Full wwPDB EM Validation Report ⓘ

Nov 5, 2024 – 09:16 pm GMT

PDB ID	:	9HAS
EMDB ID	:	EMD-52005
Title	:	pT=3 virus-like particle of ssRNA phage ESO003 coat protein
Authors	:	Kalnins, G.
Deposited on	:	2024-11-05
Resolution	:	3.20 Å(reported)
Based on initial model	:	.

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

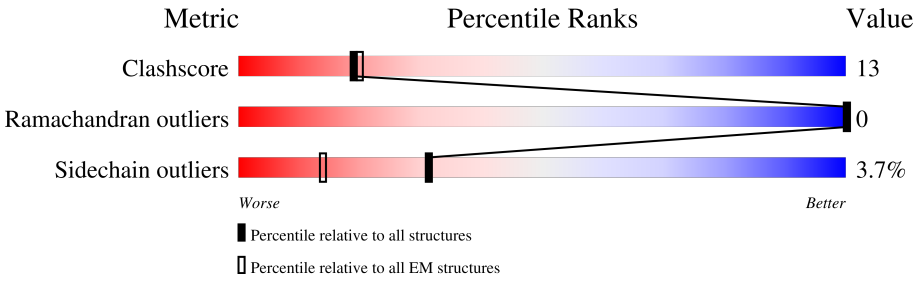
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	AA	113	14% 61% 35% ·
1	AB	113	14% 63% 37%
1	AC	113	18% 69% 28% ·
1	AD	113	17% 65% 32% ·
1	AE	113	15% 68% 31% ·
1	AF	113	18% 72% 27% ·
1	AG	113	15% 67% 31% ·
1	AH	113	12% 69% 28% ·

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Mol	Chain	Length	Quality of chain
1	AI	113	17% 75% 24%
1	AJ	113	14% 60% 37%
1	AK	113	14% 63% 35%
1	AL	113	18% 70% 28%
1	AM	113	15% 62% 35%
1	AN	113	12% 65% 32%
1	AO	113	17% 72% 28%
1	AP	113	15% 68% 30%
1	AQ	113	14% 63% 35%
1	AR	113	19% 69% 31%
1	AS	113	15% 68% 30%
1	AT	113	12% 68% 30%
1	AU	113	17% 75% 24%
1	AV	113	14% 62% 35%
1	AW	113	14% 63% 36%
1	AX	113	18% 71% 27%
1	AY	113	15% 62% 35%
1	AZ	113	13% 64% 34%
1	BA	113	17% 73% 27%
1	BB	113	15% 69% 29%
1	BC	113	12% 67% 30%
1	BD	113	17% 75% 24%
1	BE	113	15% 67% 30%
1	BF	113	14% 62% 36%
1	BG	113	19% 69% 31%

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Mol	Chain	Length	Quality of chain
1	BH	113	17% 65% 34%
1	BI	113	15% 69% 30%
1	BJ	113	18% 73% 26%
1	BK	113	15% 66% 31%
1	BL	113	13% 65% 33%
1	BM	113	17% 73% 26%
1	BN	113	15% 69% 29%
1	BO	113	12% 69% 29%
1	BP	113	16% 79% 20%
1	BQ	113	15% 67% 30%
1	BR	113	14% 62% 36%
1	BS	113	20% 70% 30%
1	BT	113	15% 63% 35%
1	BU	113	13% 64% 34%
1	BV	113	17% 73% 26%
1	BW	113	17% 65% 33%
1	BX	113	15% 69% 30%
1	BY	113	18% 73% 25%
1	BZ	113	14% 63% 34%
1	CA	113	15% 64% 35%
1	CB	113	18% 69% 28%
1	CC	113	14% 66% 31%
1	CD	113	14% 61% 37%
1	CE	113	20% 68% 32%
1	CF	113	15% 65% 32%

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Mol	Chain	Length	Quality of chain
1	CG	113	13% 65% 32%
1	CH	113	17% 73% 27%
1	CI	113	17% 65% 33%
1	CJ	113	15% 71% 28%
1	CK	113	18% 75% 22%
1	CL	113	15% 67% 31%
1	CM	113	13% 61% 37%
1	CN	113	20% 67% 33%
1	CO	113	14% 62% 35%
1	CP	113	14% 65% 34%
1	CQ	113	18% 70% 28%
1	CR	113	15% 67% 31%
1	CS	113	12% 69% 29%
1	CT	113	16% 78% 21%
1	CU	113	17% 67% 29%
1	CV	113	15% 70% 29%
1	CW	113	18% 73% 25%
1	CX	113	14% 66% 32%
1	CY	113	14% 61% 37%
1	CZ	113	20% 69% 31%
1	DA	113	14% 61% 36%
1	DB	113	14% 64% 35%
1	DC	113	18% 70% 28%
1	DD	113	17% 67% 30%
1	DE	113	15% 71% 28%

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Mol	Chain	Length	Quality of chain
1	DF	113	18% 74% 24%
1	DG	113	15% 67% 31%
1	DH	113	12% 68% 29%
1	DI	113	16% 77% 22%
1	DJ	113	15% 64% 35%
1	DK	113	12% 66% 31%
1	DL	113	16% 73% 27%
1	DM	113	14% 61% 35%
1	DN	113	15% 63% 35%
1	DO	113	18% 70% 28%
1	DP	113	15% 67% 31%
1	DQ	113	12% 69% 29%
1	DR	113	16% 80% 19%
1	DS	113	16% 65% 33%
1	DT	113	15% 71% 28%
1	DU	113	18% 75% 23%
1	DV	113	14% 62% 35%
1	DW	113	14% 63% 36%
1	DX	113	18% 68% 30%
1	DY	113	15% 67% 31%
1	DZ	113	13% 62% 36%
1	EA	113	20% 70% 30%
1	EB	113	15% 67% 30%
1	EC	113	13% 65% 33%
1	ED	113	17% 73% 26%

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Mol	Chain	Length	Quality of chain
1	EE	113	17% 66% 31%
1	EF	113	15% 69% 30%
1	EG	113	18% 73% 26%
1	EH	113	14% 62% 35%
1	EI	113	15% 64% 35%
1	EJ	113	18% 71% 27%
1	EK	113	15% 67% 30%
1	EL	113	14% 61% 37%
1	EM	113	20% 70% 30%
1	EN	113	17% 66% 30%
1	EO	113	15% 72% 27%
1	EP	113	17% 73% 26%
1	EQ	113	13% 62% 35%
1	ER	113	13% 61% 36%
1	ES	113	16% 73% 26%
1	ET	113	15% 71% 27%
1	EU	113	13% 69% 30%
1	EV	113	17% 74% 25%
1	EW	113	16% 71% 27%
1	EX	113	14% 67% 31%
1	EY	113	19% 70% 29%
1	EZ	113	17% 71% 28%
1	FA	113	15% 70% 29%
1	FB	113	17% 73% 26%
1	FC	113	13% 63% 34%

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Mol	Chain	Length	Quality of chain
1	FD	113	13% 62% 35%
1	FE	113	17% 74% 25%
1	FF	113	16% 71% 27%
1	FG	113	14% 68% 31%
1	FH	113	19% 67% 32%
1	FI	113	15% 71% 27%
1	FJ	113	13% 71% 27%
1	FK	113	17% 74% 25%
1	FL	113	14% 60% 37%
1	FM	113	14% 65% 35%
1	FN	113	19% 69% 29%
1	FO	113	13% 65% 33%
1	FP	113	13% 65% 32%
1	FQ	113	16% 75% 23%
1	FR	113	16% 70% 27%
1	FS	113	14% 67% 31%
1	FT	113	19% 74% 25%
1	FU	113	15% 71% 27%
1	FV	113	13% 67% 31%
1	FW	113	17% 78% 21%
1	FX	113	13% 64% 34%
1	FY	113	13% 62% 35%
1	FZ	113	16% 78% 20%
1	GA	113	14% 59% 38%
1	GB	113	14% 65% 35%

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Mol	Chain	Length	Quality of chain
1	GC	113	18% 68% 30%
1	GD	113	17% 69% 29%
1	GE	113	15% 72% 27%
1	GF	113	17% 73% 25%
1	GG	113	15% 71% 27%
1	GH	113	13% 67% 32%
1	GI	113	17% 76% 23%
1	GJ	113	13% 63% 35%
1	GK	113	13% 65% 32%
1	GL	113	16% 74% 25%
1	GM	113	14% 61% 37%
1	GN	113	14% 65% 35%
1	GO	113	18% 67% 31%
1	GP	113	15% 72% 26%
1	GQ	113	13% 68% 30%
1	GR	113	17% 76% 23%
1	GS	113	17% 69% 29%
1	GT	113	15% 72% 27%
1	GU	113	17% 72% 26%
1	GV	113	15% 71% 26%
1	GW	113	14% 66% 32%
1	GX	113	19% 71% 28%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 154260 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called coat protein of ssRNA phage ESO003.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AB	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AC	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AD	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AE	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AF	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AG	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AH	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AI	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AJ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AK	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AL	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AM	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AN	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AO	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AP	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AQ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AR	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AS	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AT	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AU	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AV	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AW	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AX	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AY	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	AZ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BA	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BB	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BC	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BD	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BE	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BF	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BG	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BH	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BI	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BJ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BK	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BL	113	Total	C	N	O	S	0	0
			857	536	147	172	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BM	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BN	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BO	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BP	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BQ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BR	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BS	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BT	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BU	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BV	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BW	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BX	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BY	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	BZ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CA	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CB	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CC	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CD	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CE	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CF	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CG	113	Total	C	N	O	S	0	0
			857	536	147	172	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CH	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CI	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CJ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CK	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CL	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CM	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CN	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CO	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CP	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CQ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CR	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CS	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CT	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CU	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CV	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CW	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CX	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CY	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	CZ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DA	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DB	113	Total	C	N	O	S	0	0
			857	536	147	172	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DC	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DD	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DE	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DF	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DG	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DH	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DI	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DJ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DK	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DL	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DM	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DN	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DO	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DP	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DQ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DR	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DS	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DT	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DU	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DV	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DW	113	Total	C	N	O	S	0	0
			857	536	147	172	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DX	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DY	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	DZ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EA	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EB	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EC	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	ED	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EE	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EF	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EG	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EH	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EI	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EJ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EK	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EL	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EM	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EN	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EO	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EP	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EQ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	ER	113	Total	C	N	O	S	0	0
			857	536	147	172	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	ES	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	ET	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EU	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EV	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EW	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EX	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EY	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	EZ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FA	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FB	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FC	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FD	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FE	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FF	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FG	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FH	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FI	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FJ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FK	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FL	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FM	113	Total	C	N	O	S	0	0
			857	536	147	172	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	FN	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FO	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FP	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FQ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FR	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FS	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FT	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FU	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FV	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FW	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FX	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FY	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	FZ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GA	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GB	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GC	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GD	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GE	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GF	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GG	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GH	113	Total	C	N	O	S	0	0
			857	536	147	172	2		

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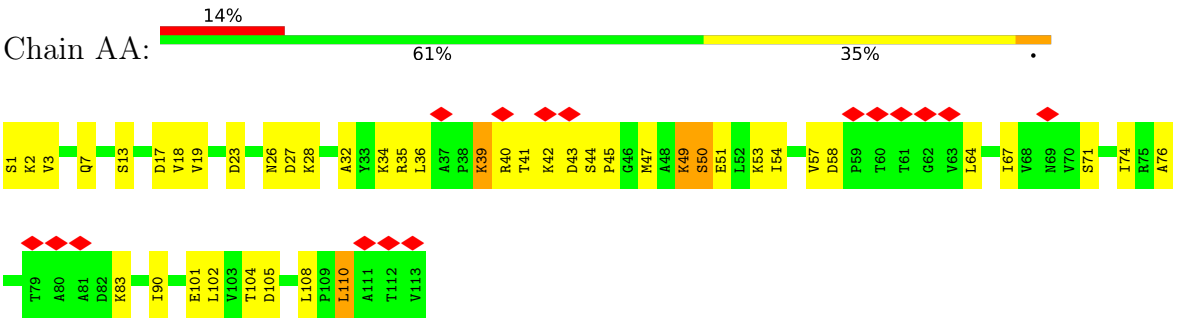
Mol	Chain	Residues	Atoms					AltConf	Trace
1	GI	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GJ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GK	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GL	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GM	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GN	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GO	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GP	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GQ	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GR	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GS	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GT	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GU	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GV	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GW	113	Total	C	N	O	S	0	0
			857	536	147	172	2		
1	GX	113	Total	C	N	O	S	0	0
			857	536	147	172	2		

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 atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

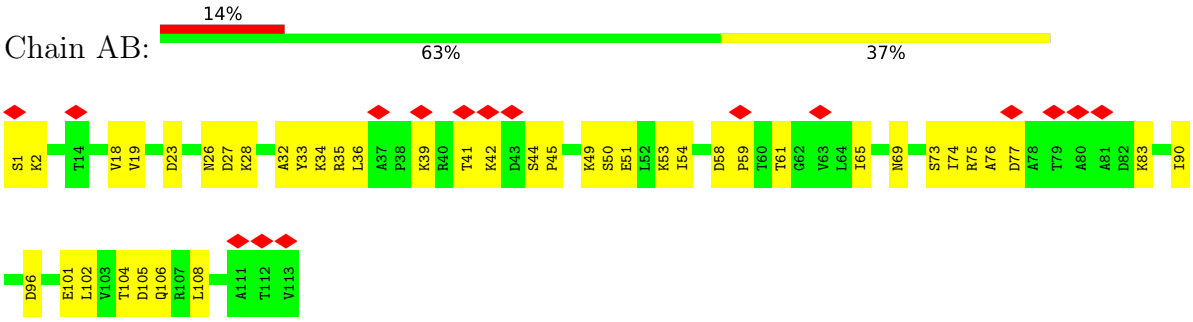
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AA:



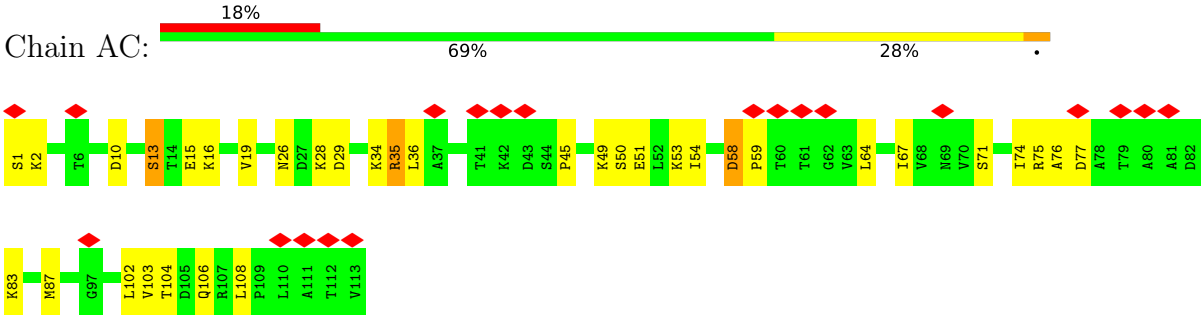
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AB:



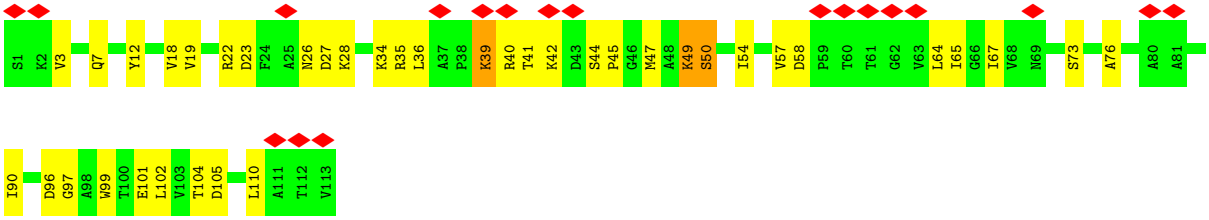
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AC:



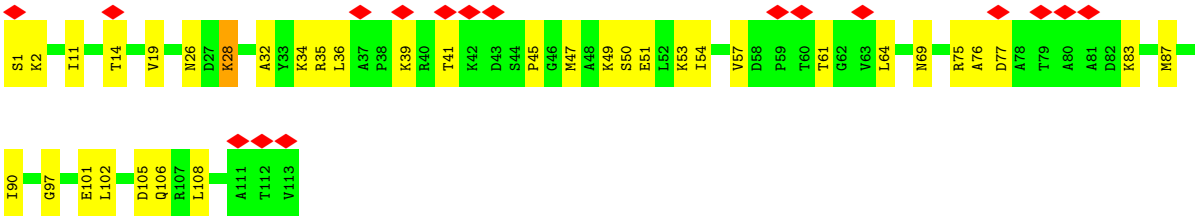
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AD:



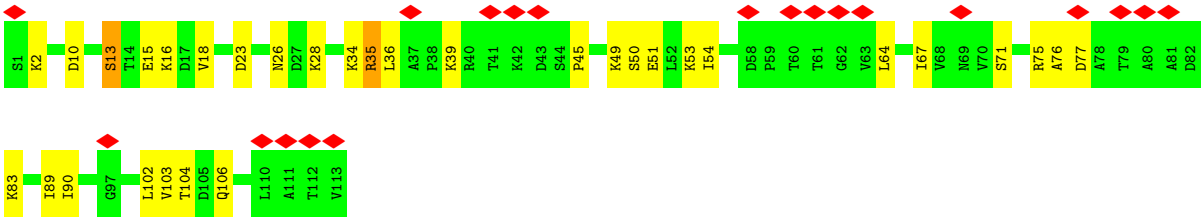
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AE:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain AF:

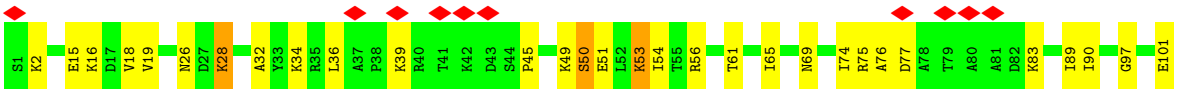


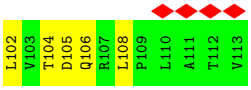
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AG:

• Molecule 1: coat protein of ssRNA phage ESO003

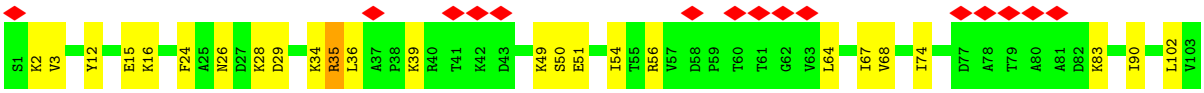
Chain AH:

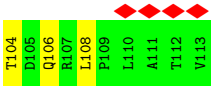




• Molecule 1: coat protein of ssRNA phage ESO003

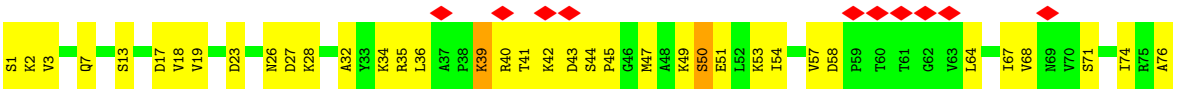
Chain AI:





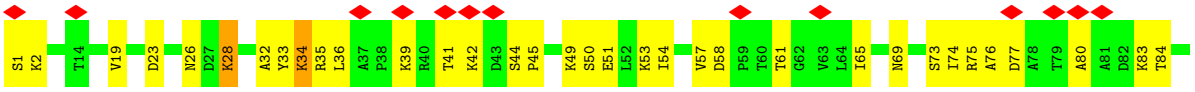
• Molecule 1: coat protein of ssRNA phage ESO003

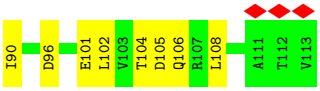
Chain AJ:



• Molecule 1: coat protein of ssRNA phage ESO003

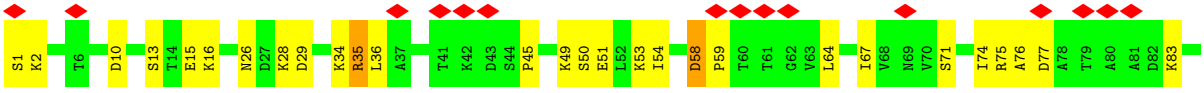
Chain AK:





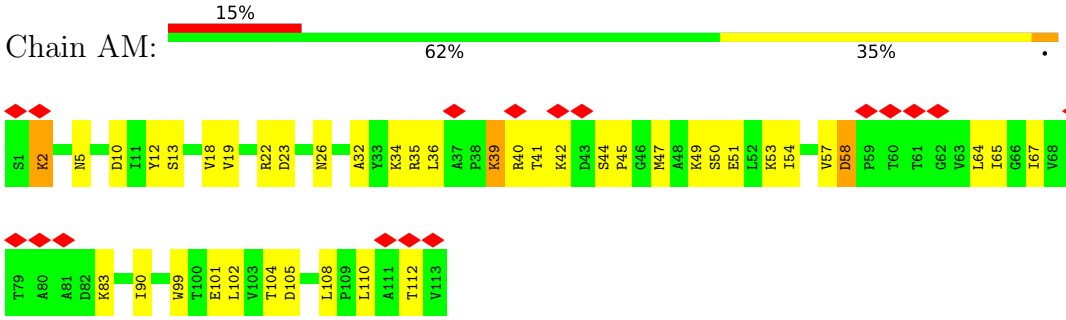
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AL:



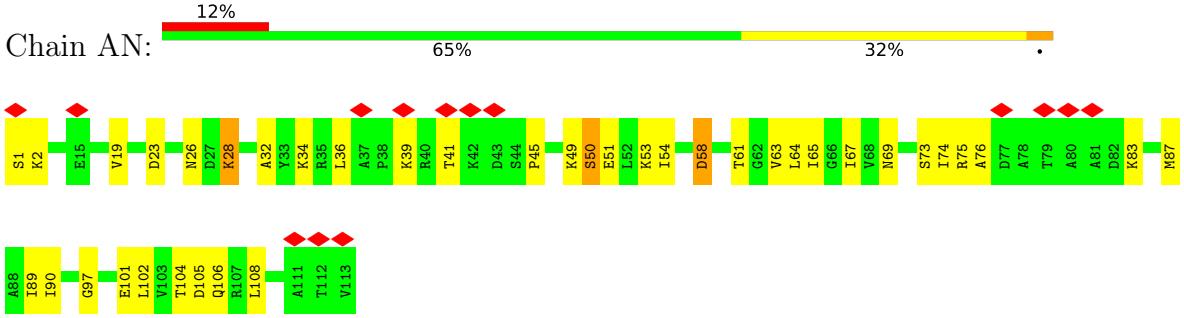
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AM:



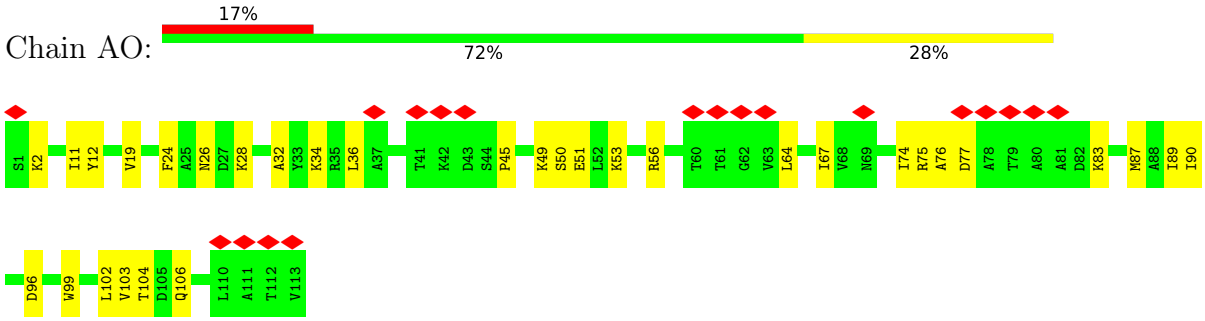
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AN:



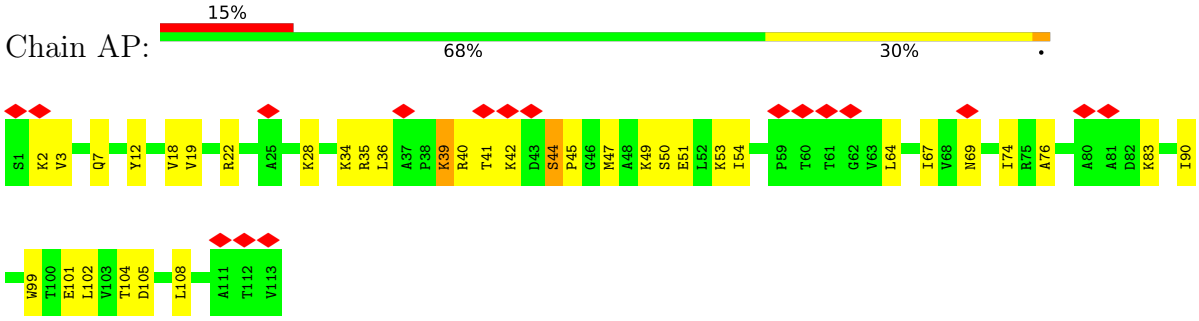
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AO:



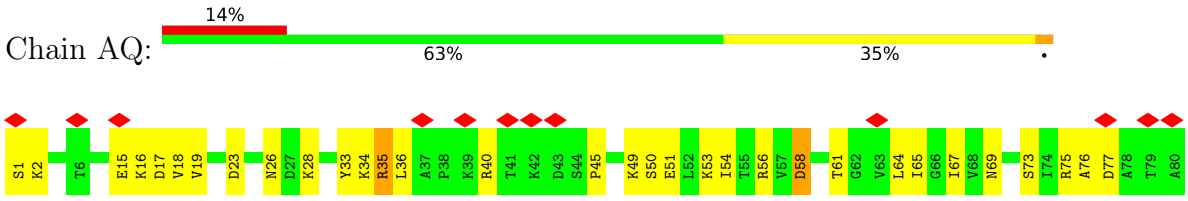
• Molecule 1: coat protein of ssRNA phage ESO003

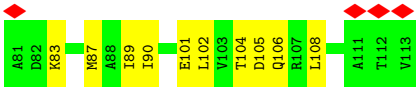
Chain AP:



• Molecule 1: coat protein of ssRNA phage ESO003

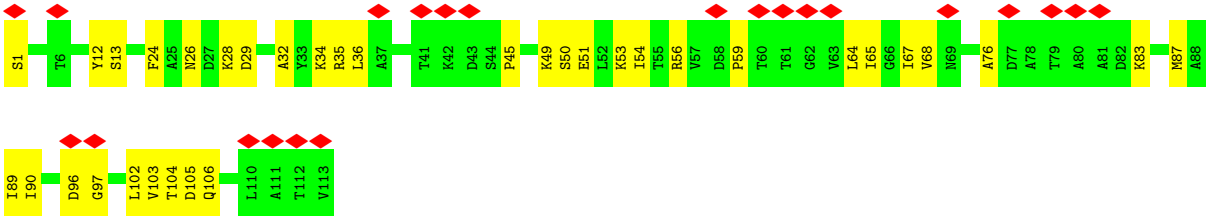
Chain AQ:





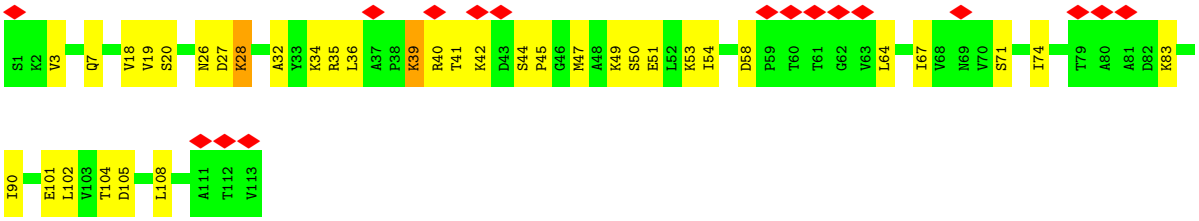
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AR:



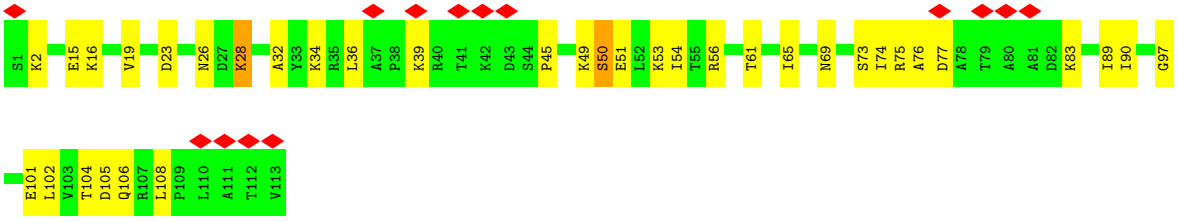
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AS:



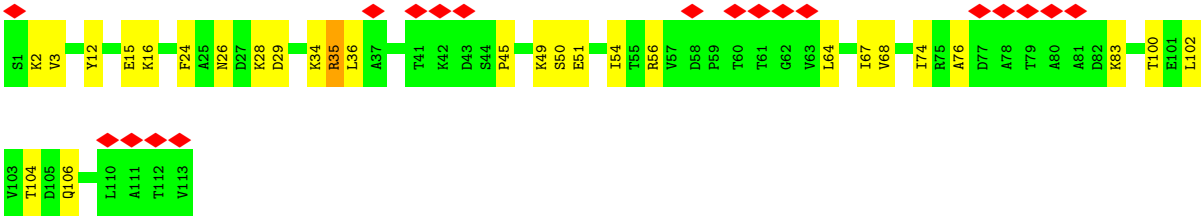
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AT:



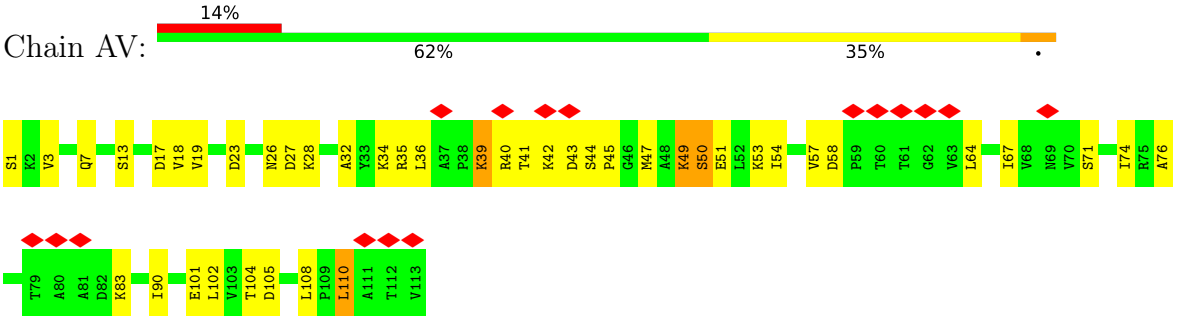
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AU:



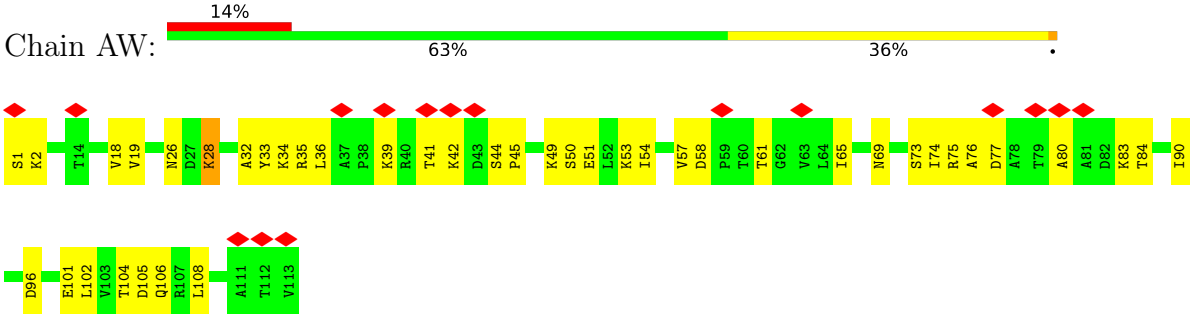
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AV:



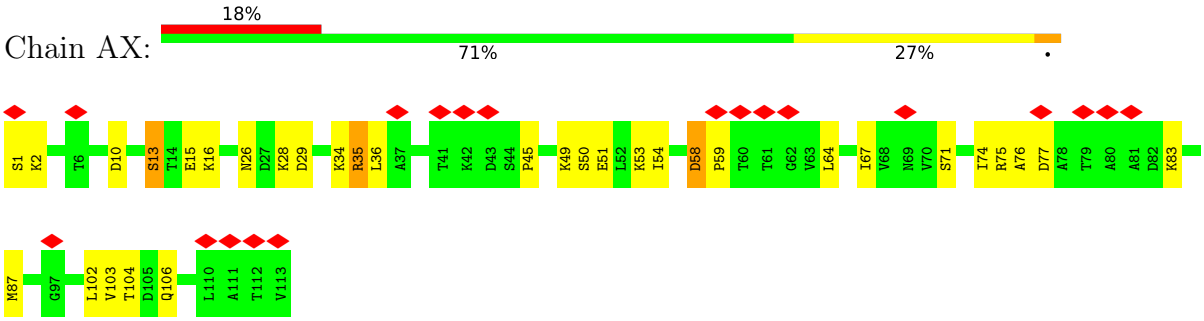
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AW:



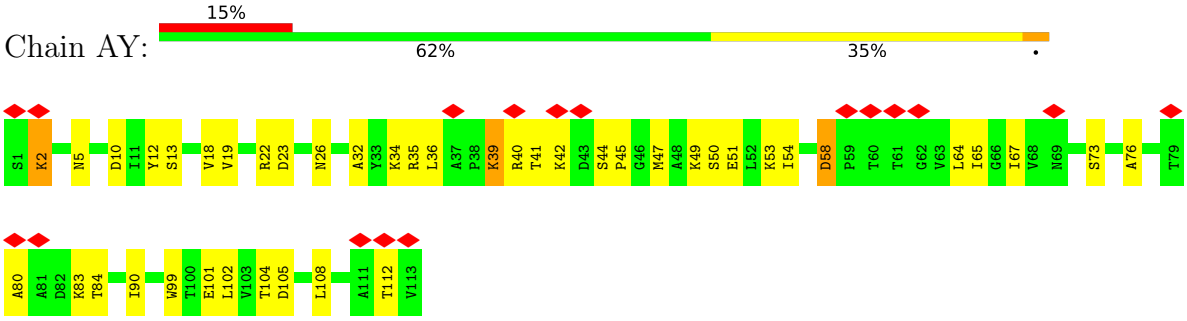
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AX:



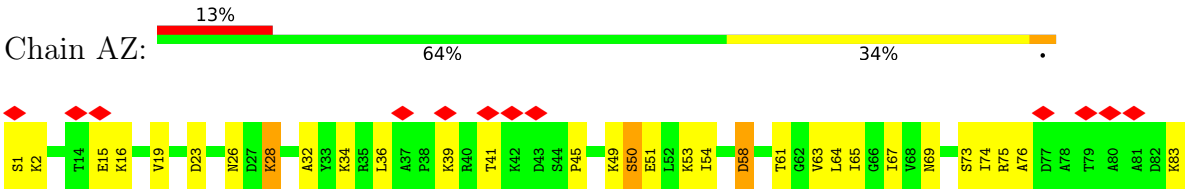
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AY:



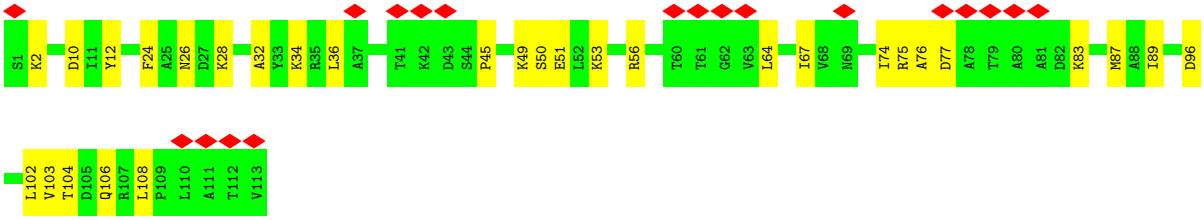
• Molecule 1: coat protein of ssRNA phage ESO003

Chain AZ:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain BA:

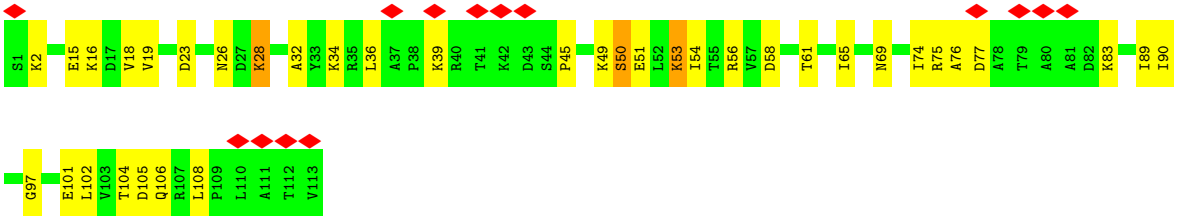


• Molecule 1: coat protein of ssRNA phage ESO003

Chain BB:

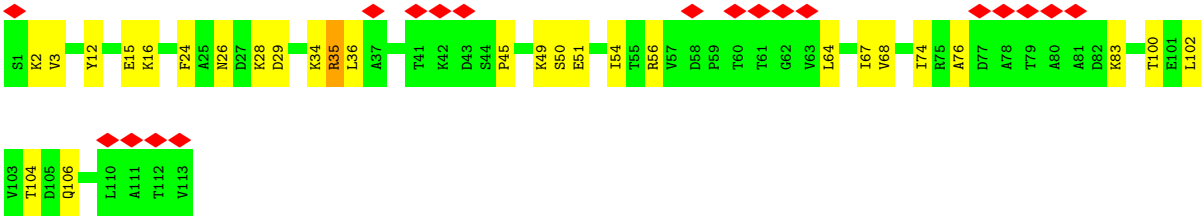
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BC:



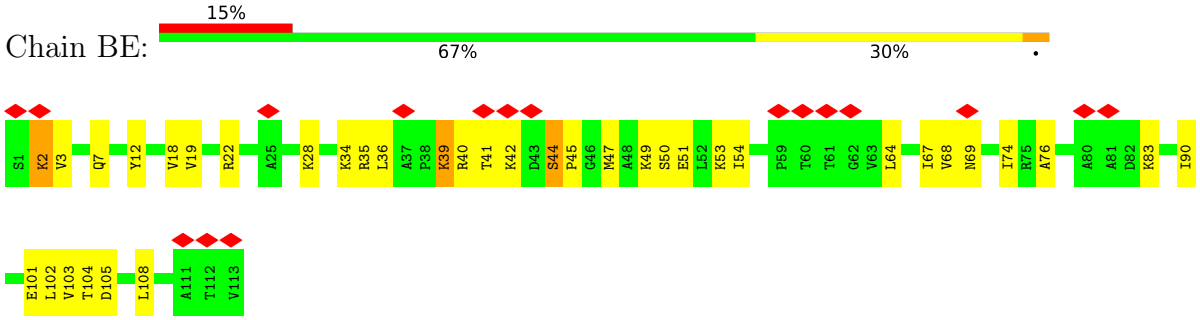
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BD:



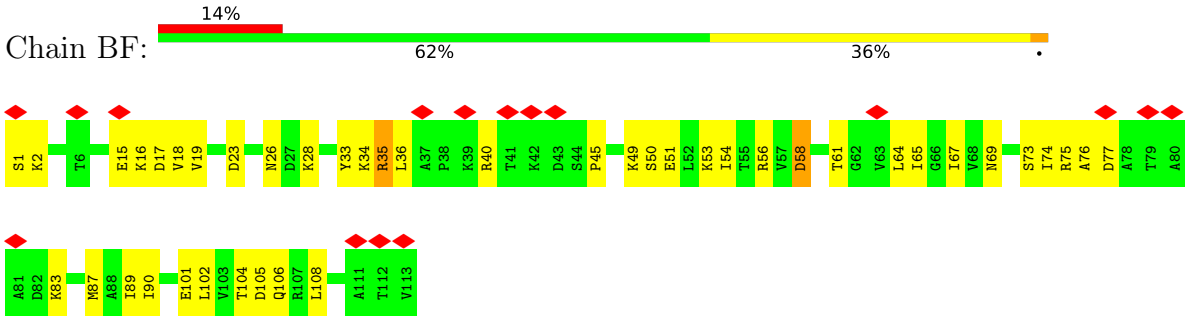
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BE:



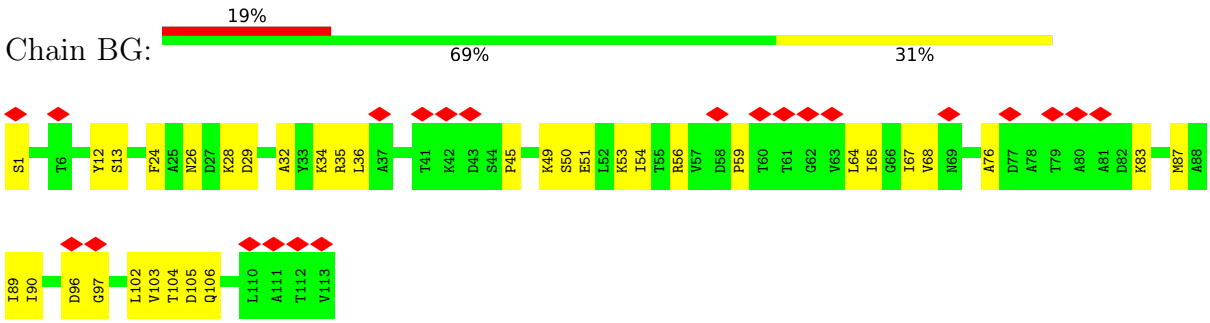
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BF:



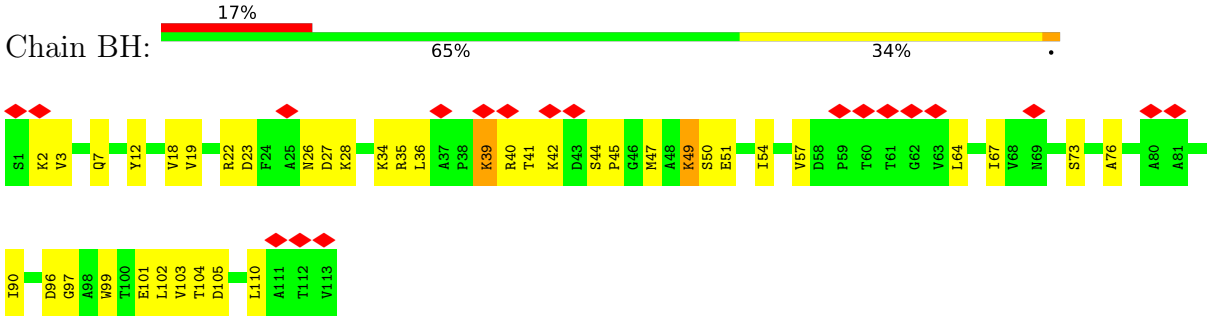
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BG:



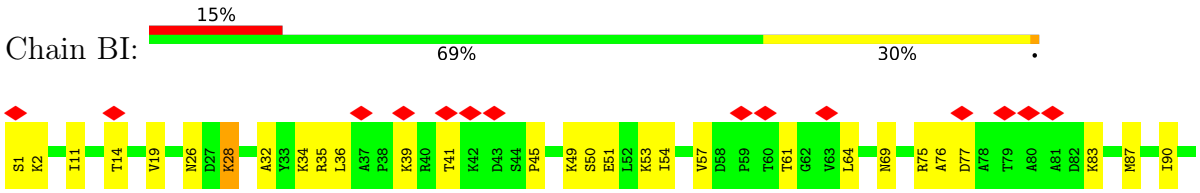
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BH:



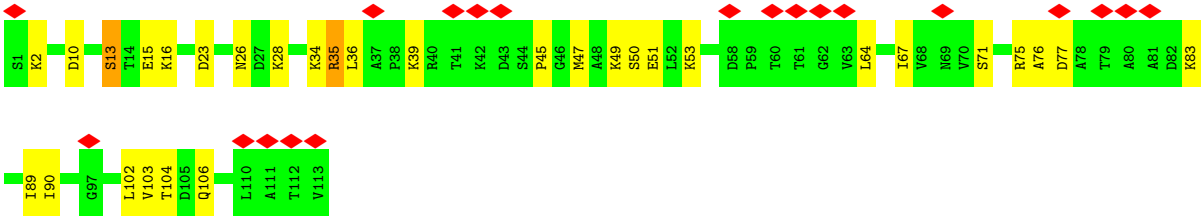
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BI:



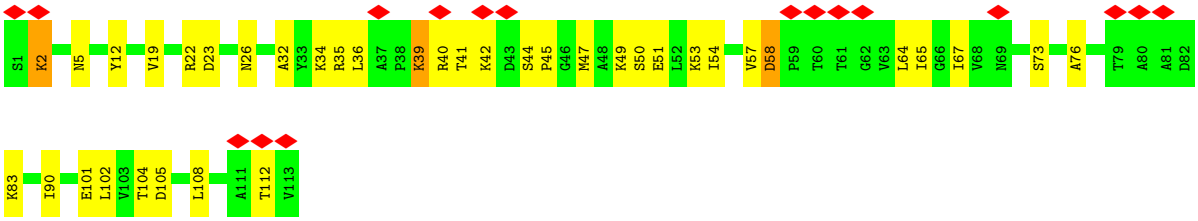
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BJ:



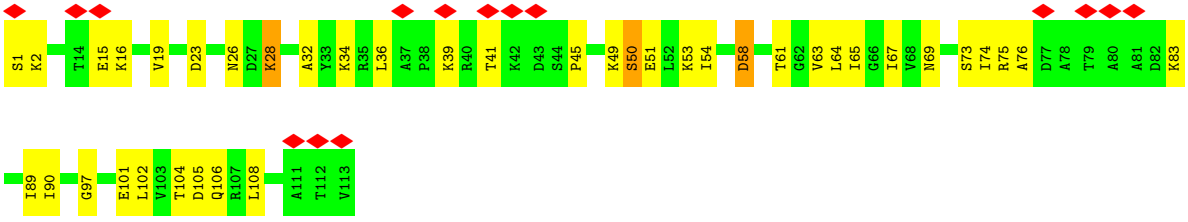
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BK:



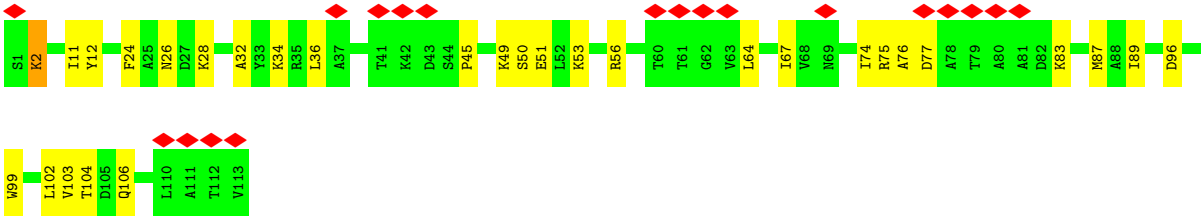
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BL:



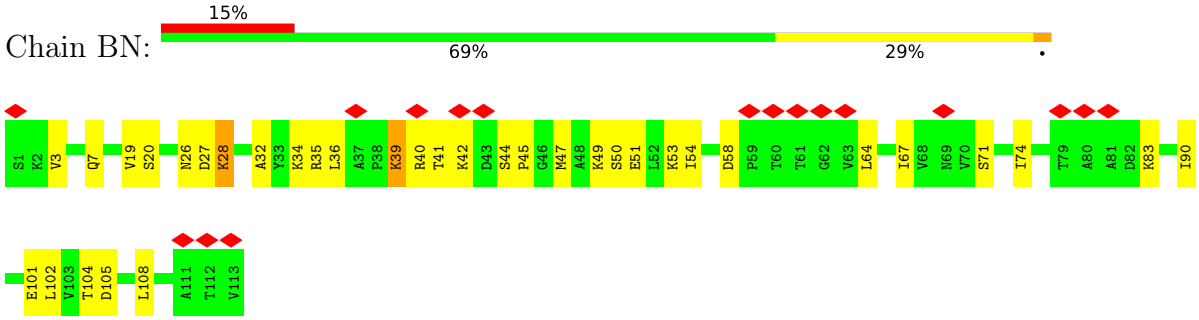
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BM:



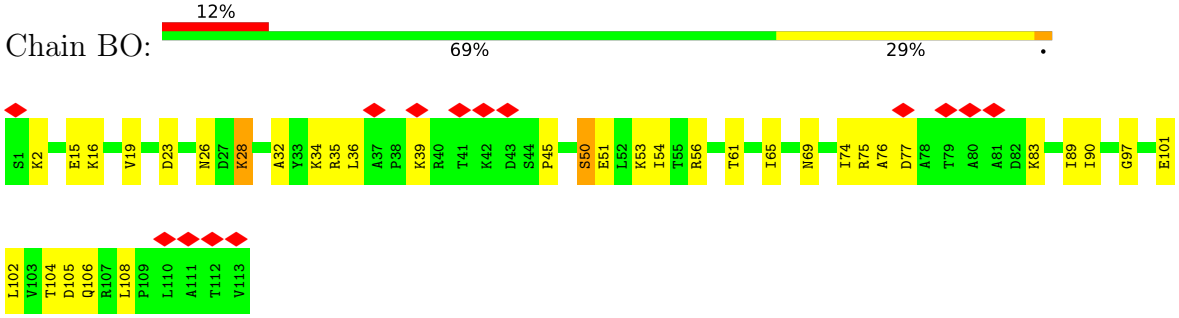
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BN:



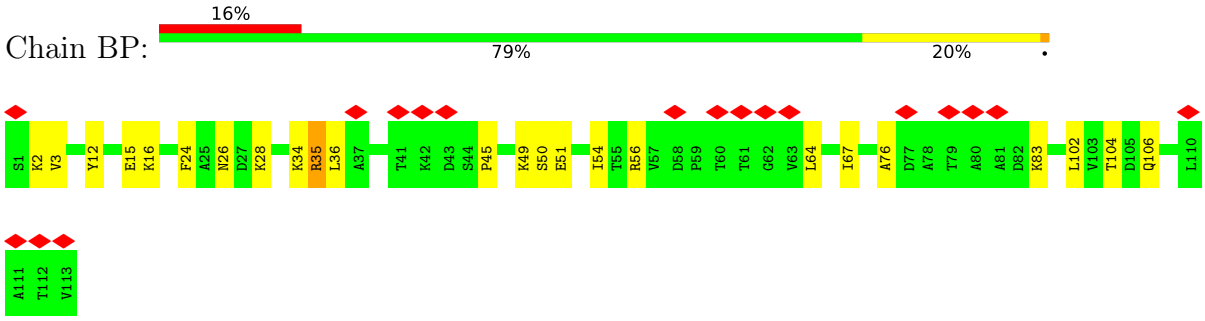
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BO:



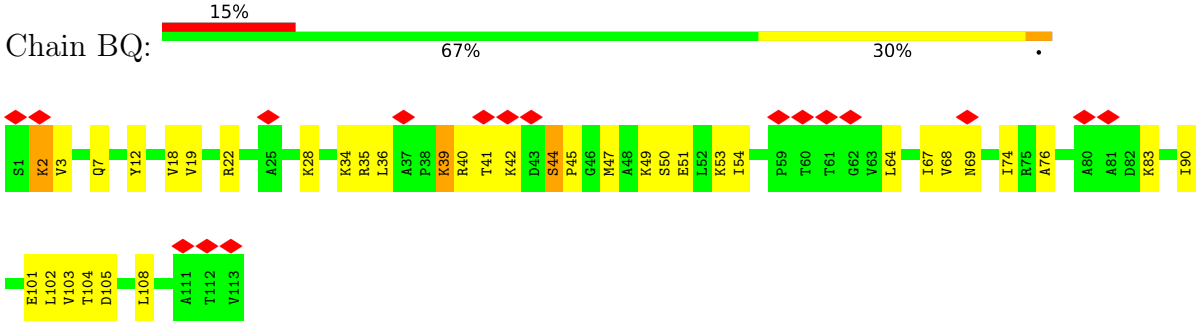
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BP:



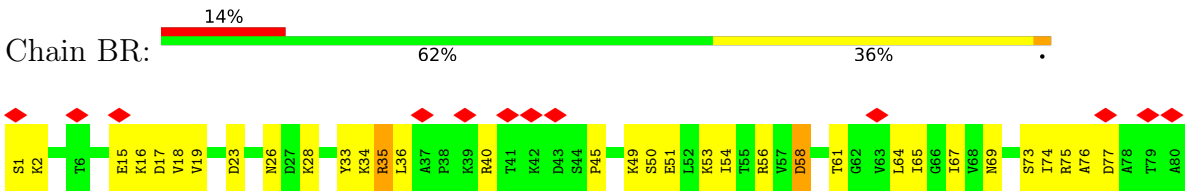
• Molecule 1: coat protein of ssRNA phage ESO003

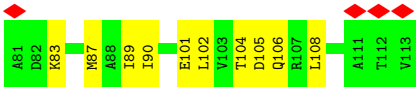
Chain BQ:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain BR:



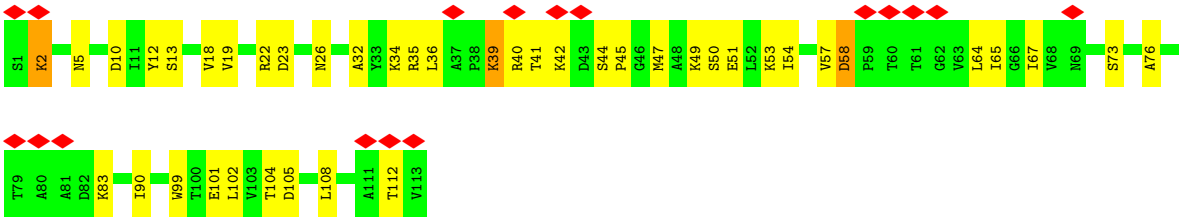


• Molecule 1: coat protein of ssRNA phage ESO003

Chain BS:

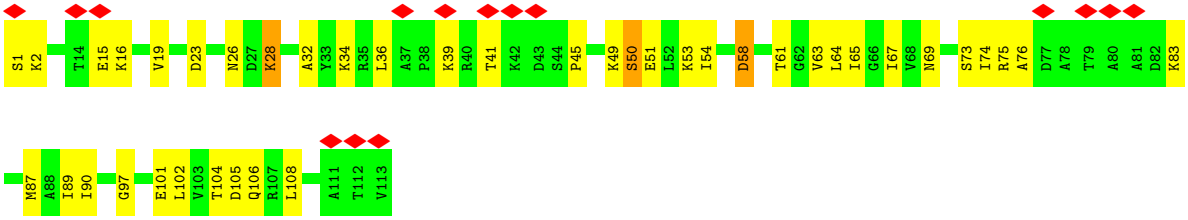
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BT:



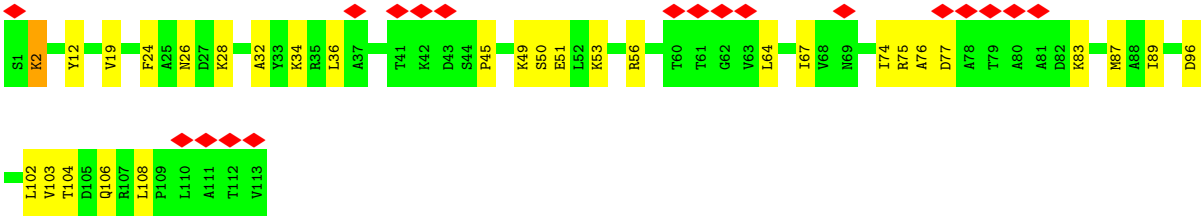
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BU:



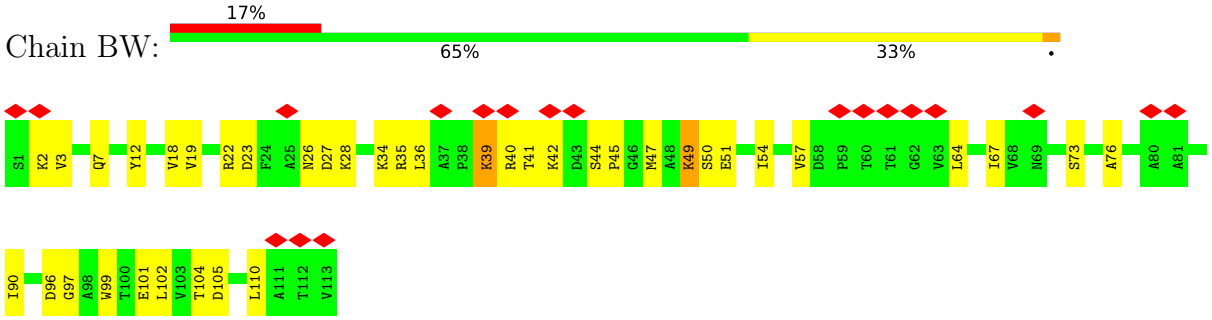
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BV:



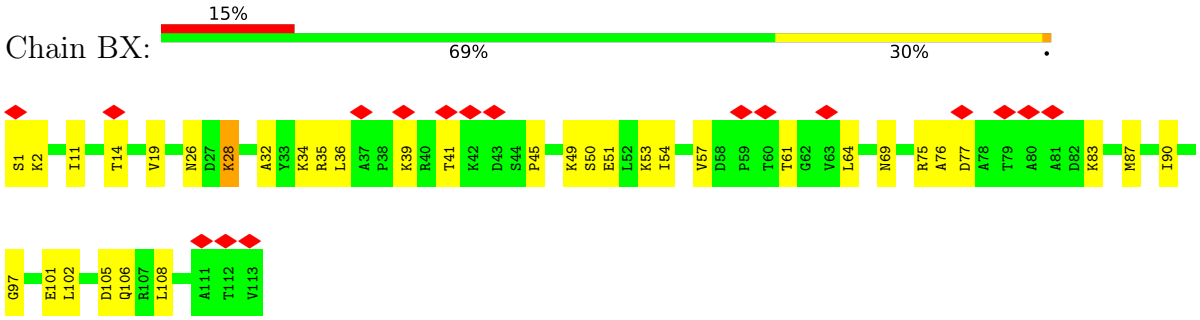
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BW:



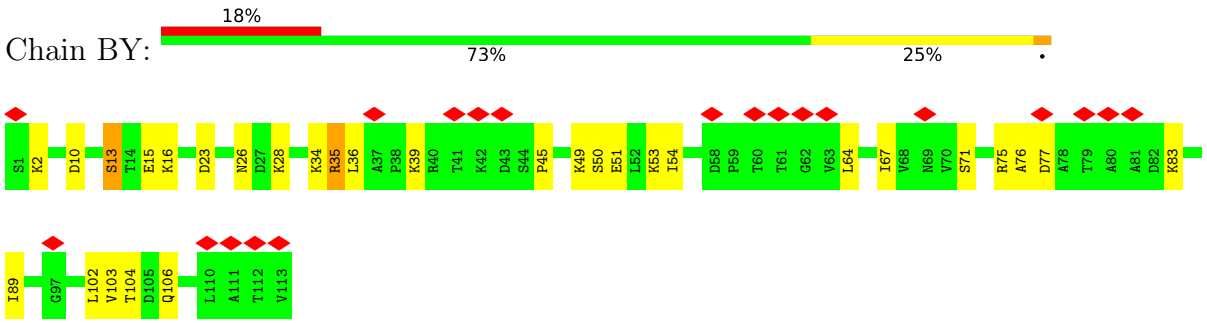
• Molecule 1: coat protein of ssRNA phage ESO003

Chain BX:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain BY:



• Molecule 1: coat protein of ssRNA phage ESO003

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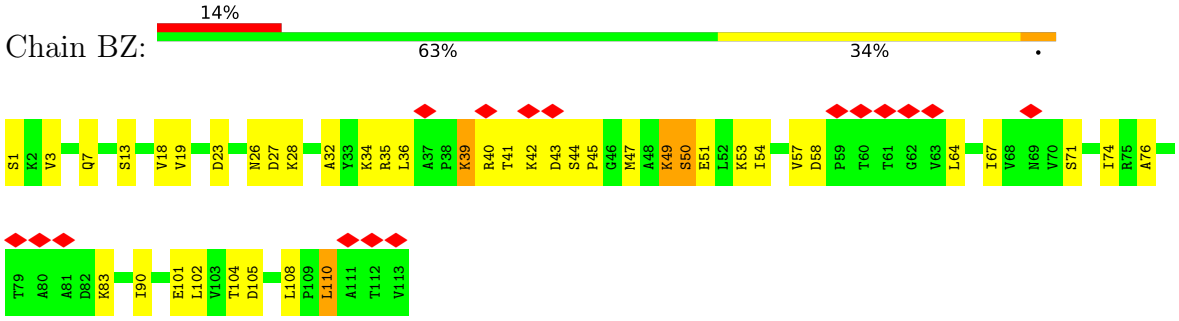
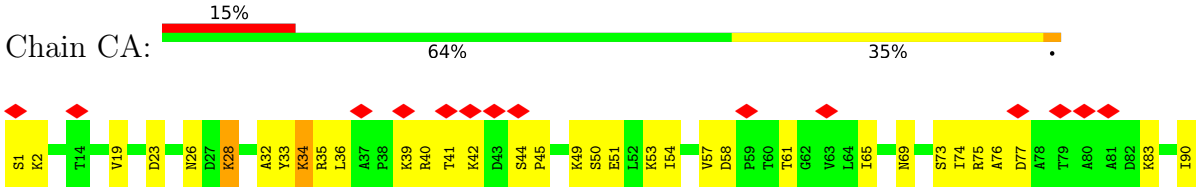


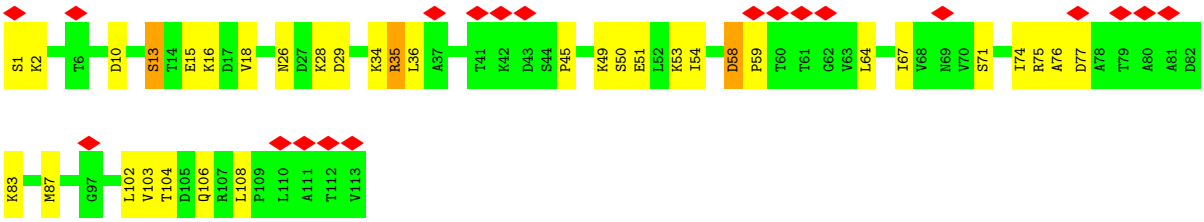
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CA:



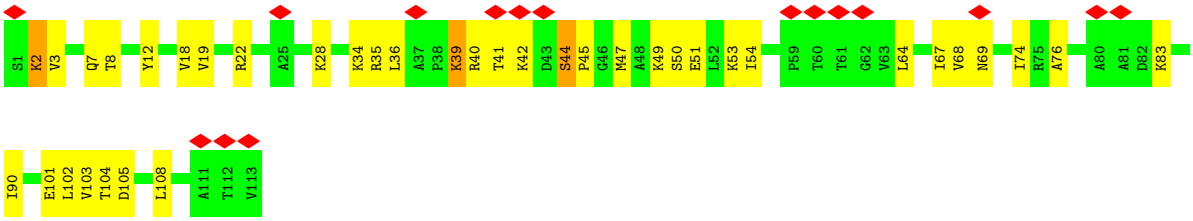
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CB:



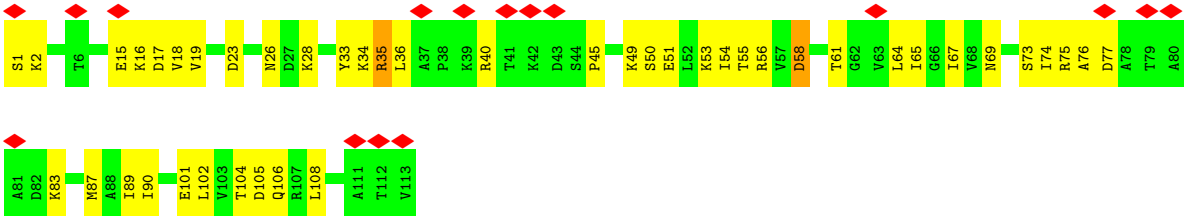
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CC:



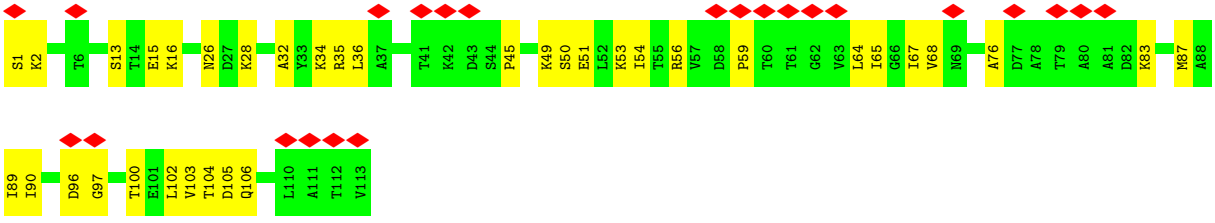
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CD:



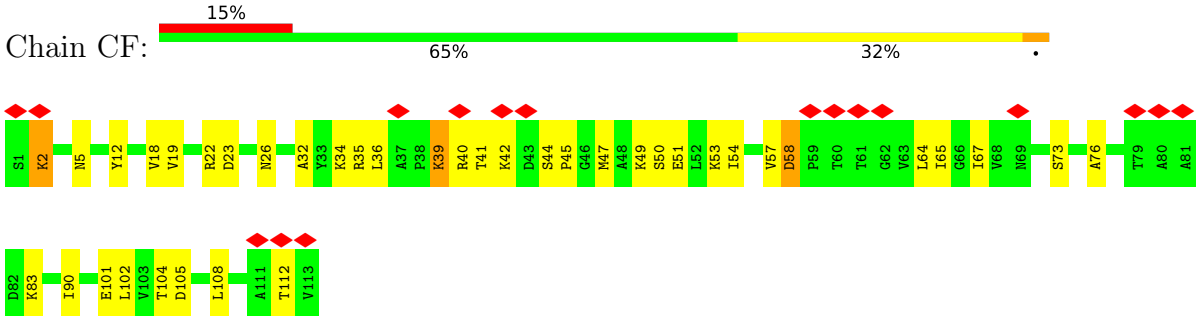
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CE:



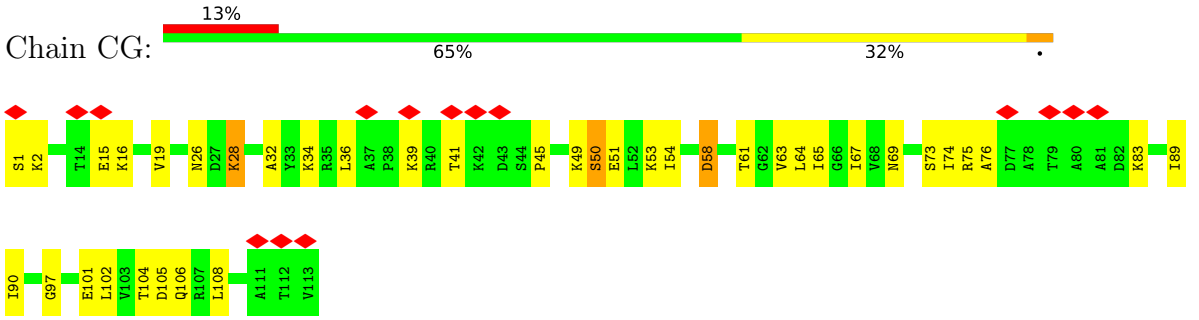
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CF:



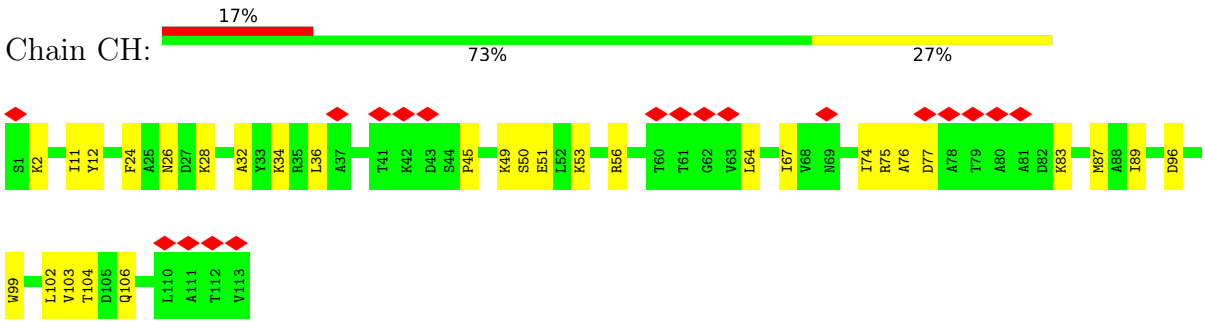
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CG:



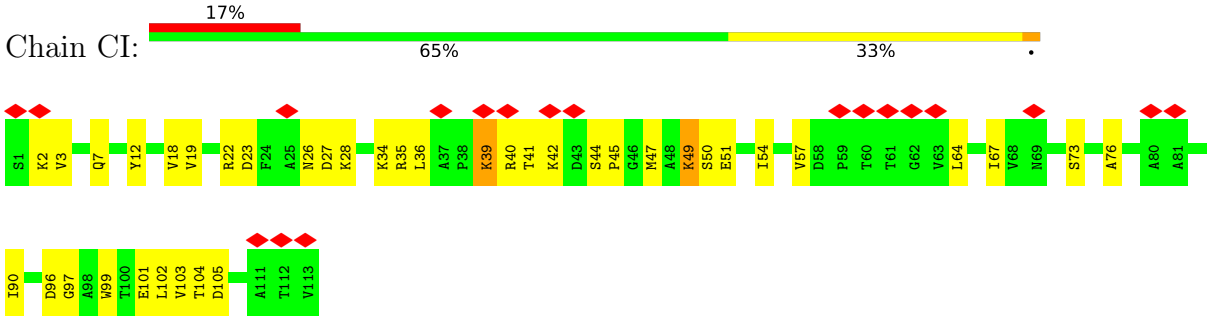
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CH:



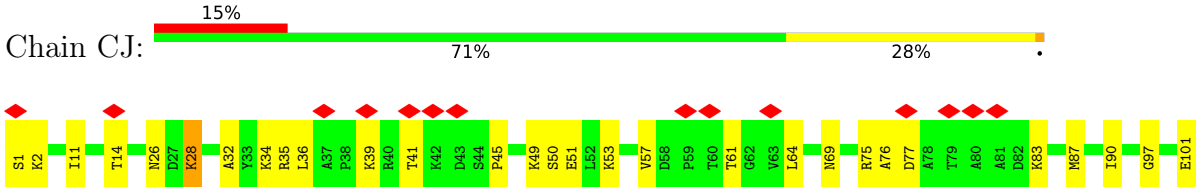
• Molecule 1: coat protein of ssRNA phage ESO003

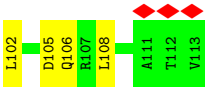
Chain CI:



• Molecule 1: coat protein of ssRNA phage ESO003

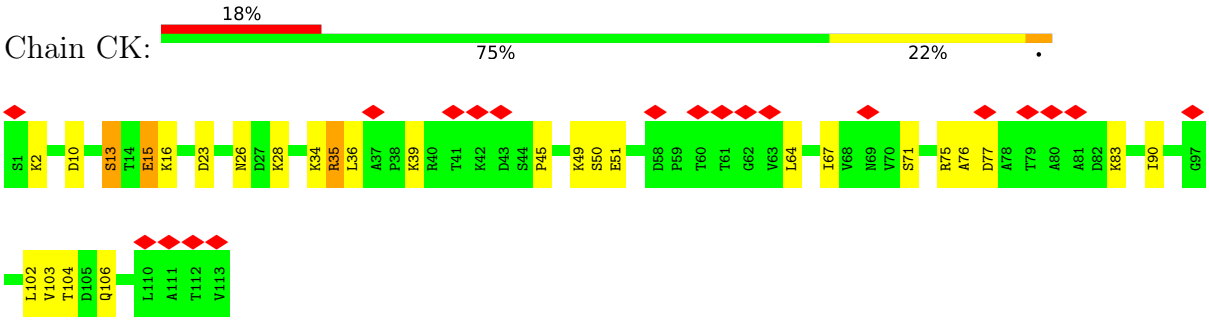
Chain CJ:





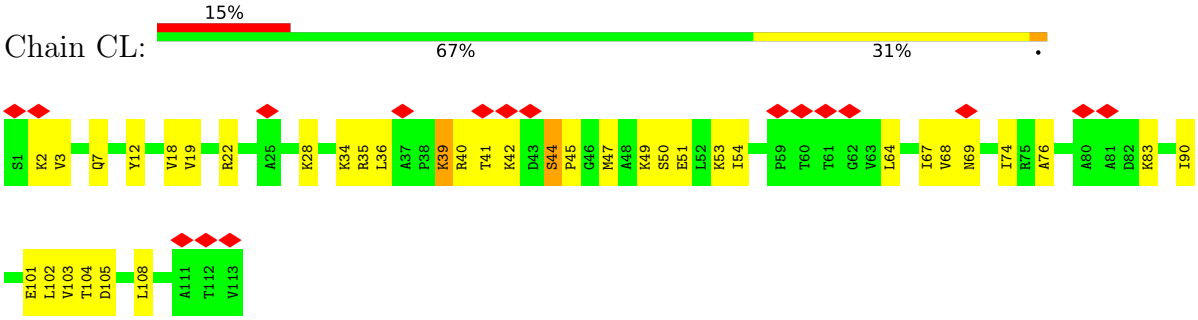
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CK:



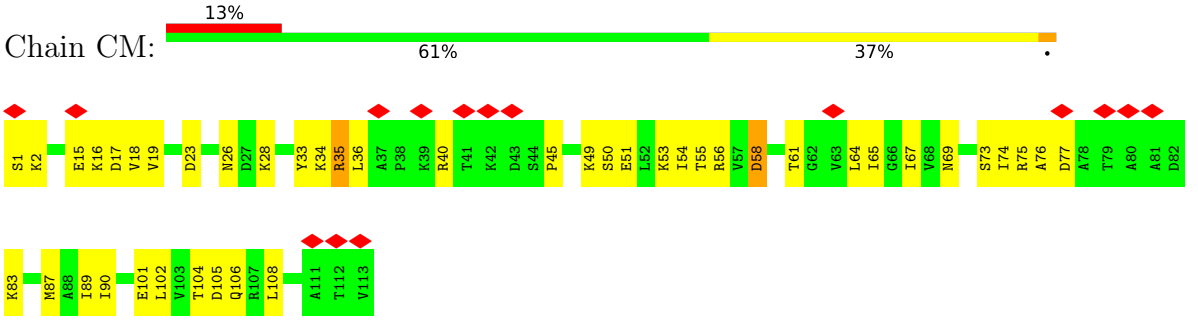
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CL:



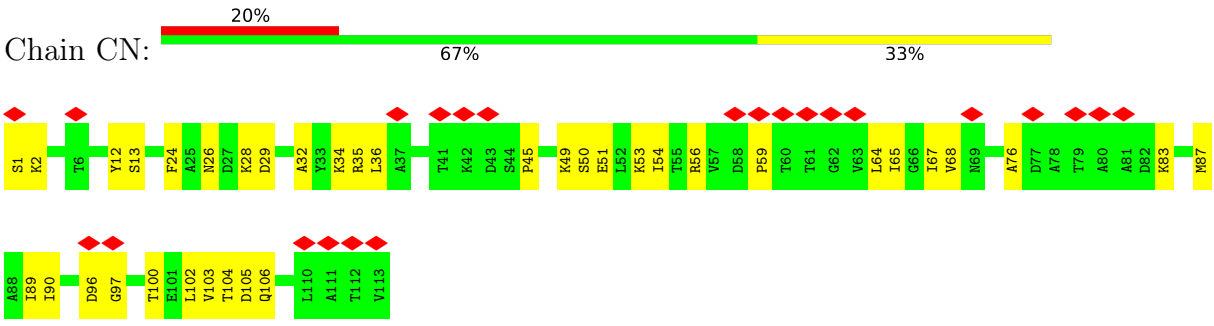
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CM:



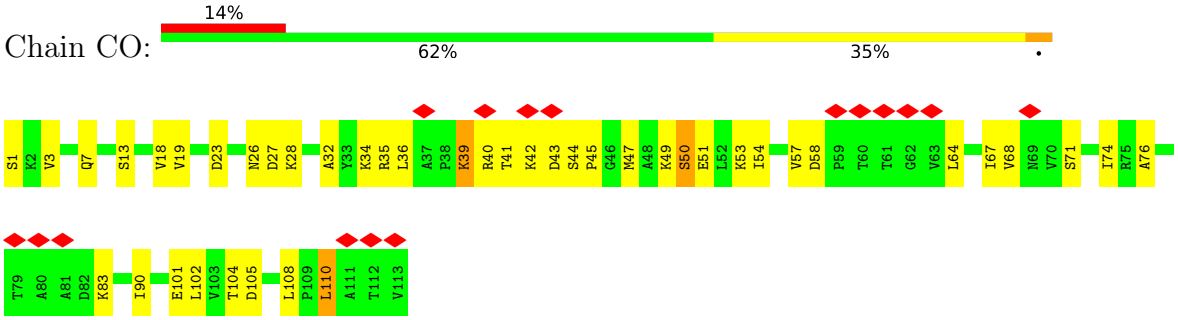
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CN:



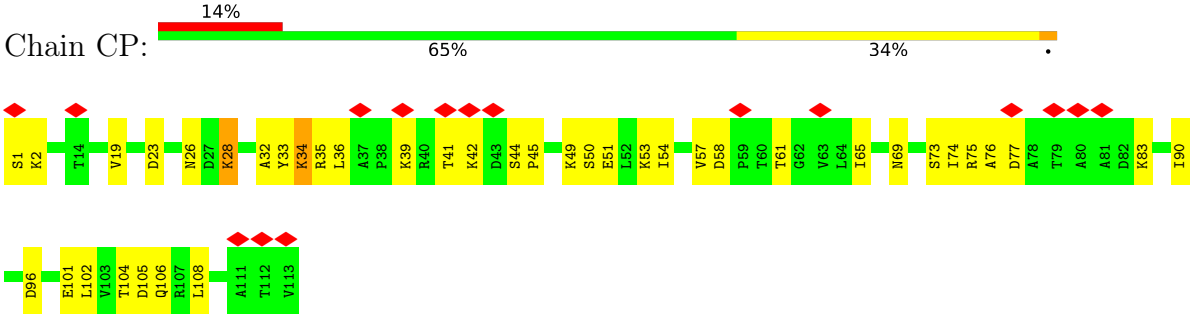
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CO:



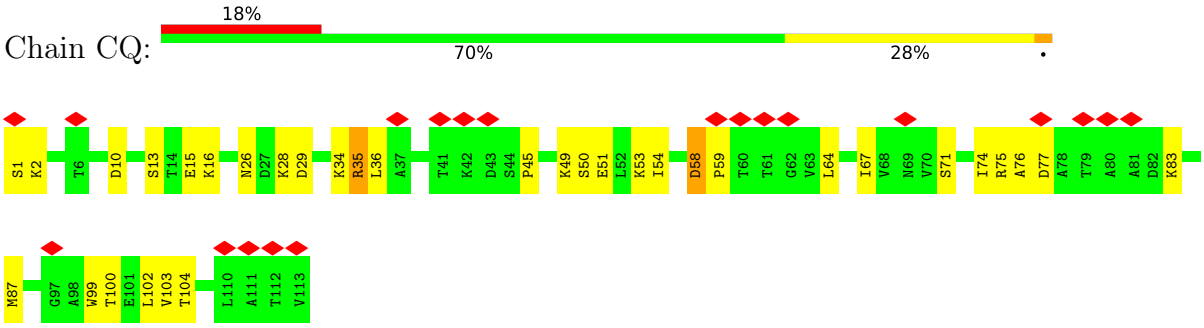
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CP:



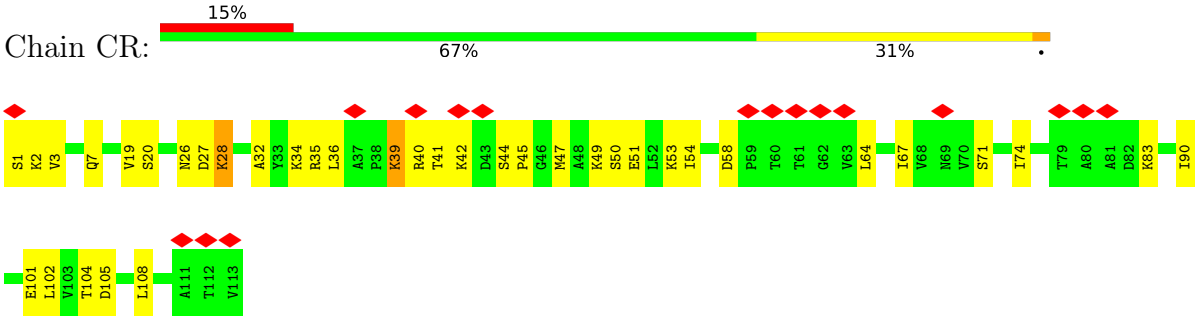
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CQ:



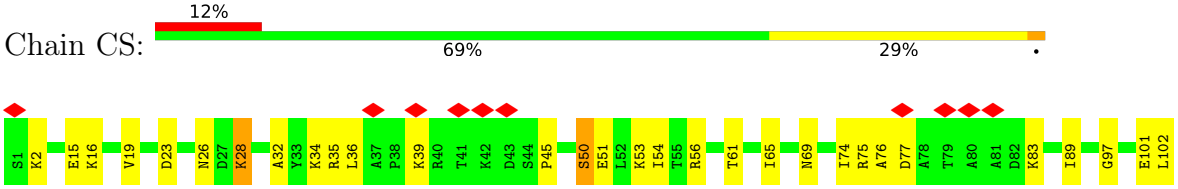
• Molecule 1: coat protein of ssRNA phage ESO003

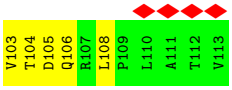
Chain CR:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain CS:





• Molecule 1: coat protein of ssRNA phage ESO003

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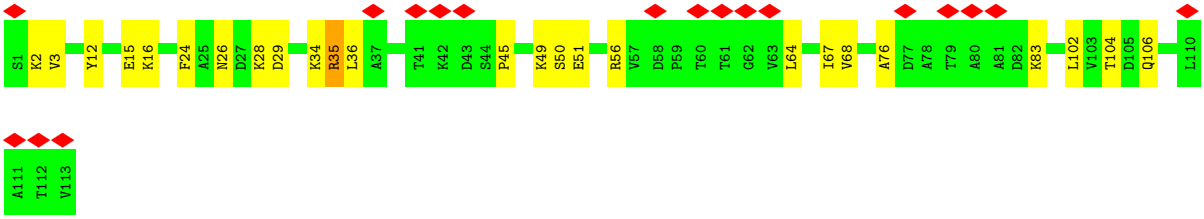
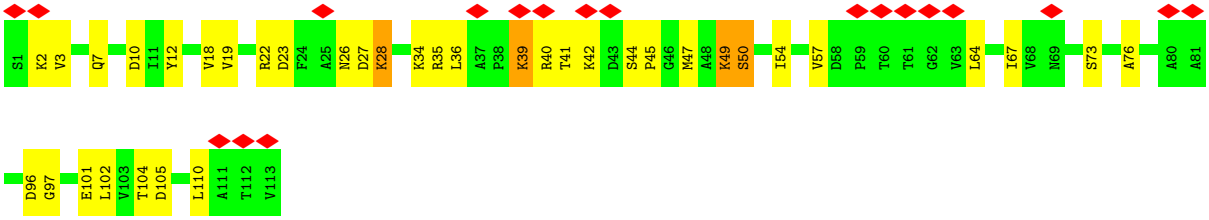


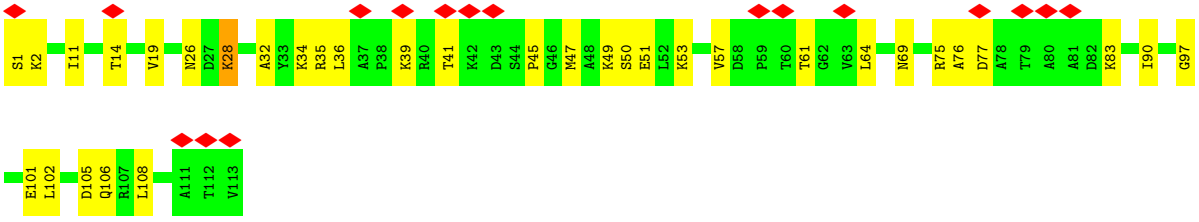
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CU:



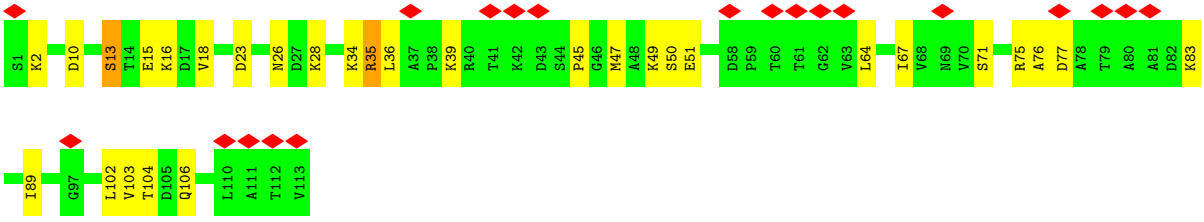
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CV:



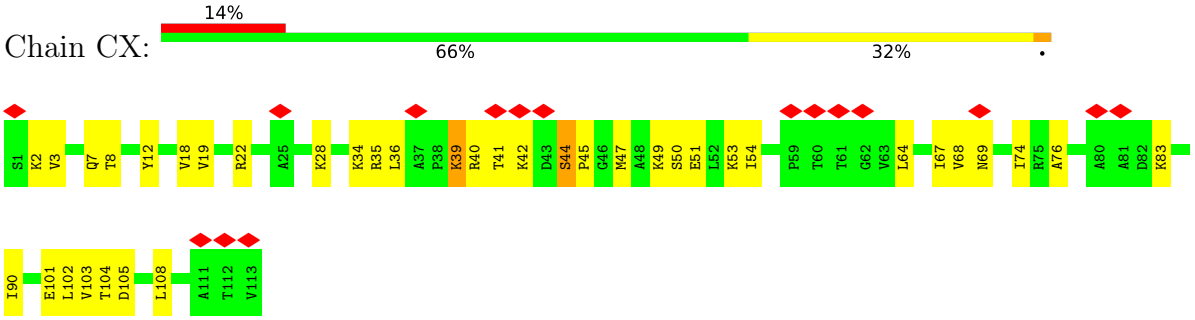
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CW:



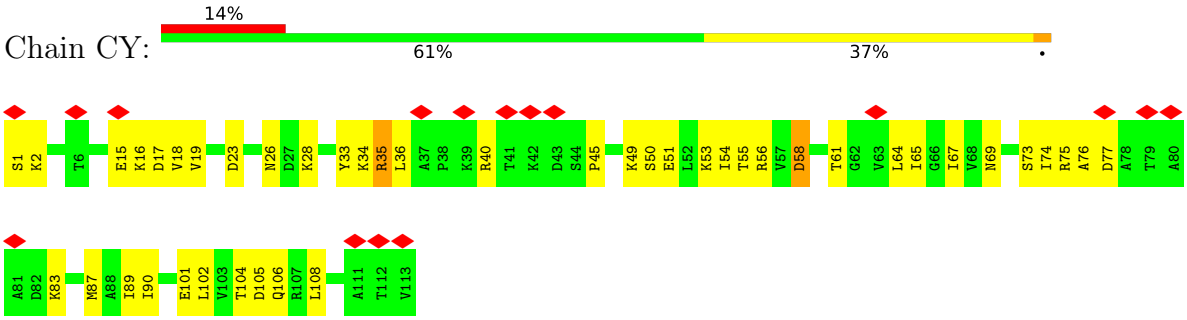
• Molecule 1: coat protein of ssRNA phage ESO003

Chain CX:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain CY:



• Molecule 1: coat protein of ssRNA phage ESO003

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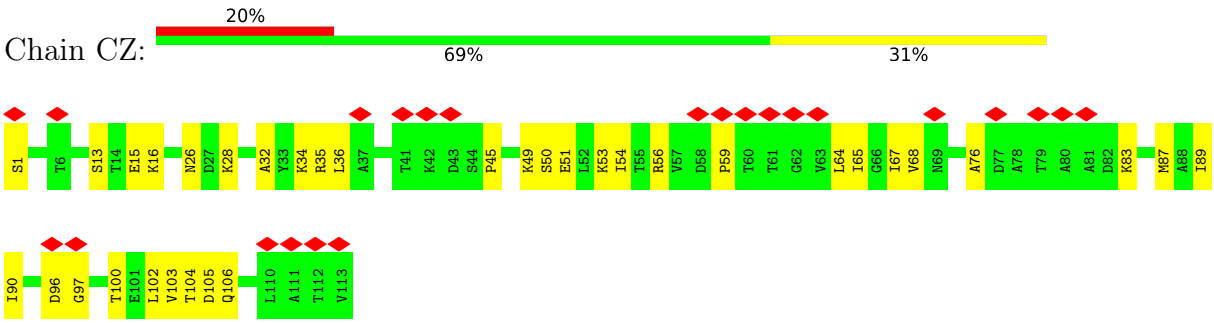
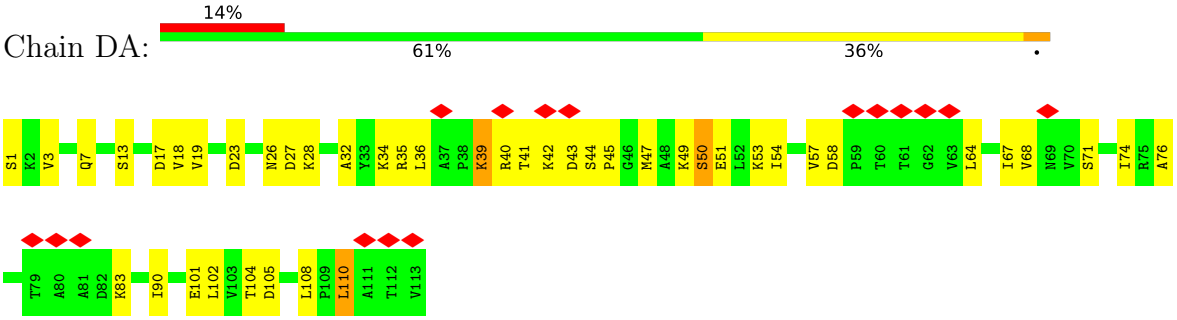


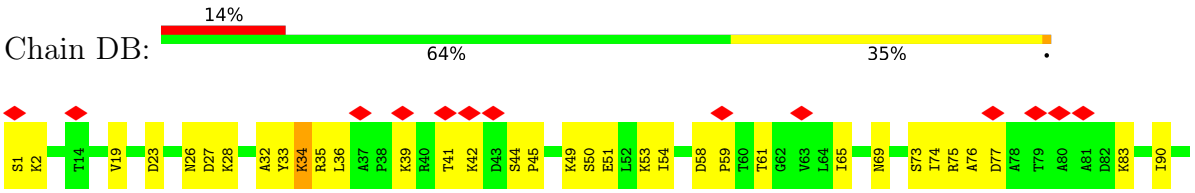
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DA:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain DB:



• Molecule 1: coat protein of ssRNA phage ESO003

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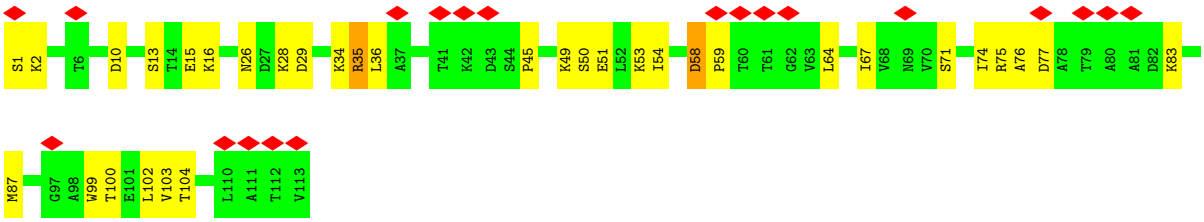
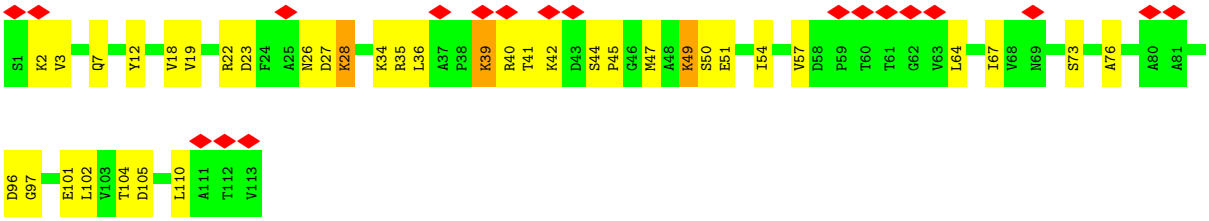


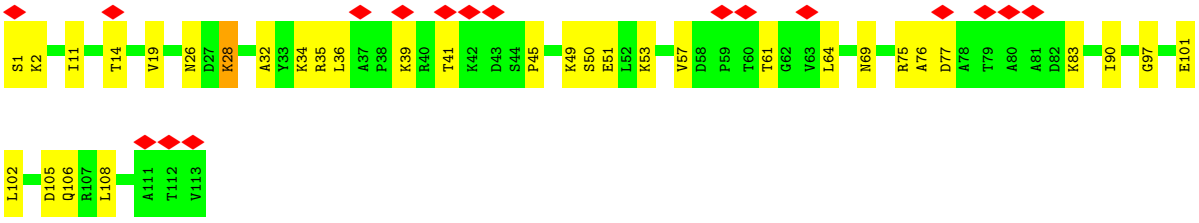
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DD:



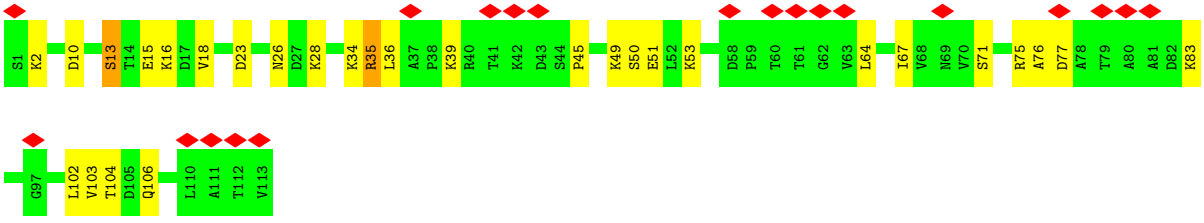
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DE:



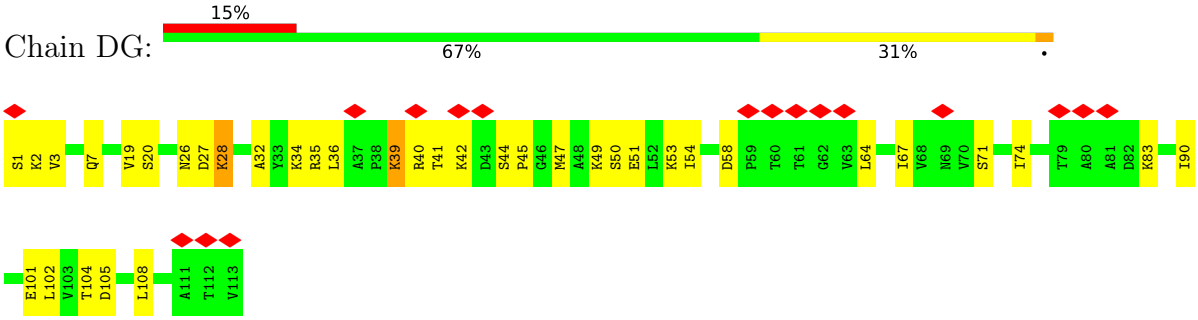
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DF:



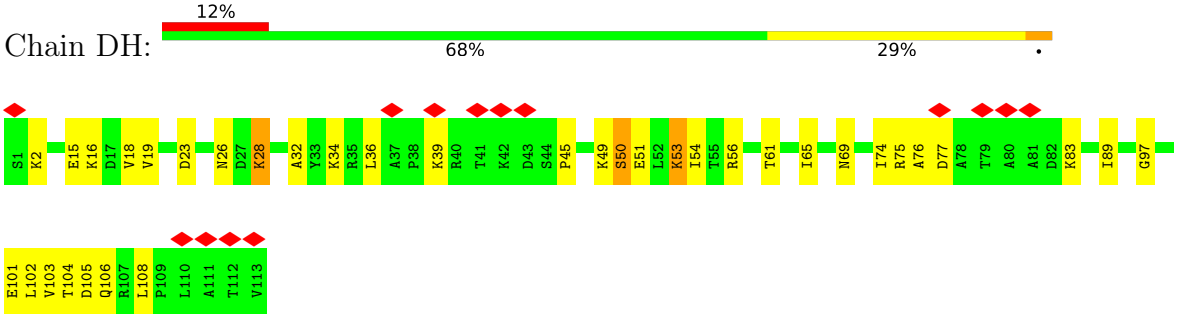
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DG:



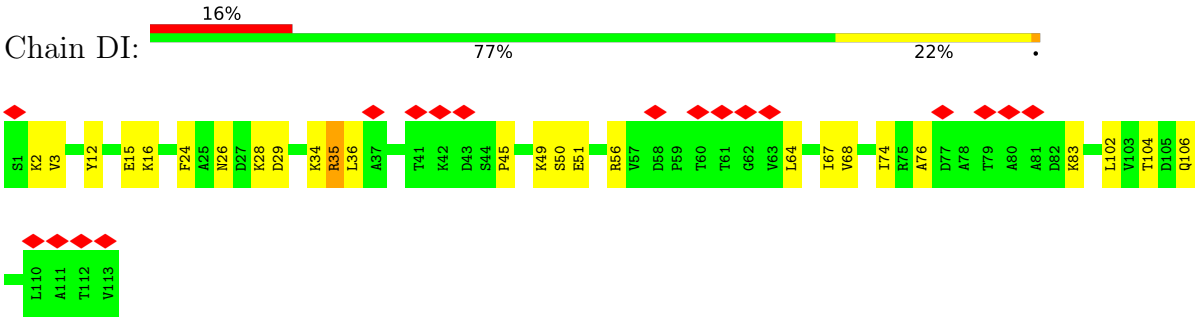
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DH:



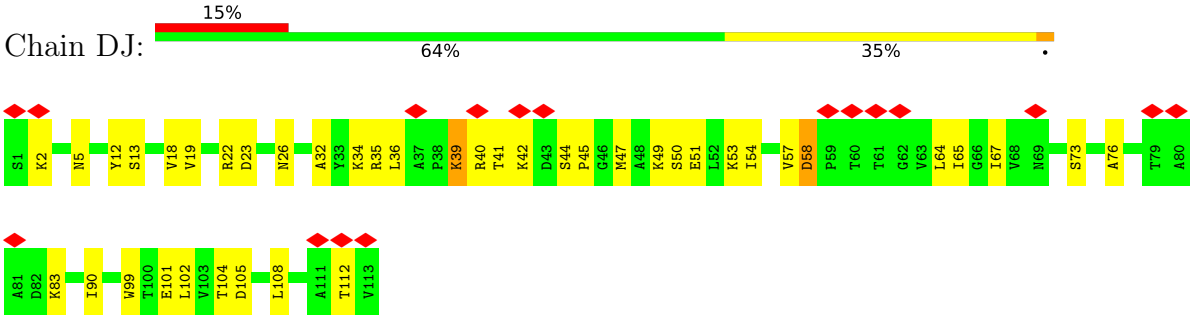
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DI:



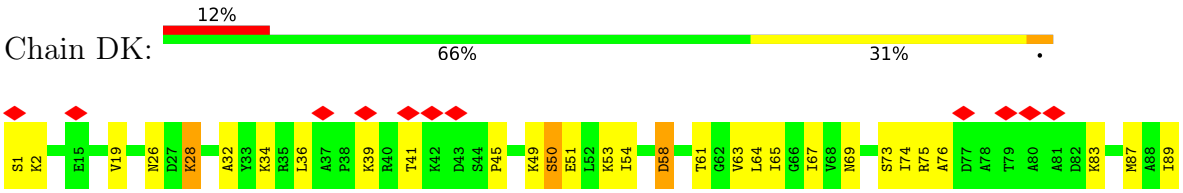
• Molecule 1: coat protein of ssRNA phage ESO003

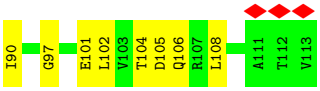
Chain DJ:



• Molecule 1: coat protein of ssRNA phage ESO003

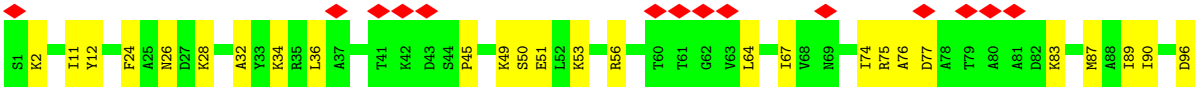
Chain DK:

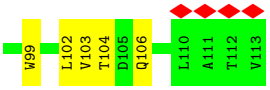




• Molecule 1: coat protein of ssRNA phage ESO003

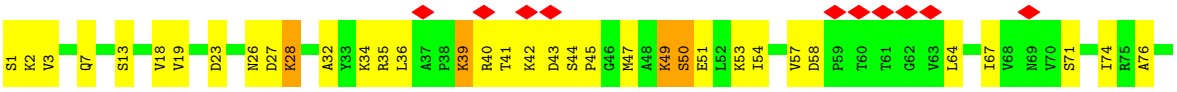
Chain DL:

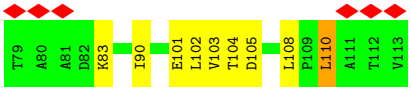




• Molecule 1: coat protein of ssRNA phage ESO003

Chain DM:





• Molecule 1: coat protein of ssRNA phage ESO003

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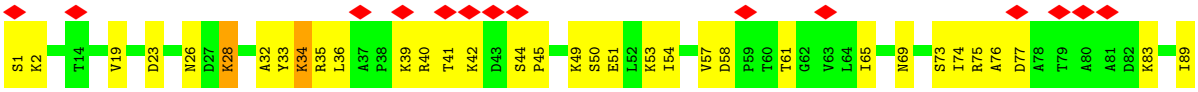

• Molecule 1: coat protein of ssRNA phage ESO003

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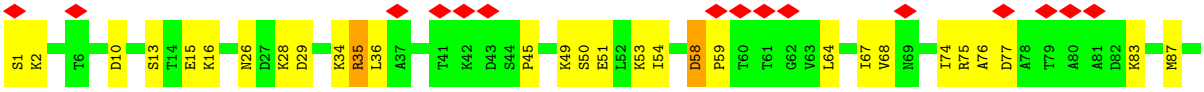
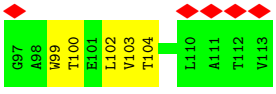
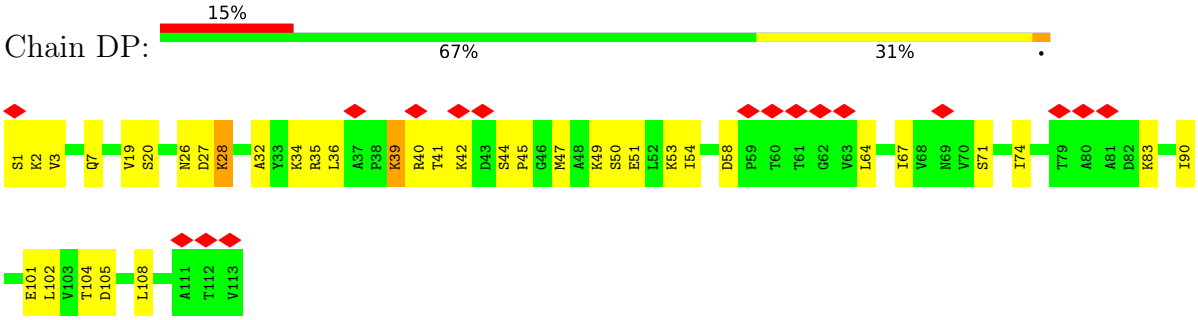




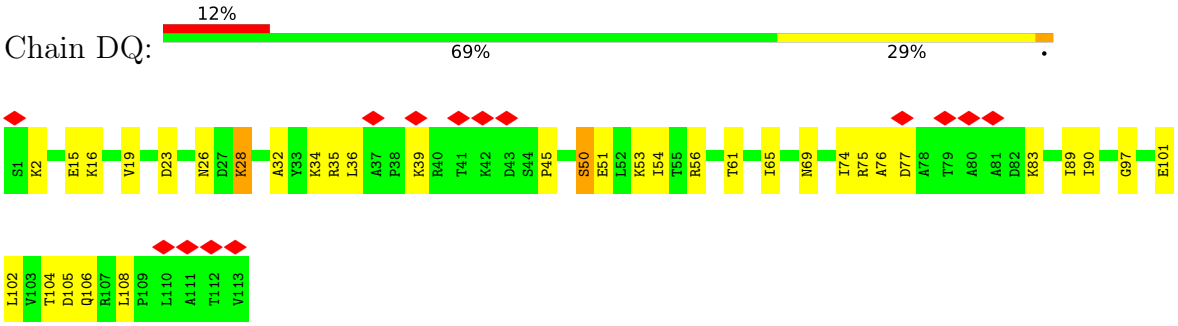
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DP:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain DQ:



• Molecule 1: coat protein of ssRNA phage ESO003

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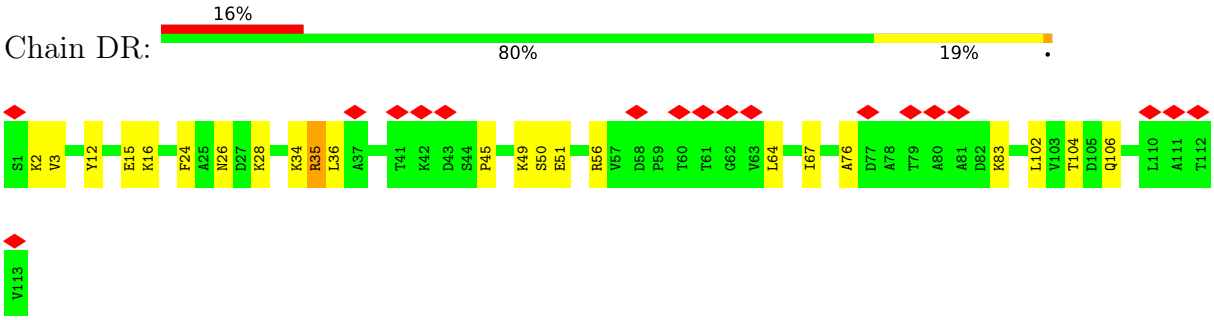
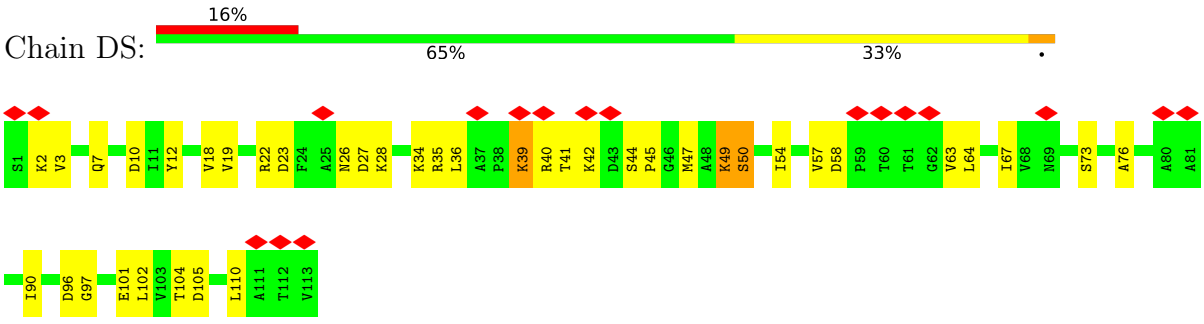


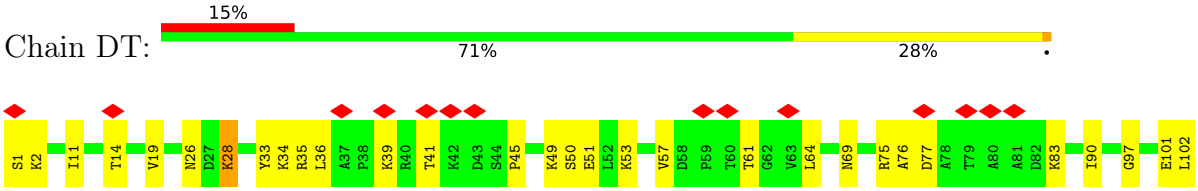
• Molecule 1: coat protein of ssRNA phage ESO003

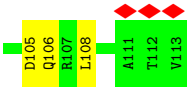
Chain DS:



• Molecule 1: coat protein of ssRNA phage ESO003

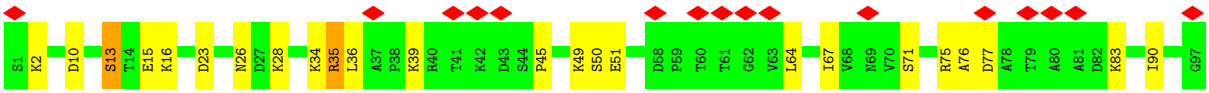
Chain DT:

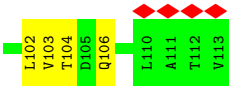




• Molecule 1: coat protein of ssRNA phage ESO003

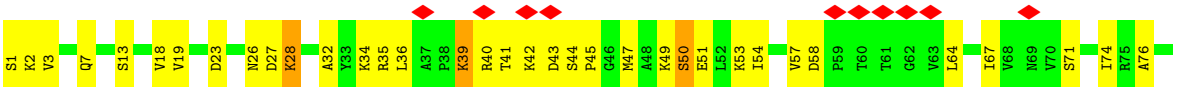
Chain DU:





• Molecule 1: coat protein of ssRNA phage ESO003

Chain DV:

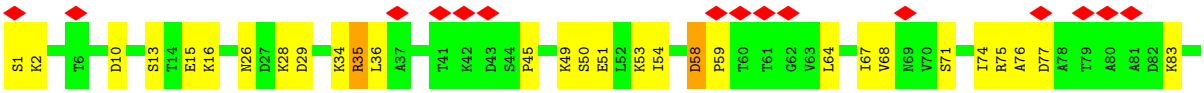


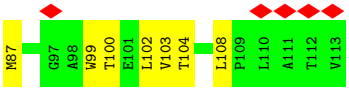
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DW:

• Molecule 1: coat protein of ssRNA phage ESO003

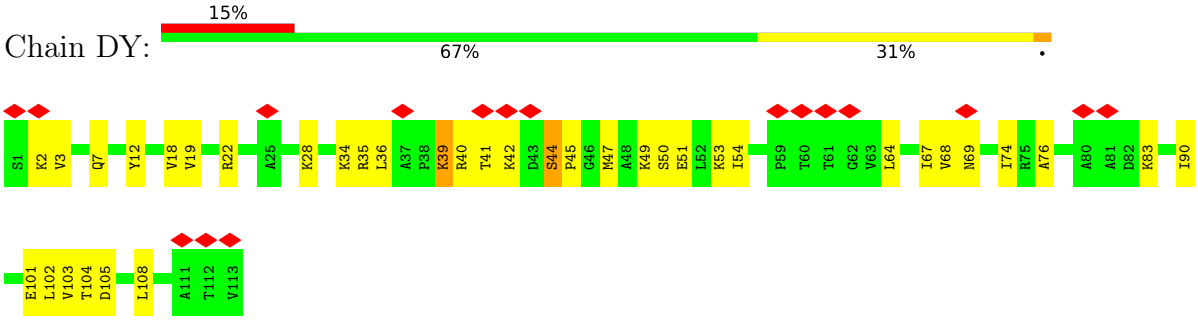
Chain DX:





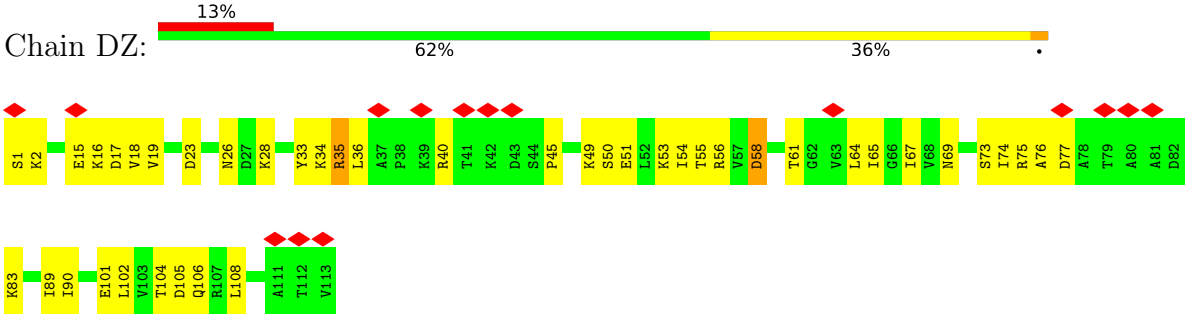
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DY:



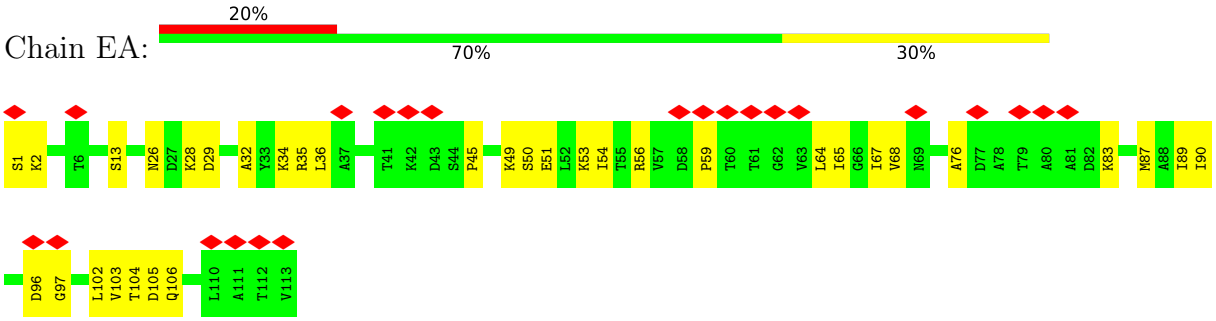
• Molecule 1: coat protein of ssRNA phage ESO003

Chain DZ:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain EA:



• Molecule 1: coat protein of ssRNA phage ESO003

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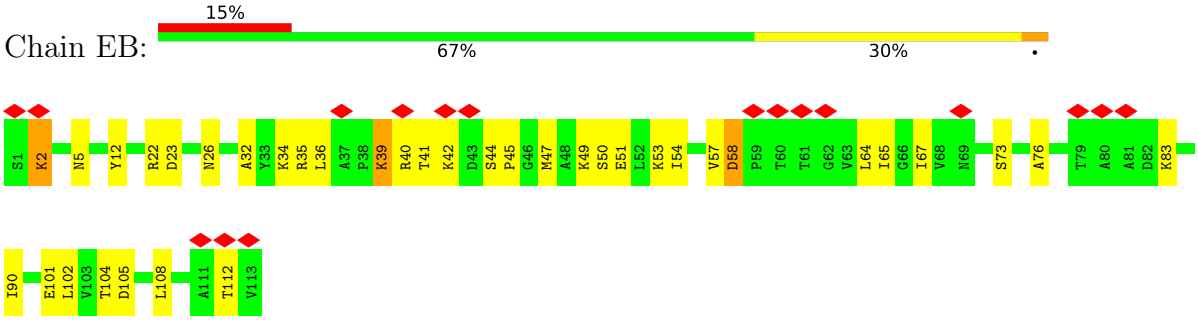
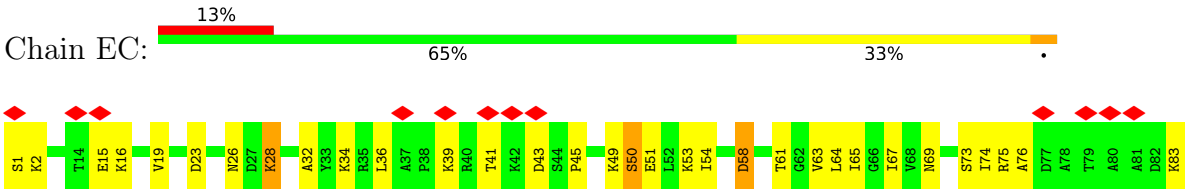


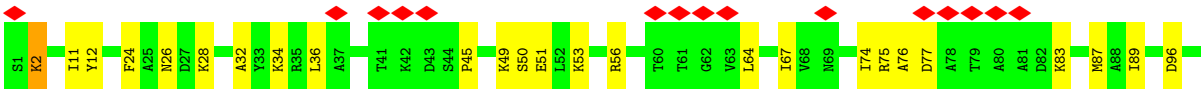
• Molecule 1: coat protein of ssRNA phage ESO003

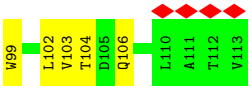
Chain EC:



• Molecule 1: coat protein of ssRNA phage ESO003

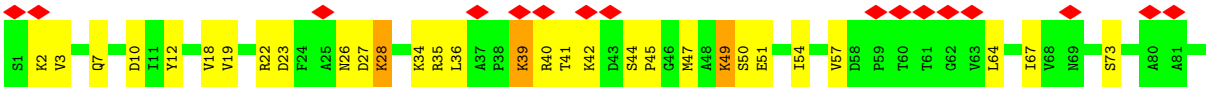
Chain ED:





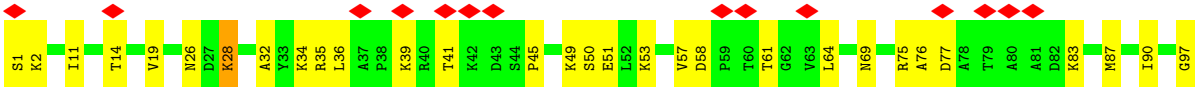
• Molecule 1: coat protein of ssRNA phage ESO003

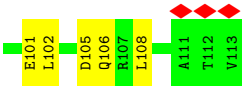
Chain EE:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain EF:





• Molecule 1: coat protein of ssRNA phage ESO003

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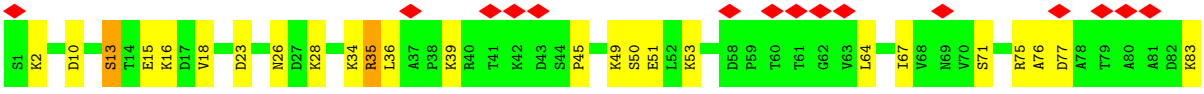
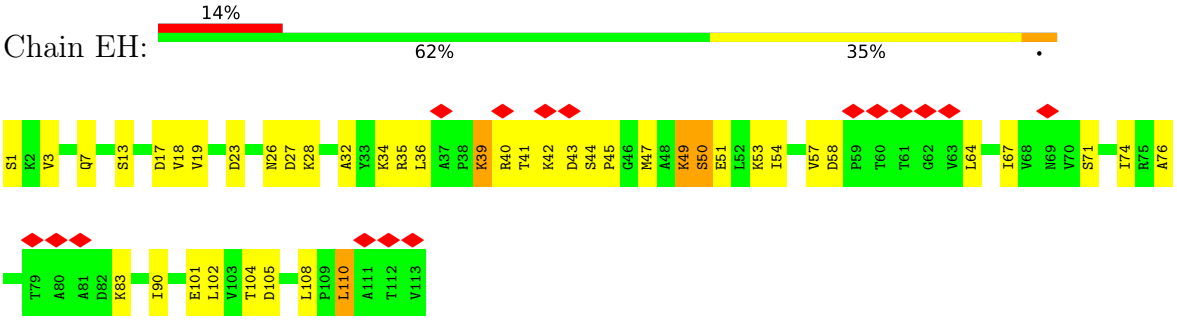


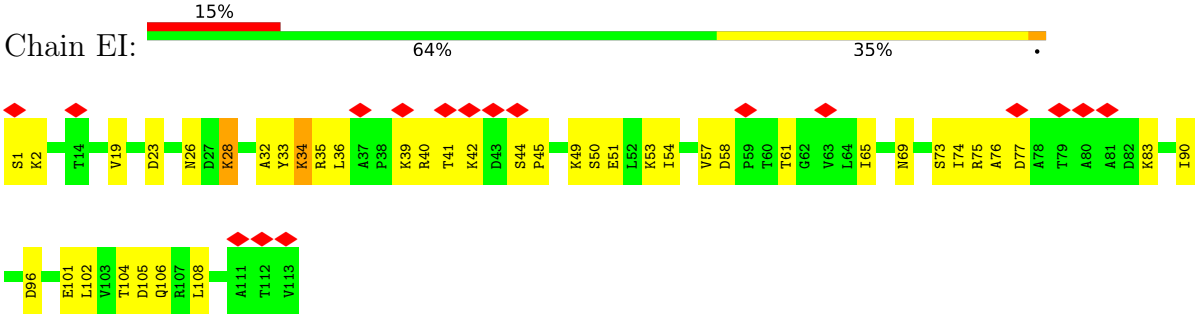
• Molecule 1: coat protein of ssRNA phage ESO003

Chain EH:



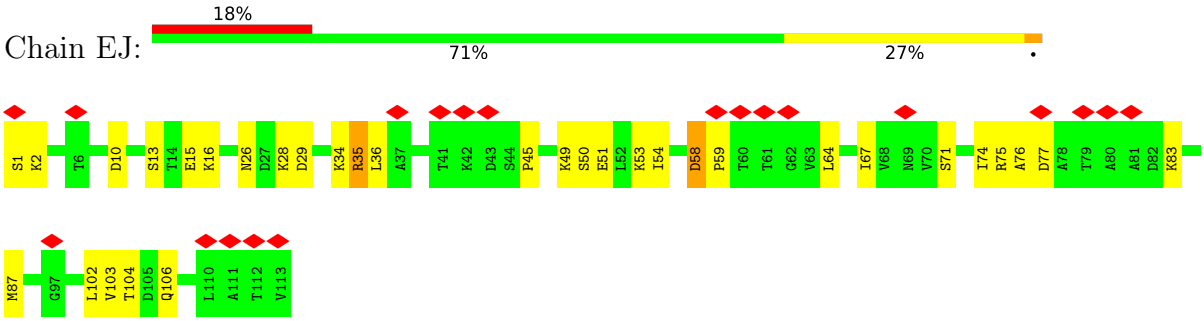
• Molecule 1: coat protein of ssRNA phage ESO003

Chain EI:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain EJ:



• Molecule 1: coat protein of ssRNA phage ESO003

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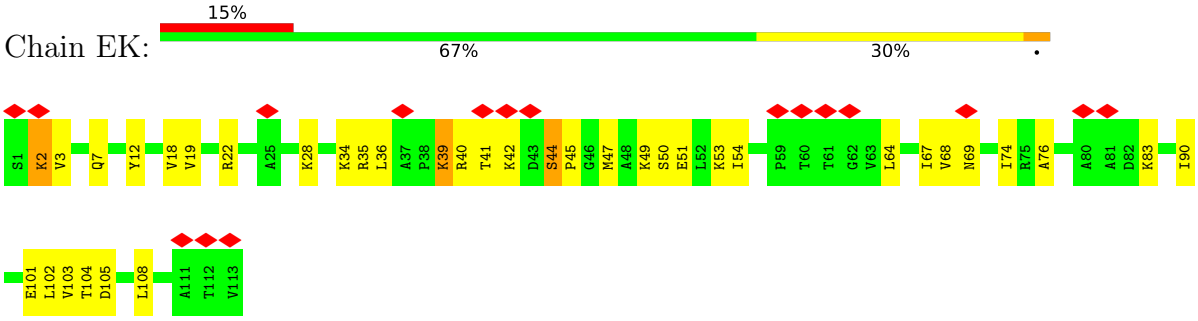
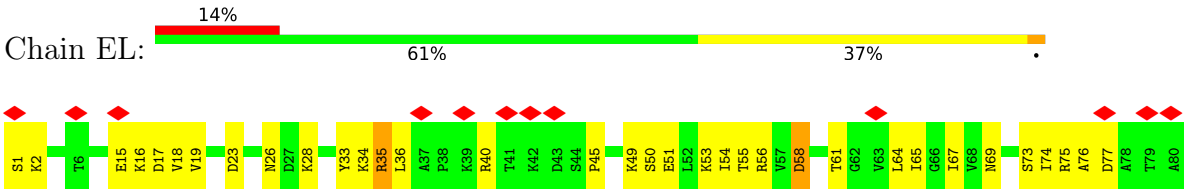
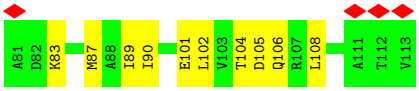


• Molecule 1: coat protein of ssRNA phage ESO003

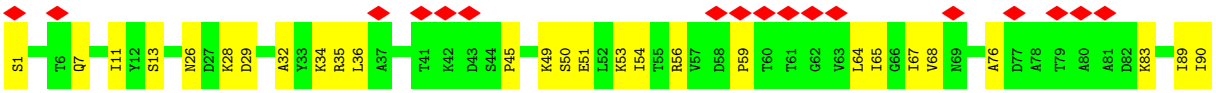
Chain EL:

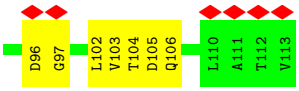




• Molecule 1: coat protein of ssRNA phage ESO003

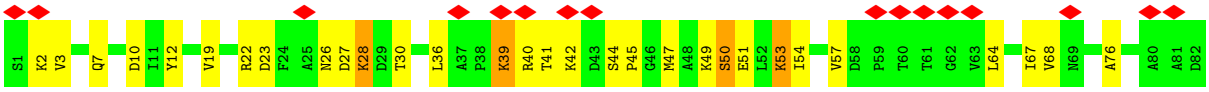
Chain EM:

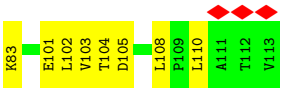




• Molecule 1: coat protein of ssRNA phage ESO003

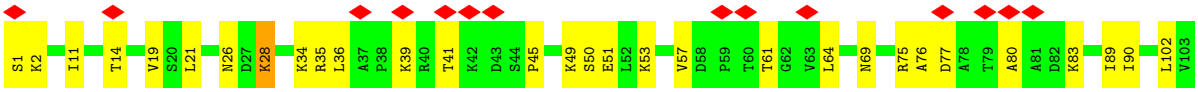
Chain EN:

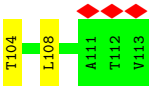




• Molecule 1: coat protein of ssRNA phage ESO003

Chain EO:





• Molecule 1: coat protein of ssRNA phage ESO003

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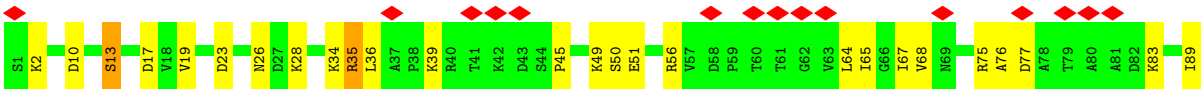
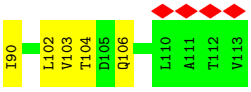
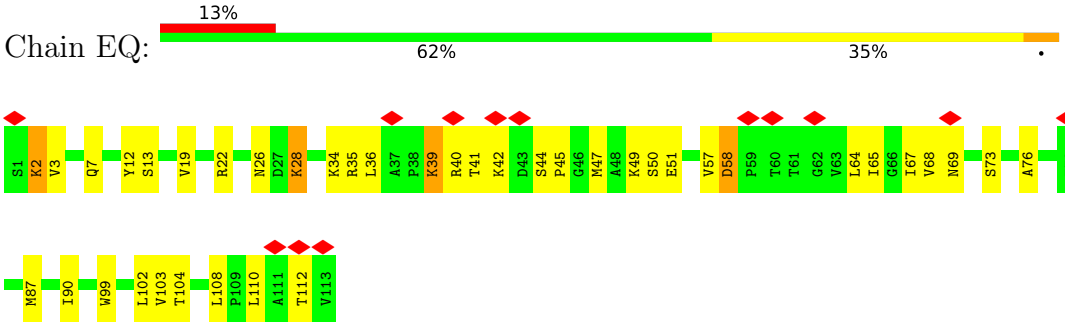




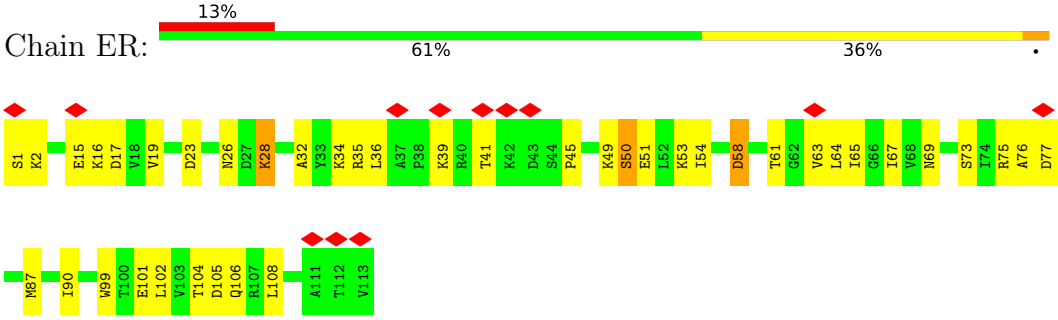
• Molecule 1: coat protein of ssRNA phage ESO003

Chain EQ:



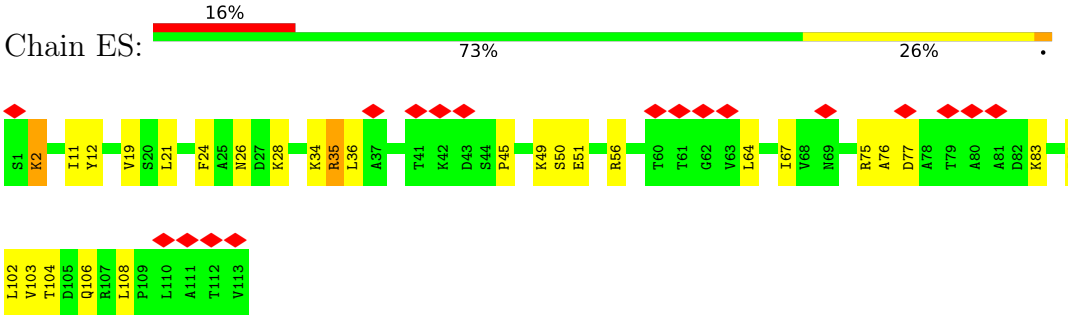
• Molecule 1: coat protein of ssRNA phage ESO003

Chain ER:



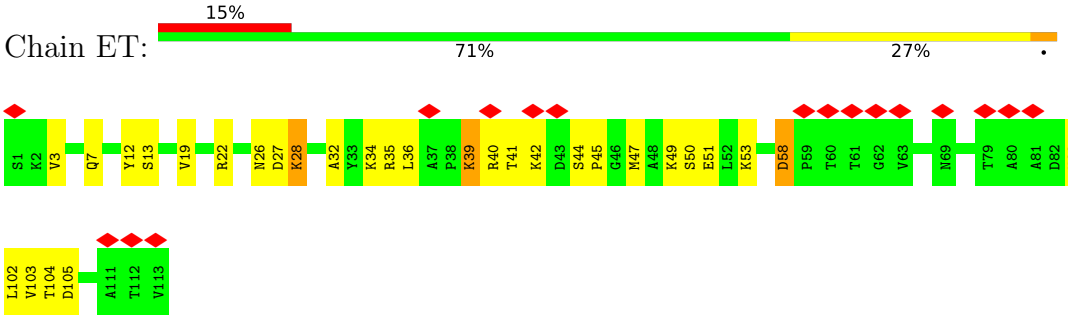
• Molecule 1: coat protein of ssRNA phage ESO003

Chain ES:



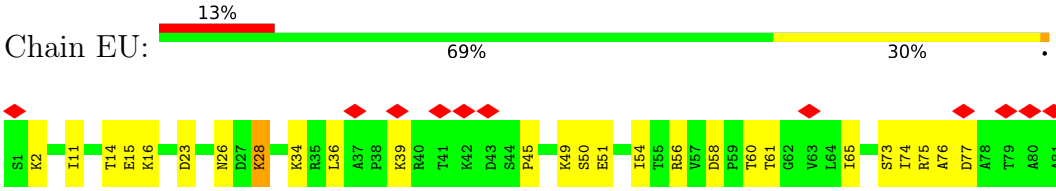
• Molecule 1: coat protein of ssRNA phage ESO003

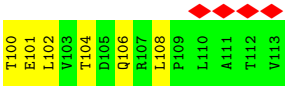
Chain ET:



• Molecule 1: coat protein of ssRNA phage ESO003

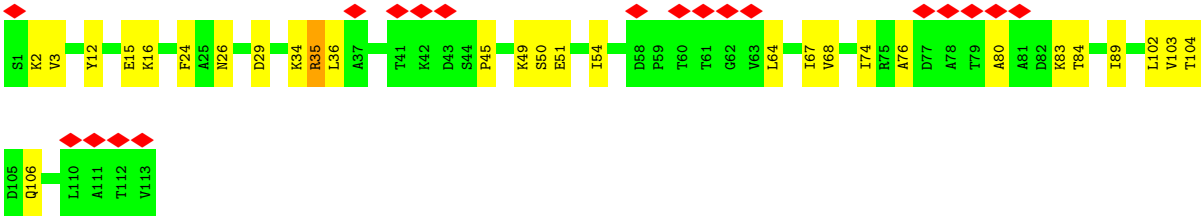
Chain EU:





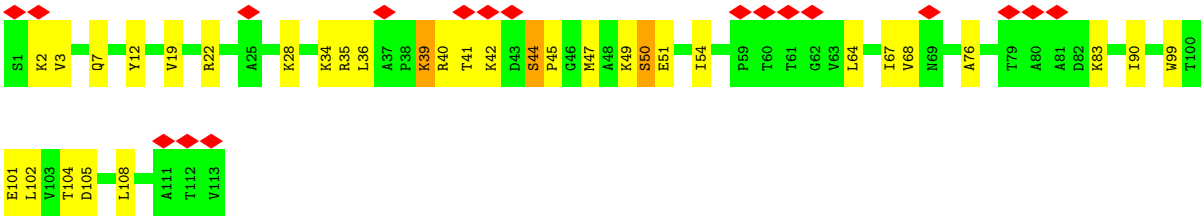
• Molecule 1: coat protein of ssRNA phage ESO003

Chain EV:



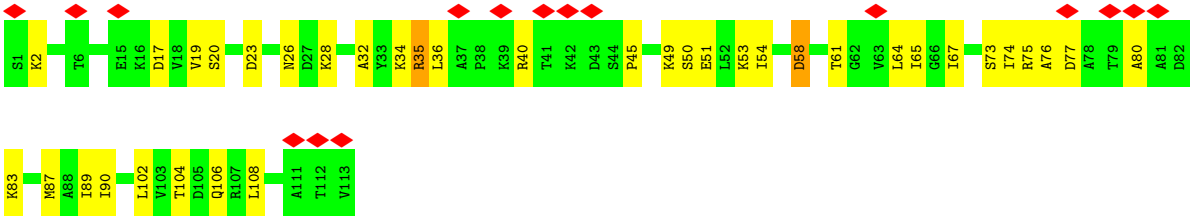
• Molecule 1: coat protein of ssRNA phage ESO003

Chain EW:



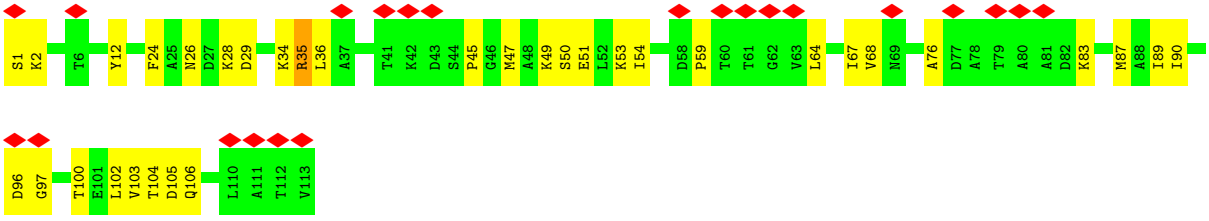
• Molecule 1: coat protein of ssRNA phage ESO003

Chain EX:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain EY:



• Molecule 1: coat protein of ssRNA phage ESO003

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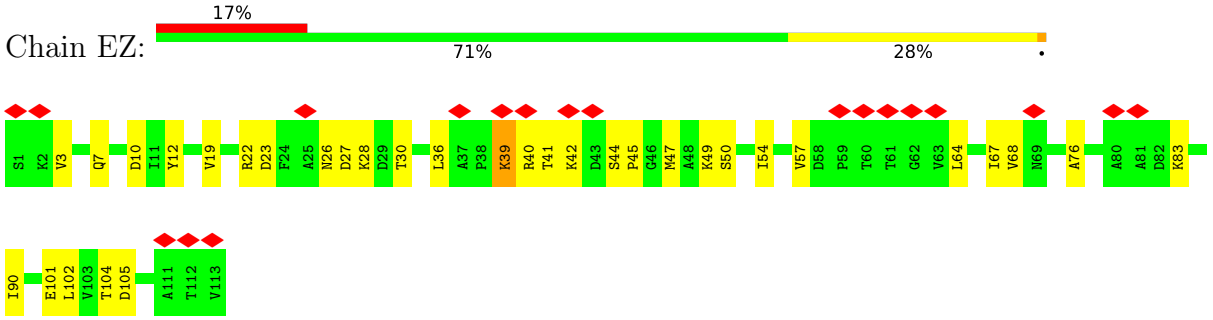

• Molecule 1: coat protein of ssRNA phage ESO003

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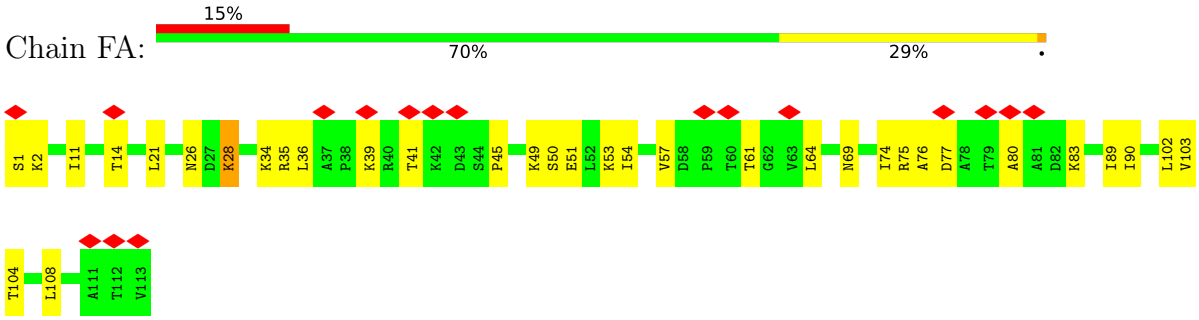
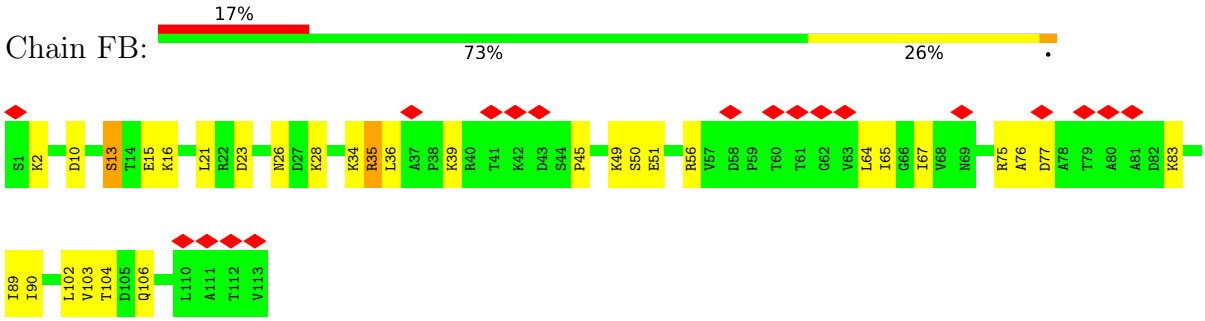


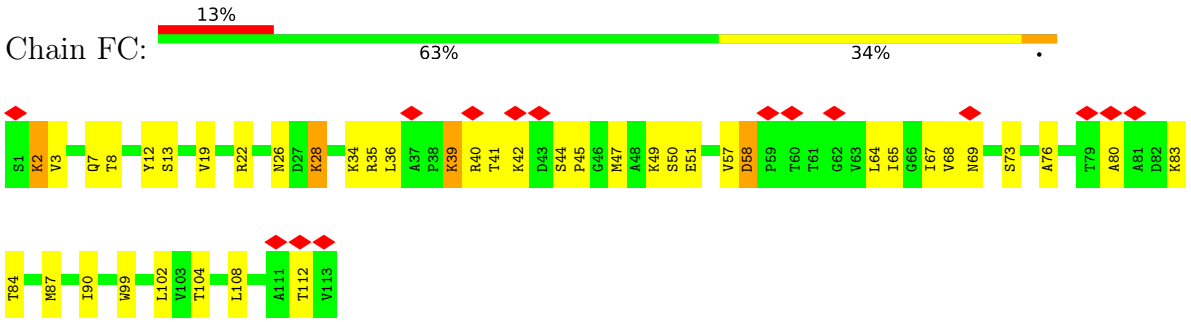
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FB:



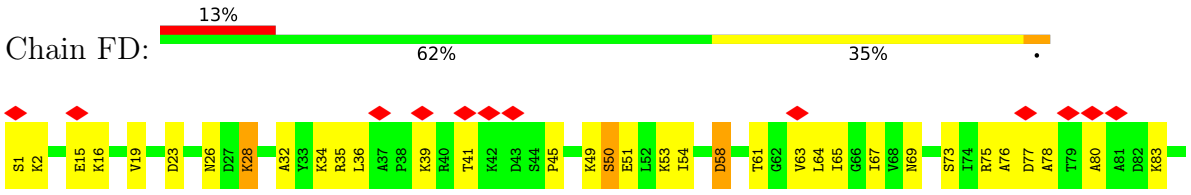
• Molecule 1: coat protein of ssRNA phage ESO003

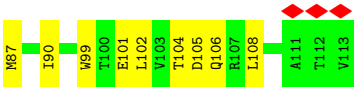
Chain FC:



• Molecule 1: coat protein of ssRNA phage ESO003

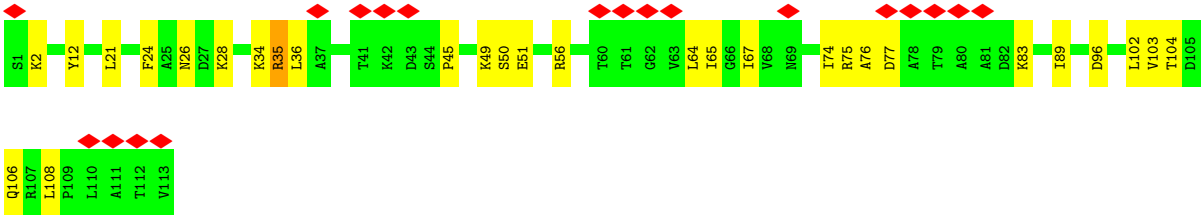
Chain FD:





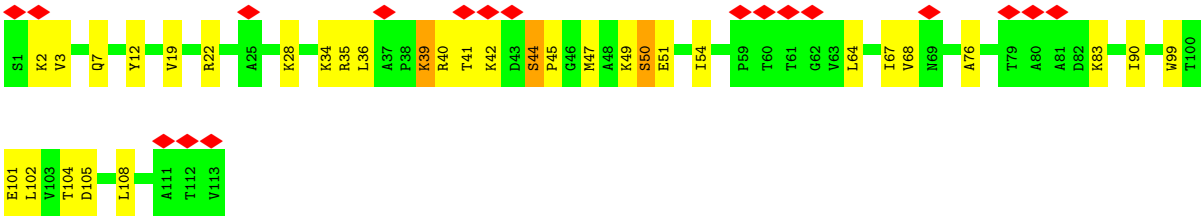
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FE:



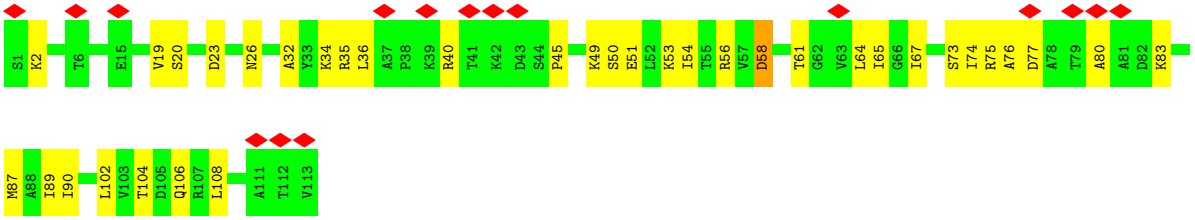
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FF:



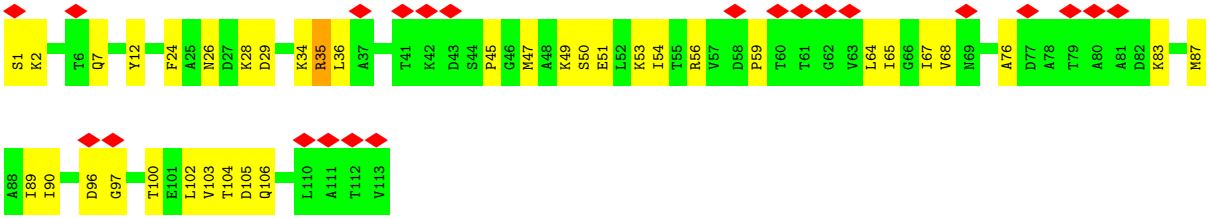
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FG:



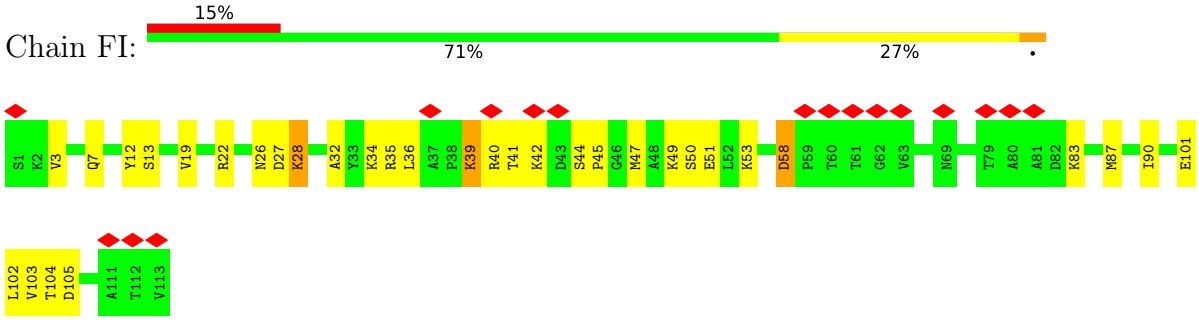
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FH:



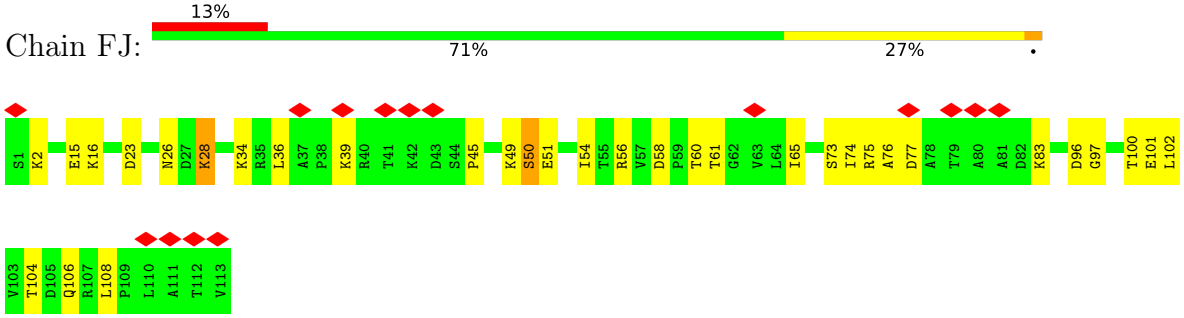
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FI:



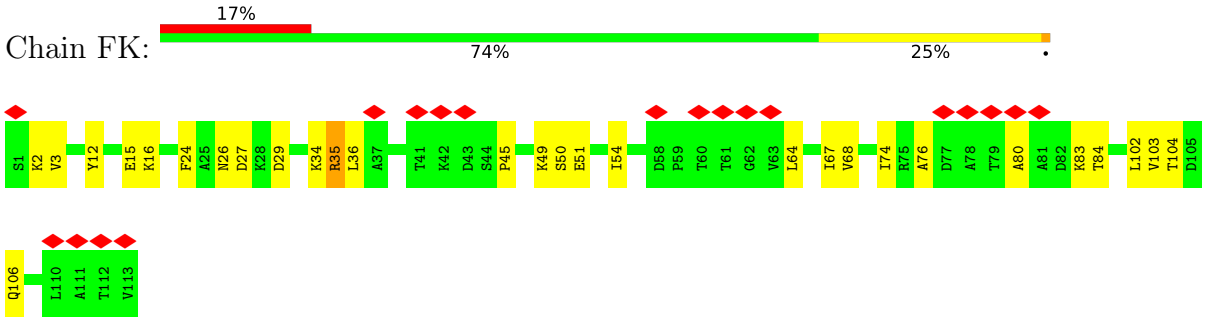
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FJ:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain FK:



• Molecule 1: coat protein of ssRNA phage ESO003

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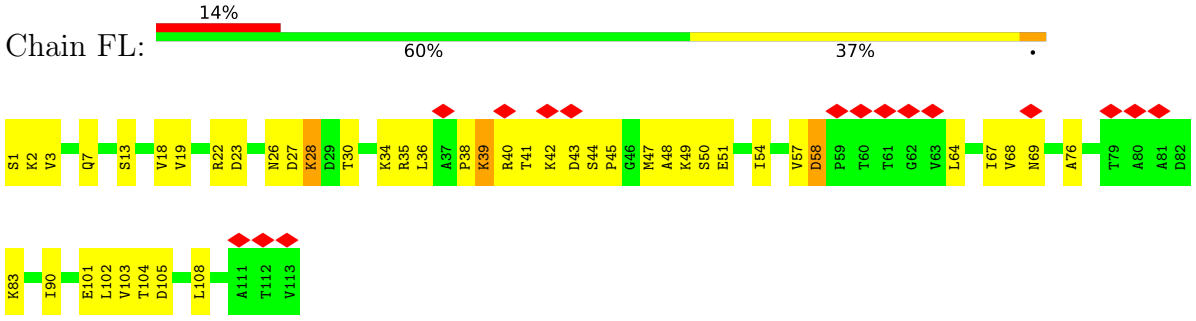
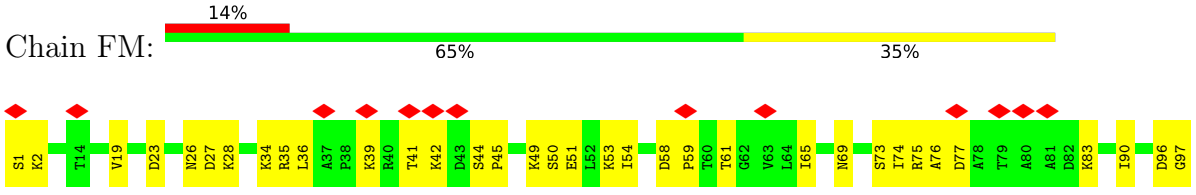
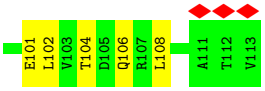


• Molecule 1: coat protein of ssRNA phage ESO003

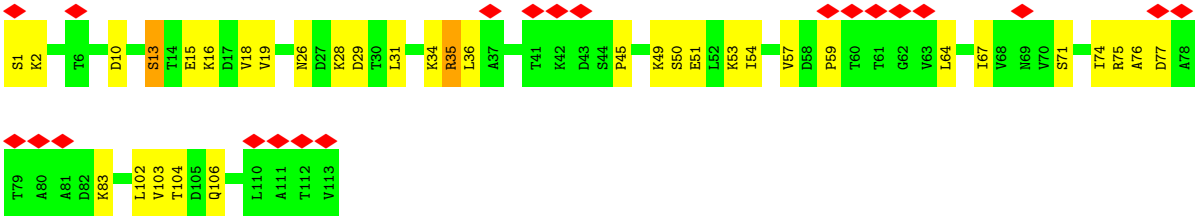
Chain FM:





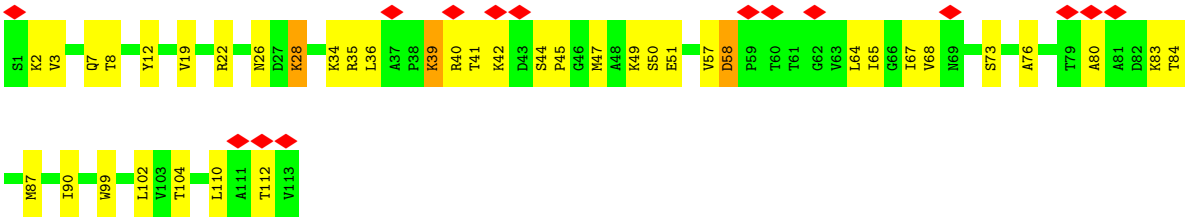
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FN:



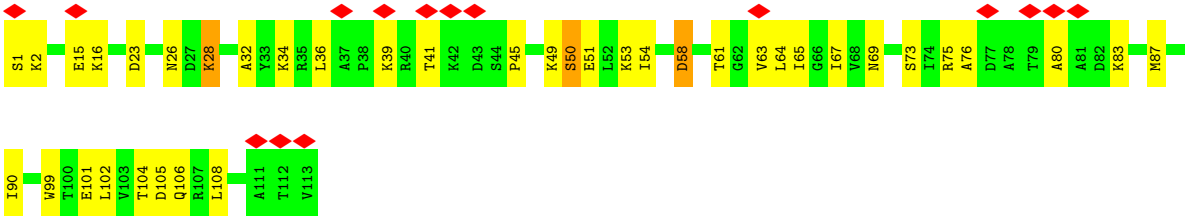
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FO:



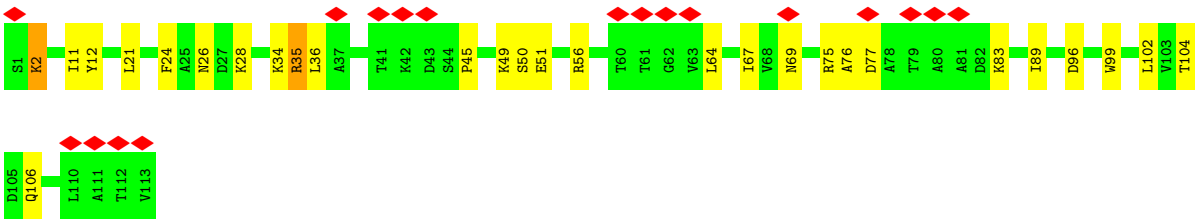
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FP:



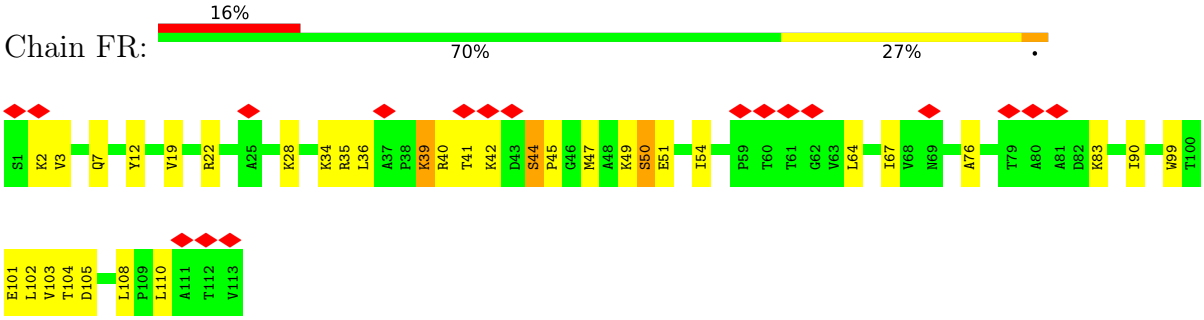
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FQ:



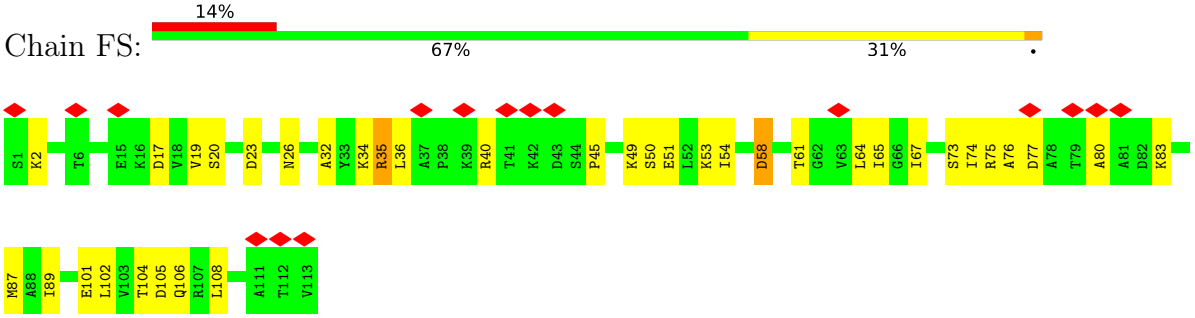
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FR:



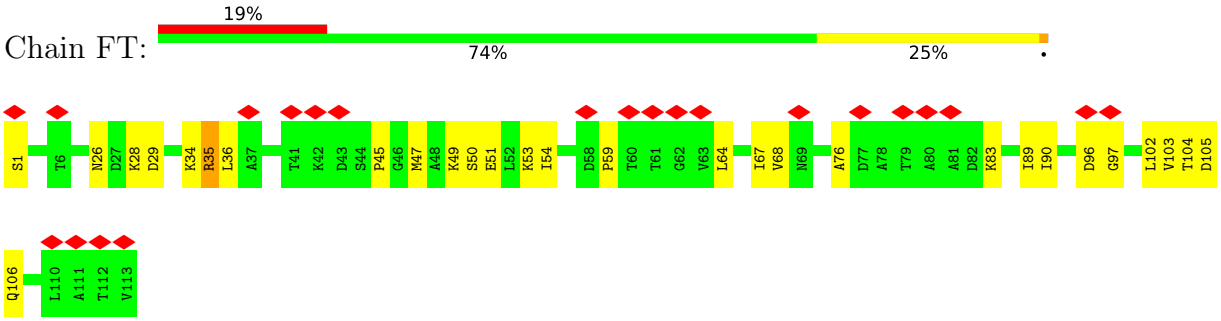
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FS:



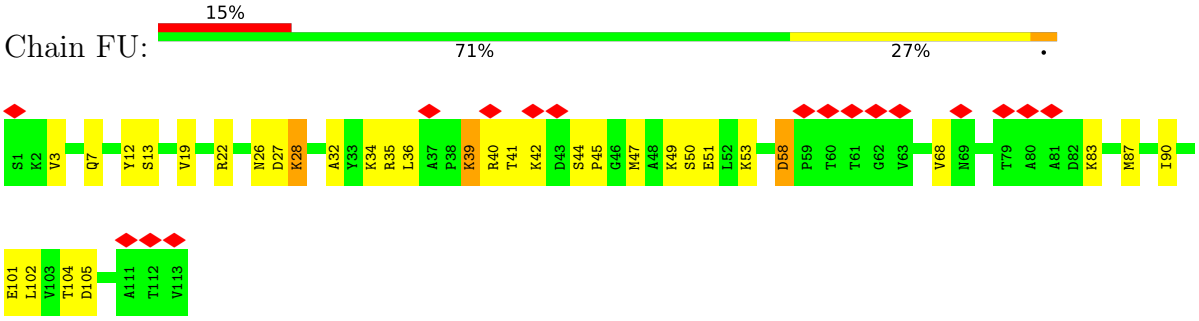
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FT:



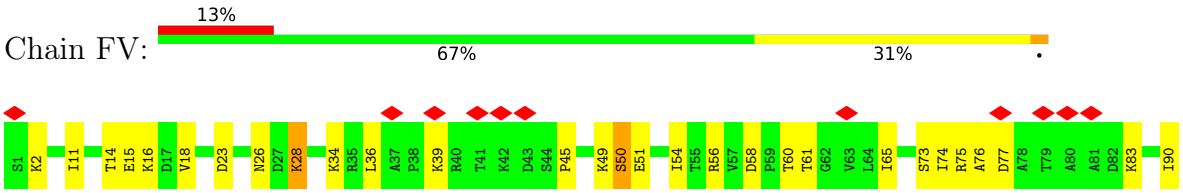
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FU:



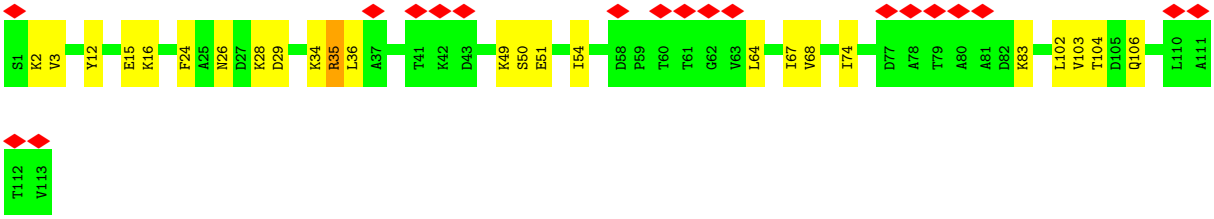
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FV:



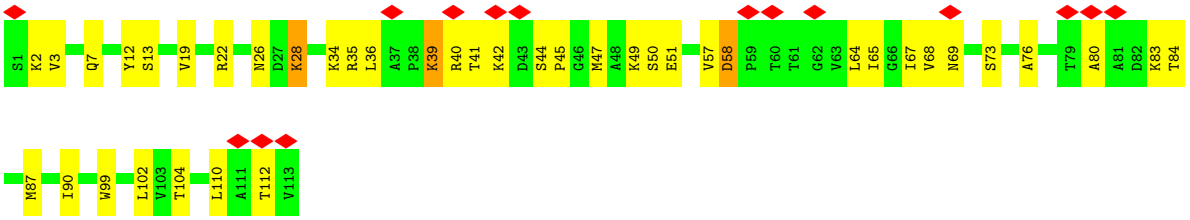
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FW:



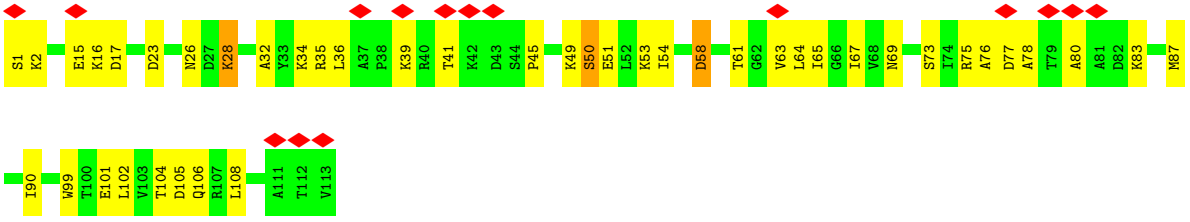
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FX:



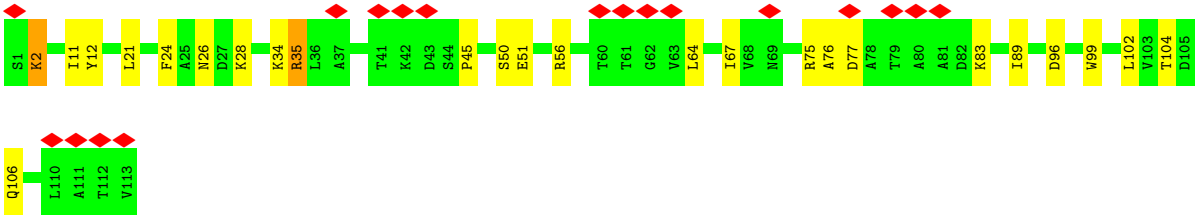
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FY:



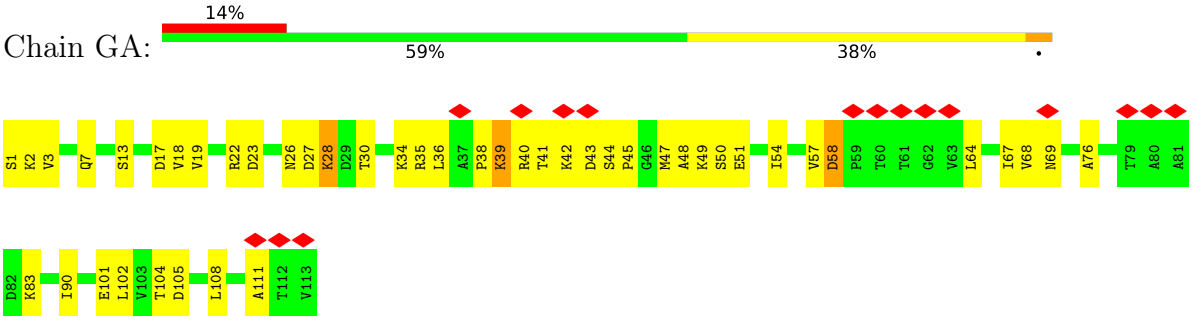
• Molecule 1: coat protein of ssRNA phage ESO003

Chain FZ:



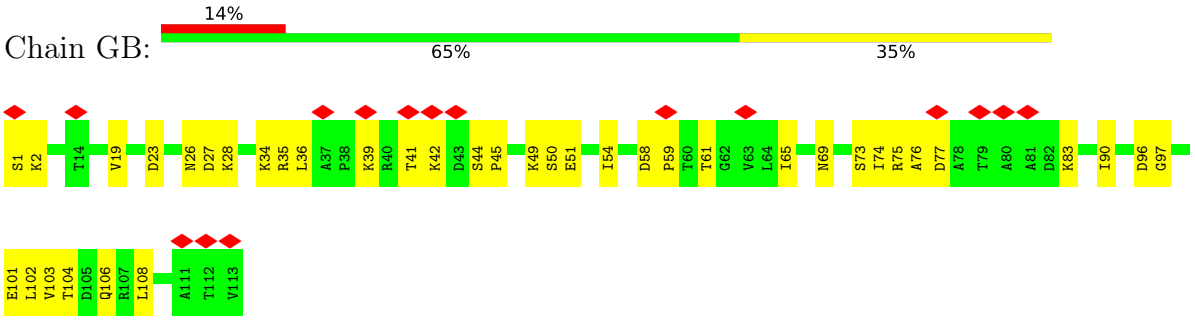
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GA:



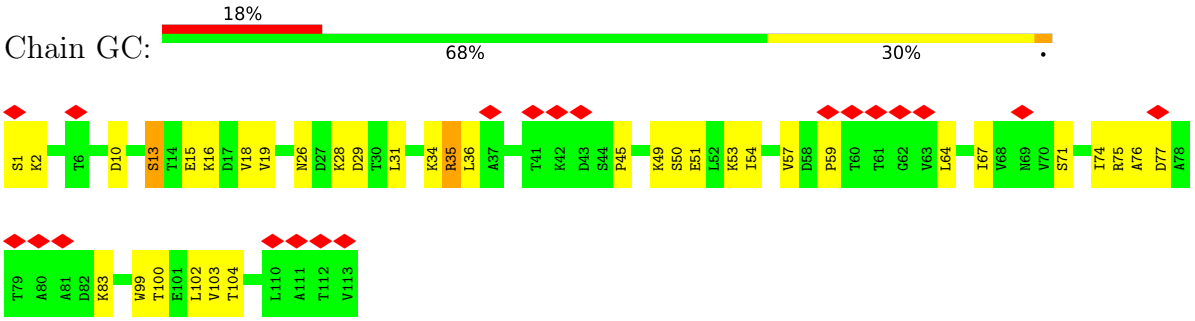
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GB:



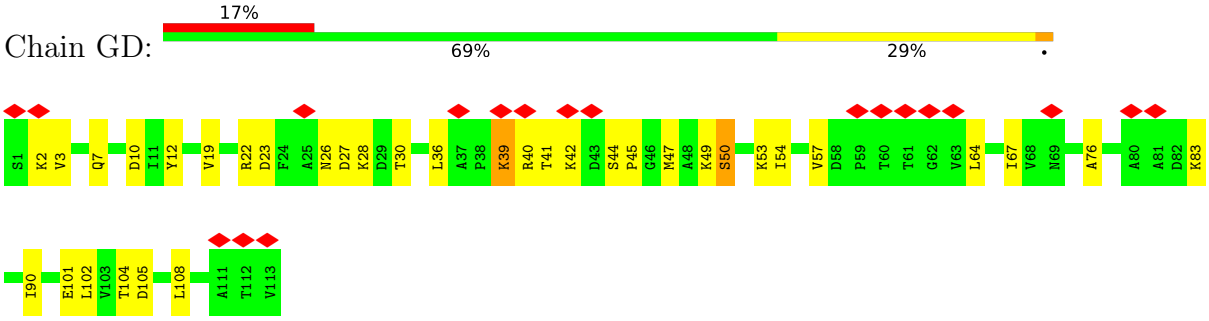
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GC:



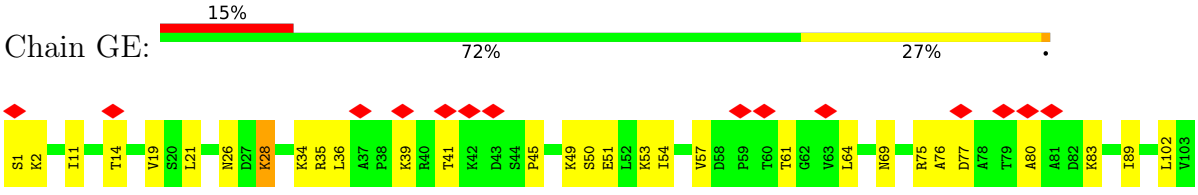
• Molecule 1: coat protein of ssRNA phage ESO003

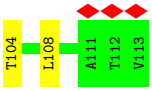
Chain GD:



• Molecule 1: coat protein of ssRNA phage ESO003

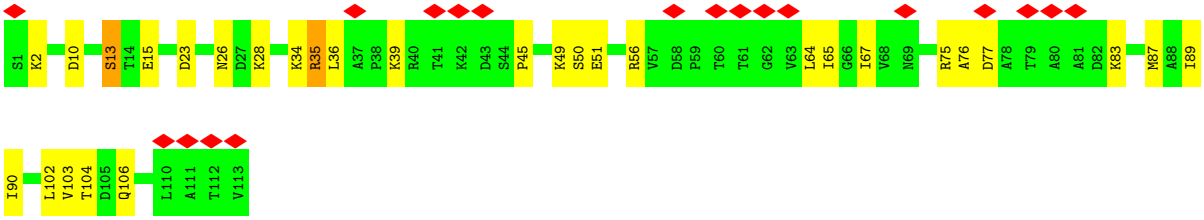
Chain GE:





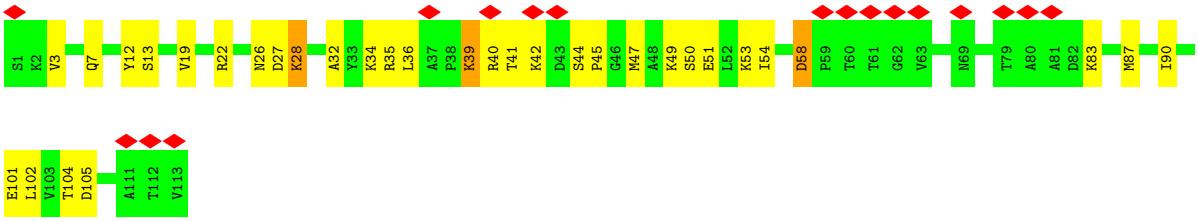
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GF:



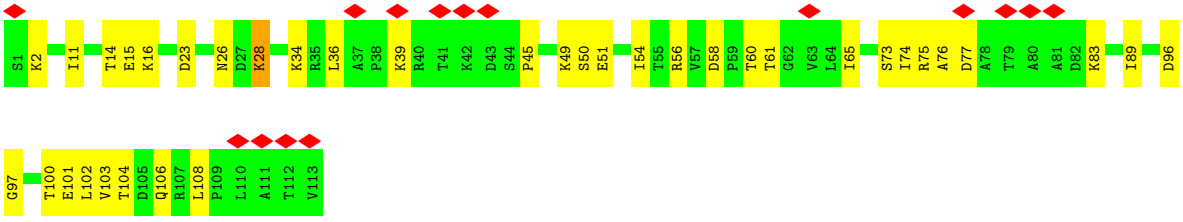
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GG:



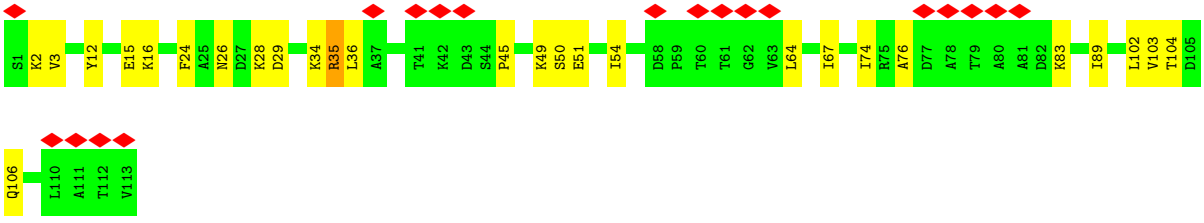
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GH:



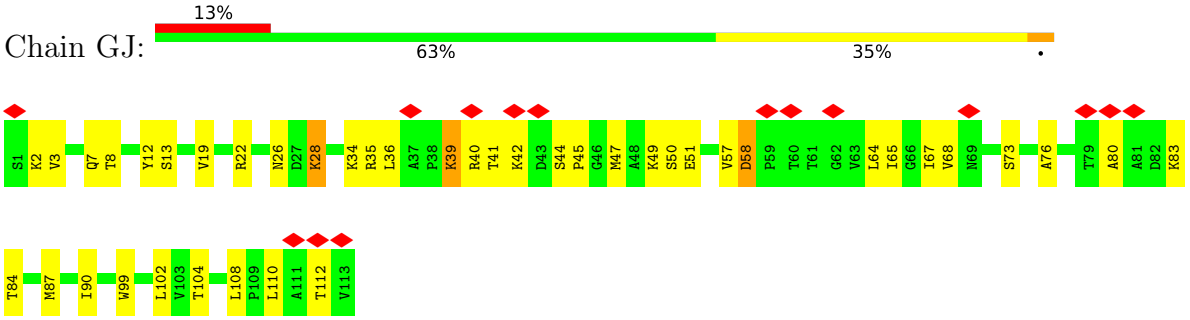
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GI:



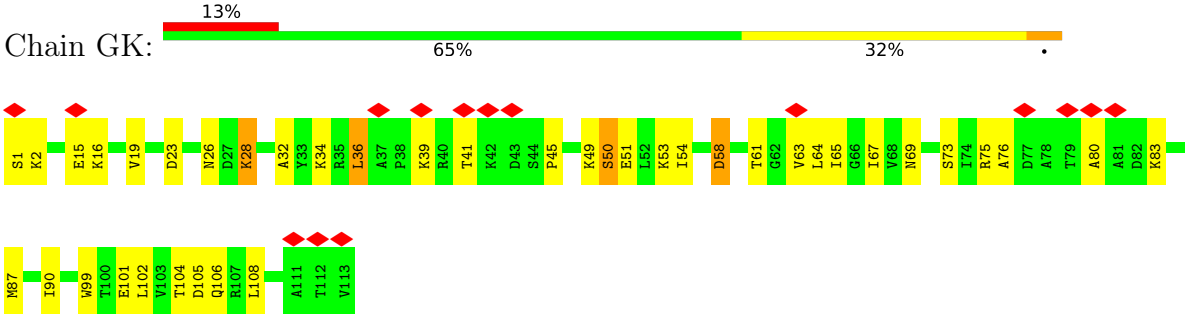
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GJ:



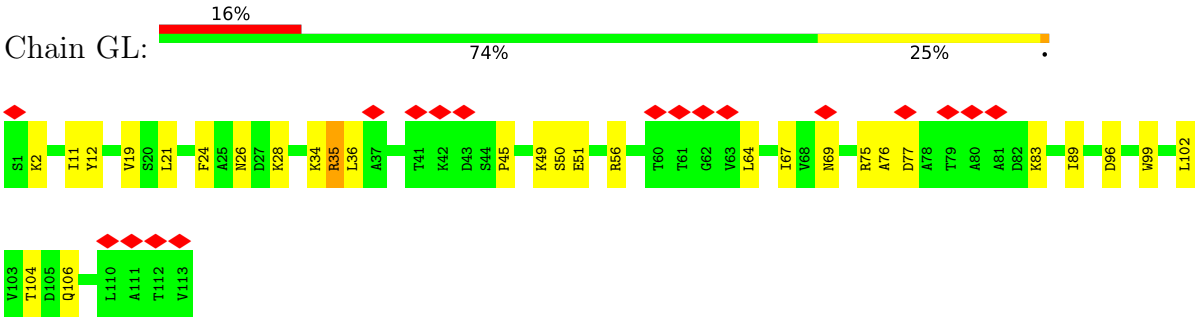
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GK:



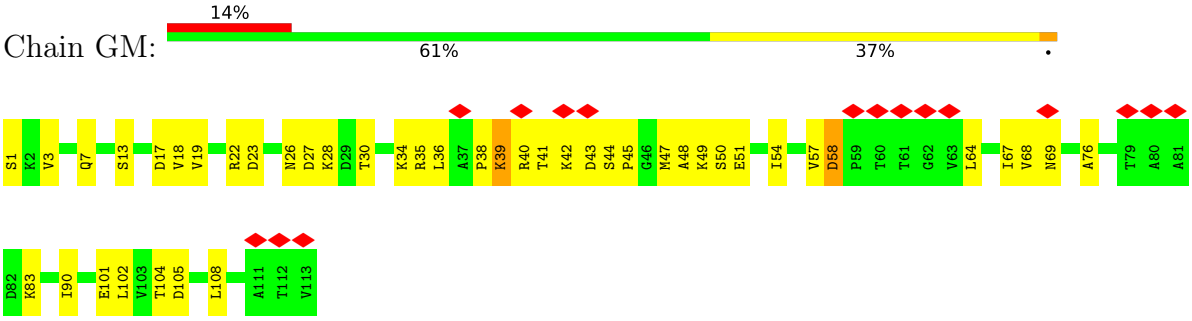
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GL:



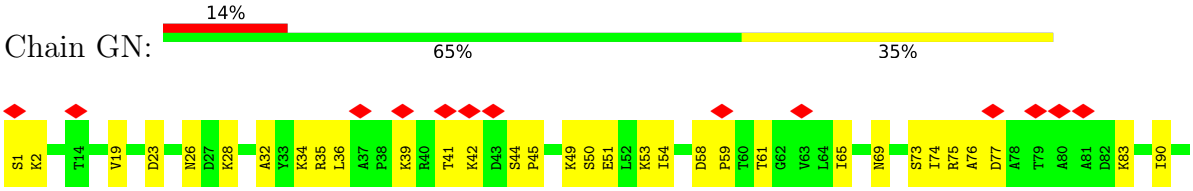
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GM:



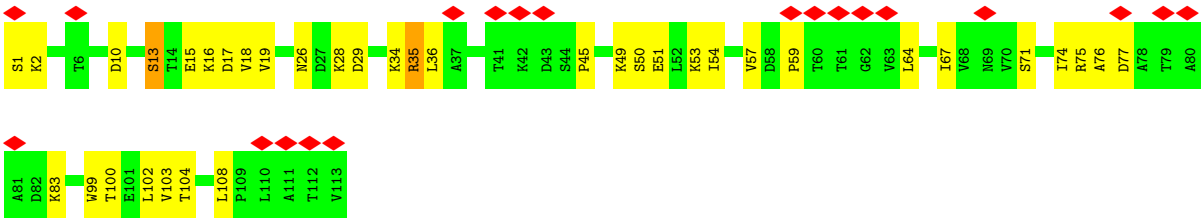
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GN:



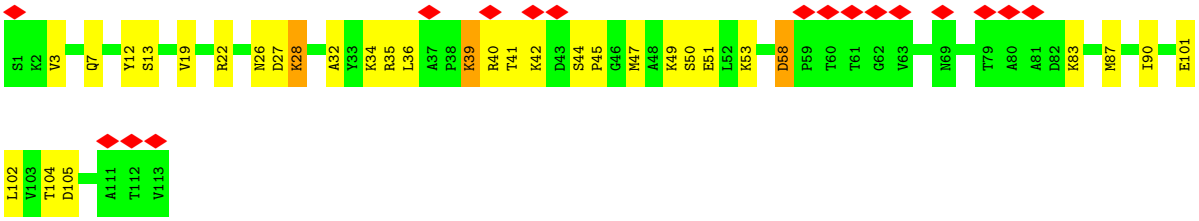
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GO:



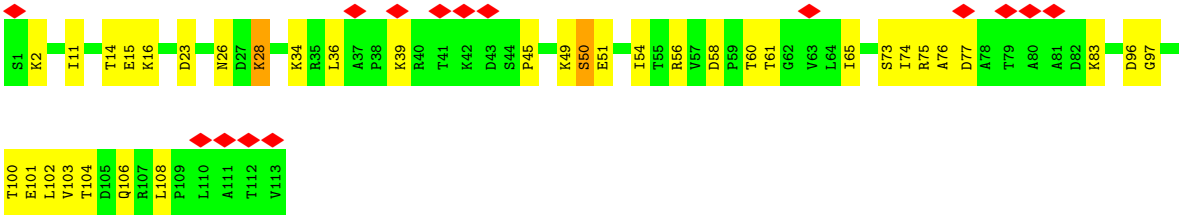
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GP:



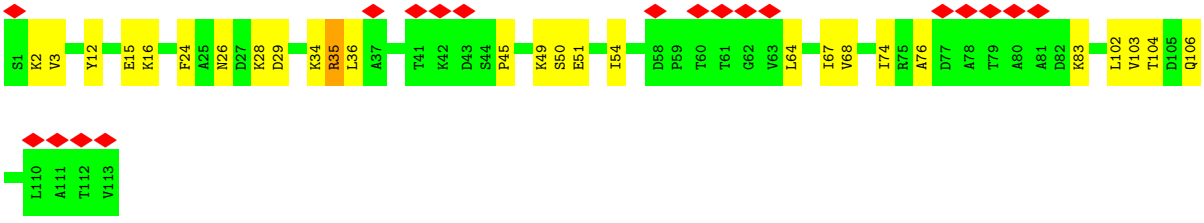
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GQ:



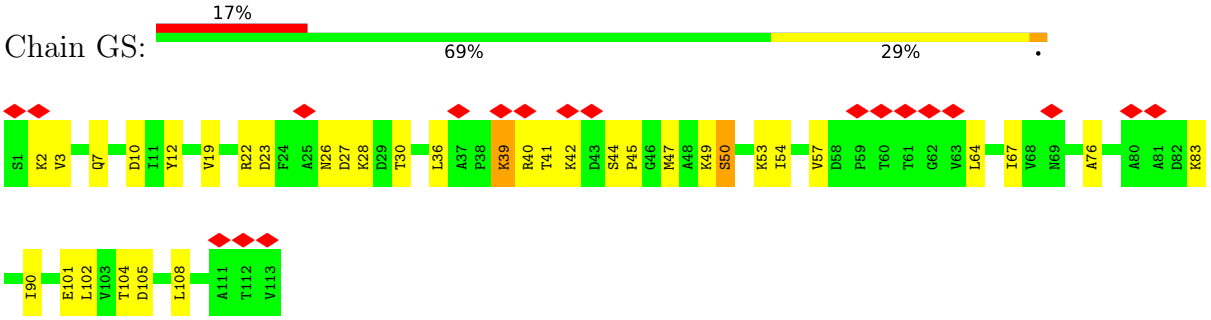
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GR:



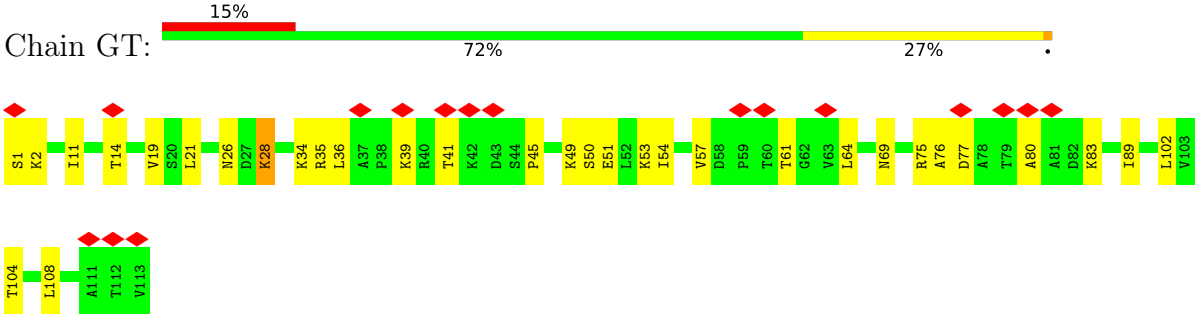
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GS:



• Molecule 1: coat protein of ssRNA phage ESO003

Chain GT:



• Molecule 1: coat protein of ssRNA phage ESO003

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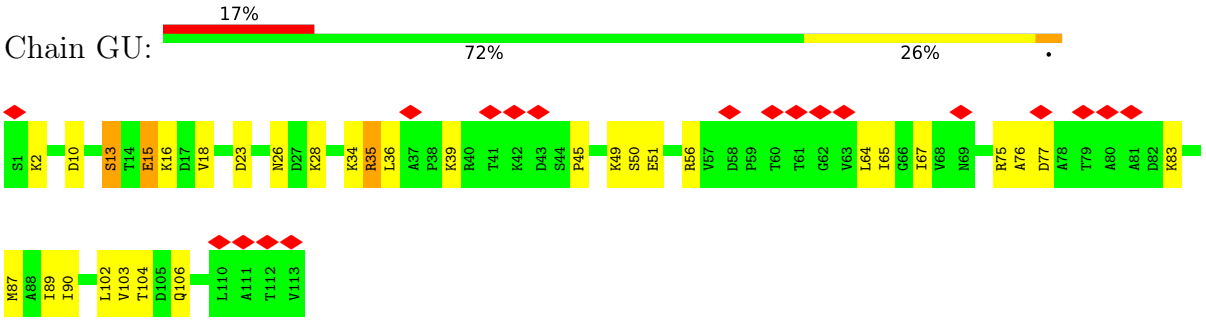
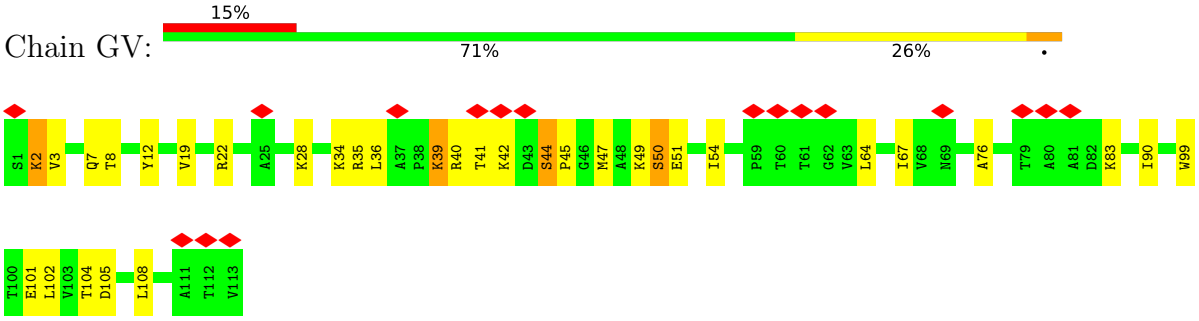


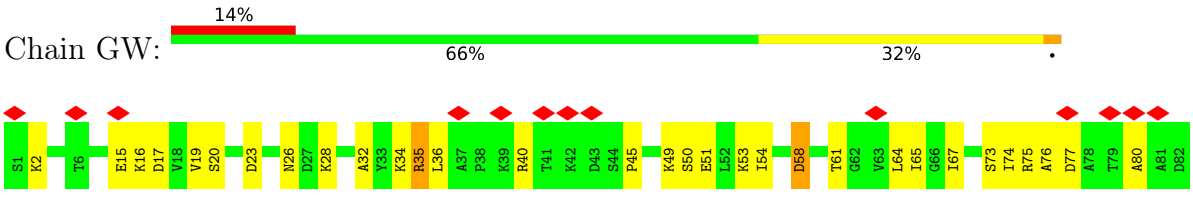
• Molecule 1: coat protein of ssRNA phage ESO003

Chain GV:

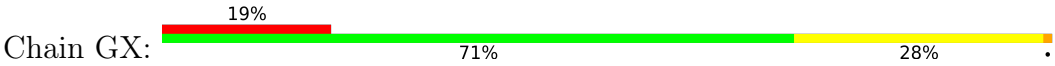


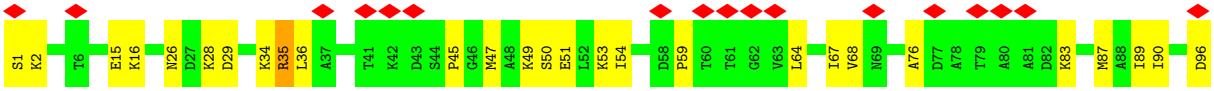
• Molecule 1: coat protein of ssRNA phage ESO003

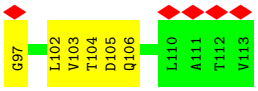
Chain GW:



• Molecule 1: coat protein of ssRNA phage ESO003







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	1297	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	1.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.044	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0095	Depositor
Map size (Å)	400.896, 400.896, 400.896	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.783, 0.783, 0.783	Depositor

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	0.31	0/867	0.62	1/1176 (0.1%)
1	AB	0.32	0/867	0.55	0/1176
1	AC	0.32	0/867	0.59	1/1176 (0.1%)
1	AD	0.32	0/867	0.57	0/1176
1	AE	0.33	0/867	0.56	0/1176
1	AF	0.32	0/867	0.57	0/1176
1	AG	0.32	0/867	0.60	1/1176 (0.1%)
1	AH	0.32	0/867	0.57	0/1176
1	AI	0.31	0/867	0.57	0/1176
1	AJ	0.31	0/867	0.62	1/1176 (0.1%)
1	AK	0.32	0/867	0.55	0/1176
1	AL	0.32	0/867	0.59	1/1176 (0.1%)
1	AM	0.32	0/867	0.61	1/1176 (0.1%)
1	AN	0.32	0/867	0.56	0/1176
1	AO	0.32	0/867	0.55	0/1176
1	AP	0.31	0/867	0.61	0/1176
1	AQ	0.33	0/867	0.56	0/1176
1	AR	0.32	0/867	0.56	0/1176
1	AS	0.32	0/867	0.61	1/1176 (0.1%)
1	AT	0.32	0/867	0.57	0/1176
1	AU	0.31	0/867	0.57	0/1176
1	AV	0.31	0/867	0.62	1/1176 (0.1%)
1	AW	0.32	0/867	0.54	0/1176
1	AX	0.32	0/867	0.59	1/1176 (0.1%)
1	AY	0.32	0/867	0.61	1/1176 (0.1%)
1	AZ	0.32	0/867	0.55	0/1176
1	BA	0.32	0/867	0.56	0/1176
1	BB	0.32	0/867	0.61	1/1176 (0.1%)
1	BC	0.32	0/867	0.56	0/1176
1	BD	0.31	0/867	0.57	0/1176
1	BE	0.31	0/867	0.60	0/1176
1	BF	0.33	0/867	0.57	0/1176
1	BG	0.32	0/867	0.56	0/1176
1	BH	0.32	0/867	0.57	0/1176

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	BI	0.33	0/867	0.55	0/1176
1	BJ	0.32	0/867	0.57	0/1176
1	BK	0.32	0/867	0.61	1/1176 (0.1%)
1	BL	0.32	0/867	0.55	0/1176
1	BM	0.32	0/867	0.55	0/1176
1	BN	0.32	0/867	0.60	1/1176 (0.1%)
1	BO	0.32	0/867	0.57	0/1176
1	BP	0.31	0/867	0.56	0/1176
1	BQ	0.31	0/867	0.60	0/1176
1	BR	0.33	0/867	0.57	0/1176
1	BS	0.32	0/867	0.56	0/1176
1	BT	0.32	0/867	0.61	1/1176 (0.1%)
1	BU	0.32	0/867	0.55	0/1176
1	BV	0.32	0/867	0.56	0/1176
1	BW	0.32	0/867	0.57	0/1176
1	BX	0.33	0/867	0.56	0/1176
1	BY	0.32	0/867	0.56	0/1176
1	BZ	0.32	0/867	0.62	1/1176 (0.1%)
1	CA	0.32	0/867	0.55	0/1176
1	CB	0.32	0/867	0.59	1/1176 (0.1%)
1	CC	0.31	0/867	0.61	0/1176
1	CD	0.33	0/867	0.57	0/1176
1	CE	0.32	0/867	0.57	0/1176
1	CF	0.32	0/867	0.61	1/1176 (0.1%)
1	CG	0.32	0/867	0.55	0/1176
1	CH	0.32	0/867	0.55	0/1176
1	CI	0.32	0/867	0.57	0/1176
1	CJ	0.33	0/867	0.56	0/1176
1	CK	0.32	0/867	0.56	0/1176
1	CL	0.31	0/867	0.60	0/1176
1	CM	0.33	0/867	0.57	0/1176
1	CN	0.32	0/867	0.56	0/1176
1	CO	0.31	0/867	0.62	1/1176 (0.1%)
1	CP	0.32	0/867	0.55	0/1176
1	CQ	0.32	0/867	0.59	1/1176 (0.1%)
1	CR	0.32	0/867	0.61	1/1176 (0.1%)
1	CS	0.32	0/867	0.57	0/1176
1	CT	0.31	0/867	0.56	0/1176
1	CU	0.32	0/867	0.57	0/1176
1	CV	0.32	0/867	0.56	0/1176
1	CW	0.32	0/867	0.57	0/1176
1	CX	0.31	0/867	0.61	0/1176
1	CY	0.33	0/867	0.57	0/1176

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	CZ	0.32	0/867	0.57	0/1176
1	DA	0.31	0/867	0.62	1/1176 (0.1%)
1	DB	0.32	0/867	0.55	0/1176
1	DC	0.32	0/867	0.59	1/1176 (0.1%)
1	DD	0.32	0/867	0.57	0/1176
1	DE	0.33	0/867	0.56	0/1176
1	DF	0.32	0/867	0.57	0/1176
1	DG	0.32	0/867	0.61	1/1176 (0.1%)
1	DH	0.32	0/867	0.57	0/1176
1	DI	0.31	0/867	0.56	0/1176
1	DJ	0.32	0/867	0.61	1/1176 (0.1%)
1	DK	0.32	0/867	0.56	0/1176
1	DL	0.32	0/867	0.55	0/1176
1	DM	0.32	0/867	0.62	1/1176 (0.1%)
1	DN	0.32	0/867	0.54	0/1176
1	DO	0.32	0/867	0.59	1/1176 (0.1%)
1	DP	0.32	0/867	0.61	1/1176 (0.1%)
1	DQ	0.32	0/867	0.57	0/1176
1	DR	0.31	0/867	0.57	0/1176
1	DS	0.32	0/867	0.57	0/1176
1	DT	0.32	0/867	0.56	0/1176
1	DU	0.32	0/867	0.56	0/1176
1	DV	0.31	0/867	0.62	1/1176 (0.1%)
1	DW	0.32	0/867	0.55	0/1176
1	DX	0.32	0/867	0.59	1/1176 (0.1%)
1	DY	0.31	0/867	0.61	0/1176
1	DZ	0.33	0/867	0.58	0/1176
1	EA	0.32	0/867	0.56	0/1176
1	EB	0.32	0/867	0.61	1/1176 (0.1%)
1	EC	0.32	0/867	0.55	0/1176
1	ED	0.32	0/867	0.55	0/1176
1	EE	0.32	0/867	0.57	0/1176
1	EF	0.33	0/867	0.55	0/1176
1	EG	0.32	0/867	0.57	0/1176
1	EH	0.32	0/867	0.63	1/1176 (0.1%)
1	EI	0.32	0/867	0.55	0/1176
1	EJ	0.32	0/867	0.59	1/1176 (0.1%)
1	EK	0.31	0/867	0.60	0/1176
1	EL	0.33	0/867	0.58	0/1176
1	EM	0.32	0/867	0.56	0/1176
1	EN	0.32	0/867	0.56	0/1176
1	EO	0.32	0/867	0.55	0/1176
1	EP	0.32	0/867	0.55	0/1176

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	EQ	0.32	0/867	0.60	1/1176 (0.1%)
1	ER	0.32	0/867	0.56	0/1176
1	ES	0.32	0/867	0.54	0/1176
1	ET	0.32	0/867	0.62	1/1176 (0.1%)
1	EU	0.32	0/867	0.55	0/1176
1	EV	0.31	0/867	0.57	0/1176
1	EW	0.31	0/867	0.60	0/1176
1	EX	0.32	0/867	0.55	0/1176
1	EY	0.32	0/867	0.55	0/1176
1	EZ	0.32	0/867	0.56	0/1176
1	FA	0.32	0/867	0.54	0/1176
1	FB	0.32	0/867	0.55	0/1176
1	FC	0.32	0/867	0.60	1/1176 (0.1%)
1	FD	0.32	0/867	0.55	0/1176
1	FE	0.32	0/867	0.55	0/1176
1	FF	0.31	0/867	0.59	0/1176
1	FG	0.32	0/867	0.55	0/1176
1	FH	0.32	0/867	0.55	0/1176
1	FI	0.32	0/867	0.62	1/1176 (0.1%)
1	FJ	0.32	0/867	0.56	0/1176
1	FK	0.31	0/867	0.57	0/1176
1	FL	0.31	0/867	0.61	1/1176 (0.1%)
1	FM	0.32	0/867	0.55	0/1176
1	FN	0.31	0/867	0.55	0/1176
1	FO	0.32	0/867	0.61	1/1176 (0.1%)
1	FP	0.32	0/867	0.55	0/1176
1	FQ	0.32	0/867	0.54	0/1176
1	FR	0.31	0/867	0.59	0/1176
1	FS	0.32	0/867	0.55	0/1176
1	FT	0.32	0/867	0.55	0/1176
1	FU	0.32	0/867	0.62	1/1176 (0.1%)
1	FV	0.32	0/867	0.56	0/1176
1	FW	0.31	0/867	0.56	0/1176
1	FX	0.32	0/867	0.60	1/1176 (0.1%)
1	FY	0.32	0/867	0.56	0/1176
1	FZ	0.32	0/867	0.54	0/1176
1	GA	0.32	0/867	0.61	1/1176 (0.1%)
1	GB	0.32	0/867	0.54	0/1176
1	GC	0.31	0/867	0.55	0/1176
1	GD	0.32	0/867	0.56	0/1176
1	GE	0.32	0/867	0.55	0/1176
1	GF	0.32	0/867	0.55	0/1176
1	GG	0.32	0/867	0.62	1/1176 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	GH	0.32	0/867	0.55	0/1176
1	GI	0.31	0/867	0.56	0/1176
1	GJ	0.32	0/867	0.61	1/1176 (0.1%)
1	GK	0.32	0/867	0.55	0/1176
1	GL	0.32	0/867	0.54	0/1176
1	GM	0.32	0/867	0.61	1/1176 (0.1%)
1	GN	0.32	0/867	0.54	0/1176
1	GO	0.31	0/867	0.55	0/1176
1	GP	0.32	0/867	0.62	1/1176 (0.1%)
1	GQ	0.32	0/867	0.56	0/1176
1	GR	0.31	0/867	0.56	0/1176
1	GS	0.32	0/867	0.56	0/1176
1	GT	0.32	0/867	0.55	0/1176
1	GU	0.32	0/867	0.56	0/1176
1	GV	0.31	0/867	0.59	0/1176
1	GW	0.32	0/867	0.55	0/1176
1	GX	0.32	0/867	0.55	0/1176
All	All	0.32	0/156060	0.57	45/211680 (0.0%)

There are no bond length outliers.

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	FU	58	ASP	CB-CG-OD2	6.70	124.33	118.30
1	GG	58	ASP	CB-CG-OD2	6.69	124.32	118.30
1	ET	58	ASP	CB-CG-OD2	6.68	124.31	118.30
1	FI	58	ASP	CB-CG-OD2	6.67	124.30	118.30
1	GP	58	ASP	CB-CG-OD2	6.67	124.30	118.30
1	FL	58	ASP	CB-CG-OD1	6.02	123.71	118.30
1	AA	58	ASP	CB-CG-OD1	5.96	123.66	118.30
1	AJ	58	ASP	CB-CG-OD1	5.95	123.66	118.30
1	CO	58	ASP	CB-CG-OD1	5.95	123.66	118.30
1	GJ	58	ASP	CB-CG-OD2	5.95	123.66	118.30
1	FO	58	ASP	CB-CG-OD2	5.95	123.66	118.30
1	DA	58	ASP	CB-CG-OD1	5.95	123.65	118.30
1	GA	58	ASP	CB-CG-OD1	5.94	123.65	118.30
1	GM	58	ASP	CB-CG-OD1	5.94	123.65	118.30
1	EQ	58	ASP	CB-CG-OD2	5.92	123.63	118.30
1	FX	58	ASP	CB-CG-OD2	5.91	123.62	118.30
1	BZ	58	ASP	CB-CG-OD1	5.89	123.61	118.30
1	DM	58	ASP	CB-CG-OD1	5.89	123.61	118.30
1	EH	58	ASP	CB-CG-OD1	5.89	123.61	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	FC	58	ASP	CB-CG-OD2	5.89	123.61	118.30
1	AV	58	ASP	CB-CG-OD1	5.89	123.60	118.30
1	DV	58	ASP	CB-CG-OD1	5.88	123.59	118.30
1	DX	58	ASP	CB-CG-OD1	5.64	123.37	118.30
1	AX	58	ASP	CB-CG-OD1	5.63	123.37	118.30
1	AC	58	ASP	CB-CG-OD1	5.62	123.36	118.30
1	CR	58	ASP	CB-CG-OD1	5.55	123.30	118.30
1	AS	58	ASP	CB-CG-OD1	5.55	123.29	118.30
1	BN	58	ASP	CB-CG-OD1	5.55	123.29	118.30
1	EJ	58	ASP	CB-CG-OD1	5.55	123.29	118.30
1	BB	58	ASP	CB-CG-OD1	5.53	123.28	118.30
1	DO	58	ASP	CB-CG-OD1	5.53	123.28	118.30
1	DP	58	ASP	CB-CG-OD1	5.53	123.28	118.30
1	DG	58	ASP	CB-CG-OD1	5.52	123.27	118.30
1	CB	58	ASP	CB-CG-OD1	5.52	123.26	118.30
1	AG	58	ASP	CB-CG-OD1	5.50	123.25	118.30
1	DJ	58	ASP	CB-CG-OD2	5.48	123.23	118.30
1	AL	58	ASP	CB-CG-OD1	5.43	123.19	118.30
1	BK	58	ASP	CB-CG-OD2	5.43	123.19	118.30
1	CF	58	ASP	CB-CG-OD2	5.43	123.19	118.30
1	CQ	58	ASP	CB-CG-OD1	5.43	123.19	118.30
1	DC	58	ASP	CB-CG-OD1	5.43	123.19	118.30
1	AM	58	ASP	CB-CG-OD2	5.43	123.19	118.30
1	AY	58	ASP	CB-CG-OD2	5.43	123.19	118.30
1	BT	58	ASP	CB-CG-OD2	5.43	123.19	118.30
1	EB	58	ASP	CB-CG-OD2	5.41	123.17	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	857	0	884	34	0
1	AB	857	0	884	33	0
1	AC	857	0	884	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AD	857	0	884	28	0
1	AE	857	0	884	26	0
1	AF	857	0	884	25	0
1	AG	857	0	884	27	0
1	AH	857	0	884	29	0
1	AI	857	0	884	25	0
1	AJ	857	0	884	35	0
1	AK	857	0	884	33	0
1	AL	857	0	884	24	0
1	AM	857	0	884	32	0
1	AN	857	0	884	31	0
1	AO	857	0	884	24	0
1	AP	857	0	884	31	0
1	AQ	857	0	884	34	0
1	AR	857	0	884	28	0
1	AS	857	0	884	29	0
1	AT	857	0	884	30	0
1	AU	857	0	884	24	0
1	AV	857	0	884	34	0
1	AW	857	0	884	35	0
1	AX	857	0	884	26	0
1	AY	857	0	884	32	0
1	AZ	857	0	884	33	0
1	BA	857	0	884	26	0
1	BB	857	0	884	28	0
1	BC	857	0	884	30	0
1	BD	857	0	884	24	0
1	BE	857	0	884	32	0
1	BF	857	0	884	36	0
1	BG	857	0	884	28	0
1	BH	857	0	884	29	0
1	BI	857	0	884	24	0
1	BJ	857	0	884	24	0
1	BK	857	0	884	31	0
1	BL	857	0	884	32	0
1	BM	857	0	884	23	0
1	BN	857	0	884	29	0
1	BO	857	0	884	29	0
1	BP	857	0	884	19	0
1	BQ	857	0	884	33	0
1	BR	857	0	884	36	0
1	BS	857	0	884	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BT	857	0	884	32	0
1	BU	857	0	884	33	0
1	BV	857	0	884	26	0
1	BW	857	0	884	28	0
1	BX	857	0	884	24	0
1	BY	857	0	884	23	0
1	BZ	857	0	884	32	0
1	CA	857	0	884	32	0
1	CB	857	0	884	28	0
1	CC	857	0	884	32	0
1	CD	857	0	884	36	0
1	CE	857	0	884	31	0
1	CF	857	0	884	32	0
1	CG	857	0	884	31	0
1	CH	857	0	884	23	0
1	CI	857	0	884	29	0
1	CJ	857	0	884	22	0
1	CK	857	0	884	21	0
1	CL	857	0	884	31	0
1	CM	857	0	884	37	0
1	CN	857	0	884	31	0
1	CO	857	0	884	32	0
1	CP	857	0	884	32	0
1	CQ	857	0	884	24	0
1	CR	857	0	884	28	0
1	CS	857	0	884	29	0
1	CT	857	0	884	19	0
1	CU	857	0	884	28	0
1	CV	857	0	884	24	0
1	CW	857	0	884	23	0
1	CX	857	0	884	32	0
1	CY	857	0	884	38	0
1	CZ	857	0	884	28	0
1	DA	857	0	884	33	0
1	DB	857	0	884	31	0
1	DC	857	0	884	26	0
1	DD	857	0	884	29	0
1	DE	857	0	884	23	0
1	DF	857	0	884	22	0
1	DG	857	0	884	28	0
1	DH	857	0	884	30	0
1	DI	857	0	884	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DJ	857	0	884	31	0
1	DK	857	0	884	30	0
1	DL	857	0	884	23	0
1	DM	857	0	884	36	0
1	DN	857	0	884	34	0
1	DO	857	0	884	26	0
1	DP	857	0	884	30	0
1	DQ	857	0	884	29	0
1	DR	857	0	884	18	0
1	DS	857	0	884	28	0
1	DT	857	0	884	22	0
1	DU	857	0	884	21	0
1	DV	857	0	884	34	0
1	DW	857	0	884	36	0
1	DX	857	0	884	27	0
1	DY	857	0	884	31	0
1	DZ	857	0	884	37	0
1	EA	857	0	884	29	0
1	EB	857	0	884	30	0
1	EC	857	0	884	31	0
1	ED	857	0	884	23	0
1	EE	857	0	884	29	0
1	EF	857	0	884	25	0
1	EG	857	0	884	25	0
1	EH	857	0	884	34	0
1	EI	857	0	884	32	0
1	EJ	857	0	884	25	0
1	EK	857	0	884	33	0
1	EL	857	0	884	37	0
1	EM	857	0	884	28	0
1	EN	857	0	884	29	0
1	EO	857	0	884	23	0
1	EP	857	0	884	27	0
1	EQ	857	0	884	33	0
1	ER	857	0	884	34	0
1	ES	857	0	884	26	0
1	ET	857	0	884	25	0
1	EU	857	0	884	29	0
1	EV	857	0	884	23	0
1	EW	857	0	884	26	0
1	EX	857	0	884	32	0
1	EY	857	0	884	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	EZ	857	0	884	23	0
1	FA	857	0	884	23	0
1	FB	857	0	884	23	0
1	FC	857	0	884	33	0
1	FD	857	0	884	35	0
1	FE	857	0	884	21	0
1	FF	857	0	884	26	0
1	FG	857	0	884	31	0
1	FH	857	0	884	30	0
1	FI	857	0	884	25	0
1	FJ	857	0	884	28	0
1	FK	857	0	884	21	0
1	FL	857	0	884	37	0
1	FM	857	0	884	34	0
1	FN	857	0	884	27	0
1	FO	857	0	884	30	0
1	FP	857	0	884	31	0
1	FQ	857	0	884	22	0
1	FR	857	0	884	28	0
1	FS	857	0	884	31	0
1	FT	857	0	884	25	0
1	FU	857	0	884	23	0
1	FV	857	0	884	30	0
1	FW	857	0	884	20	0
1	FX	857	0	884	30	0
1	FY	857	0	884	33	0
1	FZ	857	0	884	20	0
1	GA	857	0	884	38	0
1	GB	857	0	884	33	0
1	GC	857	0	884	31	0
1	GD	857	0	884	25	0
1	GE	857	0	884	22	0
1	GF	857	0	884	24	0
1	GG	857	0	884	25	0
1	GH	857	0	884	30	0
1	GI	857	0	884	22	0
1	GJ	857	0	884	31	0
1	GK	857	0	884	32	0
1	GL	857	0	884	22	0
1	GM	857	0	884	36	0
1	GN	857	0	884	35	0
1	GO	857	0	884	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GP	857	0	884	23	0
1	GQ	857	0	884	29	0
1	GR	857	0	884	22	0
1	GS	857	0	884	25	0
1	GT	857	0	884	21	0
1	GU	857	0	884	27	0
1	GV	857	0	884	27	0
1	GW	857	0	884	33	0
1	GX	857	0	884	28	0
All	All	154260	0	159120	3952	0

