLN
1	GT	97	ASN
1	GV	107	GLN
1	GW	97	ASN
1	GY	107	GLN
1	GZ	97	ASN
1	GZ	107	GLN
1	HA	97	ASN
1	HB	97	ASN
1	HB	107	GLN
1	HC	97	ASN
1	HD	97	ASN
1	HD	107	GLN
1	HE	107	GLN
1	HF	97	ASN
1	HH	107	GLN
1	HI	97	ASN
1	HL	97	ASN
1	HM	97	ASN
1	HO	97	ASN
1	HP	107	GLN
1	HQ	97	ASN

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Mol	Chain	Res	Type
1	HR	97	ASN
1	HS	97	ASN
1	HT	97	ASN
1	HT	107	GLN
1	HU	97	ASN
1	HV	97	ASN
1	HV	107	GLN
1	HW	97	ASN
1	HW	107	GLN
1	HX	97	ASN
1	HY	97	ASN
1	HY	107	GLN
1	IA	97	ASN
1	IB	107	GLN
1	IC	107	GLN
1	ID	97	ASN
1	IF	97	ASN
1	IG	97	ASN
1	II	97	ASN
1	IJ	97	ASN
1	IK	107	GLN
1	IL	97	ASN
1	IM	97	ASN
1	IN	107	GLN
1	IO	97	ASN
1	IP	97	ASN
1	IQ	97	ASN
1	IR	107	GLN
1	IS	97	ASN
1	IT	97	ASN
1	IU	97	ASN
1	IU	107	GLN
1	IV	97	ASN
1	IW	97	ASN
1	IW	107	GLN
1	IX	97	ASN
1	IX	107	GLN
1	IY	97	ASN
1	JB	97	ASN
1	JC	97	ASN
1	JE	97	ASN
1	JF	97	ASN

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Mol	Chain	Res	Type
1	JG	97	ASN
1	JG	107	GLN
1	JH	97	ASN
1	JJ	107	GLN
1	JK	97	ASN
1	JL	107	GLN
1	JM	97	ASN
1	JM	107	GLN
1	JN	97	ASN
1	JO	97	ASN
1	JP	107	GLN
1	JQ	97	ASN
1	JR	97	ASN
1	JT	97	ASN
1	JU	107	GLN
1	JV	97	ASN
1	JV	107	GLN
1	JW	97	ASN
1	JX	107	GLN
1	JY	97	ASN
1	JY	107	GLN
1	JZ	97	ASN
1	KA	107	GLN
1	KC	97	ASN
1	KD	97	ASN
1	KE	97	ASN
1	KE	107	GLN
1	KF	97	ASN
1	KG	107	GLN
1	KI	97	ASN
1	KL	97	ASN
1	KM	97	ASN
1	KN	97	ASN
1	KN	107	GLN
1	KO	97	ASN
1	KQ	107	GLN
1	KR	97	ASN
1	KT	97	ASN
1	KT	107	GLN
1	KU	97	ASN
1	KU	107	GLN
1	KV	107	GLN

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Mol	Chain	Res	Type
1	KX	97	ASN
1	KY	97	ASN
1	KZ	97	ASN
1	KZ	107	GLN
1	LA	97	ASN
1	LC	107	GLN
1	LD	97	ASN
1	LE	97	ASN
1	LE	107	GLN
1	LG	97	ASN
1	LJ	97	ASN
1	LK	97	ASN
1	LK	107	GLN
1	LM	97	ASN
1	LN	107	GLN
1	LP	97	ASN
1	LR	97	ASN
1	LR	107	GLN
1	LS	97	ASN
1	LT	97	ASN
1	LU	97	ASN
1	LU	107	GLN
1	LV	97	ASN
1	LW	97	ASN
1	LW	107	GLN
1	LX	97	ASN
1	LY	97	ASN
1	LZ	107	GLN
1	MA	97	ASN
1	MB	97	ASN
1	MC	97	ASN
1	MD	107	GLN
1	ME	97	ASN
1	MF	97	ASN
1	MH	97	ASN
1	MI	97	ASN
1	MJ	97	ASN
1	MJ	107	GLN
1	MK	97	ASN
1	ML	97	ASN
1	MM	107	GLN
1	MN	97	ASN

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Mol	Chain	Res	Type
1	MO	97	ASN
1	MQ	97	ASN
1	MR	97	ASN
1	MS	97	ASN
1	MS	107	GLN
1	MT	97	ASN
1	MU	97	ASN
1	MU	107	GLN
1	MV	97	ASN
1	MW	97	ASN
1	MX	107	GLN
1	MY	97	ASN
1	MY	107	GLN
1	MZ	97	ASN
1	NA	97	ASN
1	NB	97	ASN
1	NB	107	GLN
1	NC	97	ASN
1	ND	97	ASN
1	NF	97	ASN
1	NG	97	ASN
1	NH	97	ASN
1	NH	107	GLN
1	NI	97	ASN
1	NJ	107	GLN
1	NK	97	ASN
1	NK	107	GLN
1	NL	97	ASN
1	NM	107	GLN
1	NN	97	ASN
1	NN	107	GLN
1	NO	97	ASN
1	NQ	97	ASN
1	NQ	107	GLN
1	NR	97	ASN
1	NS	107	GLN
1	NT	97	ASN
1	NT	107	GLN
1	NU	97	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	RA	18/30 (60%)	0	0
2	RB	18/30 (60%)	0	0
2	RC	18/30 (60%)	0	0
2	RD	18/30 (60%)	0	0
2	RE	18/30 (60%)	0	0
2	RF	18/30 (60%)	0	0
2	RG	18/30 (60%)	0	0
2	RH	18/30 (60%)	0	0
2	RI	18/30 (60%)	0	0
2	RJ	18/30 (60%)	0	0
2	RK	18/30 (60%)	0	0
2	RL	18/30 (60%)	0	0
2	RM	18/30 (60%)	0	0
2	RN	18/30 (60%)	0	0
2	RO	18/30 (60%)	0	0
2	RP	18/30 (60%)	0	0
2	RQ	18/30 (60%)	0	0
2	RR	18/30 (60%)	0	0
2	RS	18/30 (60%)	0	0
2	RT	18/30 (60%)	0	0
2	RU	18/30 (60%)	0	0
2	RV	18/30 (60%)	0	0
2	RW	18/30 (60%)	0	0
2	RX	18/30 (60%)	0	0
2	RY	18/30 (60%)	0	0
2	RZ	18/30 (60%)	0	0
2	SA	18/30 (60%)	0	0
2	SB	18/30 (60%)	0	0
2	SC	18/30 (60%)	0	0
2	SD	18/30 (60%)	0	0
2	SE	18/30 (60%)	0	0
2	SF	18/30 (60%)	0	0
2	SG	18/30 (60%)	0	0
2	SH	18/30 (60%)	0	0
2	SI	18/30 (60%)	0	0
2	SJ	18/30 (60%)	0	0
2	SK	18/30 (60%)	0	0
2	SL	18/30 (60%)	0	0
2	SM	18/30 (60%)	0	0
2	SN	18/30 (60%)	0	0
2	SO	18/30 (60%)	0	0
2	SP	18/30 (60%)	0	0
2	SQ	18/30 (60%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	SR	18/30 (60%)	0	0
2	SS	18/30 (60%)	0	0
2	ST	18/30 (60%)	0	0
2	SU	18/30 (60%)	0	0
2	SV	18/30 (60%)	0	0
2	SW	18/30 (60%)	0	0
2	SX	18/30 (60%)	0	0
2	SY	18/30 (60%)	0	0
2	SZ	18/30 (60%)	0	0
2	TA	18/30 (60%)	0	0
2	TB	18/30 (60%)	0	0
2	TC	18/30 (60%)	0	0
2	TD	18/30 (60%)	0	0
2	TE	18/30 (60%)	0	0
2	TF	18/30 (60%)	0	0
2	TG	18/30 (60%)	0	0
2	TH	18/30 (60%)	0	0
All	All	1080/1800 (60%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	AA	113/113 (100%)	0.45	7 (6%)	26	16	51, 87, 163, 193	0
1	AB	113/113 (100%)	0.31	2 (1%)	67	42	49, 83, 126, 154	0
1	AC	113/113 (100%)	0.42	5 (4%)	39	21	54, 96, 147, 177	0
1	AD	113/113 (100%)	0.52	6 (5%)	32	18	51, 87, 163, 193	0
1	AE	113/113 (100%)	0.46	6 (5%)	32	18	49, 83, 126, 154	0
1	AF	113/113 (100%)	0.56	4 (3%)	47	26	54, 96, 147, 177	0
1	AG	113/113 (100%)	0.40	3 (2%)	56	33	51, 87, 163, 193	0
1	AH	113/113 (100%)	0.55	6 (5%)	32	18	49, 83, 126, 154	0
1	AI	113/113 (100%)	0.69	15 (13%)	7	6	54, 96, 147, 177	0
1	AJ	113/113 (100%)	0.49	10 (8%)	15	10	51, 87, 163, 193	0
1	AK	113/113 (100%)	0.28	3 (2%)	56	33	49, 83, 126, 154	0
1	AL	113/113 (100%)	0.67	10 (8%)	15	10	54, 96, 147, 177	0
1	AM	113/113 (100%)	0.34	4 (3%)	47	26	51, 87, 163, 193	0
1	AN	113/113 (100%)	0.48	1 (0%)	81	58	49, 83, 126, 154	0
1	AO	113/113 (100%)	0.40	5 (4%)	39	21	54, 96, 147, 177	0
1	AP	113/113 (100%)	0.78	12 (10%)	11	8	51, 87, 163, 193	0
1	AQ	113/113 (100%)	0.55	5 (4%)	39	21	49, 83, 126, 154	0
1	AR	113/113 (100%)	0.71	9 (7%)	18	12	54, 96, 147, 177	0
1	AS	113/113 (100%)	0.48	5 (4%)	39	21	51, 87, 163, 193	0
1	AT	113/113 (100%)	0.33	3 (2%)	56	33	49, 83, 126, 154	0
1	AU	113/113 (100%)	0.53	4 (3%)	47	26	54, 96, 147, 177	0
1	AV	113/113 (100%)	0.48	6 (5%)	32	18	51, 87, 163, 193	0
1	AW	113/113 (100%)	0.44	5 (4%)	39	21	49, 83, 126, 154	0
1	AX	113/113 (100%)	0.63	8 (7%)	22	14	54, 96, 147, 177	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	113/113 (100%)	0.35	3 (2%) 56 33	51, 87, 163, 193	0
1	AZ	113/113 (100%)	0.71	6 (5%) 32 18	49, 83, 126, 154	0
1	BA	113/113 (100%)	0.65	8 (7%) 22 14	54, 96, 147, 177	0
1	BB	113/113 (100%)	0.72	8 (7%) 22 14	51, 87, 163, 193	0
1	BC	113/113 (100%)	0.31	4 (3%) 47 26	49, 83, 126, 154	0
1	BD	113/113 (100%)	0.55	7 (6%) 26 16	54, 96, 147, 177	0
1	BE	113/113 (100%)	0.50	7 (6%) 26 16	51, 87, 163, 193	0
1	BF	113/113 (100%)	0.47	6 (5%) 32 18	49, 83, 126, 154	0
1	BG	113/113 (100%)	0.68	11 (9%) 13 9	54, 96, 147, 177	0
1	BH	113/113 (100%)	0.36	4 (3%) 47 26	51, 87, 163, 193	0
1	BI	113/113 (100%)	0.47	6 (5%) 32 18	49, 83, 126, 154	0
1	BJ	113/113 (100%)	0.57	4 (3%) 47 26	54, 96, 147, 177	0
1	BK	113/113 (100%)	0.42	3 (2%) 56 33	51, 87, 163, 193	0
1	BL	113/113 (100%)	0.45	7 (6%) 26 16	49, 83, 126, 154	0
1	BM	113/113 (100%)	0.66	8 (7%) 22 14	54, 96, 147, 177	0
1	BN	113/113 (100%)	0.54	6 (5%) 32 18	51, 87, 163, 193	0
1	BO	113/113 (100%)	0.42	3 (2%) 56 33	49, 83, 126, 154	0
1	BP	113/113 (100%)	0.54	8 (7%) 22 14	54, 96, 147, 177	0
1	BQ	113/113 (100%)	1.14	16 (14%) 6 5	51, 87, 163, 193	0
1	BR	113/113 (100%)	0.77	12 (10%) 11 8	49, 83, 126, 154	0
1	BS	113/113 (100%)	0.82	10 (8%) 15 10	54, 96, 147, 177	0
1	BT	113/113 (100%)	0.51	9 (7%) 18 12	51, 87, 163, 193	0
1	BU	113/113 (100%)	0.56	7 (6%) 26 16	49, 83, 126, 154	0
1	BV	113/113 (100%)	0.80	11 (9%) 13 9	54, 96, 147, 177	0
1	BW	113/113 (100%)	0.35	4 (3%) 47 26	51, 87, 163, 193	0
1	BX	113/113 (100%)	0.40	4 (3%) 47 26	49, 83, 126, 154	0
1	BY	113/113 (100%)	0.64	10 (8%) 15 10	54, 96, 147, 177	0
1	BZ	113/113 (100%)	0.33	3 (2%) 56 33	51, 87, 163, 193	0
1	CA	113/113 (100%)	0.42	8 (7%) 22 14	49, 83, 126, 154	0
1	CB	113/113 (100%)	0.45	5 (4%) 39 21	54, 96, 147, 177	0
1	CC	113/113 (100%)	0.56	10 (8%) 15 10	51, 87, 163, 193	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	CD	113/113 (100%)	0.54	6 (5%) 32 18	49, 83, 126, 154	0
1	CE	113/113 (100%)	0.68	15 (13%) 7 6	54, 96, 147, 177	0
1	CF	113/113 (100%)	0.51	6 (5%) 32 18	51, 87, 163, 193	0
1	CG	113/113 (100%)	0.63	6 (5%) 32 18	49, 83, 126, 154	0
1	CH	113/113 (100%)	0.65	12 (10%) 11 8	54, 96, 147, 177	0
1	CI	113/113 (100%)	0.46	4 (3%) 47 26	51, 87, 163, 193	0
1	CJ	113/113 (100%)	0.55	6 (5%) 32 18	49, 83, 126, 154	0
1	CK	113/113 (100%)	0.60	4 (3%) 47 26	54, 96, 147, 177	0
1	CL	113/113 (100%)	0.49	6 (5%) 32 18	51, 87, 163, 193	0
1	CM	113/113 (100%)	0.51	4 (3%) 47 26	49, 83, 126, 154	0
1	CN	113/113 (100%)	0.66	11 (9%) 13 9	54, 96, 147, 177	0
1	CO	113/113 (100%)	0.49	5 (4%) 39 21	51, 87, 163, 193	0
1	CP	113/113 (100%)	0.93	14 (12%) 8 6	49, 83, 126, 154	0
1	CQ	113/113 (100%)	0.76	5 (4%) 39 21	54, 96, 147, 177	0
1	CR	113/113 (100%)	0.63	9 (7%) 18 12	51, 87, 163, 193	0
1	CS	113/113 (100%)	0.54	4 (3%) 47 26	49, 83, 126, 154	0
1	CT	113/113 (100%)	0.64	7 (6%) 26 16	54, 96, 147, 177	0
1	CU	113/113 (100%)	0.65	7 (6%) 26 16	51, 87, 163, 193	0
1	CV	113/113 (100%)	0.53	7 (6%) 26 16	49, 83, 126, 154	0
1	CW	113/113 (100%)	0.55	5 (4%) 39 21	54, 96, 147, 177	0
1	CX	113/113 (100%)	0.70	13 (11%) 9 6	51, 87, 163, 193	0
1	CY	113/113 (100%)	0.51	7 (6%) 26 16	49, 83, 126, 154	0
1	CZ	113/113 (100%)	0.73	13 (11%) 9 6	54, 96, 147, 177	0
1	DA	113/113 (100%)	0.36	5 (4%) 39 21	51, 87, 163, 193	0
1	DB	113/113 (100%)	0.39	3 (2%) 56 33	49, 83, 126, 154	0
1	DC	113/113 (100%)	0.65	8 (7%) 22 14	54, 96, 147, 177	0
1	DD	113/113 (100%)	0.47	6 (5%) 32 18	51, 87, 163, 193	0
1	DE	113/113 (100%)	0.40	4 (3%) 47 26	49, 83, 126, 154	0
1	DF	113/113 (100%)	0.80	9 (7%) 18 12	54, 96, 147, 177	0
1	DG	113/113 (100%)	0.41	3 (2%) 56 33	51, 87, 163, 193	0
1	DH	113/113 (100%)	0.49	4 (3%) 47 26	49, 83, 126, 154	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	DI	113/113 (100%)	0.67	8 (7%) 22 14	54, 96, 147, 177	0
1	DJ	113/113 (100%)	1.13	19 (16%) 4 4	51, 87, 163, 193	0
1	DK	113/113 (100%)	0.80	7 (6%) 26 16	49, 83, 126, 154	0
1	DL	113/113 (100%)	0.62	4 (3%) 47 26	54, 96, 147, 177	0
1	DM	113/113 (100%)	0.42	5 (4%) 39 21	51, 87, 163, 193	0
1	DN	113/113 (100%)	0.25	2 (1%) 67 42	49, 83, 126, 154	0
1	DO	113/113 (100%)	0.52	6 (5%) 32 18	54, 96, 147, 177	0
1	DP	113/113 (100%)	0.42	3 (2%) 56 33	51, 87, 163, 193	0
1	DQ	113/113 (100%)	0.38	5 (4%) 39 21	49, 83, 126, 154	0
1	DR	113/113 (100%)	0.54	7 (6%) 26 16	54, 96, 147, 177	0
1	DS	113/113 (100%)	0.59	6 (5%) 32 18	51, 87, 163, 193	0
1	DT	113/113 (100%)	0.30	1 (0%) 81 58	49, 83, 126, 154	0
1	DU	113/113 (100%)	0.68	5 (4%) 39 21	54, 96, 147, 177	0
1	DV	113/113 (100%)	0.50	7 (6%) 26 16	51, 87, 163, 193	0
1	DW	113/113 (100%)	0.29	4 (3%) 47 26	49, 83, 126, 154	0
1	DX	113/113 (100%)	0.75	11 (9%) 13 9	54, 96, 147, 177	0
1	DY	113/113 (100%)	0.47	3 (2%) 56 33	51, 87, 163, 193	0
1	DZ	113/113 (100%)	0.57	11 (9%) 13 9	49, 83, 126, 154	0
1	EA	113/113 (100%)	0.32	1 (0%) 81 58	54, 96, 147, 177	0
1	EB	113/113 (100%)	0.81	9 (7%) 18 12	51, 87, 163, 193	0
1	EC	113/113 (100%)	0.99	10 (8%) 15 10	49, 83, 126, 154	0
1	ED	113/113 (100%)	0.74	6 (5%) 32 18	54, 96, 147, 177	0
1	EE	113/113 (100%)	0.65	10 (8%) 15 10	51, 87, 163, 193	0
1	EF	113/113 (100%)	0.33	1 (0%) 81 58	49, 83, 126, 154	0
1	EG	113/113 (100%)	0.57	8 (7%) 22 14	54, 96, 147, 177	0
1	EH	113/113 (100%)	0.46	7 (6%) 26 16	51, 87, 163, 193	0
1	EI	113/113 (100%)	0.44	3 (2%) 56 33	49, 83, 126, 154	0
1	EJ	113/113 (100%)	0.64	7 (6%) 26 16	54, 96, 147, 177	0
1	EK	113/113 (100%)	0.60	8 (7%) 22 14	51, 87, 163, 193	0
1	EL	113/113 (100%)	0.54	11 (9%) 13 9	49, 83, 126, 154	0
1	EM	113/113 (100%)	0.54	9 (7%) 18 12	54, 96, 147, 177	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	EN	113/113 (100%)	0.44	4 (3%)	47	26	51, 87, 163, 193	0
1	EO	113/113 (100%)	0.43	8 (7%)	22	14	49, 83, 126, 154	0
1	EP	113/113 (100%)	0.57	11 (9%)	13	9	54, 96, 147, 177	0
1	EQ	113/113 (100%)	0.61	6 (5%)	32	18	51, 87, 163, 193	0
1	ER	113/113 (100%)	0.45	4 (3%)	47	26	49, 83, 126, 154	0
1	ES	113/113 (100%)	0.80	9 (7%)	18	12	54, 96, 147, 177	0
1	ET	113/113 (100%)	0.51	7 (6%)	26	16	51, 87, 163, 193	0
1	EU	113/113 (100%)	0.75	11 (9%)	13	9	49, 83, 126, 154	0
1	EV	113/113 (100%)	0.43	5 (4%)	39	21	54, 96, 147, 177	0
1	EW	113/113 (100%)	0.61	9 (7%)	18	12	51, 87, 163, 193	0
1	EX	113/113 (100%)	0.55	5 (4%)	39	21	49, 83, 126, 154	0
1	EY	113/113 (100%)	0.69	6 (5%)	32	18	54, 96, 147, 177	0
1	EZ	113/113 (100%)	0.51	5 (4%)	39	21	51, 87, 163, 193	0
1	FA	113/113 (100%)	0.44	6 (5%)	32	18	49, 83, 126, 154	0
1	FB	113/113 (100%)	0.48	6 (5%)	32	18	54, 96, 147, 177	0
1	FC	113/113 (100%)	0.55	5 (4%)	39	21	51, 87, 163, 193	0
1	FD	113/113 (100%)	0.56	4 (3%)	47	26	49, 83, 126, 154	0
1	FE	113/113 (100%)	0.82	13 (11%)	9	6	54, 96, 147, 177	0
1	FF	113/113 (100%)	0.60	10 (8%)	15	10	51, 87, 163, 193	0
1	FG	113/113 (100%)	0.49	5 (4%)	39	21	49, 83, 126, 154	0
1	FH	113/113 (100%)	0.63	3 (2%)	56	33	54, 96, 147, 177	0
1	FI	113/113 (100%)	0.46	3 (2%)	56	33	51, 87, 163, 193	0
1	FJ	113/113 (100%)	0.44	5 (4%)	39	21	49, 83, 126, 154	0
1	FK	113/113 (100%)	0.44	5 (4%)	39	21	54, 96, 147, 177	0
1	FL	113/113 (100%)	0.44	6 (5%)	32	18	51, 87, 163, 193	0
1	FM	113/113 (100%)	0.41	2 (1%)	67	42	49, 83, 126, 154	0
1	FN	113/113 (100%)	0.46	1 (0%)	81	58	54, 96, 147, 177	0
1	FO	113/113 (100%)	0.39	3 (2%)	56	33	51, 87, 163, 193	0
1	FP	113/113 (100%)	0.53	5 (4%)	39	21	49, 83, 126, 154	0
1	FQ	113/113 (100%)	0.51	6 (5%)	32	18	54, 96, 147, 177	0
1	FR	113/113 (100%)	0.52	7 (6%)	26	16	51, 87, 163, 193	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	FS	113/113 (100%)	0.65	7 (6%) 26 16	49, 83, 126, 154	0
1	FT	113/113 (100%)	0.49	6 (5%) 32 18	54, 96, 147, 177	0
1	FU	113/113 (100%)	0.53	6 (5%) 32 18	51, 87, 163, 193	0
1	FV	113/113 (100%)	0.50	3 (2%) 56 33	49, 83, 126, 154	0
1	FW	113/113 (100%)	0.64	5 (4%) 39 21	54, 96, 147, 177	0
1	FX	113/113 (100%)	0.44	4 (3%) 47 26	51, 87, 163, 193	0
1	FY	113/113 (100%)	0.35	5 (4%) 39 21	49, 83, 126, 154	0
1	FZ	113/113 (100%)	0.67	6 (5%) 32 18	54, 96, 147, 177	0
1	GA	113/113 (100%)	0.59	8 (7%) 22 14	51, 87, 163, 193	0
1	GB	113/113 (100%)	0.76	5 (4%) 39 21	49, 83, 126, 154	0
1	GC	113/113 (100%)	0.81	8 (7%) 22 14	54, 96, 147, 177	0
1	GD	113/113 (100%)	0.64	12 (10%) 11 8	51, 87, 163, 193	0
1	GE	113/113 (100%)	0.52	4 (3%) 47 26	49, 83, 126, 154	0
1	GF	113/113 (100%)	0.63	8 (7%) 22 14	54, 96, 147, 177	0
1	GG	113/113 (100%)	0.50	7 (6%) 26 16	51, 87, 163, 193	0
1	GH	113/113 (100%)	0.50	3 (2%) 56 33	49, 83, 126, 154	0
1	GI	113/113 (100%)	0.54	6 (5%) 32 18	54, 96, 147, 177	0
1	GJ	113/113 (100%)	0.58	9 (7%) 18 12	51, 87, 163, 193	0
1	GK	113/113 (100%)	0.74	10 (8%) 15 10	49, 83, 126, 154	0
1	GL	113/113 (100%)	0.69	8 (7%) 22 14	54, 96, 147, 177	0
1	GM	113/113 (100%)	0.44	7 (6%) 26 16	51, 87, 163, 193	0
1	GN	113/113 (100%)	0.52	10 (8%) 15 10	49, 83, 126, 154	0
1	GO	113/113 (100%)	0.62	9 (7%) 18 12	54, 96, 147, 177	0
1	GP	113/113 (100%)	0.81	7 (6%) 26 16	51, 87, 163, 193	0
1	GQ	113/113 (100%)	0.41	3 (2%) 56 33	49, 83, 126, 154	0
1	GR	113/113 (100%)	0.79	8 (7%) 22 14	54, 96, 147, 177	0
1	GS	113/113 (100%)	0.47	6 (5%) 32 18	51, 87, 163, 193	0
1	GT	113/113 (100%)	0.44	4 (3%) 47 26	49, 83, 126, 154	0
1	GU	113/113 (100%)	0.68	10 (8%) 15 10	54, 96, 147, 177	0
1	GV	113/113 (100%)	0.45	5 (4%) 39 21	51, 87, 163, 193	0
1	GW	113/113 (100%)	0.40	4 (3%) 47 26	49, 83, 126, 154	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	GX	113/113 (100%)	0.72	9 (7%) 18 12	54, 96, 147, 177	0
1	GY	113/113 (100%)	0.63	11 (9%) 13 9	51, 87, 163, 193	0
1	GZ	113/113 (100%)	0.51	5 (4%) 39 21	49, 83, 126, 154	0
1	HA	113/113 (100%)	0.63	8 (7%) 22 14	54, 96, 147, 177	0
1	HB	113/113 (100%)	0.41	5 (4%) 39 21	51, 87, 163, 193	0
1	HC	113/113 (100%)	0.46	8 (7%) 22 14	49, 83, 126, 154	0
1	HD	113/113 (100%)	0.52	4 (3%) 47 26	54, 96, 147, 177	0
1	HE	113/113 (100%)	0.69	9 (7%) 18 12	51, 87, 163, 193	0
1	HF	113/113 (100%)	0.35	2 (1%) 67 42	49, 83, 126, 154	0
1	HG	113/113 (100%)	0.59	6 (5%) 32 18	54, 96, 147, 177	0
1	HH	113/113 (100%)	0.75	10 (8%) 15 10	51, 87, 163, 193	0
1	HI	113/113 (100%)	1.03	11 (9%) 13 9	49, 83, 126, 154	0
1	HJ	113/113 (100%)	0.97	12 (10%) 11 8	54, 96, 147, 177	0
1	HK	113/113 (100%)	0.30	5 (4%) 39 21	51, 87, 163, 193	0
1	HL	113/113 (100%)	0.43	2 (1%) 67 42	49, 83, 126, 154	0
1	HM	113/113 (100%)	0.64	9 (7%) 18 12	54, 96, 147, 177	0
1	HN	113/113 (100%)	0.35	1 (0%) 81 58	51, 87, 163, 193	0
1	HO	113/113 (100%)	0.57	7 (6%) 26 16	49, 83, 126, 154	0
1	HP	113/113 (100%)	0.46	5 (4%) 39 21	54, 96, 147, 177	0
1	HQ	113/113 (100%)	0.46	2 (1%) 67 42	51, 87, 163, 193	0
1	HR	113/113 (100%)	0.78	11 (9%) 13 9	49, 83, 126, 154	0
1	HS	113/113 (100%)	0.58	5 (4%) 39 21	54, 96, 147, 177	0
1	HT	113/113 (100%)	0.44	2 (1%) 67 42	51, 87, 163, 193	0
1	HU	113/113 (100%)	0.37	2 (1%) 67 42	49, 83, 126, 154	0
1	HV	113/113 (100%)	0.52	5 (4%) 39 21	54, 96, 147, 177	0
1	HW	113/113 (100%)	0.48	8 (7%) 22 14	51, 87, 163, 193	0
1	HX	113/113 (100%)	0.62	9 (7%) 18 12	49, 83, 126, 154	0
1	HY	113/113 (100%)	0.68	4 (3%) 47 26	54, 96, 147, 177	0
1	HZ	113/113 (100%)	0.43	8 (7%) 22 14	51, 87, 163, 193	0
1	IA	113/113 (100%)	0.56	8 (7%) 22 14	49, 83, 126, 154	0
1	IB	113/113 (100%)	0.65	8 (7%) 22 14	54, 96, 147, 177	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	IC	113/113 (100%)	1.08	18 (15%) 5 4	51, 87, 163, 193	0
1	ID	113/113 (100%)	0.70	6 (5%) 32 18	49, 83, 126, 154	0
1	IE	113/113 (100%)	0.81	8 (7%) 22 14	54, 96, 147, 177	0
1	IF	113/113 (100%)	0.37	6 (5%) 32 18	51, 87, 163, 193	0
1	IG	113/113 (100%)	0.56	4 (3%) 47 26	49, 83, 126, 154	0
1	IH	113/113 (100%)	0.80	7 (6%) 26 16	54, 96, 147, 177	0
1	II	113/113 (100%)	0.59	4 (3%) 47 26	51, 87, 163, 193	0
1	IJ	113/113 (100%)	0.85	7 (6%) 26 16	49, 83, 126, 154	0
1	IK	113/113 (100%)	0.57	4 (3%) 47 26	54, 96, 147, 177	0
1	IL	113/113 (100%)	0.45	7 (6%) 26 16	51, 87, 163, 193	0
1	IM	113/113 (100%)	0.42	3 (2%) 56 33	49, 83, 126, 154	0
1	IN	113/113 (100%)	0.86	17 (15%) 5 5	54, 96, 147, 177	0
1	IO	113/113 (100%)	0.57	6 (5%) 32 18	51, 87, 163, 193	0
1	IP	113/113 (100%)	0.56	5 (4%) 39 21	49, 83, 126, 154	0
1	IQ	113/113 (100%)	0.60	7 (6%) 26 16	54, 96, 147, 177	0
1	IR	113/113 (100%)	0.46	4 (3%) 47 26	51, 87, 163, 193	0
1	IS	113/113 (100%)	0.34	1 (0%) 81 58	49, 83, 126, 154	0
1	IT	113/113 (100%)	0.64	6 (5%) 32 18	54, 96, 147, 177	0
1	IU	113/113 (100%)	0.56	8 (7%) 22 14	51, 87, 163, 193	0
1	IV	113/113 (100%)	0.63	7 (6%) 26 16	49, 83, 126, 154	0