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

All (3952) 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:ET:36:LEU:HB2	1:ET:49:LYS:HB2	1.54	0.90
1:FI:36:LEU:HB2	1:FI:49:LYS:HB2	1.54	0.90
1:GP:36:LEU:HB2	1:GP:49:LYS:HB2	1.54	0.89
1:GF:34:LYS:HB3	1:GF:51:GLU:HB3	1.55	0.88
1:FU:36:LEU:HB2	1:FU:49:LYS:HB2	1.54	0.88
1:EP:34:LYS:HB3	1:EP:51:GLU:HB3	1.56	0.88
1:GU:34:LYS:HB3	1:GU:51:GLU:HB3	1.57	0.87
1:FO:36:LEU:HB2	1:FO:49:LYS:HB2	1.55	0.86
1:GJ:36:LEU:HB2	1:GJ:49:LYS:HB2	1.56	0.86
1:FB:36:LEU:HB3	1:FB:49:LYS:HB2	1.57	0.85
1:FW:36:LEU:HB3	1:FW:49:LYS:HB2	1.59	0.85
1:EY:36:LEU:HB3	1:EY:49:LYS:HB2	1.59	0.84
1:FT:36:LEU:HB3	1:FT:49:LYS:HB2	1.59	0.84
1:FH:36:LEU:HB3	1:FH:49:LYS:HB2	1.59	0.84
1:GU:36:LEU:HB3	1:GU:49:LYS:HB2	1.58	0.84
1:EP:36:LEU:HB3	1:EP:49:LYS:HB2	1.58	0.84
1:EV:36:LEU:HB3	1:EV:49:LYS:HB2	1.58	0.83
1:GR:34:LYS:HB3	1:GR:51:GLU:HB3	1.59	0.83
1:GI:36:LEU:HB3	1:GI:49:LYS:HB2	1.58	0.83
1:GF:36:LEU:HB3	1:GF:49:LYS:HB2	1.58	0.83
1:FK:36:LEU:HB3	1:FK:49:LYS:HB2	1.59	0.83
1:DF:34:LYS:HB3	1:DF:51:GLU:HB3	1.58	0.82
1:GR:36:LEU:HB3	1:GR:49:LYS:HB2	1.59	0.82
1:FW:34:LYS:HB3	1:FW:51:GLU:HB3	1.59	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GX:36:LEU:HB3	1:GX:49:LYS:HB2	1.59	0.82
1:EV:34:LYS:HB3	1:EV:51:GLU:HB3	1.61	0.82
1:CK:34:LYS:HB3	1:CK:51:GLU:HB3	1.63	0.81
1:DU:34:LYS:HB3	1:DU:51:GLU:HB3	1.63	0.81
1:AU:36:LEU:HB3	1:AU:49:LYS:HB2	1.63	0.81
1:BD:36:LEU:HB3	1:BD:49:LYS:HB2	1.63	0.80
1:GI:34:LYS:HB3	1:GI:51:GLU:HB3	1.62	0.80
1:ES:34:LYS:HB3	1:ES:51:GLU:HB3	1.64	0.80
1:FU:104:THR:HG22	1:FV:83:LYS:HG2	1.64	0.80
1:FE:34:LYS:HB3	1:FE:51:GLU:HB3	1.64	0.80
1:GP:104:THR:HG22	1:GQ:83:LYS:HG2	1.64	0.80
1:AF:34:LYS:HB3	1:AF:51:GLU:HB3	1.64	0.79
1:GG:104:THR:HG22	1:GH:83:LYS:HG2	1.63	0.79
1:GL:34:LYS:HB3	1:GL:51:GLU:HB3	1.64	0.79
1:DI:36:LEU:HB3	1:DI:49:LYS:HB2	1.63	0.79
1:CT:36:LEU:HB3	1:CT:49:LYS:HB2	1.64	0.79
1:FZ:34:LYS:HB3	1:FZ:51:GLU:HB3	1.64	0.79
1:AP:104:THR:HG22	1:AQ:83:LYS:HD2	1.64	0.79
1:DR:36:LEU:HB3	1:DR:49:LYS:HB2	1.63	0.79
1:BP:36:LEU:HB3	1:BP:49:LYS:HB2	1.63	0.78
1:CW:34:LYS:HB3	1:CW:51:GLU:HB3	1.63	0.78
1:FK:34:LYS:HB3	1:FK:51:GLU:HB3	1.64	0.78
1:CO:47:MET:HB2	1:CO:49:LYS:HZ3	1.48	0.78
1:ET:104:THR:HG22	1:EU:83:LYS:HG2	1.63	0.78
1:FX:83:LYS:HD2	1:FY:104:THR:HG22	1.66	0.78
1:FO:83:LYS:HD2	1:FP:104:THR:HG22	1.66	0.78
1:FQ:34:LYS:HB3	1:FQ:51:GLU:HB3	1.64	0.77
1:FI:104:THR:HG22	1:FJ:83:LYS:HG2	1.63	0.77
1:BQ:104:THR:HA	1:BR:83:LYS:HE3	1.66	0.77
1:CH:34:LYS:HB3	1:CH:51:GLU:HB3	1.67	0.77
1:FT:34:LYS:HB3	1:FT:51:GLU:HB3	1.67	0.77
1:CL:47:MET:HB2	1:CL:49:LYS:HZ3	1.50	0.77
1:EG:34:LYS:HB3	1:EG:51:GLU:HB3	1.66	0.77
1:EK:104:THR:HA	1:EL:83:LYS:HE3	1.66	0.77
1:EQ:83:LYS:HD2	1:ER:104:THR:HG22	1.66	0.77
1:GJ:83:LYS:HD2	1:GK:104:THR:HG22	1.66	0.77
1:AI:36:LEU:HB3	1:AI:49:LYS:HB2	1.64	0.77
1:BM:34:LYS:HB3	1:BM:51:GLU:HB3	1.67	0.77
1:ED:34:LYS:HB3	1:ED:51:GLU:HB3	1.67	0.77
1:GX:34:LYS:HB3	1:GX:51:GLU:HB3	1.66	0.77
1:EN:36:LEU:HB2	1:EN:49:LYS:HB2	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FH:34:LYS:HB3	1:FH:51:GLU:HB3	1.67	0.77
1:GG:36:LEU:HB2	1:GG:49:LYS:HB2	1.67	0.77
1:EY:34:LYS:HB3	1:EY:51:GLU:HB3	1.67	0.77
1:DJ:36:LEU:HB2	1:DJ:49:LYS:HB2	1.66	0.76
1:GD:36:LEU:HB2	1:GD:49:LYS:HB2	1.67	0.76
1:CB:83:LYS:HE3	1:GL:104:THR:HA	1.68	0.76
1:EQ:36:LEU:HB2	1:EQ:49:LYS:HB2	1.68	0.76
1:DL:34:LYS:HB3	1:DL:51:GLU:HB3	1.67	0.76
1:GS:36:LEU:HB2	1:GS:49:LYS:HB2	1.67	0.76
1:FC:83:LYS:HD2	1:FD:104:THR:HG22	1.66	0.76
1:AO:34:LYS:HB3	1:AO:51:GLU:HB3	1.67	0.76
1:CX:104:THR:HA	1:CY:83:LYS:HE3	1.66	0.76
1:DY:47:MET:HB2	1:DY:49:LYS:HZ3	1.50	0.76
1:DY:104:THR:HA	1:DZ:83:LYS:HE3	1.66	0.76
1:FE:104:THR:HA	1:FN:83:LYS:HE3	1.68	0.76
1:CF:36:LEU:HB2	1:CF:49:LYS:HB2	1.68	0.76
1:EB:36:LEU:HB2	1:EB:49:LYS:HB2	1.68	0.76
1:BV:34:LYS:HB3	1:BV:51:GLU:HB3	1.68	0.76
1:FX:36:LEU:HB2	1:FX:49:LYS:HB2	1.68	0.75
1:AJ:40:ARG:NH2	1:AZ:61:THR:OG1	2.20	0.75
1:EM:36:LEU:HB3	1:EM:49:LYS:HB2	1.68	0.75
1:AY:36:LEU:HB2	1:AY:49:LYS:HB2	1.68	0.75
1:BE:104:THR:HA	1:BF:83:LYS:HE3	1.66	0.75
1:FE:83:LYS:HE3	1:FN:104:THR:HA	1.68	0.75
1:AR:36:LEU:HB3	1:AR:49:LYS:HB2	1.68	0.75
1:AX:83:LYS:HE3	1:FZ:104:THR:HA	1.67	0.75
1:CL:104:THR:HA	1:CM:83:LYS:HE3	1.66	0.75
1:EC:61:THR:OG1	1:EH:40:ARG:NH2	2.19	0.75
1:EJ:83:LYS:HE3	1:FQ:104:THR:HA	1.67	0.75
1:BA:34:LYS:HB3	1:BA:51:GLU:HB3	1.68	0.75
1:AM:36:LEU:HB2	1:AM:49:LYS:HB2	1.68	0.75
1:CC:104:THR:HA	1:CD:83:LYS:HE3	1.66	0.75
1:DA:47:MET:HB2	1:DA:49:LYS:HZ3	1.52	0.75
1:DK:61:THR:OG1	1:GM:40:ARG:NH2	2.19	0.75
1:BK:36:LEU:HB2	1:BK:49:LYS:HB2	1.68	0.74
1:AA:40:ARG:NH2	1:FD:61:THR:OG1	2.20	0.74
1:FB:34:LYS:HB3	1:FB:51:GLU:HB3	1.68	0.74
1:FC:36:LEU:HB2	1:FC:49:LYS:HB2	1.68	0.74
1:BJ:34:LYS:HB3	1:BJ:51:GLU:HB3	1.69	0.74
1:BT:36:LEU:HB2	1:BT:49:LYS:HB2	1.68	0.74
1:AN:61:THR:OG1	1:DA:40:ARG:NH2	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:40:ARG:NH2	1:ER:61:THR:OG1	2.20	0.74
1:BE:47:MET:HB2	1:BE:49:LYS:HZ3	1.52	0.74
1:CG:61:THR:OG1	1:DM:40:ARG:NH2	2.19	0.74
1:BL:61:THR:OG1	1:BZ:40:ARG:NH2	2.19	0.74
1:BR:75:ARG:NH2	1:BR:77:ASP:OD2	2.21	0.74
1:CM:75:ARG:NH2	1:CM:77:ASP:OD2	2.21	0.74
1:BU:61:THR:OG1	1:CO:40:ARG:NH2	2.20	0.74
1:BY:34:LYS:HB3	1:BY:51:GLU:HB3	1.70	0.74
1:CD:75:ARG:NH2	1:CD:77:ASP:OD2	2.21	0.74
1:EL:75:ARG:NH2	1:EL:77:ASP:OD2	2.21	0.74
1:FG:40:ARG:HG3	1:FG:45:PRO:HA	1.70	0.74
1:GO:28:LYS:HB3	1:GO:59:PRO:HD3	1.70	0.74
1:AQ:40:ARG:HG3	1:AQ:45:PRO:HA	1.70	0.74
1:EX:40:ARG:HG3	1:EX:45:PRO:HA	1.70	0.74
1:EH:47:MET:HB2	1:EH:49:LYS:HZ3	1.52	0.74
1:FL:40:ARG:NH2	1:FY:61:THR:OG1	2.20	0.74
1:FN:28:LYS:HB3	1:FN:59:PRO:HD3	1.70	0.73
1:FP:61:THR:OG1	1:GA:40:ARG:NH2	2.20	0.73
1:GC:28:LYS:HB3	1:GC:59:PRO:HD3	1.70	0.73
1:AV:47:MET:HB2	1:AV:49:LYS:HZ3	1.52	0.73
1:AQ:75:ARG:NH2	1:AQ:77:ASP:OD2	2.21	0.73
1:BF:75:ARG:NH2	1:BF:77:ASP:OD2	2.21	0.73
1:BG:36:LEU:HB3	1:BG:49:LYS:HB2	1.70	0.73
1:CT:34:LYS:HB3	1:CT:51:GLU:HB3	1.70	0.73
1:DP:36:LEU:HB2	1:DP:49:LYS:HB2	1.70	0.73
1:DV:40:ARG:NH2	1:GK:61:THR:OG1	2.20	0.73
1:FS:40:ARG:HG3	1:FS:45:PRO:HA	1.70	0.73
1:BF:40:ARG:HG3	1:BF:45:PRO:HA	1.71	0.73
1:CQ:103:VAL:O	1:CQ:104:THR:OG1	2.07	0.73
1:CC:47:MET:HB2	1:CC:49:LYS:HZ3	1.53	0.73
1:CM:40:ARG:HG3	1:CM:45:PRO:HA	1.70	0.73
1:DZ:75:ARG:NH2	1:DZ:77:ASP:OD2	2.21	0.73
1:EE:36:LEU:HB2	1:EE:49:LYS:HB2	1.71	0.73
1:GW:40:ARG:HG3	1:GW:45:PRO:HA	1.70	0.73
1:AD:36:LEU:HB2	1:AD:49:LYS:HB2	1.71	0.73
1:CY:40:ARG:HG3	1:CY:45:PRO:HA	1.71	0.73
1:AS:36:LEU:HB2	1:AS:49:LYS:HB2	1.70	0.73
1:EX:75:ARG:NH2	1:EX:77:ASP:OD2	2.21	0.73
1:BB:36:LEU:HB2	1:BB:49:LYS:HB2	1.70	0.73
1:BN:36:LEU:HB2	1:BN:49:LYS:HB2	1.70	0.73
1:CD:40:ARG:HG3	1:CD:45:PRO:HA	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:36:LEU:HB2	1:CR:49:LYS:HB2	1.70	0.73
1:DC:103:VAL:O	1:DC:104:THR:OG1	2.07	0.73
1:DG:36:LEU:HB2	1:DG:49:LYS:HB2	1.70	0.73
1:DZ:40:ARG:HG3	1:DZ:45:PRO:HA	1.71	0.73
1:FG:75:ARG:NH2	1:FG:77:ASP:OD2	2.21	0.73
1:AG:36:LEU:HB2	1:AG:49:LYS:HB2	1.71	0.72
1:BR:40:ARG:HG3	1:BR:45:PRO:HA	1.70	0.72
1:FY:75:ARG:NH2	1:FY:77:ASP:OD2	2.22	0.72
1:GH:75:ARG:NH2	1:GH:77:ASP:OD2	2.22	0.72
1:GM:36:LEU:HB2	1:GM:49:LYS:HB2	1.71	0.72
1:GW:75:ARG:NH2	1:GW:77:ASP:OD2	2.21	0.72
1:EL:40:ARG:HG3	1:EL:45:PRO:HA	1.71	0.72
1:AA:47:MET:HB2	1:AA:49:LYS:HZ3	1.54	0.72
1:CY:75:ARG:NH2	1:CY:77:ASP:OD2	2.21	0.72
1:ER:75:ARG:NH2	1:ER:77:ASP:OD2	2.22	0.72
1:AF:103:VAL:O	1:AF:104:THR:OG1	2.08	0.72
1:AL:103:VAL:O	1:AL:104:THR:OG1	2.07	0.72
1:DD:36:LEU:HB2	1:DD:49:LYS:HB2	1.71	0.72
1:BP:34:LYS:HB3	1:BP:51:GLU:HB3	1.71	0.72
1:DR:34:LYS:HB3	1:DR:51:GLU:HB3	1.70	0.72
1:DH:75:ARG:NH2	1:DH:77:ASP:OD2	2.23	0.72
1:DQ:75:ARG:NH2	1:DQ:77:ASP:OD2	2.23	0.72
1:EA:36:LEU:HB3	1:EA:49:LYS:HB2	1.72	0.72
1:BO:75:ARG:NH2	1:BO:77:ASP:OD2	2.23	0.72
1:CS:75:ARG:NH2	1:CS:77:ASP:OD2	2.23	0.72
1:FD:75:ARG:NH2	1:FD:77:ASP:OD2	2.22	0.72
1:FS:75:ARG:NH2	1:FS:77:ASP:OD2	2.21	0.72
1:EG:103:VAL:O	1:EG:104:THR:OG1	2.08	0.72
1:AC:104:THR:HA	1:ES:83:LYS:HE3	1.72	0.71
1:GQ:75:ARG:NH2	1:GQ:77:ASP:OD2	2.23	0.71
1:BV:103:VAL:O	1:BV:104:THR:OG1	2.07	0.71
1:DO:103:VAL:O	1:DO:104:THR:OG1	2.07	0.71
1:EU:75:ARG:NH2	1:EU:77:ASP:OD2	2.23	0.71
1:BH:36:LEU:HB2	1:BH:49:LYS:HB2	1.71	0.71
1:DX:103:VAL:O	1:DX:104:THR:OG1	2.07	0.71
1:FJ:75:ARG:NH2	1:FJ:77:ASP:OD2	2.23	0.71
1:FV:74:ILE:HG21	1:FV:83:LYS:HD3	1.73	0.71
1:BC:75:ARG:NH2	1:BC:77:ASP:OD2	2.23	0.71
1:CU:36:LEU:HB2	1:CU:49:LYS:HB2	1.71	0.71
1:AG:101:GLU:O	1:AG:105:ASP:HB2	1.91	0.71
1:DF:36:LEU:HB3	1:DF:49:LYS:HB2	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DP:101:GLU:O	1:DP:105:ASP:HB2	1.91	0.71
1:BN:101:GLU:O	1:BN:105:ASP:HB2	1.91	0.71
1:BW:36:LEU:HB2	1:BW:49:LYS:HB2	1.71	0.71
1:CE:36:LEU:HB3	1:CE:49:LYS:HB2	1.72	0.71
1:CN:36:LEU:HB3	1:CN:49:LYS:HB2	1.72	0.71
1:DG:101:GLU:O	1:DG:105:ASP:HB2	1.91	0.71
1:AT:75:ARG:NH2	1:AT:77:ASP:OD2	2.23	0.71
1:BY:103:VAL:O	1:BY:104:THR:OG1	2.08	0.71
1:CR:101:GLU:O	1:CR:105:ASP:HB2	1.91	0.71
1:GB:75:ARG:NH2	1:GB:77:ASP:OD2	2.24	0.71
1:BJ:103:VAL:O	1:BJ:104:THR:OG1	2.08	0.71
1:CH:103:VAL:O	1:CH:104:THR:OG1	2.09	0.71
1:CK:36:LEU:HB3	1:CK:49:LYS:HB2	1.73	0.71
1:DA:36:LEU:HB2	1:DA:49:LYS:HB2	1.73	0.71
1:FJ:74:ILE:HG21	1:FJ:83:LYS:HD3	1.73	0.71
1:CI:36:LEU:HB2	1:CI:49:LYS:HB2	1.71	0.71
1:FM:75:ARG:NH2	1:FM:77:ASP:OD2	2.24	0.71
1:AW:75:ARG:NH2	1:AW:77:ASP:OD2	2.24	0.70
1:BS:36:LEU:HB3	1:BS:49:LYS:HB2	1.72	0.70
1:CB:104:THR:HA	1:GL:83:LYS:HE3	1.72	0.70
1:CP:75:ARG:NH2	1:CP:77:ASP:OD2	2.24	0.70
1:DS:36:LEU:HB2	1:DS:49:LYS:HB2	1.71	0.70
1:AX:104:THR:HA	1:FZ:83:LYS:HE3	1.72	0.70
1:EJ:104:THR:HA	1:FQ:83:LYS:HE3	1.72	0.70
1:CO:36:LEU:HB2	1:CO:49:LYS:HB2	1.73	0.70
1:FV:75:ARG:NH2	1:FV:77:ASP:OD2	2.23	0.70
1:AJ:36:LEU:HB2	1:AJ:49:LYS:HB2	1.73	0.70
1:CA:75:ARG:NH2	1:CA:77:ASP:OD2	2.25	0.70
1:CW:36:LEU:HB3	1:CW:49:LYS:HB2	1.74	0.70
1:EI:75:ARG:NH2	1:EI:77:ASP:OD2	2.25	0.70
1:ER:34:LYS:HB3	1:ER:51:GLU:HB3	1.74	0.70
1:DN:75:ARG:NH2	1:DN:77:ASP:OD2	2.25	0.70
1:AH:75:ARG:NH2	1:AH:77:ASP:OD2	2.23	0.70
1:GN:75:ARG:NH2	1:GN:77:ASP:OD2	2.24	0.70
1:AB:75:ARG:NH2	1:AB:77:ASP:OD2	2.24	0.70
1:EK:47:MET:HB2	1:EK:49:LYS:HZ3	1.56	0.70
1:EZ:36:LEU:HB2	1:EZ:49:LYS:HB2	1.72	0.70
1:FI:83:LYS:HD2	1:FJ:104:THR:HG22	1.73	0.70
1:GF:103:VAL:O	1:GF:104:THR:OG1	2.10	0.70
1:AK:75:ARG:NH2	1:AK:77:ASP:OD2	2.24	0.70
1:BQ:47:MET:HB2	1:BQ:49:LYS:HZ3	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DU:36:LEU:HB3	1:DU:49:LYS:HB2	1.74	0.70
1:FY:34:LYS:HB3	1:FY:51:GLU:HB3	1.74	0.70
1:AJ:47:MET:HB2	1:AJ:49:LYS:HZ3	1.57	0.70
1:CZ:36:LEU:HB3	1:CZ:49:LYS:HB2	1.72	0.70
1:FS:34:LYS:HB3	1:FS:51:GLU:HB3	1.74	0.70
1:GU:103:VAL:O	1:GU:104:THR:OG1	2.10	0.70
1:DB:75:ARG:NH2	1:DB:77:ASP:OD2	2.25	0.70
1:FV:34:LYS:HB3	1:FV:51:GLU:HB3	1.74	0.70
1:BB:101:GLU:O	1:BB:105:ASP:HB2	1.91	0.69
1:EU:74:ILE:HG21	1:EU:83:LYS:HD3	1.73	0.69
1:CJ:75:ARG:NH2	1:CJ:77:ASP:OD2	2.25	0.69
1:DT:75:ARG:NH2	1:DT:77:ASP:OD2	2.25	0.69
1:EP:103:VAL:O	1:EP:104:THR:OG1	2.10	0.69
1:ET:83:LYS:HD2	1:EU:104:THR:HG22	1.74	0.69
1:BB:40:ARG:NH2	1:EF:61:THR:OG1	2.24	0.69
1:BI:61:THR:OG1	1:DG:40:ARG:NH2	2.24	0.69
1:BJ:36:LEU:HB3	1:BJ:49:LYS:HB2	1.74	0.69
1:CV:75:ARG:NH2	1:CV:77:ASP:OD2	2.25	0.69
1:AE:75:ARG:NH2	1:AE:77:ASP:OD2	2.25	0.69
1:AS:101:GLU:O	1:AS:105:ASP:HB2	1.91	0.69
1:DE:75:ARG:NH2	1:DE:77:ASP:OD2	2.25	0.69
1:AZ:101:GLU:O	1:AZ:105:ASP:HB2	1.93	0.69
1:AA:83:LYS:HD2	1:AB:104:THR:HG22	1.74	0.69
1:AO:103:VAL:O	1:AO:104:THR:OG1	2.09	0.69
1:BA:103:VAL:O	1:BA:104:THR:OG1	2.07	0.69
1:FG:34:LYS:HB3	1:FG:51:GLU:HB3	1.74	0.69
1:FL:36:LEU:HB2	1:FL:49:LYS:HB2	1.72	0.69
1:BU:101:GLU:O	1:BU:105:ASP:HB2	1.93	0.69
1:BX:75:ARG:NH2	1:BX:77:ASP:OD2	2.25	0.69
1:BY:36:LEU:HB3	1:BY:49:LYS:HB2	1.74	0.69
1:CG:101:GLU:O	1:CG:105:ASP:HB2	1.93	0.69
1:DL:103:VAL:O	1:DL:104:THR:OG1	2.09	0.69
1:DV:83:LYS:HD2	1:DW:104:THR:HG22	1.74	0.69
1:EX:34:LYS:HB3	1:EX:51:GLU:HB3	1.74	0.69
1:FB:83:LYS:HE3	1:FK:104:THR:HA	1.75	0.69
1:FB:103:VAL:O	1:FB:104:THR:OG1	2.10	0.69
1:FU:83:LYS:HD2	1:FV:104:THR:HG22	1.74	0.69
1:GA:36:LEU:HB2	1:GA:49:LYS:HB2	1.72	0.69
1:AJ:83:LYS:HD2	1:AK:104:THR:HG22	1.74	0.69
1:BL:101:GLU:O	1:BL:105:ASP:HB2	1.93	0.69
1:DM:47:MET:HB2	1:DM:49:LYS:HZ3	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ED:103:VAL:O	1:ED:104:THR:OG1	2.09	0.69
1:GW:34:LYS:HB3	1:GW:51:GLU:HB3	1.74	0.69
1:DA:83:LYS:HD2	1:DB:104:THR:HG22	1.74	0.69
1:EU:34:LYS:HB3	1:EU:51:GLU:HB3	1.74	0.69
1:FF:47:MET:HB2	1:FF:49:LYS:HZ3	1.58	0.69
1:FJ:34:LYS:HB3	1:FJ:51:GLU:HB3	1.74	0.69
1:CB:28:LYS:HB3	1:CB:59:PRO:HD3	1.75	0.68
1:DM:83:LYS:HD2	1:DN:104:THR:HG22	1.74	0.68
1:DV:36:LEU:HB2	1:DV:49:LYS:HB2	1.75	0.68
1:EF:75:ARG:NH2	1:EF:77:ASP:OD2	2.25	0.68
1:EJ:28:LYS:HB3	1:EJ:59:PRO:HD3	1.75	0.68
1:FD:34:LYS:HB3	1:FD:51:GLU:HB3	1.74	0.68
1:GQ:74:ILE:HG21	1:GQ:83:LYS:HD3	1.73	0.68
1:AX:28:LYS:HB3	1:AX:59:PRO:HD3	1.75	0.68
1:BM:103:VAL:O	1:BM:104:THR:OG1	2.09	0.68
1:BZ:83:LYS:HD2	1:CA:104:THR:HG22	1.74	0.68
1:CQ:28:LYS:HB3	1:CQ:59:PRO:HD3	1.75	0.68
1:EC:101:GLU:O	1:EC:105:ASP:HB2	1.93	0.68
1:CK:103:VAL:O	1:CK:104:THR:OG1	2.09	0.68
1:CO:83:LYS:HD2	1:CP:104:THR:HG22	1.74	0.68
1:EG:36:LEU:HB3	1:EG:49:LYS:HB2	1.74	0.68
1:AF:36:LEU:HB3	1:AF:49:LYS:HB2	1.74	0.68
1:BZ:36:LEU:HB2	1:BZ:49:LYS:HB2	1.76	0.68
1:FK:103:VAL:O	1:FK:104:THR:OG1	2.12	0.68
1:GG:83:LYS:HD2	1:GH:104:THR:HG22	1.74	0.68
1:GP:83:LYS:HD2	1:GQ:104:THR:HG22	1.74	0.68
1:AI:104:THR:HA	1:EP:83:LYS:HE3	1.76	0.68
1:AV:83:LYS:HD2	1:AW:104:THR:HG22	1.74	0.68
1:DA:104:THR:HG22	1:DB:83:LYS:HD2	1.76	0.68
1:GM:83:LYS:HD2	1:GN:104:THR:HG22	1.76	0.68
1:BG:50:SER:HB2	1:GX:102:LEU:HG	1.76	0.68
1:DM:36:LEU:HB2	1:DM:49:LYS:HB2	1.76	0.68
1:AM:104:THR:HG22	1:AN:83:LYS:HD2	1.76	0.68
1:AN:101:GLU:O	1:AN:105:ASP:HB2	1.93	0.68
1:DK:101:GLU:O	1:DK:105:ASP:HB2	1.93	0.68
1:DU:103:VAL:O	1:DU:104:THR:OG1	2.09	0.68
1:FE:103:VAL:O	1:FE:104:THR:OG1	2.10	0.68
1:AP:47:MET:HB2	1:AP:49:LYS:HZ3	1.58	0.68
1:AY:104:THR:HG22	1:AZ:83:LYS:HD2	1.76	0.68
1:CJ:61:THR:OG1	1:DP:40:ARG:NH2	2.27	0.68
1:EE:102:LEU:HG	1:EF:50:SER:HB2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:40:ARG:NH2	1:FA:61:THR:OG1	2.27	0.67
1:AV:36:LEU:HB2	1:AV:49:LYS:HB2	1.75	0.67
1:GQ:34:LYS:HB3	1:GQ:51:GLU:HB3	1.74	0.67
1:BD:104:THR:HA	1:GU:83:LYS:HE3	1.76	0.67
1:CX:47:MET:HB2	1:CX:49:LYS:HZ3	1.58	0.67
1:DC:28:LYS:HB3	1:DC:59:PRO:HD3	1.75	0.67
1:EH:83:LYS:HD2	1:EI:104:THR:HG22	1.74	0.67
1:EZ:104:THR:HA	1:FA:83:LYS:HE3	1.76	0.67
1:BX:61:THR:OG1	1:CR:40:ARG:NH2	2.27	0.67
1:DO:28:LYS:HB3	1:DO:59:PRO:HD3	1.75	0.67
1:ES:103:VAL:O	1:ES:104:THR:OG1	2.11	0.67
1:DX:28:LYS:HB3	1:DX:59:PRO:HD3	1.75	0.67
1:AA:104:THR:HG22	1:AB:83:LYS:HD2	1.76	0.67
1:AU:104:THR:HA	1:GF:83:LYS:HE3	1.76	0.67
1:DN:40:ARG:HG3	1:DN:45:PRO:HA	1.76	0.67
1:GH:34:LYS:HB3	1:GH:51:GLU:HB3	1.75	0.67
1:GH:74:ILE:HG21	1:GH:83:LYS:HD3	1.73	0.67
1:GM:18:VAL:HG22	1:GM:34:LYS:HG3	1.76	0.67
1:AA:36:LEU:HB2	1:AA:49:LYS:HB2	1.75	0.67
1:CW:103:VAL:O	1:CW:104:THR:OG1	2.09	0.67
1:DJ:104:THR:HG22	1:DK:83:LYS:HD2	1.77	0.67
1:DS:102:LEU:HG	1:DT:50:SER:HB2	1.76	0.67
1:DF:103:VAL:O	1:DF:104:THR:OG1	2.09	0.67
1:EH:36:LEU:HB2	1:EH:49:LYS:HB2	1.76	0.67
1:AC:28:LYS:HB3	1:AC:59:PRO:HD3	1.75	0.67
1:AJ:104:THR:HG22	1:AK:83:LYS:HD2	1.76	0.67
1:AL:28:LYS:HB3	1:AL:59:PRO:HD3	1.75	0.67
1:BT:104:THR:HG22	1:BU:83:LYS:HD2	1.76	0.67
1:CI:102:LEU:HG	1:CJ:50:SER:HB2	1.76	0.67
1:EM:50:SER:HB2	1:FT:102:LEU:HG	1.76	0.67
1:FL:18:VAL:HG22	1:FL:34:LYS:HG3	1.77	0.67
1:AV:104:THR:HG22	1:AW:83:LYS:HD2	1.76	0.67
1:EV:103:VAL:O	1:EV:104:THR:OG1	2.13	0.67
1:AP:36:LEU:HB2	1:AP:49:LYS:HB2	1.77	0.67
1:BQ:36:LEU:HB2	1:BQ:49:LYS:HB2	1.77	0.67
1:CA:40:ARG:HG3	1:CA:45:PRO:HA	1.76	0.67
1:EK:36:LEU:HB2	1:EK:49:LYS:HB2	1.77	0.67
1:FF:36:LEU:HB2	1:FF:49:LYS:HB2	1.77	0.67
1:BV:96:ASP:OD1	1:GO:1:SER:OG	2.14	0.66
1:BZ:47:MET:HB2	1:BZ:49:LYS:HZ3	1.60	0.66
1:DD:102:LEU:HG	1:DE:50:SER:HB2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GN:34:LYS:HB3	1:GN:51:GLU:HB3	1.77	0.66
1:AO:96:ASP:OD1	1:DX:1:SER:OG	2.13	0.66
1:BE:36:LEU:HB2	1:BE:49:LYS:HB2	1.77	0.66
1:BI:75:ARG:NH2	1:BI:77:ASP:OD2	2.25	0.66
1:CC:36:LEU:HB2	1:CC:49:LYS:HB2	1.77	0.66
1:CO:104:THR:HG22	1:CP:83:LYS:HD2	1.76	0.66
1:DL:96:ASP:OD1	1:DO:1:SER:OG	2.13	0.66
1:DY:36:LEU:HB2	1:DY:49:LYS:HB2	1.77	0.66
1:GC:103:VAL:O	1:GC:104:THR:OG1	2.11	0.66
1:AU:34:LYS:HB3	1:AU:51:GLU:HB3	1.76	0.66
1:CL:36:LEU:HB2	1:CL:49:LYS:HB2	1.77	0.66
1:CU:102:LEU:HG	1:CV:50:SER:HB2	1.77	0.66
1:EH:104:THR:HG22	1:EI:83:LYS:HD2	1.76	0.66
1:GK:34:LYS:HB3	1:GK:51:GLU:HB3	1.77	0.66
1:AX:2:LYS:NZ	1:AX:10:ASP:OD1	2.29	0.66
1:BZ:104:THR:HG22	1:CA:83:LYS:HD2	1.76	0.66
1:FN:103:VAL:O	1:FN:104:THR:OG1	2.11	0.66
1:GV:36:LEU:HB2	1:GV:49:LYS:HB2	1.77	0.66
1:BN:40:ARG:NH2	1:DT:61:THR:OG1	2.28	0.66
1:DV:104:THR:HG22	1:DW:83:LYS:HD2	1.76	0.66
1:DW:75:ARG:NH2	1:DW:77:ASP:OD2	2.25	0.66
1:FO:12:TYR:HB2	1:FO:22:ARG:HG3	1.78	0.66
1:GD:104:THR:HA	1:GE:83:LYS:HE3	1.76	0.66
1:GV:104:THR:HA	1:GW:83:LYS:HE3	1.78	0.66
1:BH:102:LEU:HG	1:BI:50:SER:HB2	1.76	0.66
1:EI:40:ARG:HG3	1:EI:45:PRO:HA	1.76	0.66
1:EJ:2:LYS:NZ	1:EJ:10:ASP:OD1	2.29	0.66
1:FW:103:VAL:O	1:FW:104:THR:OG1	2.13	0.66
1:BW:102:LEU:HG	1:BX:50:SER:HB2	1.76	0.66
1:EN:104:THR:HA	1:EO:83:LYS:HE3	1.76	0.66
1:FL:83:LYS:HD2	1:FM:104:THR:HG22	1.76	0.66
1:FR:36:LEU:HB2	1:FR:49:LYS:HB2	1.77	0.66
1:GA:83:LYS:HD2	1:GB:104:THR:HG22	1.76	0.66
1:AB:18:VAL:HG22	1:AB:34:LYS:HG3	1.78	0.66
1:AB:61:THR:OG1	1:FR:40:ARG:NH2	2.29	0.66
1:AC:2:LYS:NZ	1:AC:10:ASP:OD1	2.29	0.66
1:AL:1:SER:OG	1:ED:96:ASP:OD1	2.13	0.66
1:CB:2:LYS:NZ	1:CB:10:ASP:OD1	2.29	0.66
1:CE:34:LYS:HB3	1:CE:51:GLU:HB3	1.78	0.66
1:DA:101:GLU:O	1:DA:105:ASP:HB2	1.96	0.66
1:GS:104:THR:HA	1:GT:83:LYS:HE3	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:83:LYS:HE3	1:DX:104:THR:HG22	1.78	0.66
1:CN:34:LYS:HB3	1:CN:51:GLU:HB3	1.78	0.66
1:DL:83:LYS:HE3	1:DO:104:THR:HG22	1.78	0.66
1:EF:34:LYS:HB3	1:EF:51:GLU:HB3	1.78	0.66
1:FX:12:TYR:HB2	1:FX:22:ARG:HG3	1.78	0.66
1:GB:34:LYS:NZ	1:GB:36:LEU:HD13	2.11	0.66
1:FC:12:TYR:HB2	1:FC:22:ARG:HG3	1.78	0.66
1:GB:34:LYS:HB3	1:GB:51:GLU:HB3	1.77	0.66
1:GW:32:ALA:HB3	1:GW:53:LYS:HG2	1.78	0.66
1:AD:102:LEU:HG	1:AE:50:SER:HB2	1.76	0.65
1:CV:34:LYS:HB3	1:CV:51:GLU:HB3	1.78	0.65
1:CX:36:LEU:HB2	1:CX:49:LYS:HB2	1.77	0.65
1:DE:34:LYS:HB3	1:DE:51:GLU:HB3	1.78	0.65
1:DM:104:THR:HG22	1:DN:83:LYS:HD2	1.76	0.65
1:GN:34:LYS:NZ	1:GN:36:LEU:HD13	2.11	0.65
1:AJ:101:GLU:O	1:AJ:105:ASP:HB2	1.96	0.65
1:BM:83:LYS:HE3	1:DC:104:THR:HG22	1.78	0.65
1:CH:83:LYS:HE3	1:CQ:104:THR:HG22	1.78	0.65
1:EQ:12:TYR:HB2	1:EQ:22:ARG:HG3	1.78	0.65
1:FM:34:LYS:NZ	1:FM:36:LEU:HD13	2.12	0.65
1:GJ:12:TYR:HB2	1:GJ:22:ARG:HG3	1.78	0.65
1:EH:101:GLU:O	1:EH:105:ASP:HB2	1.96	0.65
1:DM:101:GLU:O	1:DM:105:ASP:HB2	1.96	0.65
1:FP:34:LYS:HB3	1:FP:51:GLU:HB3	1.77	0.65
1:CV:61:THR:OG1	1:GP:40:ARG:NH2	2.29	0.65
1:DE:61:THR:OG1	1:GG:40:ARG:NH2	2.29	0.65
1:DJ:12:TYR:HB2	1:DJ:22:ARG:HG3	1.79	0.65
1:EN:40:ARG:NH2	1:GW:61:THR:OG1	2.30	0.65
1:AL:2:LYS:NZ	1:AL:10:ASP:OD1	2.30	0.65
1:DC:2:LYS:NZ	1:DC:10:ASP:OD1	2.30	0.65
1:EK:18:VAL:HG22	1:EK:34:LYS:HG3	1.79	0.65
1:GA:18:VAL:HG22	1:GA:34:LYS:HG3	1.79	0.65
1:BI:34:LYS:HB3	1:BI:51:GLU:HB3	1.78	0.65
1:CH:106:GLN:O	1:CQ:35:ARG:NH1	2.29	0.65
1:EG:2:LYS:NZ	1:EG:10:ASP:OD2	2.30	0.65
1:FR:35:ARG:NH1	1:FS:106:GLN:O	2.29	0.65
1:AA:101:GLU:O	1:AA:105:ASP:HB2	1.97	0.65
1:AE:61:THR:OG1	1:FU:40:ARG:NH2	2.29	0.65
1:AW:18:VAL:HG22	1:AW:34:LYS:HG3	1.78	0.65
1:BQ:18:VAL:HG22	1:BQ:34:LYS:HG3	1.79	0.65
1:EB:12:TYR:HB2	1:EB:22:ARG:HG3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FR:47:MET:HB2	1:FR:49:LYS:HZ3	1.61	0.65
1:AV:101:GLU:O	1:AV:105:ASP:HB2	1.97	0.65
1:BM:96:ASP:OD1	1:DC:1:SER:OG	2.13	0.65
1:BX:34:LYS:HB3	1:BX:51:GLU:HB3	1.79	0.65
1:CC:35:ARG:NH1	1:CD:106:GLN:O	2.29	0.65
1:CF:12:TYR:HB2	1:CF:22:ARG:HG3	1.78	0.65
1:EW:36:LEU:HB2	1:EW:49:LYS:HB2	1.79	0.65
1:EW:47:MET:HB2	1:EW:49:LYS:HZ3	1.62	0.65
1:CO:101:GLU:O	1:CO:105:ASP:HB2	1.96	0.64
1:DU:2:LYS:NZ	1:DU:10:ASP:OD2	2.30	0.64
1:DV:101:GLU:O	1:DV:105:ASP:HB2	1.97	0.64
1:DX:2:LYS:NZ	1:DX:10:ASP:OD1	2.30	0.64
1:GG:47:MET:HB2	1:GG:49:LYS:HZ3	1.62	0.64
1:AD:40:ARG:NH2	1:EX:61:THR:OG1	2.30	0.64
1:BS:35:ARG:NH1	1:CZ:106:GLN:O	2.30	0.64
1:BZ:101:GLU:O	1:BZ:105:ASP:HB2	1.96	0.64
1:CQ:2:LYS:NZ	1:CQ:10:ASP:OD1	2.30	0.64
1:DB:61:THR:OG1	1:GV:40:ARG:NH2	2.29	0.64
1:DO:2:LYS:NZ	1:DO:10:ASP:OD1	2.30	0.64
1:EX:32:ALA:HB3	1:EX:53:LYS:HG2	1.78	0.64
1:FF:104:THR:HA	1:FG:83:LYS:HE3	1.78	0.64
1:FO:35:ARG:NH1	1:FP:106:GLN:O	2.27	0.64
1:FR:104:THR:HA	1:FS:83:LYS:HE3	1.78	0.64
1:AE:34:LYS:HB3	1:AE:51:GLU:HB3	1.78	0.64
1:BA:96:ASP:OD1	1:GC:1:SER:OG	2.14	0.64
1:EP:2:LYS:NZ	1:EP:10:ASP:OD2	2.31	0.64
1:FS:32:ALA:HB3	1:FS:53:LYS:HG2	1.78	0.64
1:FS:61:THR:OG1	1:GD:40:ARG:NH2	2.30	0.64
1:AP:18:VAL:HG22	1:AP:34:LYS:HG3	1.79	0.64
1:BK:12:TYR:HB2	1:BK:22:ARG:HG3	1.78	0.64