1	IW	113/113 (100%)	0.68	4 (3%) 47 26	54, 96, 147, 177	0
1	IX	113/113 (100%)	0.43	6 (5%) 32 18	51, 87, 163, 193	0
1	IY	113/113 (100%)	0.50	6 (5%) 32 18	49, 83, 126, 154	0
1	IZ	113/113 (100%)	0.53	6 (5%) 32 18	54, 96, 147, 177	0
1	JA	113/113 (100%)	0.70	11 (9%) 13 9	51, 87, 163, 193	0
1	JB	113/113 (100%)	0.37	4 (3%) 47 26	49, 83, 126, 154	0
1	JC	113/113 (100%)	0.67	3 (2%) 56 33	54, 96, 147, 177	0
1	JD	113/113 (100%)	0.75	6 (5%) 32 18	51, 87, 163, 193	0
1	JE	113/113 (100%)	0.46	3 (2%) 56 33	49, 83, 126, 154	0
1	JF	113/113 (100%)	0.87	16 (14%) 6 5	54, 96, 147, 177	0
1	JG	113/113 (100%)	0.37	4 (3%) 47 26	51, 87, 163, 193	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	JH	113/113 (100%)	0.35	4 (3%)	47	26	49, 83, 126, 154	0
1	JI	113/113 (100%)	0.69	6 (5%)	32	18	54, 96, 147, 177	0
1	JJ	113/113 (100%)	0.56	5 (4%)	39	21	51, 87, 163, 193	0
1	JK	113/113 (100%)	0.51	7 (6%)	26	16	49, 83, 126, 154	0
1	JL	113/113 (100%)	0.66	8 (7%)	22	14	54, 96, 147, 177	0
1	JM	113/113 (100%)	0.32	4 (3%)	47	26	51, 87, 163, 193	0
1	JN	113/113 (100%)	0.35	1 (0%)	81	58	49, 83, 126, 154	0
1	JO	113/113 (100%)	0.54	5 (4%)	39	21	54, 96, 147, 177	0
1	JP	113/113 (100%)	0.53	5 (4%)	39	21	51, 87, 163, 193	0
1	JQ	113/113 (100%)	0.47	3 (2%)	56	33	49, 83, 126, 154	0
1	JR	113/113 (100%)	0.67	7 (6%)	26	16	54, 96, 147, 177	0
1	JS	113/113 (100%)	0.45	5 (4%)	39	21	51, 87, 163, 193	0
1	JT	113/113 (100%)	0.45	5 (4%)	39	21	49, 83, 126, 154	0
1	JU	113/113 (100%)	0.56	5 (4%)	39	21	54, 96, 147, 177	0
1	JV	113/113 (100%)	0.55	5 (4%)	39	21	51, 87, 163, 193	0
1	JW	113/113 (100%)	0.46	4 (3%)	47	26	49, 83, 126, 154	0
1	JX	113/113 (100%)	0.63	11 (9%)	13	9	54, 96, 147, 177	0
1	JY	113/113 (100%)	0.39	6 (5%)	32	18	51, 87, 163, 193	0
1	JZ	113/113 (100%)	0.35	4 (3%)	47	26	49, 83, 126, 154	0
1	KA	113/113 (100%)	0.65	5 (4%)	39	21	54, 96, 147, 177	0
1	KB	113/113 (100%)	0.40	6 (5%)	32	18	51, 87, 163, 193	0
1	KC	113/113 (100%)	0.43	4 (3%)	47	26	49, 83, 126, 154	0
1	KD	113/113 (100%)	0.50	8 (7%)	22	14	54, 96, 147, 177	0
1	KE	113/113 (100%)	0.46	5 (4%)	39	21	51, 87, 163, 193	0
1	KF	113/113 (100%)	0.55	6 (5%)	32	18	49, 83, 126, 154	0
1	KG	113/113 (100%)	0.51	9 (7%)	18	12	54, 96, 147, 177	0
1	KH	113/113 (100%)	0.57	5 (4%)	39	21	51, 87, 163, 193	0
1	KI	113/113 (100%)	0.59	9 (7%)	18	12	49, 83, 126, 154	0
1	KJ	113/113 (100%)	0.74	12 (10%)	11	8	54, 96, 147, 177	0
1	KK	113/113 (100%)	0.45	3 (2%)	56	33	51, 87, 163, 193	0
1	KL	113/113 (100%)	0.37	4 (3%)	47	26	49, 83, 126, 154	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	KM	113/113 (100%)	0.66	8 (7%) 22 14	54, 96, 147, 177	0
1	KN	113/113 (100%)	0.53	11 (9%) 13 9	51, 87, 163, 193	0
1	KO	113/113 (100%)	0.50	4 (3%) 47 26	49, 83, 126, 154	0
1	KP	113/113 (100%)	0.57	2 (1%) 67 42	54, 96, 147, 177	0
1	KQ	113/113 (100%)	0.33	5 (4%) 39 21	51, 87, 163, 193	0
1	KR	113/113 (100%)	0.33	2 (1%) 67 42	49, 83, 126, 154	0
1	KS	113/113 (100%)	0.51	5 (4%) 39 21	54, 96, 147, 177	0
1	KT	113/113 (100%)	0.64	7 (6%) 26 16	51, 87, 163, 193	0
1	KU	113/113 (100%)	0.65	3 (2%) 56 33	49, 83, 126, 154	0
1	KV	113/113 (100%)	0.77	12 (10%) 11 8	54, 96, 147, 177	0
1	KW	113/113 (100%)	0.66	10 (8%) 15 10	51, 87, 163, 193	0
1	KX	113/113 (100%)	0.59	11 (9%) 13 9	49, 83, 126, 154	0
1	KY	113/113 (100%)	0.55	5 (4%) 39 21	54, 96, 147, 177	0
1	KZ	113/113 (100%)	0.39	6 (5%) 32 18	51, 87, 163, 193	0
1	LA	113/113 (100%)	0.59	6 (5%) 32 18	49, 83, 126, 154	0
1	LB	113/113 (100%)	0.71	12 (10%) 11 8	54, 96, 147, 177	0
1	LC	113/113 (100%)	0.51	2 (1%) 67 42	51, 87, 163, 193	0
1	LD	113/113 (100%)	0.49	4 (3%) 47 26	49, 83, 126, 154	0
1	LE	113/113 (100%)	0.54	7 (6%) 26 16	54, 96, 147, 177	0
1	LF	113/113 (100%)	0.66	5 (4%) 39 21	51, 87, 163, 193	0
1	LG	113/113 (100%)	0.30	2 (1%) 67 42	49, 83, 126, 154	0
1	LH	113/113 (100%)	0.66	12 (10%) 11 8	54, 96, 147, 177	0
1	LI	113/113 (100%)	0.47	8 (7%) 22 14	51, 87, 163, 193	0
1	LJ	113/113 (100%)	0.55	1 (0%) 81 58	49, 83, 126, 154	0
1	LK	113/113 (100%)	0.64	6 (5%) 32 18	54, 96, 147, 177	0
1	LL	113/113 (100%)	0.60	5 (4%) 39 21	51, 87, 163, 193	0
1	LM	113/113 (100%)	0.41	2 (1%) 67 42	49, 83, 126, 154	0
1	LN	113/113 (100%)	0.55	4 (3%) 47 26	54, 96, 147, 177	0
1	LO	113/113 (100%)	0.58	9 (7%) 18 12	51, 87, 163, 193	0
1	LP	113/113 (100%)	0.53	7 (6%) 26 16	49, 83, 126, 154	0
1	LQ	113/113 (100%)	0.81	11 (9%) 13 9	54, 96, 147, 177	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	LR	113/113 (100%)	0.59	3 (2%)	56	33	51, 87, 163, 193	0
1	LS	113/113 (100%)	0.44	3 (2%)	56	33	49, 83, 126, 154	0
1	LT	113/113 (100%)	0.62	9 (7%)	18	12	54, 96, 147, 177	0
1	LU	113/113 (100%)	0.64	13 (11%)	9	6	51, 87, 163, 193	0
1	LV	113/113 (100%)	0.59	10 (8%)	15	10	49, 83, 126, 154	0
1	LW	113/113 (100%)	0.68	9 (7%)	18	12	54, 96, 147, 177	0
1	LX	113/113 (100%)	0.78	9 (7%)	18	12	51, 87, 163, 193	0
1	LY	113/113 (100%)	0.31	3 (2%)	56	33	49, 83, 126, 154	0
1	LZ	113/113 (100%)	0.58	5 (4%)	39	21	54, 96, 147, 177	0
1	MA	113/113 (100%)	0.49	7 (6%)	26	16	51, 87, 163, 193	0
1	MB	113/113 (100%)	0.46	2 (1%)	67	42	49, 83, 126, 154	0
1	MC	113/113 (100%)	0.50	2 (1%)	67	42	54, 96, 147, 177	0
1	MD	113/113 (100%)	0.44	5 (4%)	39	21	51, 87, 163, 193	0
1	ME	113/113 (100%)	0.55	4 (3%)	47	26	49, 83, 126, 154	0
1	MF	113/113 (100%)	0.59	4 (3%)	47	26	54, 96, 147, 177	0
1	MG	113/113 (100%)	0.41	4 (3%)	47	26	51, 87, 163, 193	0
1	MH	113/113 (100%)	0.52	3 (2%)	56	33	49, 83, 126, 154	0
1	MI	113/113 (100%)	0.72	9 (7%)	18	12	54, 96, 147, 177	0
1	MJ	113/113 (100%)	0.44	9 (7%)	18	12	51, 87, 163, 193	0
1	MK	113/113 (100%)	0.52	4 (3%)	47	26	49, 83, 126, 154	0
1	ML	113/113 (100%)	0.53	2 (1%)	67	42	54, 96, 147, 177	0
1	MM	113/113 (100%)	1.20	24 (21%)	2	3	51, 87, 163, 193	0
1	MN	113/113 (100%)	0.82	9 (7%)	18	12	49, 83, 126, 154	0
1	MO	113/113 (100%)	0.66	10 (8%)	15	10	54, 96, 147, 177	0
1	MP	113/113 (100%)	0.49	4 (3%)	47	26	51, 87, 163, 193	0
1	MQ	113/113 (100%)	0.42	3 (2%)	56	33	49, 83, 126, 154	0
1	MR	113/113 (100%)	0.72	7 (6%)	26	16	54, 96, 147, 177	0
1	MS	113/113 (100%)	0.63	4 (3%)	47	26	51, 87, 163, 193	0
1	MT	113/113 (100%)	0.38	5 (4%)	39	21	49, 83, 126, 154	0
1	MU	113/113 (100%)	0.54	4 (3%)	47	26	54, 96, 147, 177	0
1	MV	113/113 (100%)	0.56	6 (5%)	32	18	51, 87, 163, 193	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	MW	113/113 (100%)	0.52	4 (3%)	47	26	49, 83, 126, 154	0
1	MX	113/113 (100%)	0.63	9 (7%)	18	12	54, 96, 147, 177	0
1	MY	113/113 (100%)	0.44	8 (7%)	22	14	51, 87, 163, 193	0
1	MZ	113/113 (100%)	0.64	8 (7%)	22	14	49, 83, 126, 154	0
1	NA	113/113 (100%)	0.58	7 (6%)	26	16	54, 96, 147, 177	0
1	NB	113/113 (100%)	0.48	3 (2%)	56	33	51, 87, 163, 193	0
1	NC	113/113 (100%)	0.44	6 (5%)	32	18	49, 83, 126, 154	0
1	ND	113/113 (100%)	0.55	5 (4%)	39	21	54, 96, 147, 177	0
1	NE	113/113 (100%)	0.60	9 (7%)	18	12	51, 87, 163, 193	0
1	NF	113/113 (100%)	0.57	4 (3%)	47	26	49, 83, 126, 154	0
1	NG	113/113 (100%)	0.40	5 (4%)	39	21	54, 96, 147, 177	0
1	NH	113/113 (100%)	0.30	5 (4%)	39	21	51, 87, 163, 193	0
1	NI	113/113 (100%)	0.49	3 (2%)	56	33	49, 83, 126, 154	0
1	NJ	113/113 (100%)	0.62	8 (7%)	22	14	54, 96, 147, 177	0
1	NK	113/113 (100%)	0.60	7 (6%)	26	16	51, 87, 163, 193	0
1	NL	113/113 (100%)	0.78	6 (5%)	32	18	49, 83, 126, 154	0
1	NM	113/113 (100%)	0.78	13 (11%)	9	6	54, 96, 147, 177	0
1	NN	113/113 (100%)	0.40	4 (3%)	47	26	51, 87, 163, 193	0
1	NO	113/113 (100%)	0.54	4 (3%)	47	26	49, 83, 126, 154	0
1	NP	113/113 (100%)	0.49	5 (4%)	39	21	54, 96, 147, 177	0
1	NQ	113/113 (100%)	0.53	5 (4%)	39	21	51, 87, 163, 193	0
1	NR	113/113 (100%)	0.43	1 (0%)	81	58	49, 83, 126, 154	0
1	NS	113/113 (100%)	0.49	7 (6%)	26	16	54, 96, 147, 177	0
1	NT	113/113 (100%)	0.66	4 (3%)	47	26	51, 87, 163, 193	0
1	NU	113/113 (100%)	0.54	4 (3%)	47	26	49, 83, 126, 154	0
1	NV	113/113 (100%)	0.83	16 (14%)	6	5	54, 96, 147, 177	0
2	RA	20/30 (66%)	0.96	3 (15%)	5	5	137, 172, 234, 256	0
2	RB	20/30 (66%)	0.98	2 (10%)	12	8	137, 172, 234, 256	0
2	RC	20/30 (66%)	0.87	2 (10%)	12	8	137, 172, 234, 256	0
2	RD	20/30 (66%)	0.63	2 (10%)	12	8	137, 172, 234, 256	0
2	RE	20/30 (66%)	0.63	1 (5%)	34	19	137, 172, 234, 256	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	RF	20/30 (66%)	1.15	3 (15%) 5 5	137, 172, 234, 256	0
2	RG	20/30 (66%)	0.61	1 (5%) 34 19	137, 172, 234, 256	0
2	RH	20/30 (66%)	0.52	0 100 100	137, 172, 234, 256	0
2	RI	20/30 (66%)	0.73	2 (10%) 12 8	137, 172, 234, 256	0
2	RJ	20/30 (66%)	0.84	2 (10%) 12 8	137, 172, 234, 256	0
2	RK	20/30 (66%)	0.91	3 (15%) 5 5	137, 172, 234, 256	0
2	RL	20/30 (66%)	0.88	2 (10%) 12 8	137, 172, 234, 256	0
2	RM	20/30 (66%)	1.14	2 (10%) 12 8	137, 172, 234, 256	0
2	RN	20/30 (66%)	0.62	2 (10%) 12 8	137, 172, 234, 256	0
2	RO	20/30 (66%)	1.44	5 (25%) 2 2	137, 172, 234, 256	0
2	RP	20/30 (66%)	0.84	1 (5%) 34 19	137, 172, 234, 256	0
2	RQ	20/30 (66%)	0.87	1 (5%) 34 19	137, 172, 234, 256	0
2	RR	20/30 (66%)	0.90	3 (15%) 5 5	137, 172, 234, 256	0
2	RS	20/30 (66%)	1.03	3 (15%) 5 5	137, 172, 234, 256	0
2	RT	20/30 (66%)	0.92	2 (10%) 12 8	137, 172, 234, 256	0
2	RU	20/30 (66%)	1.40	3 (15%) 5 5	137, 172, 234, 256	0
2	RV	20/30 (66%)	0.78	1 (5%) 34 19	137, 172, 234, 256	0
2	RW	20/30 (66%)	1.08	3 (15%) 5 5	137, 172, 234, 256	0
2	RX	20/30 (66%)	0.76	0 100 100	137, 172, 234, 256	0
2	RY	20/30 (66%)	0.92	2 (10%) 12 8	137, 172, 234, 256	0
2	RZ	20/30 (66%)	0.85	4 (20%) 3 3	137, 172, 234, 256	0
2	SA	20/30 (66%)	0.51	0 100 100	137, 172, 234, 256	0
2	SB	20/30 (66%)	1.03	3 (15%) 5 5	137, 172, 234, 256	0
2	SC	20/30 (66%)	0.63	1 (5%) 34 19	137, 172, 234, 256	0
2	SD	20/30 (66%)	0.93	1 (5%) 34 19	137, 172, 234, 256	0
2	SE	20/30 (66%)	0.88	2 (10%) 12 8	137, 172, 234, 256	0
2	SF	20/30 (66%)	1.08	1 (5%) 34 19	137, 172, 234, 256	0
2	SG	20/30 (66%)	0.59	1 (5%) 34 19	137, 172, 234, 256	0
2	SH	20/30 (66%)	1.24	4 (20%) 3 3	137, 172, 234, 256	0
2	SI	20/30 (66%)	0.80	2 (10%) 12 8	137, 172, 234, 256	0
2	SJ	20/30 (66%)	0.96	2 (10%) 12 8	137, 172, 234, 256	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	SK	20/30 (66%)	0.94	5 (25%) 2 2	137, 172, 234, 256	0
2	SL	20/30 (66%)	1.08	2 (10%) 12 8	137, 172, 234, 256	0
2	SM	20/30 (66%)	0.64	0 100 100	137, 172, 234, 256	0
2	SN	20/30 (66%)	0.86	3 (15%) 5 5	137, 172, 234, 256	0
2	SO	20/30 (66%)	1.15	2 (10%) 12 8	137, 172, 234, 256	0
2	SP	20/30 (66%)	0.76	1 (5%) 34 19	137, 172, 234, 256	0
2	SQ	20/30 (66%)	1.17	4 (20%) 3 3	137, 172, 234, 256	0
2	SR	20/30 (66%)	1.45	4 (20%) 3 3	137, 172, 234, 256	0
2	SS	20/30 (66%)	0.71	2 (10%) 12 8	137, 172, 234, 256	0
2	ST	20/30 (66%)	0.78	2 (10%) 12 8	137, 172, 234, 256	0
2	SU	20/30 (66%)	1.05	2 (10%) 12 8	137, 172, 234, 256	0
2	SV	20/30 (66%)	0.94	2 (10%) 12 8	137, 172, 234, 256	0
2	SW	20/30 (66%)	0.99	2 (10%) 12 8	137, 172, 234, 256	0
2	SX	20/30 (66%)	1.43	3 (15%) 5 5	137, 172, 234, 256	0
2	SY	20/30 (66%)	0.75	1 (5%) 34 19	137, 172, 234, 256	0
2	SZ	20/30 (66%)	0.93	1 (5%) 34 19	137, 172, 234, 256	0
2	TA	20/30 (66%)	0.74	2 (10%) 12 8	137, 172, 234, 256	0
2	TB	20/30 (66%)	1.01	4 (20%) 3 3	137, 172, 234, 256	0
2	TC	20/30 (66%)	0.83	0 100 100	137, 172, 234, 256	0
2	TD	20/30 (66%)	0.60	0 100 100	137, 172, 234, 256	0
2	TE	20/30 (66%)	0.75	2 (10%) 12 8	137, 172, 234, 256	0
2	TF	20/30 (66%)	0.66	2 (10%) 12 8	137, 172, 234, 256	0
2	TG	20/30 (66%)	0.77	2 (10%) 12 8	137, 172, 234, 256	0
2	TH	20/30 (66%)	0.96	3 (15%) 5 5	137, 172, 234, 256	0
All	All	41880/42480 (98%)	0.57	2425 (5%) 29 17	49, 89, 154, 256	0

All (2425) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BS	65	GLY	9.4
1	IE	65	GLY	7.8
1	GJ	64	ALA	7.2
1	JX	65	GLY	6.6
1	GG	64	ALA	6.1

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Mol	Chain	Res	Type	RSRZ
1	FX	64	ALA	5.8
1	DX	40	GLY	5.7
1	GR	40	GLY	5.7
1	NK	64	ALA	5.5
1	MF	40	GLY	5.5
1	JU	40	GLY	5.4
1	HJ	40	GLY	5.4
1	DP	64	ALA	5.4
1	HY	64	ALA	5.3
1	DK	113	PHE	5.3
1	LW	40	GLY	5.2
1	KY	40	GLY	5.1
1	FW	40	GLY	4.9
1	BM	40	GLY	4.9
1	HM	64	ALA	4.9
1	HI	45	LYS	4.9
1	MJ	41	LYS	4.8
1	DK	112	GLY	4.8
1	LH	40	GLY	4.8
1	IC	40	GLY	4.7
1	FA	38	SER	4.7
1	KG	40	GLY	4.7
1	FQ	65	GLY	4.7
1	GD	64	ALA	4.7
1	LA	1	SER	4.6
1	JI	51	ALA	4.6
1	AR	40	GLY	4.6
1	EQ	40	GLY	4.6
1	IO	63	VAL	4.6
1	NE	72	ALA	4.6
1	LP	110	GLN	4.6
1	IX	64	ALA	4.5
1	JX	44	ALA	4.5
1	BV	64	ALA	4.5
1	ME	9	GLY	4.5
1	BQ	44	ALA	4.5
1	HC	1	SER	4.4
1	JL	32	ARG	4.5
1	AP	41	LYS	4.4
1	DG	40	GLY	4.4
1	IC	44	ALA	4.4
1	HA	36	LYS	4.4

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Mol	Chain	Res	Type	RSRZ
1	NA	40	GLY	4.4
1	MZ	41	LYS	4.3
1	AV	64	ALA	4.3
1	GU	1	SER	4.3
1	CC	38	SER	4.3
1	GP	1	SER	4.3
1	MT	52	ALA	4.3
1	CL	64	ALA	4.2
1	KZ	38	SER	4.2
1	DU	26	ARG	4.2
1	JF	40	GLY	4.2
1	DL	40	GLY	4.2
1	EG	65	GLY	4.2
1	FQ	64	ALA	4.2
1	KB	40	GLY	4.1
1	FF	64	ALA	4.1
1	AJ	66	LEU	4.1
1	GY	64	ALA	4.1
1	CE	65	GLY	4.1
1	JC	26	ARG	4.1
1	DO	20	TYR	4.1
2	RZ	29	U	4.1
1	JK	40	GLY	4.1
1	DD	64	ALA	4.1
1	CX	19	GLY	4.1
1	LQ	41	LYS	4.0
1	GA	40	GLY	4.0
1	HH	41	LYS	4.0
1	DJ	40	GLY	4.0
1	DX	1	SER	4.0
1	FW	45	LYS	4.0
1	BQ	42	PHE	4.0
2	SX	30	A	4.0
1	BQ	38	SER	4.0
1	ND	82	ARG	4.0
1	AP	63	VAL	3.9
1	BE	41	LYS	3.9
1	MQ	1	SER	3.9
1	IU	40	GLY	3.9
1	AI	72	ALA	3.9
1	FL	72	ALA	3.9
1	LI	38	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	IU	41	LYS	3.9
1	NS	111	GLY	3.9
1	CV	52	ALA	3.9
1	CV	40	GLY	3.9
1	NJ	65	GLY	3.9
1	DA	38	SER	3.9
1	DJ	38	SER	3.9
1	LL	45	LYS	3.9
2	SQ	30	A	3.9
1	HE	38	SER	3.9
1	LL	38	SER	3.9
1	EV	65	GLY	3.9
1	NI	41	LYS	3.9
1	CX	38	SER	3.8
1	MY	41	LYS	3.8
1	FE	19	GLY	3.8
1	FQ	26	ARG	3.8
1	EL	52	ALA	3.8
1	ES	18	PRO	3.8
1	MP	63	VAL	3.8
1	BT	41	LYS	3.8
1	MG	41	LYS	3.8
1	MD	38	SER	3.8
1	AY	64	ALA	3.8
1	EW	45	LYS	3.8
2	SF	30	A	3.8
1	EE	38	SER	3.8
1	EK	48	ARG	3.8
1	AI	40	GLY	3.8
1	CU	64	ALA	3.8
1	ME	112	GLY	3.8
1	HM	18	PRO	3.8
1	EH	66	LEU	3.7
1	GM	5	SER	3.7
1	EC	1	SER	3.7
1	LQ	38	SER	3.7
1	KE	64	ALA	3.7
1	EI	38	SER	3.7
1	GQ	38	SER	3.7
1	CC	64	ALA	3.7
1	FU	64	ALA	3.7
1	LB	41	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
1	KS	50	THR	3.7
1	GR	38	SER	3.7
1	LH	38	SER	3.7
1	HJ	41	LYS	3.7
1	EQ	64	ALA	3.7
1	JH	44	ALA	3.7
1	EP	40	GLY	3.7
1	ID	65	GLY	3.7
2	RL	30	A	3.7
1	BQ	10	SER	3.7
1	FK	1	SER	3.7
1	JL	1	SER	3.7
1	CV	72	ALA	3.7
1	BL	40	GLY	3.7
1	GD	63	VAL	3.7
1	KJ	48	ARG	3.7
1	BN	1	SER	3.7
1	MI	18	PRO	3.7
1	MJ	64	ALA	3.6
1	HE	19	GLY	3.6
1	IN	40	GLY	3.6
1	DW	1	SER	3.6
1	BG	20	TYR	3.6
1	EK	64	ALA	3.6
1	LP	86	ALA	3.6
1	GC	65	GLY	3.6
1	EQ	63	VAL	3.6
1	ID	113	PHE	3.6
1	JH	45	LYS	3.6
1	LV	45	LYS	3.6
1	CR	70	SER	3.6
1	HS	72	ALA	3.6
1	II	64	ALA	3.6
1	AP	45	LYS	3.6
1	GS	45	LYS	3.6
1	KC	41	LYS	3.6
1	CZ	38	SER	3.6
1	CS	73	GLU	3.6
1	IF	64	ALA	3.6
1	FQ	27	GLY	3.6
1	GR	41	LYS	3.6
1	LP	16	THR	3.6

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Mol	Chain	Res	Type	RSRZ
1	DD	63	VAL	3.6
1	KO	1	SER	3.6
1	BE	64	ALA	3.6
1	CA	51	ALA	3.6
1	HM	44	ALA	3.6
1	KN	82	ARG	3.6
1	BW	42	PHE	3.6
1	FW	42	PHE	3.6
1	MD	63	VAL	3.6
1	MR	38	SER	3.6
2	RU	30	A	3.6
1	DG	41	LYS	3.6
1	GY	45	LYS	3.6
1	FC	64	ALA	3.6
1	JA	51	ALA	3.6
1	NT	63	VAL	3.6
1	LR	38	SER	3.6
1	LY	1	SER	3.6
1	CF	64	ALA	3.5
1	CU	66	LEU	3.5
1	JY	64	ALA	3.5
1	KD	26	ARG	3.5
1	CZ	65	GLY	3.5
1	MY	63	VAL	3.5
1	GJ	38	SER	3.5
2	SD	10	U	3.5
2	SN	30	A	3.5
1	IR	41	LYS	3.5
1	GK	72	ALA	3.5
1	HY	113	PHE	3.5
1	FI	63	VAL	3.5
1	FX	63	VAL	3.5
1	II	63	VAL	3.5
1	IZ	40	GLY	3.5
1	HX	1	SER	3.5
1	KK	1	SER	3.5
1	MM	38	SER	3.5
1	NG	67	PRO	3.5
1	AJ	64	ALA	3.5
1	GN	81	GLY	3.5
1	JA	76	ILE	3.5
1	KT	38	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	JO	26	ARG	3.5
1	BL	45	LYS	3.5
1	DJ	83	GLY	3.5
1	MM	40	GLY	3.5
1	MO	40	GLY	3.5
1	HR	10	SER	3.5
1	LO	38	SER	3.5
1	LT	38	SER	3.5
1	NR	1	SER	3.5
2	RR	10	U	3.5
1	BI	113	PHE	3.5
1	IC	63	VAL	3.5
1	NO	19	GLY	3.5
1	BQ	48	ARG	3.5
1	MX	32	ARG	3.5
1	AS	38	SER	3.4
1	JD	70	SER	3.4
1	LU	65	GLY	3.4
1	IL	2	THR	3.4
1	HI	110	GLN	3.4
1	HJ	42	PHE	3.4
1	EB	72	ALA	3.4
1	KW	64	ALA	3.4
1	CR	19	GLY	3.4
1	LP	112	GLY	3.4
2	RY	30	A	3.4
1	EU	56	LEU	3.4
1	FL	66	LEU	3.4
1	LI	64	ALA	3.4
1	NV	70	SER	3.4
1	HG	41	LYS	3.4
1	IU	67	PRO	3.4
1	FR	64	ALA	3.4
1	LC	63	VAL	3.4
1	HD	1	SER	3.4
1	MM	10	SER	3.4
1	KX	19	GLY	3.4
1	NE	112	GLY	3.4
1	DO	113	PHE	3.4
1	MI	26	ARG	3.4
2	RN	30	A	3.4
1	KD	18	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	MR	1	SER	3.4
1	AJ	19	GLY	3.4
1	KA	90	ASP	3.4
1	EQ	67	PRO	3.4
1	IN	18	PRO	3.4
1	EB	64	ALA	3.4
1	HI	72	ALA	3.4
2	SP	10	U	3.4
1	DN	38	SER	3.4
1	GA	38	SER	3.4
1	GD	47	GLY	3.3
1	JN	19	GLY	3.3
1	MQ	40	GLY	3.3
1	NV	36	LYS	3.4
1	EP	44	ALA	3.3
1	JG	64	ALA	3.3
1	NQ	72	ALA	3.3
1	DS	63	VAL	3.3
1	HJ	43	ASN	3.3
1	IX	63	VAL	3.3
1	NN	63	VAL	3.3
1	ED	41	LYS	3.3
1	HW	41	LYS	3.3
1	NK	42	PHE	3.3
1	DZ	9	GLY	3.3
1	FT	27	GLY	3.3
1	CX	46	THR	3.3
1	GK	86	ALA	3.3
1	IO	64	ALA	3.3
1	KT	67	PRO	3.3
1	FU	41	LYS	3.3
1	AV	26	ARG	3.3
1	CU	38	SER	3.3
1	GE	1	SER	3.3
1	JU	1	SER	3.3
1	BG	40	GLY	3.3
1	AH	2	THR	3.3
1	ML	16	THR	3.3
1	CR	72	ALA	3.3
1	HK	67	PRO	3.3
1	EZ	26	ARG	3.3
1	FT	26	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
1	IC	38	SER	3.3
1	LP	38	SER	3.3
1	CP	19	GLY	3.3
1	MI	19	GLY	3.3
1	IJ	1	SER	3.3
1	IV	1	SER	3.3
1	JZ	1	SER	3.3
1	KT	40	GLY	3.3
1	IW	79	THR	3.3
1	BR	45	LYS	3.3
1	FF	41	LYS	3.3
1	LM	45	LYS	3.3
1	KH	82	ARG	3.3
1	NQ	66	LEU	3.3
1	KH	112	GLY	3.3
1	JF	20	TYR	3.3
1	MP	45	LYS	3.3
1	NT	42	PHE	3.2
1	EE	48	ARG	3.2
1	EQ	72	ALA	3.2
1	GO	64	ALA	3.2
1	LU	82	ARG	3.2
1	GY	63	VAL	3.2
1	HJ	38	SER	3.2
1	IE	70	SER	3.2
1	MX	1	SER	3.2
2	RT	10	U	3.2
1	DQ	41	LYS	3.2
1	GX	41	LYS	3.2
2	RM	30	A	3.2
1	LH	42	PHE	3.2
1	LH	64	ALA	3.2
1	LL	41	LYS	3.2
1	FG	40	GLY	3.2
1	JD	40	GLY	3.2
1	NK	47	GLY	3.2
1	IV	73	GLU	3.2
2	SN	10	U	3.2
1	GD	74	VAL	3.2
1	AI	67	PRO	3.2
1	CK	41	LYS	3.2
2	RB	30	A	3.2

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Mol	Chain	Res	Type	RSRZ
2	SI	30	A	3.2
2	ST	30	A	3.2
2	TF	30	A	3.2
1	JA	19	GLY	3.2
1	JD	66	LEU	3.2
1	NL	9	GLY	3.2
1	IN	50	THR	3.2
1	EE	42	PHE	3.2
1	BE	63	VAL	3.2
1	EE	64	ALA	3.2
1	NJ	44	ALA	3.2
1	NK	44	ALA	3.2
1	CL	38	SER	3.2
1	IG	38	SER	3.2
1	ET	67	PRO	3.2
1	KN	45	LYS	3.2
1	MO	36	LYS	3.2
2	TB	10	U	3.2
1	GJ	112	GLY	3.2
1	NJ	43	ASN	3.2
1	JF	32	ARG	3.2
1	KX	20	TYR	3.2
1	NF	34	GLN	3.2
1	EJ	54	SER	3.2
1	JY	66	LEU	3.2
1	CX	37	ILE	3.2
1	KO	40	GLY	3.2
1	MM	42	PHE	3.2
1	IH	33	ASN	3.2
1	DJ	45	LYS	3.2
1	EK	41	LYS	3.2
1	CG	1	SER	3.2
1	DE	38	SER	3.2
1	IA	1	SER	3.2
1	KJ	38	SER	3.2
1	LB	72	ALA	3.2
2	RS	10	U	3.2
2	SB	10	U	3.2
1	DC	40	GLY	3.1
1	KC	40	GLY	3.1
2	RA	30	A	3.1
2	RI	30	A	3.1

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Mol	Chain	Res	Type	RSRZ
2	SL	30	A	3.1
1	CE	36	LYS	3.1
1	CM	45	LYS	3.1
1	IC	45	LYS	3.1
1	NM	41	LYS	3.1
1	EI	52	ALA	3.1
1	HN	64	ALA	3.1
1	LT	86	ALA	3.1
1	MN	5	SER	3.1
1	AS	42	PHE	3.1
1	GO	113	PHE	3.1
1	AQ	26	ARG	3.1
1	BI	83	GLY	3.1
1	JE	40	GLY	3.1
1	NM	32	ARG	3.1
1	GD	41	LYS	3.1
1	JF	36	LYS	3.1
1	JB	72	ALA	3.1
1	LM	1	SER	3.1
2	TB	30	A	3.1
1	AP	67	PRO	3.1
1	HV	26	ARG	3.1
1	DJ	47	GLY	3.1
1	EB	40	GLY	3.1
1	EZ	65	GLY	3.1
1	JQ	41	LYS	3.1
1	GM	64	ALA	3.1
1	KI	72	ALA	3.1
1	KL	1	SER	3.1
2	SH	6	U	3.1
1	IH	113	PHE	3.1
1	LV	18	PRO	3.1
1	AC	45	LYS	3.1
1	AU	26	ARG	3.1
1	AA	40	GLY	3.1
1	CU	27	GLY	3.1
1	GF	40	GLY	3.1
1	NA	39	GLY	3.1
1	HJ	50	THR	3.1
2	RF	30	A	3.1
1	NK	63	VAL	3.1
1	AI	113	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
1	LH	113	PHE	3.1
1	LH	41	LYS	3.1
1	NA	27	GLY	3.1
1	EU	10	SER	3.1
1	NB	38	SER	3.1
1	AL	73	GLU	3.1
1	EG	42	PHE	3.1
1	KB	42	PHE	3.1
1	LB	42	PHE	3.1
1	HJ	36	LYS	3.1
1	AR	48	ARG	3.1
1	AV	67	PRO	3.1
1	BU	32	ARG	3.1
1	GU	18	PRO	3.1
1	LQ	48	ARG	3.1
1	IB	40	GLY	3.1
1	CZ	24	SER	3.0
1	IR	63	VAL	3.0
1	JG	38	SER	3.0
1	JV	38	SER	3.0
1	KX	1	SER	3.0
1	AX	64	ALA	3.0
1	DV	64	ALA	3.0
1	NJ	64	ALA	3.0
1	JK	43	ASN	3.0
1	CO	41	LYS	3.0
1	NV	82	ARG	3.0
2	SV	10	U	3.0
1	DF	19	GLY	3.0
1	EY	40	GLY	3.0
1	IQ	27	GLY	3.0
1	NV	40	GLY	3.0
1	FR	38	SER	3.0
1	GJ	70	SER	3.0
1	JS	1	SER	3.0
1	LF	1	SER	3.0
1	BS	64	ALA	3.0
1	CJ	41	LYS	3.0
1	EX	45	LYS	3.0
1	FP	45	LYS	3.0
1	GK	42	PHE	3.0
1	LS	113	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	HR	11	ASN	3.0
1	AK	40	GLY	3.0
1	GT	40	GLY	3.0
1	LI	19	GLY	3.0
1	MM	39	GLY	3.0
1	MS	9	GLY	3.0
1	FS	113	PHE	3.0
1	ET	64	ALA	3.0
1	KN	64	ALA	3.0
1	LL	64	ALA	3.0
1	NN	44	ALA	3.0
1	HA	20	TYR	3.0
1	DM	9	GLY	3.0
1	BP	41	LYS	3.0
1	BT	45	LYS	3.0
1	EN	41	LYS	3.0
1	IW	1	SER	3.0
1	KY	113	PHE	3.0
1	LI	1	SER	3.0
1	NE	38	SER	3.0
1	JJ	64	ALA	3.0
1	CN	26	ARG	3.0
2	RM	10	U	3.0
2	SH	10	U	3.0
1	KW	41	LYS	3.0
1	LO	41	LYS	3.0
1	LU	45	LYS	3.0
1	BU	83	GLY	3.0
1	MO	27	GLY	3.0
1	NV	19	GLY	3.0
1	IJ	110	GLN	3.0
1	BS	1	SER	3.0
1	GL	4	SER	3.0
1	KW	63	VAL	3.0
1	LD	38	SER	3.0
1	BA	26	ARG	3.0
1	KL	72	ALA	3.0
1	MV	64	ALA	3.0
1	NJ	26	ARG	3.0
2	SB	30	A	3.0
2	SV	30	A	3.0
1	AT	73	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	DY	67	PRO	3.0
1	GE	18	PRO	3.0
1	BF	41	LYS	3.0
1	EJ	27	GLY	3.0
1	IC	111	GLY	3.0
1	MM	19	GLY	3.0
1	DU	79	THR	3.0
1	EG	4	SER	3.0
1	EK	38	SER	3.0
1	KN	63	VAL	3.0
1	FE	32	ARG	3.0
1	LV	26	ARG	3.0
1	DM	64	ALA	3.0
1	FE	44	ALA	3.0
1	HB	64	ALA	3.0
1	IE	64	ALA	3.0
1	LE	45	LYS	2.9
1	MM	11	ASN	2.9
1	GK	73	GLU	2.9
1	MK	73	GLU	2.9
1	JI	19	GLY	2.9
1	LN	40	GLY	2.9
1	EM	82	ARG	2.9
1	FP	38	SER	2.9
1	MI	1	SER	2.9
1	KK	64	ALA	2.9
1	KS	41	LYS	2.9
1	MV	41	LYS	2.9
1	NN	45	LYS	2.9
1	CK	67	PRO	2.9
1	DF	113	PHE	2.9
1	MZ	113	PHE	2.9
2	SQ	10	U	2.9
1	EC	9	GLY	2.9
1	BR	38	SER	2.9
1	CL	26	ARG	2.9
1	GK	1	SER	2.9
1	KV	1	SER	2.9
1	LZ	26	ARG	2.9
1	NG	26	ARG	2.9
1	CE	51	ALA	2.9
1	DC	64	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	EL	72	ALA	2.9
1	EZ	44	ALA	2.9
1	FC	44	ALA	2.9
1	HK	64	ALA	2.9
1	FZ	41	LYS	2.9
1	MM	90	ASP	2.9
1	CP	20	TYR	2.9
1	AA	67	PRO	2.9
1	BM	42	PHE	2.9
1	DC	42	PHE	2.9
1	ER	43	ASN	2.9
1	AU	65	GLY	2.9
1	BY	26	ARG	2.9
1	DV	1	SER	2.9
1	FE	26	ARG	2.9
1	HB	38	SER	2.9
1	HH	48	ARG	2.9
1	IR	38	SER	2.9
1	JV	63	VAL	2.9
1	KJ	46	THR	2.9
1	EU	72	ALA	2.9
1	LC	64	ALA	2.9
1	LI	51	ALA	2.9
1	GN	41	LYS	2.9
1	LW	36	LYS	2.9
1	CY	77	ILE	2.9
1	FA	42	PHE	2.9
1	JX	42	PHE	2.9
1	FH	18	PRO	2.9
1	LY	48	ARG	2.9
1	MI	32	ARG	2.9
1	AH	1	SER	2.9
1	DV	63	VAL	2.9
1	FZ	27	GLY	2.9
1	GY	1	SER	2.9
1	HH	1	SER	2.9
1	JA	112	GLY	2.9
1	JB	38	SER	2.9
1	AK	41	LYS	2.9
1	CD	41	LYS	2.9
1	NC	45	LYS	2.9
1	AO	44	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	KN	44	ALA	2.9
2	RE	30	A	2.9
1	EG	67	PRO	2.9
1	EY	18	PRO	2.9
1	IB	32	ARG	2.9
1	JO	45	LYS	2.9
1	KD	38	SER	2.9
2	SR	10	U	2.9
1	BL	41	LYS	2.9
1	BT	63	VAL	2.9
1	CE	19	GLY	2.9
1	KW	45	LYS	2.9
1	LU	63	VAL	2.9
1	JR	16	THR	2.9
1	DJ	44	ALA	2.9
1	EZ	64	ALA	2.9
1	GX	44	ALA	2.9
1	IT	108	ILE	2.9
1	JS	64	ALA	2.9
1	MZ	72	ALA	2.9
1	GP	66	LEU	2.9
1	AC	67	PRO	2.9
1	AQ	32	ARG	2.9
1	MN	26	ARG	2.9
1	CU	63	VAL	2.8
1	DJ	63	VAL	2.8
1	FU	1	SER	2.8
1	GD	1	SER	2.8
1	IE	38	SER	2.8
1	KU	1	SER	2.8
1	KW	1	SER	2.8
1	MT	38	SER	2.8
2	RT	30	A	2.8
1	CC	72	ALA	2.8
1	CP	86	ALA	2.8
1	DV	2	THR	2.8
1	FJ	72	ALA	2.8
1	HW	64	ALA	2.8
1	KA	50	THR	2.8
1	JU	113	PHE	2.8
2	RK	10	U	2.8
2	TE	10	U	2.8

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Mol	Chain	Res	Type	RSRZ
1	CW	82	ARG	2.8
1	NV	26	ARG	2.8
1	BW	41	LYS	2.8
1	FE	41	LYS	2.8
1	GO	67	PRO	2.8
1	MV	45	LYS	2.8
1	GG	1	SER	2.8
1	HI	1	SER	2.8
1	JJ	63	VAL	2.8
1	BY	27	GLY	2.8
1	DA	65	GLY	2.8
1	LQ	66	LEU	2.8
1	LT	95	ASP	2.8
1	GV	86	ALA	2.8
1	HH	2	THR	2.8
1	HH	50	THR	2.8
1	LX	44	ALA	2.8
1	NH	79	THR	2.8
2	RQ	30	A	2.8
2	TB	7	A	2.8
2	TH	30	A	2.8
1	CE	41	LYS	2.8
1	CI	41	LYS	2.8
1	HC	41	LYS	2.8
1	JV	41	LYS	2.8
1	MM	32	ARG	2.8
1	AR	73	GLU	2.8
1	GM	63	VAL	2.8
1	LE	73	GLU	2.8
1	BP	65	GLY	2.8
1	ES	39	GLY	2.8
1	EU	9	GLY	2.8
1	EW	40	GLY	2.8
1	FP	40	GLY	2.8
1	JQ	40	GLY	2.8
2	SL	23	U	2.8
2	TG	10	U	2.8
1	AD	64	ALA	2.8
1	BB	51	ALA	2.8
1	BD	44	ALA	2.8
1	CZ	86	ALA	2.8
1	DS	64	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	GN	52	ALA	2.8
1	NM	64	ALA	2.8
1	NM	72	ALA	2.8
1	BB	42	PHE	2.8
1	CZ	82	ARG	2.8
1	BJ	1	SER	2.8
1	ET	63	VAL	2.8
1	FF	70	SER	2.8
1	MD	67	PRO	2.8
1	BA	40	GLY	2.8
1	CN	19	GLY	2.8
1	DJ	39	GLY	2.8
1	HX	73	GLU	2.8
1	JW	112	GLY	2.8
1	LS	83	GLY	2.8
1	MX	73	GLU	2.8
1	GP	64	ALA	2.8
1	CY	113	PHE	2.8
1	DD	41	LYS	2.8
1	MT	45	LYS	2.8
1	BA	32	ARG	2.8
1	NU	26	ARG	2.8
1	LF	66	LEU	2.8
1	DD	38	SER	2.8
1	DW	38	SER	2.8
1	HJ	49	VAL	2.8
1	HZ	63	VAL	2.8
1	MU	1	SER	2.8
1	DJ	88	ASN	2.8
1	DU	27	GLY	2.8
1	DU	112	GLY	2.8
1	HC	83	GLY	2.8
1	IZ	19	GLY	2.8
1	LQ	19	GLY	2.8
1	CF	71	ALA	2.8
1	DJ	64	ALA	2.8
1	DS	113	PHE	2.8
1	IM	72	ALA	2.8
1	JX	64	ALA	2.8
1	AZ	26	ARG	2.8
1	BE	26	ARG	2.8
1	EY	26	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	FS	101	ASP	2.8
1	HG	48	ARG	2.8
1	MM	101	ASP	2.8
1	CN	18	PRO	2.8
1	CP	1	SER	2.8
1	EB	63	VAL	2.8
1	GP	38	SER	2.8
1	MY	5	SER	2.8
2	SU	24	A	2.8
1	IN	67	PRO	2.8
1	JG	63	VAL	2.8
1	BV	20	TYR	2.8
1	AP	42	PHE	2.8
1	BC	19	GLY	2.8
1	CV	110	GLN	2.8
1	DZ	113	PHE	2.8
1	FL	73	GLU	2.8
1	GN	113	PHE	2.8
1	HI	3	PHE	2.8
1	CP	52	ALA	2.8
1	DJ	2	THR	2.8
1	EQ	41	LYS	2.8
1	IU	64	ALA	2.8
1	JK	41	LYS	2.8
2	RF	10	U	2.8
2	RO	27	U	2.8
1	GN	48	ARG	2.7
1	IN	48	ARG	2.7
1	JF	104	ARG	2.7
1	MM	82	ARG	2.7
1	MO	26	ARG	2.7
1	MR	48	ARG	2.7
1	FK	90	ASP	2.7
1	GY	90	ASP	2.7
1	BC	38	SER	2.7
1	CF	63	VAL	2.7
1	CN	91	VAL	2.7
1	EL	38	SER	2.7
1	FR	63	VAL	2.7
1	CG	42	PHE	2.7
1	FE	20	TYR	2.7
1	IZ	36	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	JK	45	LYS	2.7
1	LP	113	PHE	2.7
1	LW	41	LYS	2.7
1	NE	41	LYS	2.7
1	BU	81	GLY	2.7
1	DR	40	GLY	2.7
1	HI	19	GLY	2.7
1	KQ	9	GLY	2.7
1	HG	64	ALA	2.7
1	HX	51	ALA	2.7
1	LE	44	ALA	2.7
1	FX	66	LEU	2.7
1	HA	32	ARG	2.7
1	HE	66	LEU	2.7
1	LN	26	ARG	2.7
2	SC	30	A	2.7
1	KE	90	ASP	2.7
1	ND	95	ASP	2.7
1	EM	1	SER	2.7
1	FW	1	SER	2.7
1	GQ	1	SER	2.7
1	LK	38	SER	2.7
2	RA	21	U	2.7
2	RC	10	U	2.7
1	HK	63	VAL	2.7
1	BQ	41	LYS	2.7
1	DM	41	LYS	2.7
1	FF	42	PHE	2.7
1	AH	83	GLY	2.7
1	CQ	40	GLY	2.7
1	GW	34	GLN	2.7
1	EO	52	ALA	2.7
1	EU	65	GLY	2.7
1	AP	48	ARG	2.7
1	GD	66	LEU	2.7
1	HW	44	ALA	2.7
1	IA	71	ALA	2.7
1	KX	72	ALA	2.7
1	LB	73	GLU	2.7
1	GI	26	ARG	2.7
1	KG	82	ARG	2.7
1	BD	38	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	EM	41	LYS	2.7
1	GS	38	SER	2.7
1	HH	63	VAL	2.7
1	HV	41	LYS	2.7
1	MY	38	SER	2.7
1	NE	70	SER	2.7
1	AH	42	PHE	2.7
1	FU	63	VAL	2.7
2	SS	30	A	2.7
1	BX	81	GLY	2.7
1	BS	82	ARG	2.7
1	CD	48	ARG	2.7
1	ED	26	ARG	2.7
1	FA	86	ALA	2.7
1	KV	112	GLY	2.7
1	GR	82	ARG	2.7
1	CW	98	THR	2.7
1	HO	12	THR	2.7
1	DO	41	LYS	2.7
1	JF	45	LYS	2.7
1	EN	38	SER	2.7
1	GK	10	SER	2.7
1	IJ	38	SER	2.7
1	IN	1	SER	2.7
1	KX	113	PHE	2.7
1	LE	113	PHE	2.7
1	GZ	101	ASP	2.7
1	BV	67	PRO	2.7
1	CX	67	PRO	2.7
1	EE	67	PRO	2.7
1	AC	26	ARG	2.7
1	BA	51	ALA	2.7
1	BJ	64	ALA	2.7
1	CY	52	ALA	2.7
1	GC	27	GLY	2.7
1	IB	26	ARG	2.7
1	JA	64	ALA	2.7
1	HE	16	THR	2.7
1	BJ	45	LYS	2.7
1	AC	38	SER	2.7
1	AQ	1	SER	2.7
1	BO	38	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	GM	4	SER	2.7
1	GO	38	SER	2.7
1	HA	113	PHE	2.7
1	HO	1	SER	2.7
1	JY	38	SER	2.7
1	GS	63	VAL	2.7
1	HM	91	VAL	2.7
1	MJ	63	VAL	2.7
1	MV	63	VAL	2.7
1	BF	18	PRO	2.7
1	GJ	67	PRO	2.7
2	SZ	10	U	2.7
1	HI	32	ARG	2.7
1	KF	106	ASP	2.7
1	DF	27	GLY	2.7
1	GE	52	ALA	2.7
1	KJ	44	ALA	2.7
1	MN	19	GLY	2.7
1	EC	2	THR	2.7
1	KN	46	THR	2.7
1	DJ	11	ASN	2.7
1	IB	45	LYS	2.7
1	IL	42	PHE	2.7
1	GT	38	SER	2.7
1	HQ	38	SER	2.7
1	IN	38	SER	2.7
1	KN	38	SER	2.7
1	KX	38	SER	2.7
1	GN	82	ARG	2.6
1	HG	26	ARG	2.6
1	IC	26	ARG	2.6
1	IK	26	ARG	2.6
1	JO	18	PRO	2.6
1	HC	72	ALA	2.6
1	IF	65	GLY	2.6
1	MW	45	LYS	2.6
1	JT	73	GLU	2.6
2	RY	10	U	2.6
2	SJ	10	U	2.6
2	SO	25	U	2.6
1	AS	109	LEU	2.6
1	KX	42	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	AD	1	SER	2.6
1	AT	1	SER	2.6
1	CQ	38	SER	2.6
1	DU	1	SER	2.6
1	EY	10	SER	2.6
1	FA	1	SER	2.6
1	GT	1	SER	2.6
1	GW	1	SER	2.6
1	HZ	1	SER	2.6
1	JW	1	SER	2.6
1	JY	1	SER	2.6
1	GE	32	ARG	2.6
1	IT	26	ARG	2.6
1	JU	82	ARG	2.6
1	KV	32	ARG	2.6
1	AM	64	ALA	2.6
1	BD	41	LYS	2.6
1	CH	40	GLY	2.6
1	CH	45	LYS	2.6
1	DL	36	LYS	2.6
1	FC	65	GLY	2.6
1	IN	19	GLY	2.6
1	JJ	41	LYS	2.6
1	JT	41	LYS	2.6
1	KM	39	GLY	2.6
1	LF	41	LYS	2.6
1	LV	19	GLY	2.6
1	NS	112	GLY	2.6
1	HR	50	THR	2.6
1	KC	16	THR	2.6
1	MM	2	THR	2.6
1	CT	1	SER	2.6
1	KF	38	SER	2.6
1	LZ	70	SER	2.6
1	NA	38	SER	2.6
1	BA	82	ARG	2.6
1	CK	26	ARG	2.6
1	NC	48	ARG	2.6
2	SH	7	A	2.6
1	CF	67	PRO	2.6
1	GA	41	LYS	2.6
1	GM	41	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	JA	45	LYS	2.6
1	JF	41	LYS	2.6
1	BD	111	GLY	2.6
1	GA	64	ALA	2.6
1	HO	40	GLY	2.6
1	KF	86	ALA	2.6
1	KJ	65	GLY	2.6
1	KT	64	ALA	2.6
1	MI	27	GLY	2.6
1	ES	101	ASP	2.6
1	LK	113	PHE	2.6
1	DI	10	SER	2.6
1	HM	1	SER	2.6
1	HP	4	SER	2.6
1	LQ	43	ASN	2.6
1	NJ	4	SER	2.6
1	DX	63	VAL	2.6
1	EK	63	VAL	2.6
1	CX	48	ARG	2.6
1	DB	82	ARG	2.6
1	FN	32	ARG	2.6
1	GI	32	ARG	2.6
1	KY	82	ARG	2.6
1	LX	32	ARG	2.6
1	BG	36	LYS	2.6
1	MD	41	LYS	2.6
1	JX	67	PRO	2.6
1	CI	64	ALA	2.6
1	IF	71	ALA	2.6
1	MF	64	ALA	2.6
1	NP	86	ALA	2.6
1	DS	112	GLY	2.6
1	HE	83	GLY	2.6
1	MO	65	GLY	2.6
1	CF	113	PHE	2.6
1	DK	25	THR	2.6
1	FL	113	PHE	2.6
1	MC	16	THR	2.6
1	AL	1	SER	2.6
1	EO	38	SER	2.6
1	FB	70	SER	2.6
1	FL	38	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	GM	38	SER	2.6
1	GS	1	SER	2.6
1	HV	38	SER	2.6
1	JQ	1	SER	2.6
1	NL	1	SER	2.6
1	NL	5	SER	2.6
2	RP	10	U	2.6
1	AL	26	ARG	2.6
1	GJ	63	VAL	2.6
1	JR	82	ARG	2.6
1	KQ	63	VAL	2.6
1	AE	41	LYS	2.6
1	AG	45	LYS	2.6
1	AR	41	LYS	2.6
1	HZ	41	LYS	2.6
1	KD	45	LYS	2.6
1	KG	41	LYS	2.6
1	AJ	67	PRO	2.6
1	CF	80	LEU	2.6
1	CM	18	PRO	2.6
1	DC	67	PRO	2.6
1	HB	18	PRO	2.6
1	IV	72	ALA	2.6
1	JM	64	ALA	2.6
1	MY	64	ALA	2.6
1	NB	66	LEU	2.6
1	BO	81	GLY	2.6
1	CC	65	GLY	2.6
1	MO	20	TYR	2.6
1	AF	38	SER	2.6
1	FJ	38	SER	2.6
1	GK	54	SER	2.6
1	GN	38	SER	2.6
1	JP	38	SER	2.6
1	KL	38	SER	2.6
1	KM	1	SER	2.6
1	HU	26	ARG	2.6
1	IN	90	ASP	2.6
1	NL	10	SER	2.6
1	AJ	41	LYS	2.6
1	CR	63	VAL	2.6
1	CY	26	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	DJ	32	ARG	2.6
1	GN	45	LYS	2.6
1	IO	26	ARG	2.6
1	IT	48	ARG	2.6
1	JV	48	ARG	2.6
1	JX	26	ARG	2.6
1	CT	18	PRO	2.6
1	FM	44	ALA	2.6
1	GX	71	ALA	2.6
1	ND	64	ALA	2.6
2	RZ	30	A	2.6
1	BF	40	GLY	2.6
1	BT	47	GLY	2.6
1	EO	83	GLY	2.6
1	GG	3	PHE	2.6
1	GX	42	PHE	2.6
1	HM	65	GLY	2.6
1	IZ	27	GLY	2.6
1	JI	113	PHE	2.6
1	KV	113	PHE	2.6
1	KW	47	GLY	2.6
1	ND	27	GLY	2.6
2	RJ	10	U	2.6
1	BE	2	THR	2.5
1	DQ	16	THR	2.5
1	AZ	32	ARG	2.5
1	BQ	1	SER	2.5
1	BZ	1	SER	2.5
1	DY	36	LYS	2.5
1	EC	5	SER	2.5
1	EW	48	ARG	2.5
1	FS	1	SER	2.5
1	HY	1	SER	2.5
1	IE	26	ARG	2.5
1	IK	1	SER	2.5
1	IQ	32	ARG	2.5
1	NN	41	LYS	2.5
1	BG	63	VAL	2.5
1	BH	63	VAL	2.5
1	CN	7	VAL	2.5
1	MR	74	VAL	2.5
1	NA	91	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	BR	56	LEU	2.5
1	DQ	42	PHE	2.5
1	MX	64	ALA	2.5
1	HO	9	GLY	2.5
1	LQ	40	GLY	2.5
1	NO	81	GLY	2.5
1	IB	108	ILE	2.5
1	MO	62	THR	2.5
1	GV	45	LYS	2.5
1	LB	45	LYS	2.5
1	LW	20	TYR	2.5
1	BI	26	ARG	2.5
1	CC	48	ARG	2.5
1	CG	38	SER	2.5
1	EO	82	ARG	2.5
1	ET	38	SER	2.5
1	EX	5	SER	2.5
1	HW	5	SER	2.5
1	IQ	82	ARG	2.5
1	KI	1	SER	2.5
1	LB	38	SER	2.5
1	MN	32	ARG	2.5
1	NQ	38	SER	2.5
1	ES	73	GLU	2.5
1	IM	73	GLU	2.5
1	JJ	74	VAL	2.5
2	SK	30	A	2.5
2	SQ	29	U	2.5
2	SU	30	A	2.5
1	FR	11	ASN	2.5
1	AA	64	ALA	2.5
1	CX	113	PHE	2.5
1	LD	51	ALA	2.5
1	LZ	113	PHE	2.5
1	GX	27	GLY	2.5
1	LW	19	GLY	2.5
1	CA	45	LYS	2.5
1	EJ	36	LYS	2.5
1	IC	41	LYS	2.5
1	LK	41	LYS	2.5
1	GM	2	THR	2.5
1	DF	82	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	IE	82	ARG	2.5
1	IN	26	ARG	2.5
1	EG	38	SER	2.5
1	EJ	38	SER	2.5
1	IA	38	SER	2.5
1	KN	1	SER	2.5
1	JF	74	VAL	2.5
1	AE	42	PHE	2.5
1	BF	113	PHE	2.5
1	GJ	113	PHE	2.5
1	KM	90	ASP	2.5
1	NJ	113	PHE	2.5
1	AI	103	ALA	2.5
1	BQ	64	ALA	2.5
1	FI	64	ALA	2.5
1	HX	52	ALA	2.5
1	KE	67	PRO	2.5
1	AX	65	GLY	2.5
1	BV	40	GLY	2.5
1	CW	65	GLY	2.5
1	EO	41	LYS	2.5
1	JR	36	LYS	2.5
1	KG	36	LYS	2.5
1	NF	45	LYS	2.5
2	RD	30	A	2.5
2	RO	10	U	2.5
2	SX	10	U	2.5
1	CX	32	ARG	2.5
1	GF	26	ARG	2.5
1	GP	2	THR	2.5
1	IQ	26	ARG	2.5
1	AI	20	TYR	2.5
1	DV	38	SER	2.5
1	IX	66	LEU	2.5
1	MS	38	SER	2.5
1	IV	74	VAL	2.5
1	KL	73	GLU	2.5
1	DJ	42	PHE	2.5
1	FC	113	PHE	2.5
1	FE	43	ASN	2.5
1	JH	42	PHE	2.5
1	KG	113	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	LR	113	PHE	2.5
1	CR	45	LYS	2.5
1	CU	41	LYS	2.5
1	FB	52	ALA	2.5
1	FY	107	GLN	2.5
1	GS	64	ALA	2.5
1	JX	45	LYS	2.5
1	MR	41	LYS	2.5
1	NT	44	ALA	2.5
1	HC	112	GLY	2.5
1	HR	83	GLY	2.5
1	LK	27	GLY	2.5
1	AW	26	ARG	2.5
1	BY	32	ARG	2.5
1	GK	26	ARG	2.5
1	KM	26	ARG	2.5
1	DX	2	THR	2.5
1	AM	1	SER	2.5
1	CU	1	SER	2.5
1	JX	4	SER	2.5
1	NH	38	SER	2.5
1	BU	73	GLU	2.5
1	EP	42	PHE	2.5
1	IC	42	PHE	2.5
2	RB	10	U	2.5
1	FE	36	LYS	2.5
1	HR	45	LYS	2.5
1	JF	97	ASN	2.5
1	AS	64	ALA	2.5
1	EC	110	GLN	2.5
1	EH	64	ALA	2.5
1	FA	89	ALA	2.5
1	KX	44	ALA	2.5
1	LB	86	ALA	2.5
1	EB	67	PRO	2.5
1	GR	67	PRO	2.5
1	KP	67	PRO	2.5
1	BU	82	ARG	2.5
1	DI	32	ARG	2.5
1	DO	26	ARG	2.5
1	DZ	19	GLY	2.5
1	GC	112	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	GF	27	GLY	2.5
1	KD	32	ARG	2.5
1	DC	62	THR	2.5
1	AD	38	SER	2.5
1	BZ	38	SER	2.5
1	KA	1	SER	2.5
1	LG	38	SER	2.5
1	IQ	113	PHE	2.4
1	JD	45	LYS	2.4
1	JF	73	GLU	2.4
1	JZ	73	GLU	2.4
1	LO	113	PHE	2.4
1	LV	42	PHE	2.4
1	CQ	36	LYS	2.4
1	KT	41	LYS	2.4
1	LV	73	GLU	2.4
1	EL	51	ALA	2.4
1	GL	71	ALA	2.4
1	HO	11	ASN	2.4
1	IR	52	ALA	2.4
1	LU	64	ALA	2.4
1	MP	64	ALA	2.4
1	AX	67	PRO	2.4
1	BP	82	ARG	2.4
1	CN	32	ARG	2.4
1	EA	26	ARG	2.4
1	EC	32	ARG	2.4
1	FI	32	ARG	2.4
1	GD	67	PRO	2.4
1	NE	66	LEU	2.4
1	GU	32	ARG	2.4
1	HJ	26	ARG	2.4
1	KW	48	ARG	2.4
1	LZ	32	ARG	2.4
1	MA	48	ARG	2.4
1	CP	9	GLY	2.4
1	DO	40	GLY	2.4
1	IO	65	GLY	2.4
1	JC	19	GLY	2.4
1	BE	38	SER	2.4
1	CQ	1	SER	2.4
1	DJ	10	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	KQ	16	THR	2.4
2	TF	10	U	2.4
1	DP	63	VAL	2.4
2	RR	30	A	2.4
1	CA	113	PHE	2.4
1	DL	20	TYR	2.4
1	GB	3	PHE	2.4
1	JJ	113	PHE	2.4
1	NM	36	LYS	2.4
1	NO	113	PHE	2.4
1	EU	73	GLU	2.4
1	KO	73	GLU	2.4
1	AW	86	ALA	2.4
1	BK	64	ALA	2.4
1	CX	64	ALA	2.4
1	BF	32	ARG	2.4
1	GB	43	ASN	2.4
1	KA	64	ALA	2.4
1	LV	44	ALA	2.4
1	MN	34	GLN	2.4
1	JF	18	PRO	2.4
1	ED	27	GLY	2.4
1	HS	27	GLY	2.4
1	LA	81	GLY	2.4
1	LX	112	GLY	2.4
1	HP	60	ASP	2.4
1	IC	79	THR	2.4
1	IK	38	SER	2.4
1	JL	79	THR	2.4
1	KF	1	SER	2.4
1	BB	41	LYS	2.4
1	BK	113	PHE	2.4
1	DR	41	LYS	2.4
1	DX	91	VAL	2.4
1	ED	42	PHE	2.4
1	FW	36	LYS	2.4
1	GU	36	LYS	2.4
1	HE	63	VAL	2.4
1	HM	63	VAL	2.4
1	IW	41	LYS	2.4
1	LG	45	LYS	2.4
1	LT	91	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	LX	41	LYS	2.4
1	NS	45	LYS	2.4
1	BN	37	ILE	2.4
1	MB	20	TYR	2.4
1	GJ	66	LEU	2.4
1	GY	66	LEU	2.4
1	JM	66	LEU	2.4
1	DI	48	ARG	2.4
1	ED	82	ARG	2.4
1	EY	64	ALA	2.4
1	GB	86	ALA	2.4
1	GL	26	ARG	2.4
1	HP	103	ALA	2.4
1	JF	26	ARG	2.4
1	NS	26	ARG	2.4
2	RI	10	U	2.4
1	EM	43	ASN	2.4
1	GF	78	MET	2.4
1	GL	67	PRO	2.4
2	RO	28	A	2.4
2	RO	30	A	2.4
2	TE	30	A	2.4
1	BW	40	GLY	2.4
1	CM	65	GLY	2.4
1	CZ	27	GLY	2.4
1	HH	40	GLY	2.4
1	HM	40	GLY	2.4
1	KM	27	GLY	2.4
1	LU	47	GLY	2.4
1	MM	47	GLY	2.4
1	AX	38	SER	2.4
1	AY	38	SER	2.4
1	BH	38	SER	2.4
1	BO	41	LYS	2.4
1	BU	45	LYS	2.4
1	BX	41	LYS	2.4
1	FU	2	THR	2.4
1	FZ	45	LYS	2.4
1	HC	45	LYS	2.4
1	HL	38	SER	2.4
1	KB	41	LYS	2.4
1	KX	45	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	MM	94	SER	2.4
1	MZ	38	SER	2.4
1	CN	113	PHE	2.4
1	IL	63	VAL	2.4
1	NQ	63	VAL	2.4
1	AL	90	ASP	2.4
1	CE	66	LEU	2.4
1	CS	20	TYR	2.4
1	FV	96	LEU	2.4
1	AL	82	ARG	2.4
1	AZ	107	GLN	2.4
1	BV	51	ALA	2.4
1	CB	26	ARG	2.4
1	CO	64	ALA	2.4
1	EK	44	ALA	2.4
1	IS	82	ARG	2.4
1	HS	110	GLN	2.4
1	IY	52	ALA	2.4
1	KI	48	ARG	2.4
1	MH	32	ARG	2.4
1	AP	65	GLY	2.4
1	BB	83	GLY	2.4
1	FH	19	GLY	2.4
1	AA	1	SER	2.4
1	AI	1	SER	2.4
1	AO	1	SER	2.4
1	BZ	41	LYS	2.4
1	DB	19	GLY	2.4
1	HJ	27	GLY	2.4
1	HM	45	LYS	2.4
1	JF	112	GLY	2.4
1	IE	1	SER	2.4
1	KB	38	SER	2.4
1	KV	41	LYS	2.4
1	LX	19	GLY	2.4
1	CA	38	SER	2.4
1	EH	38	SER	2.4
1	EU	38	SER	2.4
1	FO	38	SER	2.4
1	AA	63	VAL	2.4
1	BP	91	VAL	2.4
1	CS	113	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	FQ	113	PHE	2.4
1	GU	46	THR	2.4
1	IJ	2	THR	2.4
1	MI	74	VAL	2.4
2	RW	6	U	2.4
2	RW	10	U	2.4
2	TA	10	U	2.4
1	FT	60	ASP	2.4
1	DX	20	TYR	2.4
2	SJ	30	A	2.4
2	SR	30	A	2.4
1	AI	64	ALA	2.4
1	DA	52	ALA	2.4
1	FE	72	ALA	2.4
1	GL	107	GLN	2.4
1	KV	44	ALA	2.4
1	EB	41	LYS	2.4
1	AL	27	GLY	2.4
1	BB	40	GLY	2.4
1	BV	39	GLY	2.4
1	CH	65	GLY	2.4
1	CJ	18	PRO	2.4
1	CL	65	GLY	2.4
1	FF	40	GLY	2.4
1	FF	67	PRO	2.4
1	IN	45	LYS	2.4
1	GK	27	GLY	2.4
1	HV	39	GLY	2.4
1	HY	65	GLY	2.4
1	LV	27	GLY	2.4
1	AF	113	PHE	2.4
1	DH	1	SER	2.4
1	JD	113	PHE	2.4
1	KA	42	PHE	2.4
1	AT	7	VAL	2.4
1	BM	32	ARG	2.4
1	DJ	104	ARG	2.4
1	DZ	82	ARG	2.4
1	ET	104	ARG	2.4
1	FK	82	ARG	2.4
1	IZ	82	ARG	2.4
1	AR	64	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	DE	72	ALA	2.4
1	EP	64	ALA	2.4
1	JW	52	ALA	2.4
1	LT	64	ALA	2.4
1	FT	45	LYS	2.4
1	KE	41	LYS	2.4
1	NV	34	GLN	2.3
2	RU	21	U	2.3
2	RV	10	U	2.3
2	RZ	10	U	2.3
1	AE	38	SER	2.3
1	AJ	4	SER	2.3
1	AP	47	GLY	2.3
1	IG	1	SER	2.3
1	IJ	40	GLY	2.3
1	IY	1	SER	2.3
1	JI	27	GLY	2.3
1	LF	113	PHE	2.3
1	LK	65	GLY	2.3
1	LQ	18	PRO	2.3
1	BC	1	SER	2.3
1	BS	38	SER	2.3
1	CM	38	SER	2.3
1	CN	1	SER	2.3
1	ES	1	SER	2.3
1	GH	1	SER	2.3
1	MJ	65	GLY	2.3
1	MM	1	SER	2.3
1	BL	96	LEU	2.3
1	KH	66	LEU	2.3
2	SW	30	A	2.3
1	FR	7	VAL	2.3
1	GJ	2	THR	2.3
1	GZ	16	THR	2.3
1	IU	79	THR	2.3
1	CZ	48	ARG	2.3
1	GN	26	ARG	2.3
1	HD	26	ARG	2.3
1	IC	48	ARG	2.3
1	IH	48	ARG	2.3
1	NV	32	ARG	2.3
1	BM	45	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	CA	41	LYS	2.3
1	CQ	41	LYS	2.3
1	FO	45	LYS	2.3
1	CJ	73	GLU	2.3
1	EW	64	ALA	2.3
1	JK	73	GLU	2.3
1	JM	52	ALA	2.3
1	CH	113	PHE	2.3
1	EV	113	PHE	2.3
1	GW	113	PHE	2.3
1	BC	83	GLY	2.3
1	BR	109	LEU	2.3
1	HH	42	PHE	2.3
1	JT	42	PHE	2.3
1	ME	113	PHE	2.3
1	CP	40	GLY	2.3
1	DJ	9	GLY	2.3
1	DX	19	GLY	2.3
1	FD	38	SER	2.3
1	GY	67	PRO	2.3
1	HR	38	SER	2.3
1	JK	1	SER	2.3
1	JR	84	ILE	2.3
1	KD	102	PRO	2.3
1	KH	67	PRO	2.3
1	LL	67	PRO	2.3
1	MA	38	SER	2.3
1	IE	43	ASN	2.3
1	EN	7	VAL	2.3
1	GG	2	THR	2.3
1	HO	2	THR	2.3
1	LO	2	THR	2.3
1	BG	82	ARG	2.3
1	BJ	82	ARG	2.3
1	DC	26	ARG	2.3
1	EO	32	ARG	2.3
1	IY	26	ARG	2.3
1	LD	55	ARG	2.3
2	RW	25	U	2.3
2	SE	8	U	2.3
2	SN	21	U	2.3
2	TB	8	U	2.3

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Mol	Chain	Res	Type	RSRZ
1	AW	45	LYS	2.3
1	ES	20	TYR	2.3
1	LA	52	ALA	2.3
1	FG	73	GLU	2.3
1	HI	106	ASP	2.3
1	HU	110	GLN	2.3
1	GU	113	PHE	2.3
1	MA	66	LEU	2.3
1	BP	81	GLY	2.3
1	CP	10	SER	2.3
1	DV	67	PRO	2.3
1	EW	1	SER	2.3
1	FR	9	GLY	2.3
1	FT	38	SER	2.3
1	HR	9	GLY	2.3
1	KK	40	GLY	2.3
1	KR	38	SER	2.3
1	LB	67	PRO	2.3
1	NB	1	SER	2.3
1	NP	47	GLY	2.3
1	BM	2	THR	2.3
1	BQ	46	THR	2.3
1	DR	16	THR	2.3
1	HZ	2	THR	2.3
1	CB	82	ARG	2.3
1	CL	41	LYS	2.3
1	CP	36	LYS	2.3
1	DW	26	ARG	2.3
1	EH	41	LYS	2.3
1	EL	32	ARG	2.3
1	EP	41	LYS	2.3
1	FB	41	LYS	2.3
1	IL	41	LYS	2.3
1	KI	41	LYS	2.3
1	KP	32	ARG	2.3
1	LV	48	ARG	2.3
1	MO	48	ARG	2.3
1	NC	82	ARG	2.3
1	AS	66	LEU	2.3
1	DZ	52	ALA	2.3
1	EE	52	ALA	2.3
1	NH	52	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	EO	110	GLN	2.3
1	GA	42	PHE	2.3
1	CE	70	SER	2.3
1	DZ	1	SER	2.3
1	KV	38	SER	2.3
1	MV	1	SER	2.3
1	FG	39	GLY	2.3
1	JY	67	PRO	2.3
1	KS	40	GLY	2.3
1	LI	65	GLY	2.3
1	MM	9	GLY	2.3
1	AJ	63	VAL	2.3
1	CT	63	VAL	2.3
1	AG	2	THR	2.3
1	GA	2	THR	2.3
1	GH	43	ASN	2.3
1	AJ	45	LYS	2.3
1	CN	36	LYS	2.3
1	DX	41	LYS	2.3
1	FM	41	LYS	2.3
1	GB	41	LYS	2.3
1	GX	48	ARG	2.3
1	HE	45	LYS	2.3
1	IP	45	LYS	2.3
1	MA	26	ARG	2.3
1	MJ	26	ARG	2.3
2	TH	28	A	2.3
1	MJ	66	LEU	2.3
1	CE	44	ALA	2.3
1	CE	64	ALA	2.3
1	CO	42	PHE	2.3
1	CP	113	PHE	2.3
1	EW	44	ALA	2.3
1	FF	44	ALA	2.3
1	IB	20	TYR	2.3
1	IN	51	ALA	2.3
1	AE	73	GLU	2.3
1	AO	38	SER	2.3
1	CR	1	SER	2.3
1	EL	1	SER	2.3
1	EP	38	SER	2.3
1	GA	1	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	HF	38	SER	2.3
1	KT	1	SER	2.3
1	AJ	40	GLY	2.3
1	BG	67	PRO	2.3
1	BQ	47	GLY	2.3
1	DZ	112	GLY	2.3
1	HA	27	GLY	2.3
1	HD	40	GLY	2.3
1	IA	63	VAL	2.3
1	JP	63	VAL	2.3
1	JS	49	VAL	2.3
1	KO	74	VAL	2.3
1	KW	40	GLY	2.3
1	KX	27	GLY	2.3
1	LO	63	VAL	2.3
1	LU	81	GLY	2.3
1	ET	41	LYS	2.3
1	AW	46	THR	2.3
1	BR	26	ARG	2.3
1	CB	50	THR	2.3
1	JE	26	ARG	2.3
1	KN	48	ARG	2.3
1	KY	26	ARG	2.3
1	MJ	25	THR	2.3
1	LU	80	LEU	2.3
2	SS	10	U	2.3
1	BG	113	PHE	2.3
1	EX	113	PHE	2.3
1	KU	113	PHE	2.3
1	MS	113	PHE	2.3
1	BP	64	ALA	2.3
1	BS	71	ALA	2.3
1	BW	64	ALA	2.3
1	DE	44	ALA	2.3
1	EP	71	ALA	2.3
1	FP	72	ALA	2.3
1	IT	75	ALA	2.3
1	NE	64	ALA	2.3
1	BG	107	GLN	2.3
1	KS	107	GLN	2.3
1	CE	38	SER	2.3
1	DI	73	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	FQ	4	SER	2.3
1	JA	54	SER	2.3
2	SK	28	A	2.3
2	ST	26	A	2.3
2	SY	30	A	2.3
1	AC	18	PRO	2.3
1	BG	18	PRO	2.3
1	CZ	45	LYS	2.3
1	DL	41	LYS	2.3
1	EE	19	GLY	2.3
1	EM	45	LYS	2.3
1	EV	41	LYS	2.3
1	FJ	40	GLY	2.3
1	FZ	67	PRO	2.3
1	IO	67	PRO	2.3
1	JS	67	PRO	2.3
1	KB	63	VAL	2.3
1	KY	41	LYS	2.3
1	LT	40	GLY	2.3
1	LT	41	LYS	2.3
1	NE	63	VAL	2.3
1	NK	41	LYS	2.3
1	CH	26	ARG	2.3
1	EB	48	ARG	2.3
1	GL	32	ARG	2.3
1	HC	82	ARG	2.3
1	IP	48	ARG	2.3
1	JT	32	ARG	2.3
1	KI	26	ARG	2.3
1	LQ	82	ARG	2.3
1	FS	2	THR	2.2
1	JX	43	ASN	2.2
1	MU	12	THR	2.2
1	MY	16	THR	2.2
1	NT	43	ASN	2.2
1	AH	113	PHE	2.2
1	BV	113	PHE	2.2
1	DC	113	PHE	2.2
1	GC	108	ILE	2.2
1	BV	103	ALA	2.2
1	LO	64	ALA	2.2
1	AQ	20	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	DH	34	GLN	2.2
1	HJ	20	TYR	2.2
1	JR	20	TYR	2.2
1	AA	38	SER	2.2
1	AW	38	SER	2.2
1	BT	1	SER	2.2
1	BU	1	SER	2.2
1	GF	1	SER	2.2
1	IF	1	SER	2.2
1	JF	10	SER	2.2
1	KE	38	SER	2.2
1	KQ	38	SER	2.2
1	AE	26	ARG	2.2
1	AP	31	PRO	2.2
1	BS	26	ARG	2.2
1	CE	27	GLY	2.2
1	DH	48	ARG	2.2
1	DM	63	VAL	2.2
1	FE	18	PRO	2.2
1	FJ	26	ARG	2.2
1	FT	82	ARG	2.2
1	GO	91	VAL	2.2
1	GP	7	VAL	2.2
1	GU	26	ARG	2.2
1	GY	65	GLY	2.2
1	HW	47	GLY	2.2
1	IL	67	PRO	2.2
1	IT	40	GLY	2.2
1	IV	32	ARG	2.2
1	JX	112	GLY	2.2
1	KX	26	ARG	2.2
1	LQ	67	PRO	2.2
2	RN	21	U	2.2
2	SR	27	U	2.2
2	SX	25	U	2.2
1	LB	50	THR	2.2
1	CP	8	ILE	2.2
1	DK	108	ILE	2.2
1	FB	113	PHE	2.2
1	MI	42	PHE	2.2
2	RZ	28	A	2.2
2	SH	5	A	2.2

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Mol	Chain	Res	Type	RSRZ
1	GI	52	ALA	2.2
1	GL	72	ALA	2.2
1	KS	64	ALA	2.2
1	KT	51	ALA	2.2
1	KZ	64	ALA	2.2
1	MR	51	ALA	2.2
1	AF	45	LYS	2.2
1	DN	41	LYS	2.2
1	DW	41	LYS	2.2
1	GW	110	GLN	2.2
1	IM	41	LYS	2.2
1	ID	38	SER	2.2
1	IN	20	TYR	2.2
1	IV	41	LYS	2.2
1	IV	45	LYS	2.2
1	BD	70	SER	2.2
1	DQ	1	SER	2.2
1	MO	38	SER	2.2
1	CD	26	ARG	2.2
1	AL	18	PRO	2.2
1	AM	67	PRO	2.2
1	BA	65	GLY	2.2
1	DZ	81	GLY	2.2
1	EV	48	ARG	2.2
1	EN	66	LEU	2.2
1	FS	40	GLY	2.2
1	HS	82	ARG	2.2
1	KJ	82	ARG	2.2
1	KM	55	ARG	2.2
1	KV	82	ARG	2.2
1	JL	18	PRO	2.2
1	MM	6	LEU	2.2
1	NM	83	GLY	2.2
1	FV	50	THR	2.2
1	HB	25	THR	2.2
1	HI	16	THR	2.2
1	MY	46	THR	2.2
1	NC	46	THR	2.2
1	BT	43	ASN	2.2
1	ES	90	ASP	2.2
1	IX	113	PHE	2.2
1	KG	43	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	MM	3	PHE	2.2
1	AG	64	ALA	2.2
1	AU	64	ALA	2.2
1	CH	72	ALA	2.2
1	CZ	36	LYS	2.2
1	DJ	71	ALA	2.2
1	DR	45	LYS	2.2
1	EM	64	ALA	2.2
1	IJ	45	LYS	2.2
1	JT	52	ALA	2.2
1	MN	45	LYS	2.2
1	NA	45	LYS	2.2
1	ND	41	LYS	2.2
1	NE	52	ALA	2.2
2	SE	10	U	2.2
1	GX	107	GLN	2.2
1	EE	1	SER	2.2
1	GI	10	SER	2.2
1	KG	20	TYR	2.2
1	MK	1	SER	2.2
1	AJ	82	ARG	2.2
1	CC	63	VAL	2.2
1	CO	48	ARG	2.2
1	CX	63	VAL	2.2
1	DF	91	VAL	2.2
1	DI	26	ARG	2.2
1	DR	26	ARG	2.2
1	EE	91	VAL	2.2
1	EL	26	ARG	2.2
1	HB	63	VAL	2.2
1	ID	26	ARG	2.2
1	KB	66	LEU	2.2
1	MF	26	ARG	2.2
1	MJ	48	ARG	2.2
1	AV	65	GLY	2.2
1	BR	9	GLY	2.2
1	CD	112	GLY	2.2
1	CH	73	GLU	2.2
1	DD	67	PRO	2.2
1	FU	65	GLY	2.2
1	FY	81	GLY	2.2
1	GQ	65	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	HI	102	PRO	2.2
1	ID	19	GLY	2.2
1	JO	65	GLY	2.2
1	KI	73	GLU	2.2
1	MG	67	PRO	2.2
1	MZ	83	GLY	2.2
2	RG	30	A	2.2
2	SB	5	A	2.2
1	EO	16	THR	2.2
1	CP	42	PHE	2.2
1	EM	42	PHE	2.2
1	JU	42	PHE	2.2
1	KW	42	PHE	2.2
1	MU	113	PHE	2.2
1	CV	45	LYS	2.2
1	EB	36	LYS	2.2
1	EE	41	LYS	2.2
1	HR	36	LYS	2.2
1	AI	71	ALA	2.2
1	AP	44	ALA	2.2
1	AX	51	ALA	2.2
1	BV	72	ALA	2.2
1	CA	72	ALA	2.2
1	CC	44	ALA	2.2
1	CS	72	ALA	2.2
1	ES	103	ALA	2.2
1	KG	64	ALA	2.2
1	LE	51	ALA	2.2
1	LI	52	ALA	2.2
1	MA	64	ALA	2.2
1	MM	64	ALA	2.2
1	DE	1	SER	2.2
1	DK	110	GLN	2.2
1	FE	38	SER	2.2
1	GF	38	SER	2.2
1	BB	48	ARG	2.2
1	BM	109	LEU	2.2
1	NI	1	SER	2.2
1	BN	26	ARG	2.2
1	BN	104	ARG	2.2
1	BQ	26	ARG	2.2
1	MX	26	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	NV	20	TYR	2.2
1	CK	49	VAL	2.2
1	AL	67	PRO	2.2
1	CT	27	GLY	2.2
1	DK	83	GLY	2.2
1	GU	40	GLY	2.2
1	HP	102	PRO	2.2
1	KJ	27	GLY	2.2
1	KV	27	GLY	2.2
1	LW	18	PRO	2.2
1	MK	19	GLY	2.2
1	MU	40	GLY	2.2
1	NC	40	GLY	2.2
1	NG	27	GLY	2.2
1	NM	40	GLY	2.2
1	AE	113	PHE	2.2
1	AR	113	PHE	2.2
1	CC	46	THR	2.2
1	ET	46	THR	2.2
1	FK	113	PHE	2.2
1	IC	46	THR	2.2
1	II	2	THR	2.2
1	JD	12	THR	2.2
1	KZ	2	THR	2.2
1	LU	50	THR	2.2
2	RK	8	U	2.2
2	SK	10	U	2.2
1	AI	41	LYS	2.2
1	CY	45	LYS	2.2
1	DV	45	LYS	2.2
1	LX	45	LYS	2.2
1	MH	41	LYS	2.2
1	BG	97	ASN	2.2
1	AD	44	ALA	2.2
1	BD	64	ALA	2.2
1	CW	64	ALA	2.2
1	GY	72	ALA	2.2
1	IP	44	ALA	2.2
1	JA	44	ALA	2.2
1	LP	103	ALA	2.2
1	NG	64	ALA	2.2
1	BI	82	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	BM	1	SER	2.2
1	BM	10	SER	2.2
1	BP	1	SER	2.2
1	BQ	32	ARG	2.2
1	BV	1	SER	2.2
1	CB	1	SER	2.2
1	DF	1	SER	2.2
1	EF	1	SER	2.2
1	EL	48	ARG	2.2
1	EW	38	SER	2.2
1	FG	1	SER	2.2
1	HX	38	SER	2.2
1	IA	66	LEU	2.2
1	GO	26	ARG	2.2
1	IX	38	SER	2.2
1	LN	82	ARG	2.2
1	LV	82	ARG	2.2
1	MW	1	SER	2.2
1	MX	54	SER	2.2
1	BQ	49	VAL	2.2
1	CJ	20	TYR	2.2
1	DT	20	TYR	2.2
1	EH	63	VAL	2.2
1	AI	65	GLY	2.2
1	BI	81	GLY	2.2
1	BR	83	GLY	2.2
1	BS	83	GLY	2.2
1	BX	83	GLY	2.2
1	CG	81	GLY	2.2
1	HX	81	GLY	2.2
1	IA	73	GLU	2.2
1	IX	65	GLY	2.2
1	KR	81	GLY	2.2
1	KV	39	GLY	2.2
1	IN	42	PHE	2.2
1	KV	73	GLU	2.2
1	MO	39	GLY	2.2
1	LJ	113	PHE	2.2
1	NM	113	PHE	2.2
1	AR	50	THR	2.2
1	BQ	45	LYS	2.2
1	DO	36	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	GU	45	LYS	2.2
1	HK	62	THR	2.2
1	LH	45	LYS	2.2
1	AH	96	LEU	2.2
1	BD	109	LEU	2.2
1	CH	103	ALA	2.1
1	DF	71	ALA	2.1
1	FR	66	LEU	2.2
1	GG	86	ALA	2.1
1	IG	52	ALA	2.1
1	KW	44	ALA	2.1
1	MM	44	ALA	2.1
1	NV	56	LEU	2.2
1	AZ	104	ARG	2.1
1	BF	101	ASP	2.1
1	BY	54	SER	2.1
1	BY	82	ARG	2.1
1	DI	90	ASP	2.1
1	DM	38	SER	2.1
1	DQ	32	ARG	2.1
1	EC	4	SER	2.1
1	EU	48	ARG	2.1
1	FD	34	GLN	2.1
1	FE	48	ARG	2.1
1	GR	1	SER	2.1
1	GY	38	SER	2.1
1	HA	38	SER	2.1
1	HS	24	SER	2.1
1	II	1	SER	2.1
1	IL	101	ASP	2.1
1	KJ	110	GLN	2.1
1	LE	38	SER	2.1
1	LT	82	ARG	2.1
1	NA	26	ARG	2.1
2	SQ	21	U	2.1
1	CH	8	ILE	2.1
1	FS	91	VAL	2.1
1	HR	35	ILE	2.1
1	MN	7	VAL	2.1
1	AQ	18	PRO	2.1
1	BG	112	GLY	2.1
1	CZ	39	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	FB	40	GLY	2.1
1	FC	19	GLY	2.1
1	GT	42	PHE	2.1
1	LE	65	GLY	2.1
1	LO	42	PHE	2.1
1	GB	36	LYS	2.1
1	JP	41	LYS	2.1
1	MM	45	LYS	2.1
1	MV	65	GLY	2.1
1	MX	112	GLY	2.1
1	MY	45	LYS	2.1
1	EM	50	THR	2.1
1	HD	2	THR	2.1
2	RC	30	A	2.1
2	SO	26	A	2.1
1	AL	109	LEU	2.1
1	CH	71	ALA	2.1
1	EC	33	ASN	2.1
1	GN	51	ALA	2.1
1	IF	44	ALA	2.1
1	JA	43	ASN	2.1
1	JH	86	ALA	2.1
1	KZ	71	ALA	2.1
1	NS	52	ALA	2.1
1	AO	26	ARG	2.1
1	IW	26	ARG	2.1
1	LQ	26	ARG	2.1
1	BR	110	GLN	2.1
1	BY	38	SER	2.1
1	CV	1	SER	2.1
1	EU	54	SER	2.1
1	IY	38	SER	2.1
1	KG	38	SER	2.1
1	KJ	1	SER	2.1
1	BQ	101	ASP	2.1
1	HX	101	ASP	2.1
1	AY	63	VAL	2.1
1	BQ	63	VAL	2.1
1	AF	41	LYS	2.1
1	BR	20	TYR	2.1
1	BY	45	LYS	2.1
1	CY	41	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	EL	45	LYS	2.1
1	EP	45	LYS	2.1
1	GU	41	LYS	2.1
1	HZ	45	LYS	2.1
1	NS	41	LYS	2.1
1	BP	40	GLY	2.1
1	DB	112	GLY	2.1
1	FZ	18	PRO	2.1
1	GL	102	PRO	2.1
1	GV	67	PRO	2.1
1	HC	40	GLY	2.1
1	HV	67	PRO	2.1
1	IT	111	GLY	2.1
1	JF	67	PRO	2.1
1	KC	83	GLY	2.1
1	KD	67	PRO	2.1
1	KF	83	GLY	2.1
1	LN	39	GLY	2.1
1	MT	65	GLY	2.1
1	AR	79	THR	2.1
1	CE	50	THR	2.1
1	FF	62	THR	2.1
1	GR	50	THR	2.1
1	JL	2	THR	2.1
1	KN	2	THR	2.1
1	EX	96	LEU	2.1
1	LX	66	LEU	2.1
2	RL	10	U	2.1
2	RS	21	U	2.1
1	CG	44	ALA	2.1
1	CP	51	ALA	2.1
1	DJ	51	ALA	2.1
1	FA	26	ARG	2.1
1	GC	26	ARG	2.1
1	HX	44	ALA	2.1
1	HZ	26	ARG	2.1
1	IH	26	ARG	2.1
1	IH	64	ALA	2.1
1	IY	82	ARG	2.1
1	JG	52	ALA	2.1
1	JP	64	ALA	2.1
1	KF	52	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	LA	26	ARG	2.1
1	LS	82	ARG	2.1
1	LT	44	ALA	2.1
1	MD	64	ALA	2.1
1	NV	64	ALA	2.1
1	BA	70	SER	2.1
1	DD	1	SER	2.1
1	DP	1	SER	2.1
1	GG	38	SER	2.1
1	GZ	1	SER	2.1
1	IC	10	SER	2.1
1	JF	1	SER	2.1
1	LA	54	SER	2.1
1	LW	1	SER	2.1
1	MT	1	SER	2.1
1	GR	110	GLN	2.1
1	HR	8	ILE	2.1
1	AZ	101	ASP	2.1
1	CE	113	PHE	2.1
1	CR	41	LYS	2.1
1	CW	113	PHE	2.1
1	ER	45	LYS	2.1
1	FG	45	LYS	2.1
1	GX	45	LYS	2.1
1	IA	68	VAL	2.1
1	KZ	63	VAL	2.1
1	LU	41	LYS	2.1
1	MA	41	LYS	2.1
2	RA	22	A	2.1
2	RJ	7	A	2.1
1	AB	20	TYR	2.1
1	BB	9	GLY	2.1
1	EJ	40	GLY	2.1
1	FF	19	GLY	2.1
1	LB	39	GLY	2.1
1	LH	39	GLY	2.1
1	DX	67	PRO	2.1
1	BY	66	LEU	2.1
1	FL	56	LEU	2.1
1	MW	56	LEU	2.1
1	GK	2	THR	2.1
1	FB	26	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	FX	48	ARG	2.1
1	HF	26	ARG	2.1
1	HX	82	ARG	2.1
1	LF	48	ARG	2.1
1	NL	32	ARG	2.1
1	NM	26	ARG	2.1
1	DZ	71	ALA	2.1
1	GF	71	ALA	2.1
1	GV	64	ALA	2.1
1	BY	1	SER	2.1
1	BY	22	SER	2.1
1	CJ	1	SER	2.1
1	CX	1	SER	2.1
1	DG	1	SER	2.1
1	DH	38	SER	2.1
1	EC	8	ILE	2.1
1	FD	94	SER	2.1
1	IC	1	SER	2.1
1	IH	70	SER	2.1
1	IY	5	SER	2.1
1	JR	38	SER	2.1
1	KU	5	SER	2.1
1	KZ	1	SER	2.1
1	LB	1	SER	2.1
1	LO	1	SER	2.1
1	ME	38	SER	2.1
1	NM	1	SER	2.1
1	DA	41	LYS	2.1
1	JA	41	LYS	2.1
1	HG	63	VAL	2.1
1	HT	113	PHE	2.1
1	HZ	113	PHE	2.1
1	IN	91	VAL	2.1
1	IU	63	VAL	2.1
1	LH	91	VAL	2.1
2	RD	10	U	2.1
2	RS	8	U	2.1
1	AX	81	GLY	2.1
1	BK	40	GLY	2.1
1	CJ	83	GLY	2.1
1	CZ	81	GLY	2.1
1	EI	40	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	GF	20	TYR	2.1
1	ID	106	ASP	2.1
1	NM	101	ASP	2.1
1	GI	65	GLY	2.1
1	GO	27	GLY	2.1
1	MQ	83	GLY	2.1
1	NM	27	GLY	2.1
1	NQ	19	GLY	2.1
1	BL	78	MET	2.1
1	CL	67	PRO	2.1
1	EH	67	PRO	2.1
1	HH	18	PRO	2.1
1	HZ	67	PRO	2.1
1	JL	67	PRO	2.1
1	KJ	18	PRO	2.1
1	MR	78	MET	2.1
1	HI	98	THR	2.1
1	ES	104	ARG	2.1
1	FY	82	ARG	2.1
1	GO	32	ARG	2.1
1	MW	48	ARG	2.1
1	AI	36	LYS	2.1
1	AP	64	ALA	2.1
1	BH	44	ALA	2.1
1	DS	72	ALA	2.1
1	EL	37	ILE	2.1
1	GO	72	ALA	2.1
1	HE	86	ALA	2.1
1	HQ	64	ALA	2.1
1	KH	44	ALA	2.1
1	KV	64	ALA	2.1
2	SR	3	A	2.1
1	CV	38	SER	2.1
1	CY	1	SER	2.1
1	DI	1	SER	2.1
1	GY	41	LYS	2.1
1	HL	1	SER	2.1
1	IG	41	LYS	2.1
1	JB	1	SER	2.1
1	KJ	70	SER	2.1
1	LH	36	LYS	2.1
1	LU	38	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	CZ	42	PHE	2.1
1	EG	43	ASN	2.1
1	EK	42	PHE	2.1
1	JE	42	PHE	2.1
1	MN	113	PHE	2.1
1	AI	63	VAL	2.1
1	AV	63	VAL	2.1
1	GC	91	VAL	2.1
1	GD	49	VAL	2.1
1	CC	105	LEU	2.1
1	BS	40	GLY	2.1
1	CN	20	TYR	2.1
1	FY	83	GLY	2.1
1	HJ	19	GLY	2.1
1	JR	19	GLY	2.1
1	LY	19	GLY	2.1
1	MI	20	TYR	2.1
1	DR	18	PRO	2.1
1	HW	67	PRO	2.1
1	IB	18	PRO	2.1
1	IC	67	PRO	2.1
1	KM	67	PRO	2.1
1	LZ	102	PRO	2.1
1	AI	73	GLU	2.1
1	AP	98	THR	2.1
1	DK	16	THR	2.1
1	AR	32	ARG	2.1
1	BT	48	ARG	2.1
1	GD	48	ARG	2.1
1	ML	26	ARG	2.1
1	NP	26	ARG	2.1
1	AL	41	LYS	2.1
1	DZ	45	LYS	2.1
1	IQ	45	LYS	2.1
1	NV	41	LYS	2.1
2	RK	21	U	2.1
2	RU	25	U	2.1
2	SG	10	U	2.1
2	SK	27	U	2.1
2	TH	10	U	2.1
1	AV	70	SER	2.1
1	BE	1	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	CG	89	ALA	2.1
1	CP	71	ALA	2.1
1	CR	64	ALA	2.1
1	DC	52	ALA	2.1
1	EU	71	ALA	2.1
1	EW	103	ALA	2.1
1	EX	1	SER	2.1
1	FF	1	SER	2.1
1	FO	94	SER	2.1
1	IF	70	SER	2.1
1	IH	5	SER	2.1
1	JP	1	SER	2.1
1	LX	38	SER	2.1
1	LX	75	ALA	2.1
1	MF	38	SER	2.1
1	MK	38	SER	2.1
1	NF	75	ALA	2.1
1	NO	38	SER	2.1
1	NV	54	SER	2.1
1	CC	42	PHE	2.1
1	CX	34	GLN	2.1
1	ER	113	PHE	2.1
1	IC	88	ASN	2.1
1	JW	110	GLN	2.1
1	CI	63	VAL	2.1
1	IU	66	LEU	2.1
1	JA	63	VAL	2.1
1	JM	63	VAL	2.1
1	MG	63	VAL	2.1
1	BL	83	GLY	2.0
1	CA	40	GLY	2.0
1	DZ	21	TYR	2.0
1	EW	47	GLY	2.0
1	FK	83	GLY	2.0
1	GZ	19	GLY	2.0
1	HE	112	GLY	2.0
1	HG	27	GLY	2.0
1	IP	39	GLY	2.0
1	JL	65	GLY	2.0
1	LO	112	GLY	2.0
1	MZ	40	GLY	2.0
1	NV	47	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	DA	67	PRO	2.0
2	RO	7	A	2.0
2	TG	30	A	2.0
1	BN	2	THR	2.0
1	CA	82	ARG	2.0
1	CE	26	ARG	2.0
1	CI	32	ARG	2.0
1	FS	82	ARG	2.0
1	GG	106	ASP	2.0
1	GX	26	ARG	2.0
1	GZ	82	ARG	2.0
1	BB	45	LYS	2.0
1	CH	36	LYS	2.0
1	CT	73	GLU	2.0
1	DS	45	LYS	2.0
1	DX	45	LYS	2.0
1	FP	41	LYS	2.0
1	GH	41	LYS	2.0
1	GP	37	ILE	2.0
1	GV	41	LYS	2.0
1	HA	73	GLU	2.0
1	IA	82	ARG	2.0
1	IP	82	ARG	2.0
1	JZ	32	ARG	2.0
1	KD	73	GLU	2.0
1	MS	2	THR	2.0
1	MZ	82	ARG	2.0
1	MC	41	LYS	2.0
1	AM	38	SER	2.0
1	BA	22	SER	2.0
1	BL	1	SER	2.0
1	BT	64	ALA	2.0
1	BV	44	ALA	2.0
1	CE	52	ALA	2.0
1	CB	113	PHE	2.0
1	DF	38	SER	2.0
1	DY	38	SER	2.0
1	EC	38	SER	2.0
1	EJ	5	SER	2.0
1	EM	38	SER	2.0
1	ER	89	ALA	2.0
1	EV	64	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	GC	1	SER	2.0
1	HH	64	ALA	2.0
1	HK	38	SER	2.0
1	HP	38	SER	2.0
1	IL	1	SER	2.0
1	IN	71	ALA	2.0
1	LH	44	ALA	2.0
1	LR	64	ALA	2.0
1	LU	42	PHE	2.0
1	MA	1	SER	2.0
1	MP	1	SER	2.0
1	NH	64	ALA	2.0
1	NI	42	PHE	2.0
1	NU	38	SER	2.0
1	NV	113	PHE	2.0
1	BN	107	GLN	2.0
1	EK	74	VAL	2.0
1	GA	49	VAL	2.0
1	JI	107	GLN	2.0
1	NM	91	VAL	2.0
1	IN	43	ASN	2.0
2	RR	21	U	2.0
1	AO	27	GLY	2.0
1	BR	40	GLY	2.0
1	EB	19	GLY	2.0
1	FJ	112	GLY	2.0
1	FV	83	GLY	2.0
1	IK	27	GLY	2.0
1	IQ	81	GLY	2.0
1	JC	65	GLY	2.0
1	JY	65	GLY	2.0
1	MZ	19	GLY	2.0
1	NJ	27	GLY	2.0
1	BX	82	ARG	2.0
1	CH	102	PRO	2.0
1	EJ	82	ARG	2.0
1	EU	36	LYS	2.0
1	FD	82	ARG	2.0
1	HA	67	PRO	2.0
1	JZ	20	TYR	2.0
1	IJ	104	ARG	2.0
1	JB	45	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	JO	82	ARG	2.0
1	KI	32	ARG	2.0
1	KN	32	ARG	2.0
1	KQ	67	PRO	2.0
1	LK	55	ARG	2.0
1	LU	48	ARG	2.0
1	LW	67	PRO	2.0
1	MH	104	ARG	2.0
1	NH	48	ARG	2.0
1	AA	62	THR	2.0
1	BH	2	THR	2.0
1	BR	73	GLU	2.0
1	CZ	60	ASP	2.0
1	IC	101	ASP	2.0
1	LW	73	GLU	2.0
1	AD	52	ALA	2.0
1	AK	1	SER	2.0
1	EG	44	ALA	2.0
1	EP	10	SER	2.0
1	EY	38	SER	2.0
1	FE	66	LEU	2.0
1	FY	72	ALA	2.0
1	FZ	52	ALA	2.0
1	GC	70	SER	2.0
1	GD	42	PHE	2.0
1	IB	64	ALA	2.0
1	IO	66	LEU	2.0
1	IZ	38	SER	2.0
1	KM	113	PHE	2.0
1	JK	56	LEU	2.0
1	JX	5	SER	2.0
1	NF	54	SER	2.0
1	NP	38	SER	2.0
1	NU	42	PHE	2.0
1	KJ	109	LEU	2.0
1	BI	34	GLN	2.0
1	BT	49	VAL	2.0
1	DF	49	VAL	2.0
1	HW	63	VAL	2.0
1	LA	68	VAL	2.0
1	LB	91	VAL	2.0
2	RF	24	A	2.0

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Mol	Chain	Res	Type	RSRZ
2	SW	28	A	2.0
2	TA	30	A	2.0
1	FH	78	MET	2.0
1	AB	26	ARG	2.0
1	AN	19	GLY	2.0
1	AU	27	GLY	2.0
1	CD	83	GLY	2.0
1	CN	45	LYS	2.0
1	DR	19	GLY	2.0
1	AI	31	PRO	2.0
1	BS	48	ARG	2.0
1	CR	48	ARG	2.0
1	CT	26	ARG	2.0
1	DI	39	GLY	2.0
1	DX	26	ARG	2.0
1	EL	40	GLY	2.0
1	EP	26	ARG	2.0
1	EP	82	ARG	2.0
1	GD	65	GLY	2.0
1	GS	40	GLY	2.0
1	HO	82	ARG	2.0
1	IC	9	GLY	2.0
1	JL	48	ARG	2.0
1	JV	82	ARG	2.0
1	LH	27	GLY	2.0
1	MJ	32	ARG	2.0
1	MM	26	ARG	2.0
1	MM	104	ARG	2.0
1	MN	65	GLY	2.0
1	NC	39	GLY	2.0
1	NU	39	GLY	2.0
1	GI	108	ILE	2.0
1	LI	67	PRO	2.0
1	MX	18	PRO	2.0
1	AX	16	THR	2.0
1	CO	46	THR	2.0
1	KI	25	THR	2.0
1	AD	113	PHE	2.0
1	AX	95	ASP	2.0
1	BR	113	PHE	2.0
1	CX	42	PHE	2.0
1	EZ	113	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	HR	42	PHE	2.0
1	HT	42	PHE	2.0
1	HW	66	LEU	2.0
1	JI	73	GLU	2.0
1	JS	113	PHE	2.0
1	MG	42	PHE	2.0
1	NS	73	GLU	2.0
1	AZ	94	SER	2.0
1	CD	38	SER	2.0
1	ED	1	SER	2.0
1	EG	5	SER	2.0
1	EH	70	SER	2.0
1	IU	1	SER	2.0
1	KI	10	SER	2.0
1	LD	52	ALA	2.0
1	NG	1	SER	2.0
1	NK	1	SER	2.0
1	NP	1	SER	2.0
1	NV	10	SER	2.0
2	SI	10	U	2.0
2	SK	29	U	2.0
1	CT	74	VAL	2.0
1	MB	7	VAL	2.0
1	MM	49	VAL	2.0
1	MX	63	VAL	2.0
1	NL	7	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.