1:EW:104:THR:HA	1:EX:83:LYS:HE3	1.78	0.64
1:FG:58:ASP:HB3	1:FG:65:ILE:HD11	1.78	0.64
1:GO:103:VAL:O	1:GO:104:THR:OG1	2.11	0.64
1:AF:2:LYS:NZ	1:AF:10:ASP:OD2	2.30	0.64
1:AP:101:GLU:O	1:AP:105:ASP:HB2	1.97	0.64
1:BV:83:LYS:HE3	1:GO:104:THR:HG22	1.79	0.64
1:BY:2:LYS:NZ	1:BY:10:ASP:OD2	2.30	0.64
1:CE:102:LEU:HG	1:CN:50:SER:HB2	1.80	0.64
1:CH:96:ASP:OD1	1:CQ:1:SER:OG	2.13	0.64
1:CJ:34:LYS:HB3	1:CJ:51:GLU:HB3	1.78	0.64
1:DV:47:MET:HB2	1:DV:49:LYS:HZ3	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FG:32:ALA:HB3	1:FG:53:LYS:HG2	1.78	0.64
1:AR:34:LYS:HB3	1:AR:51:GLU:HB3	1.78	0.64
1:AR:50:SER:HB2	1:EA:102:LEU:HG	1.80	0.64
1:BB:54:ILE:HD13	1:BC:89:ILE:HG21	1.80	0.64
1:BE:18:VAL:HG22	1:BE:34:LYS:HG3	1.79	0.64
1:BJ:2:LYS:NZ	1:BJ:10:ASP:OD2	2.30	0.64
1:CC:18:VAL:HG22	1:CC:34:LYS:HG3	1.79	0.64
1:CE:50:SER:HB2	1:CN:102:LEU:HG	1.80	0.64
1:CI:40:ARG:NH2	1:CM:61:THR:OG1	2.30	0.64
1:CW:2:LYS:NZ	1:CW:10:ASP:OD2	2.30	0.64
1:DF:2:LYS:NZ	1:DF:10:ASP:OD2	2.30	0.64
1:DW:18:VAL:HG22	1:DW:34:LYS:HG3	1.77	0.64
1:EK:35:ARG:NH1	1:EL:106:GLN:O	2.29	0.64
1:EW:40:ARG:NH2	1:FM:61:THR:OG1	2.29	0.64
1:FF:40:ARG:NH2	1:GB:61:THR:OG1	2.30	0.64
1:FM:34:LYS:HB3	1:FM:51:GLU:HB3	1.79	0.64
1:AL:104:THR:HG22	1:ED:83:LYS:HE3	1.78	0.64
1:AS:54:ILE:HD13	1:AT:89:ILE:HG21	1.80	0.64
1:BM:87:MET:HE1	1:DC:100:THR:HG23	1.78	0.64
1:CF:35:ARG:NH1	1:CG:106:GLN:O	2.26	0.64
1:CK:2:LYS:NZ	1:CK:10:ASP:OD2	2.30	0.64
1:DT:34:LYS:HB3	1:DT:51:GLU:HB3	1.79	0.64
1:EA:34:LYS:HB3	1:EA:51:GLU:HB3	1.78	0.64
1:GJ:35:ARG:NH1	1:GK:106:GLN:O	2.27	0.64
1:GO:26:ASN:ND2	1:GO:29:ASP:OD2	2.30	0.64
1:AF:106:GLN:O	1:EV:35:ARG:NH1	2.30	0.64
1:DY:40:ARG:NH2	1:GN:61:THR:OG1	2.30	0.64
1:FP:36:LEU:HB2	1:FP:49:LYS:HB2	1.80	0.64
1:AG:35:ARG:NH1	1:AH:106:GLN:O	2.30	0.64
1:AP:40:ARG:NH2	1:AW:61:THR:OG1	2.29	0.64
1:BN:104:THR:HG22	1:BO:83:LYS:HD2	1.80	0.64
1:BQ:35:ARG:NH1	1:BR:106:GLN:O	2.29	0.64
1:CL:18:VAL:HG22	1:CL:34:LYS:HG3	1.79	0.64
1:CX:35:ARG:NH1	1:CY:106:GLN:O	2.29	0.64
1:CZ:34:LYS:HB3	1:CZ:51:GLU:HB3	1.78	0.64
1:DF:106:GLN:O	1:DR:35:ARG:NH1	2.30	0.64
1:AG:54:ILE:HD13	1:AH:89:ILE:HG21	1.80	0.63
1:AY:35:ARG:NH1	1:AZ:106:GLN:O	2.26	0.63
1:BD:83:LYS:HE3	1:GU:104:THR:HA	1.80	0.63
1:CX:18:VAL:HG22	1:CX:34:LYS:HG3	1.79	0.63
1:FB:2:LYS:NZ	1:FB:10:ASP:OD2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:83:LYS:HE3	1:GC:104:THR:HG22	1.79	0.63
1:CR:104:THR:HG22	1:CS:83:LYS:HD2	1.80	0.63
1:DP:104:THR:HG22	1:DQ:83:LYS:HD2	1.80	0.63
1:AI:83:LYS:HE3	1:EP:104:THR:HA	1.80	0.63
1:AU:83:LYS:HE3	1:GF:104:THR:HA	1.80	0.63
1:BS:34:LYS:HB3	1:BS:51:GLU:HB3	1.78	0.63
1:CB:103:VAL:O	1:CB:104:THR:OG1	2.16	0.63
1:DG:104:THR:HG22	1:DH:83:LYS:HD2	1.80	0.63
1:DV:35:ARG:NH1	1:DW:106:GLN:O	2.31	0.63
1:FN:2:LYS:NZ	1:FN:10:ASP:OD1	2.30	0.63
1:AS:40:ARG:NH2	1:EO:61:THR:OG1	2.31	0.63
1:BN:54:ILE:HD13	1:BO:89:ILE:HG21	1.80	0.63
1:BP:35:ARG:NH1	1:CW:106:GLN:O	2.30	0.63
1:BS:102:LEU:HG	1:CZ:50:SER:HB2	1.80	0.63
1:GF:2:LYS:NZ	1:GF:10:ASP:OD2	2.31	0.63
1:GO:2:LYS:NZ	1:GO:10:ASP:OD1	2.31	0.63
1:AD:64:LEU:HD11	1:AD:67:ILE:HG13	1.81	0.63
1:BE:40:ARG:NH2	1:EI:61:THR:OG1	2.32	0.63
1:BQ:40:ARG:NH2	1:DN:61:THR:OG1	2.32	0.63
1:DG:54:ILE:HD13	1:DH:89:ILE:HG21	1.80	0.63
1:DW:61:THR:OG1	1:EK:40:ARG:NH2	2.32	0.63
1:GU:2:LYS:NZ	1:GU:10:ASP:OD2	2.31	0.63
1:CY:58:ASP:HB3	1:CY:65:ILE:HD11	1.81	0.63
1:DD:64:LEU:HD11	1:DD:67:ILE:HG13	1.81	0.63
1:EL:58:ASP:HB3	1:EL:65:ILE:HD11	1.81	0.63
1:AC:103:VAL:O	1:AC:104:THR:OG1	2.16	0.63
1:AK:61:THR:OG1	1:CX:40:ARG:NH2	2.32	0.63
1:BK:35:ARG:NH1	1:BL:106:GLN:O	2.26	0.63
1:BT:35:ARG:NH1	1:BU:106:GLN:O	2.26	0.63
1:CE:35:ARG:NH1	1:CN:106:GLN:O	2.30	0.63
1:DM:35:ARG:NH1	1:DN:106:GLN:O	2.31	0.63
1:DS:64:LEU:HD11	1:DS:67:ILE:HG13	1.79	0.63
1:FB:106:GLN:O	1:FK:35:ARG:NH1	2.31	0.63
1:GO:34:LYS:HB3	1:GO:51:GLU:HB3	1.79	0.63
1:AZ:32:ALA:HB3	1:AZ:53:LYS:HG2	1.81	0.63
1:BR:58:ASP:HB3	1:BR:65:ILE:HD11	1.81	0.63
1:DY:18:VAL:HG22	1:DY:34:LYS:HG3	1.79	0.63
1:GC:34:LYS:HB3	1:GC:51:GLU:HB3	1.79	0.63
1:GD:102:LEU:HG	1:GE:50:SER:HB2	1.81	0.62
1:GS:102:LEU:HG	1:GT:50:SER:HB2	1.81	0.62
1:AA:35:ARG:NH1	1:AB:106:GLN:O	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:35:ARG:NH1	1:AN:106:GLN:O	2.26	0.62
1:AR:106:GLN:O	1:EA:35:ARG:NH1	2.30	0.62
1:EM:35:ARG:NH1	1:FT:106:GLN:O	2.32	0.62
1:AJ:35:ARG:NH1	1:AK:106:GLN:O	2.31	0.62
1:AL:35:ARG:NH1	1:ED:106:GLN:O	2.29	0.62
1:AZ:36:LEU:HB2	1:AZ:49:LYS:HB2	1.81	0.62
1:BS:50:SER:HB2	1:CZ:102:LEU:HG	1.79	0.62
1:CG:36:LEU:HB2	1:CG:49:LYS:HB2	1.81	0.62
1:EB:35:ARG:NH1	1:EC:106:GLN:O	2.26	0.62
1:EM:102:LEU:HG	1:FT:50:SER:HB2	1.81	0.62
1:FI:40:ARG:NH2	1:GE:61:THR:OG1	2.31	0.62
1:AN:32:ALA:HB3	1:AN:53:LYS:HG2	1.81	0.62
1:BI:101:GLU:O	1:BI:105:ASP:HB2	1.99	0.62
1:BM:106:GLN:O	1:DC:35:ARG:NH1	2.29	0.62
1:DK:32:ALA:HB3	1:DK:53:LYS:HG2	1.81	0.62
1:GC:26:ASN:ND2	1:GC:29:ASP:OD2	2.30	0.62
1:AG:104:THR:HG22	1:AH:83:LYS:HD2	1.80	0.62
1:AX:106:GLN:O	1:FZ:35:ARG:NH1	2.31	0.62
1:CW:75:ARG:NH2	1:CW:77:ASP:OD2	2.32	0.62
1:EC:32:ALA:HB3	1:EC:53:LYS:HG2	1.81	0.62
1:ET:40:ARG:NH2	1:GT:61:THR:OG1	2.31	0.62
1:FN:34:LYS:HB3	1:FN:51:GLU:HB3	1.80	0.62
1:GC:2:LYS:NZ	1:GC:10:ASP:OD1	2.31	0.62
1:GK:36:LEU:HB2	1:GK:49:LYS:HB2	1.81	0.62
1:AM:12:TYR:HB2	1:AM:22:ARG:HG3	1.82	0.62
1:AR:102:LEU:HG	1:EA:50:SER:HB2	1.79	0.62
1:AS:104:THR:HG22	1:AT:83:LYS:HD2	1.80	0.62
1:BW:64:LEU:HD11	1:BW:67:ILE:HG13	1.81	0.62
1:CA:61:THR:OG1	1:CL:40:ARG:NH2	2.32	0.62
1:CE:106:GLN:O	1:CN:35:ARG:NH1	2.30	0.62
1:EJ:106:GLN:O	1:FQ:35:ARG:NH1	2.31	0.62
1:EY:102:LEU:HG	1:FH:50:SER:HB2	1.81	0.62
1:BB:104:THR:HG22	1:BC:83:LYS:HD2	1.80	0.62
1:BX:101:GLU:O	1:BX:105:ASP:HB2	2.00	0.62
1:DF:75:ARG:NH2	1:DF:77:ASP:OD2	2.32	0.62
1:DJ:35:ARG:NH1	1:DK:106:GLN:O	2.26	0.62
1:EC:36:LEU:HB2	1:EC:49:LYS:HB2	1.81	0.62
1:EE:64:LEU:HD11	1:EE:67:ILE:HG13	1.81	0.62
1:EY:50:SER:HB2	1:FH:102:LEU:HG	1.81	0.62
1:AE:101:GLU:O	1:AE:105:ASP:HB2	1.99	0.62
1:BH:64:LEU:HD11	1:BH:67:ILE:HG13	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:40:ARG:NH2	1:CP:61:THR:OG1	2.32	0.62
1:CU:64:LEU:HD11	1:CU:67:ILE:HG13	1.81	0.62
1:EF:101:GLU:O	1:EF:105:ASP:HB2	1.99	0.62
1:CB:35:ARG:NH1	1:GL:106:GLN:O	2.31	0.62
1:FN:26:ASN:ND2	1:FN:29:ASP:OD2	2.30	0.62
1:BG:106:GLN:O	1:GX:35:ARG:NH1	2.31	0.62
1:CJ:101:GLU:O	1:CJ:105:ASP:HB2	2.00	0.62
1:FC:35:ARG:NH1	1:FD:106:GLN:O	2.29	0.62
1:AH:32:ALA:HB3	1:AH:53:LYS:HG3	1.81	0.61
1:BG:34:LYS:HB3	1:BG:51:GLU:HB3	1.82	0.61
1:CI:64:LEU:HD11	1:CI:67:ILE:HG13	1.81	0.61
1:EG:106:GLN:O	1:FW:35:ARG:NH1	2.30	0.61
1:EJ:35:ARG:NH1	1:FQ:106:GLN:O	2.32	0.61
1:AO:106:GLN:O	1:DX:35:ARG:NH1	2.29	0.61
1:AQ:101:GLU:O	1:AQ:105:ASP:HB2	2.00	0.61
1:BF:18:VAL:HG22	1:BF:34:LYS:HG3	1.82	0.61
1:CP:101:GLU:O	1:CP:105:ASP:HB2	2.01	0.61
1:CW:15:GLU:HG3	1:CW:16:LYS:N	2.14	0.61
1:DT:101:GLU:O	1:DT:105:ASP:HB2	2.00	0.61
1:AX:35:ARG:NH1	1:FZ:106:GLN:O	2.32	0.61
1:BS:83:LYS:HD2	1:CZ:104:THR:HG22	1.83	0.61
1:BU:36:LEU:HB2	1:BU:49:LYS:HB2	1.81	0.61
1:CA:101:GLU:O	1:CA:105:ASP:HB2	2.01	0.61
1:CB:106:GLN:O	1:GL:35:ARG:NH1	2.31	0.61
1:DG:35:ARG:NH1	1:DH:106:GLN:O	2.29	0.61
1:DL:106:GLN:O	1:DO:35:ARG:NH1	2.29	0.61
1:DZ:18:VAL:HG22	1:DZ:34:LYS:HG3	1.82	0.61
1:EZ:102:LEU:HG	1:FA:50:SER:HB2	1.81	0.61
1:AQ:58:ASP:HB3	1:AQ:65:ILE:HD11	1.81	0.61
1:AW:101:GLU:O	1:AW:105:ASP:HB2	2.01	0.61
1:BF:101:GLU:O	1:BF:105:ASP:HB2	2.00	0.61
1:BK:102:LEU:HG	1:BL:50:SER:HB2	1.82	0.61
1:BK:104:THR:HG22	1:BL:83:LYS:HD2	1.82	0.61
1:BL:32:ALA:HB3	1:BL:53:LYS:HG2	1.81	0.61
1:BL:36:LEU:HB2	1:BL:49:LYS:HB2	1.81	0.61
1:BV:106:GLN:HB3	1:GO:35:ARG:HD3	1.82	0.61
1:BZ:35:ARG:NH1	1:CA:106:GLN:O	2.31	0.61
1:CE:104:THR:HG22	1:CN:83:LYS:HD2	1.83	0.61
1:CH:87:MET:HE1	1:CQ:100:THR:HG23	1.83	0.61
1:DH:32:ALA:HB3	1:DH:53:LYS:HG3	1.81	0.61
1:DK:36:LEU:HB2	1:DK:49:LYS:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DN:101:GLU:O	1:DN:105:ASP:HB2	2.01	0.61
1:DW:101:GLU:O	1:DW:105:ASP:HB2	2.01	0.61
1:DZ:61:THR:OG1	1:EE:40:ARG:NH2	2.32	0.61
1:EB:104:THR:HG22	1:EC:83:LYS:HD2	1.82	0.61
1:EI:101:GLU:O	1:EI:105:ASP:HB2	2.01	0.61
1:BA:106:GLN:HB3	1:GC:35:ARG:HD3	1.82	0.61
1:BF:58:ASP:HB3	1:BF:65:ILE:HD11	1.81	0.61
1:CD:58:ASP:HB3	1:CD:65:ILE:HD11	1.81	0.61
1:CO:35:ARG:NH1	1:CP:106:GLN:O	2.31	0.61
1:EM:34:LYS:HB3	1:EM:51:GLU:HB3	1.83	0.61
1:GV:35:ARG:NH1	1:GW:106:GLN:O	2.29	0.61
1:AN:36:LEU:HB2	1:AN:49:LYS:HB2	1.81	0.61
1:BT:102:LEU:HG	1:BU:50:SER:HB2	1.82	0.61
1:BU:32:ALA:HB3	1:BU:53:LYS:HG2	1.81	0.61
1:CK:75:ARG:NH2	1:CK:77:ASP:OD2	2.32	0.61
1:CR:35:ARG:NH1	1:CS:106:GLN:O	2.30	0.61
1:DJ:102:LEU:HG	1:DK:50:SER:HB2	1.81	0.61
1:DU:75:ARG:NH2	1:DU:77:ASP:OD2	2.32	0.61
1:EQ:35:ARG:NH1	1:ER:106:GLN:O	2.29	0.61
1:BV:87:MET:HE1	1:GO:100:THR:HG23	1.82	0.61
1:CD:18:VAL:HG22	1:CD:34:LYS:HG3	1.82	0.61
1:CF:102:LEU:HG	1:CG:50:SER:HB2	1.82	0.61
1:CG:32:ALA:HB3	1:CG:53:LYS:HG2	1.81	0.61
1:AP:102:LEU:HG	1:AQ:50:SER:HB2	1.81	0.61
1:AQ:18:VAL:HG22	1:AQ:34:LYS:HG3	1.83	0.61
1:AV:35:ARG:NH1	1:AW:106:GLN:O	2.31	0.61
1:BN:83:LYS:HD2	1:BO:104:THR:HG22	1.83	0.61
1:BR:101:GLU:O	1:BR:105:ASP:HB2	2.00	0.61
1:BT:12:TYR:HB2	1:BT:22:ARG:HG3	1.82	0.61
1:CM:18:VAL:HG22	1:CM:34:LYS:HG3	1.83	0.61
1:CV:101:GLU:O	1:CV:105:ASP:HB2	1.99	0.61
1:DP:83:LYS:HD2	1:DQ:104:THR:HG22	1.83	0.61
1:DY:35:ARG:NH1	1:DZ:106:GLN:O	2.29	0.61
1:EL:101:GLU:O	1:EL:105:ASP:HB2	2.00	0.61
1:AR:1:SER:OG	1:EA:96:ASP:OD2	2.18	0.61
1:AR:104:THR:HG22	1:EA:83:LYS:HD2	1.82	0.61
1:AY:12:TYR:HB2	1:AY:22:ARG:HG3	1.82	0.61
1:CE:1:SER:OG	1:CN:96:ASP:OD2	2.17	0.61
1:CR:54:ILE:HD13	1:CS:89:ILE:HG21	1.82	0.61
1:CY:101:GLU:O	1:CY:105:ASP:HB2	2.01	0.61
1:DB:101:GLU:O	1:DB:105:ASP:HB2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DE:101:GLU:O	1:DE:105:ASP:HB2	2.00	0.61
1:DY:101:GLU:O	1:DY:105:ASP:HB2	2.01	0.61
1:EB:102:LEU:HG	1:EC:50:SER:HB2	1.82	0.61
1:AU:35:ARG:NH1	1:GF:106:GLN:O	2.32	0.61
1:BS:106:GLN:O	1:CZ:35:ARG:NH1	2.30	0.61
1:CS:32:ALA:HB3	1:CS:53:LYS:HG3	1.82	0.61
1:DP:54:ILE:HD13	1:DQ:89:ILE:HG21	1.82	0.61
1:EH:35:ARG:NH1	1:EI:106:GLN:O	2.31	0.61
1:BJ:106:GLN:O	1:GR:35:ARG:NH1	2.30	0.60
1:CE:83:LYS:HD2	1:CN:104:THR:HG22	1.83	0.60
1:EN:64:LEU:HD11	1:EN:67:ILE:HG13	1.83	0.60
1:AK:101:GLU:O	1:AK:105:ASP:HB2	2.01	0.60
1:BE:101:GLU:O	1:BE:105:ASP:HB2	2.01	0.60
1:BS:104:THR:HG22	1:CZ:83:LYS:HD2	1.83	0.60
1:BY:50:SER:HB2	1:GI:102:LEU:HG	1.83	0.60
1:CF:104:THR:HG22	1:CG:83:LYS:HD2	1.82	0.60
1:CL:102:LEU:HG	1:CM:50:SER:HB2	1.83	0.60
1:DQ:32:ALA:HB3	1:DQ:53:LYS:HG3	1.82	0.60
1:EN:102:LEU:HG	1:EO:50:SER:HB2	1.81	0.60
1:AC:106:GLN:O	1:ES:35:ARG:NH1	2.31	0.60
1:BC:32:ALA:HB3	1:BC:53:LYS:HG3	1.81	0.60
1:CC:102:LEU:HG	1:CD:50:SER:HB2	1.84	0.60
1:EK:102:LEU:HG	1:EL:50:SER:HB2	1.83	0.60
1:AB:101:GLU:O	1:AB:105:ASP:HB2	2.01	0.60
1:DP:35:ARG:NH1	1:DQ:106:GLN:O	2.30	0.60
1:EG:50:SER:HB2	1:FW:102:LEU:HG	1.84	0.60
1:EL:18:VAL:HG22	1:EL:34:LYS:HG3	1.82	0.60
1:FF:35:ARG:NH1	1:FG:106:GLN:O	2.29	0.60
1:BO:32:ALA:HB3	1:BO:53:LYS:HG3	1.82	0.60
1:BQ:102:LEU:HG	1:BR:50:SER:HB2	1.83	0.60
1:DI:35:ARG:NH1	1:DU:106:GLN:O	2.29	0.60
1:DY:102:LEU:HG	1:DZ:50:SER:HB2	1.83	0.60
1:GS:64:LEU:HD11	1:GS:67:ILE:HG13	1.83	0.60
1:BE:35:ARG:NH1	1:BF:106:GLN:O	2.29	0.60
1:BJ:50:SER:HB2	1:GR:102:LEU:HG	1.84	0.60
1:BR:18:VAL:HG22	1:BR:34:LYS:HG3	1.83	0.60
1:DL:87:MET:HE1	1:DO:100:THR:HG23	1.84	0.60
1:EM:96:ASP:OD2	1:FT:1:SER:OG	2.18	0.60
1:GD:64:LEU:HD11	1:GD:67:ILE:HG13	1.83	0.60
1:AC:35:ARG:NH1	1:ES:106:GLN:O	2.31	0.60
1:AL:26:ASN:ND2	1:AL:29:ASP:OD2	2.29	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:34:LYS:NZ	1:AW:36:LEU:HD13	2.17	0.60
1:CQ:34:LYS:HB3	1:CQ:51:GLU:HB3	1.84	0.60
1:CY:18:VAL:HG22	1:CY:34:LYS:HG3	1.82	0.60
1:AL:34:LYS:HB3	1:AL:51:GLU:HB3	1.84	0.60
1:AM:102:LEU:HG	1:AN:50:SER:HB2	1.83	0.60
1:AY:102:LEU:HG	1:AZ:50:SER:HB2	1.83	0.60
1:BN:35:ARG:NH1	1:BO:106:GLN:O	2.30	0.60
1:BY:106:GLN:O	1:GI:35:ARG:NH1	2.30	0.60
1:CD:101:GLU:O	1:CD:105:ASP:HB2	2.01	0.60
1:CM:101:GLU:O	1:CM:105:ASP:HB2	2.00	0.60
1:EK:101:GLU:O	1:EK:105:ASP:HB2	2.01	0.60
1:AC:26:ASN:ND2	1:AC:29:ASP:OD2	2.29	0.60
1:BC:61:THR:HA	1:DJ:45:PRO:HB3	1.84	0.60
1:DI:83:LYS:HE3	1:DU:104:THR:HA	1.84	0.60
1:EZ:64:LEU:HD11	1:EZ:67:ILE:HG13	1.83	0.60
1:AP:35:ARG:NH1	1:AQ:106:GLN:O	2.29	0.60
1:BQ:101:GLU:O	1:BQ:105:ASP:HB2	2.02	0.60
1:BS:96:ASP:OD2	1:CZ:1:SER:OG	2.17	0.60
1:BT:101:GLU:O	1:BT:105:ASP:HB2	2.02	0.60
1:CC:101:GLU:O	1:CC:105:ASP:HB2	2.01	0.60
1:CK:106:GLN:O	1:CT:35:ARG:NH1	2.30	0.60
1:CX:101:GLU:O	1:CX:105:ASP:HB2	2.01	0.60
1:DW:34:LYS:NZ	1:DW:36:LEU:HD13	2.17	0.60
1:GF:75:ARG:NH2	1:GF:77:ASP:OD2	2.35	0.60
1:GR:103:VAL:O	1:GR:104:THR:OG1	2.13	0.60
1:GV:47:MET:HB2	1:GV:49:LYS:HZ3	1.67	0.60
1:AF:50:SER:HB2	1:EV:102:LEU:HG	1.84	0.59
1:CE:96:ASP:OD2	1:CN:1:SER:OG	2.18	0.59
1:CK:104:THR:HA	1:CT:83:LYS:HE3	1.84	0.59
1:FA:75:ARG:NH2	1:FA:77:ASP:OD2	2.35	0.59
1:AS:83:LYS:HD2	1:AT:104:THR:HG22	1.83	0.59
1:AY:83:LYS:HD2	1:AZ:104:THR:HG22	1.85	0.59
1:CL:101:GLU:O	1:CL:105:ASP:HB2	2.02	0.59
1:FA:34:LYS:HB3	1:FA:51:GLU:HB3	1.84	0.59
1:AC:34:LYS:HB3	1:AC:51:GLU:HB3	1.84	0.59
1:AM:101:GLU:O	1:AM:105:ASP:HB2	2.02	0.59
1:AT:32:ALA:HB3	1:AT:53:LYS:HG3	1.82	0.59
1:AZ:34:LYS:HB3	1:AZ:51:GLU:HB3	1.85	0.59
1:BD:35:ARG:NH1	1:GU:106:GLN:O	2.33	0.59
1:CB:34:LYS:HB3	1:CB:51:GLU:HB3	1.85	0.59
1:DG:83:LYS:HD2	1:DH:104:THR:HG22	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EG:83:LYS:HD2	1:FW:104:THR:HG22	1.84	0.59
1:GI:103:VAL:O	1:GI:104:THR:OG1	2.13	0.59
1:AG:83:LYS:HD2	1:AH:104:THR:HG22	1.83	0.59
1:AR:35:ARG:NH1	1:EA:106:GLN:O	2.30	0.59
1:BB:35:ARG:NH1	1:BC:106:GLN:O	2.29	0.59
1:BB:83:LYS:HD2	1:BC:104:THR:HG22	1.83	0.59
1:BG:102:LEU:HG	1:GX:50:SER:HB2	1.84	0.59
1:GU:75:ARG:NH2	1:GU:77:ASP:OD2	2.36	0.59
1:AB:34:LYS:NZ	1:AB:36:LEU:HD13	2.17	0.59
1:AO:87:MET:HE1	1:DX:100:THR:HG23	1.85	0.59
1:CG:34:LYS:HB3	1:CG:51:GLU:HB3	1.84	0.59
1:CR:83:LYS:HD2	1:CS:104:THR:HG22	1.83	0.59
1:GE:34:LYS:HB3	1:GE:51:GLU:HB3	1.85	0.59
1:GT:34:LYS:HB3	1:GT:51:GLU:HB3	1.85	0.59
1:AX:15:GLU:HG3	1:AX:16:LYS:N	2.18	0.59
1:BV:106:GLN:O	1:GO:35:ARG:NH1	2.32	0.59
1:CQ:26:ASN:ND2	1:CQ:29:ASP:OD2	2.29	0.59
1:CX:102:LEU:HG	1:CY:50:SER:HB2	1.84	0.59
1:DA:40:ARG:NH1	1:DA:42:LYS:O	2.36	0.59
1:DD:42:LYS:HG3	1:DD:44:SER:H	1.68	0.59
1:DJ:83:LYS:HD2	1:DK:104:THR:HG22	1.85	0.59
1:EJ:15:GLU:HG3	1:EJ:16:LYS:N	2.18	0.59
1:AJ:40:ARG:NH1	1:AJ:42:LYS:O	2.36	0.59
1:BE:102:LEU:HG	1:BF:50:SER:HB2	1.83	0.59
1:CB:15:GLU:HG3	1:CB:16:LYS:N	2.18	0.59
1:CB:26:ASN:ND2	1:CB:29:ASP:OD2	2.29	0.59
1:CF:83:LYS:HD2	1:CG:104:THR:HG22	1.85	0.59
1:CQ:15:GLU:HG3	1:CQ:16:LYS:N	2.18	0.59
1:DM:40:ARG:NH1	1:DM:42:LYS:O	2.36	0.59
1:DQ:101:GLU:O	1:DQ:105:ASP:HB2	2.03	0.59
1:DZ:101:GLU:O	1:DZ:105:ASP:HB2	2.02	0.59
1:EG:15:GLU:HG3	1:EG:16:LYS:N	2.18	0.59
1:EM:1:SER:OG	1:FT:96:ASP:OD2	2.18	0.59
1:GW:74:ILE:HG21	1:GW:83:LYS:HD3	1.85	0.59
1:AM:83:LYS:HD2	1:AN:104:THR:HG22	1.85	0.59
1:BJ:83:LYS:HD2	1:GR:104:THR:HG22	1.85	0.59
1:DX:34:LYS:HB3	1:DX:51:GLU:HB3	1.84	0.59
1:EB:83:LYS:HD2	1:EC:104:THR:HG22	1.85	0.59
1:EH:40:ARG:NH1	1:EH:42:LYS:O	2.36	0.59
1:EO:34:LYS:HB3	1:EO:51:GLU:HB3	1.85	0.59
1:EW:35:ARG:NH1	1:EX:106:GLN:O	2.30	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EZ:57:VAL:HG22	1:EZ:64:LEU:HA	1.84	0.59
1:FS:74:ILE:HG21	1:FS:83:LYS:HD3	1.85	0.59
1:GP:12:TYR:HB2	1:GP:22:ARG:HG3	1.85	0.59
1:AL:15:GLU:HG3	1:AL:16:LYS:N	2.18	0.59
1:AR:83:LYS:HD2	1:EA:104:THR:HG22	1.83	0.59
1:AS:35:ARG:NH1	1:AT:106:GLN:O	2.31	0.59
1:AU:50:SER:HB2	1:GF:102:LEU:HG	1.84	0.59
1:BA:106:GLN:O	1:GC:35:ARG:NH1	2.32	0.59
1:BO:101:GLU:O	1:BO:105:ASP:HB2	2.03	0.59
1:BY:83:LYS:HD2	1:GI:104:THR:HG22	1.85	0.59
1:BZ:40:ARG:NH1	1:BZ:42:LYS:O	2.36	0.59
1:CO:40:ARG:NH1	1:CO:42:LYS:O	2.36	0.59
1:DC:15:GLU:HG3	1:DC:16:LYS:N	2.18	0.59
1:DO:34:LYS:HB3	1:DO:51:GLU:HB3	1.84	0.59
1:EM:104:THR:HG22	1:FT:83:LYS:HD2	1.85	0.59
1:GM:40:ARG:NH1	1:GM:42:LYS:O	2.36	0.59
1:AA:40:ARG:NH1	1:AA:42:LYS:O	2.36	0.59
1:AC:15:GLU:HG3	1:AC:16:LYS:N	2.18	0.59
1:AZ:15:GLU:HG2	1:AZ:16:LYS:H	1.68	0.59
1:BC:101:GLU:O	1:BC:105:ASP:HB2	2.03	0.59
1:BN:50:SER:HB2	1:BO:102:LEU:HG	1.85	0.59
1:CI:42:LYS:HG3	1:CI:44:SER:H	1.68	0.59
1:DH:101:GLU:O	1:DH:105:ASP:HB2	2.03	0.59
1:EC:34:LYS:HB3	1:EC:51:GLU:HB3	1.84	0.59
1:EJ:26:ASN:ND2	1:EJ:29:ASP:OD2	2.29	0.59
1:EY:96:ASP:OD2	1:FH:1:SER:OG	2.18	0.59
1:GG:12:TYR:HB2	1:GG:22:ARG:HG3	1.85	0.59
1:AF:83:LYS:HD2	1:EV:104:THR:HG22	1.85	0.58
1:AG:50:SER:HB2	1:AH:102:LEU:HG	1.85	0.58
1:AY:101:GLU:O	1:AY:105:ASP:HB2	2.02	0.58
1:BT:83:LYS:HD2	1:BU:104:THR:HG22	1.85	0.58
1:BV:50:SER:HB2	1:GO:102:LEU:HG	1.85	0.58
1:CS:101:GLU:O	1:CS:105:ASP:HB2	2.03	0.58
1:DP:50:SER:HB2	1:DQ:102:LEU:HG	1.85	0.58
1:DV:40:ARG:NH1	1:DV:42:LYS:O	2.36	0.58
1:EY:106:GLN:O	1:FH:35:ARG:NH1	2.33	0.58
1:EZ:42:LYS:HG3	1:EZ:44:SER:H	1.68	0.58
1:FE:106:GLN:O	1:FN:35:ARG:NH1	2.33	0.58
1:GE:75:ARG:NH2	1:GE:77:ASP:OD2	2.35	0.58
1:GT:75:ARG:NH2	1:GT:77:ASP:OD2	2.35	0.58
1:AT:101:GLU:O	1:AT:105:ASP:HB2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BV:104:THR:HA	1:GO:83:LYS:HE3	1.84	0.58
1:DJ:101:GLU:O	1:DJ:105:ASP:HB2	2.03	0.58
1:AV:40:ARG:NH1	1:AV:42:LYS:O	2.36	0.58
1:BG:104:THR:HG22	1:GX:83:LYS:HD2	1.85	0.58
1:BK:83:LYS:HD2	1:BL:104:THR:HG22	1.85	0.58
1:CL:35:ARG:NH1	1:CM:106:GLN:O	2.29	0.58
1:DF:15:GLU:HG3	1:DF:16:LYS:H	1.68	0.58
1:DI:50:SER:HB2	1:DU:102:LEU:HG	1.85	0.58
1:DO:26:ASN:ND2	1:DO:29:ASP:OD2	2.29	0.58
1:EM:106:GLN:O	1:FT:35:ARG:NH1	2.33	0.58
1:EY:1:SER:OG	1:FH:96:ASP:OD2	2.18	0.58
1:AG:102:LEU:HG	1:AH:50:SER:HB2	1.86	0.58
1:BD:50:SER:HB2	1:GU:102:LEU:HG	1.85	0.58
1:BS:1:SER:OG	1:CZ:96:ASP:OD2	2.18	0.58
1:BU:15:GLU:HG2	1:BU:16:LYS:H	1.68	0.58
1:FL:40:ARG:NH1	1:FL:42:LYS:O	2.36	0.58
1:AX:26:ASN:ND2	1:AX:29:ASP:OD2	2.29	0.58
1:BB:50:SER:HB2	1:BC:102:LEU:HG	1.85	0.58
1:CK:102:LEU:HG	1:CT:50:SER:HB2	1.85	0.58
1:DS:12:TYR:HB2	1:DS:22:ARG:HG3	1.86	0.58
1:DX:26:ASN:ND2	1:DX:29:ASP:OD2	2.29	0.58
1:GB:34:LYS:HZ1	1:GB:36:LEU:HD13	1.68	0.58
1:AS:50:SER:HB2	1:AT:102:LEU:HG	1.85	0.58
1:AX:34:LYS:HB3	1:AX:51:GLU:HB3	1.84	0.58
1:BL:34:LYS:HB3	1:BL:51:GLU:HB3	1.84	0.58
1:CB:75:ARG:NH2	1:CB:77:ASP:OD2	2.37	0.58
1:DC:34:LYS:HB3	1:DC:51:GLU:HB3	1.84	0.58
1:EN:57:VAL:HG22	1:EN:64:LEU:HA	1.84	0.58
1:EY:104:THR:HG22	1:FH:83:LYS:HD2	1.85	0.58
1:FI:12:TYR:HB2	1:FI:22:ARG:HG3	1.85	0.58
1:GA:40:ARG:NH1	1:GA:42:LYS:O	2.36	0.58
1:BP:83:LYS:HE3	1:CW:104:THR:HA	1.84	0.58
1:DF:104:THR:HA	1:DR:83:LYS:HE3	1.84	0.58
1:DI:34:LYS:HB3	1:DI:51:GLU:HB3	1.86	0.58
1:EG:75:ARG:NH2	1:EG:77:ASP:OD2	2.35	0.58
1:ET:12:TYR:HB2	1:ET:22:ARG:HG3	1.85	0.58
1:EY:35:ARG:NH1	1:FH:106:GLN:O	2.33	0.58
1:FE:89:ILE:HG21	1:FN:54:ILE:HD13	1.84	0.58
1:GC:36:LEU:HB3	1:GC:49:LYS:HB2	1.86	0.58
1:GS:57:VAL:HG22	1:GS:64:LEU:HA	1.84	0.58
1:AC:36:LEU:HB3	1:AC:49:LYS:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:75:ARG:NH2	1:AF:77:ASP:OD2	2.35	0.58
1:AN:34:LYS:HB3	1:AN:51:GLU:HB3	1.84	0.58
1:CK:15:GLU:HG3	1:CK:16:LYS:H	1.69	0.58
1:DC:26:ASN:ND2	1:DC:29:ASP:OD2	2.29	0.58
1:FL:50:SER:HB2	1:FM:102:LEU:HG	1.86	0.58
1:FN:15:GLU:HG3	1:FN:16:LYS:N	2.19	0.58
1:GA:50:SER:HB2	1:GB:102:LEU:HG	1.86	0.58
1:GD:57:VAL:HG22	1:GD:64:LEU:HA	1.84	0.58
1:AH:101:GLU:O	1:AH:105:ASP:HB2	2.03	0.58
1:DK:34:LYS:HB3	1:DK:51:GLU:HB3	1.84	0.58
1:DP:42:LYS:HG3	1:DP:44:SER:H	1.69	0.58
1:EY:83:LYS:HD2	1:FH:104:THR:HG22	1.85	0.58
1:EY:96:ASP:OD1	1:EY:97:GLY:N	2.37	0.58
1:FB:75:ARG:NH2	1:FB:77:ASP:OD2	2.35	0.58
1:FX:35:ARG:NH1	1:FY:106:GLN:O	2.29	0.58
1:GC:15:GLU:HG3	1:GC:16:LYS:N	2.19	0.58
1:BA:104:THR:HA	1:GC:83:LYS:HE3	1.84	0.58
1:BJ:75:ARG:NH2	1:BJ:77:ASP:OD2	2.35	0.58
1:BN:42:LYS:HG3	1:BN:44:SER:H	1.69	0.58
1:DF:102:LEU:HG	1:DR:50:SER:HB2	1.85	0.58
1:EJ:34:LYS:HB3	1:EJ:51:GLU:HB3	1.85	0.58
1:FP:32:ALA:HB3	1:FP:53:LYS:HG2	1.86	0.58
1:AI:35:ARG:NH1	1:EP:106:GLN:O	2.33	0.57
1:BB:102:LEU:HG	1:BC:50:SER:HB2	1.86	0.57
1:BG:83:LYS:HD2	1:GX:104:THR:HG22	1.84	0.57
1:BP:50:SER:HB2	1:CW:102:LEU:HG	1.85	0.57
1:BU:34:LYS:HB3	1:BU:51:GLU:HB3	1.85	0.57
1:BW:42:LYS:HG3	1:BW:44:SER:H	1.68	0.57
1:BY:75:ARG:NH2	1:BY:77:ASP:OD2	2.35	0.57
1:FG:74:ILE:HG21	1:FG:83:LYS:HD3	1.85	0.57
1:FM:51:GLU:HG3	1:FM:69:ASN:HD21	1.68	0.57
1:GO:15:GLU:HG3	1:GO:16:LYS:N	2.19	0.57
1:AC:75:ARG:NH2	1:AC:77:ASP:OD2	2.37	0.57
1:AQ:61:THR:O	1:CU:40:ARG:NE	2.35	0.57
1:AS:102:LEU:HG	1:AT:50:SER:HB2	1.86	0.57
1:AV:34:LYS:HB3	1:AV:51:GLU:HB3	1.86	0.57
1:BF:61:THR:O	1:DD:40:ARG:NE	2.35	0.57
1:BH:12:TYR:HB2	1:BH:22:ARG:HG3	1.86	0.57
1:DV:34:LYS:HB3	1:DV:51:GLU:HB3	1.86	0.57
1:EP:75:ARG:NH2	1:EP:77:ASP:OD2	2.35	0.57
1:ET:42:LYS:HG3	1:ET:44:SER:H	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FI:42:LYS:HG3	1:FI:44:SER:H	1.69	0.57
1:FN:36:LEU:HB3	1:FN:49:LYS:HB2	1.86	0.57
1:FU:42:LYS:HG3	1:FU:44:SER:H	1.69	0.57
1:GJ:64:LEU:HD11	1:GJ:67:ILE:HG13	1.86	0.57
1:GM:50:SER:HB2	1:GN:102:LEU:HG	1.86	0.57
1:AB:32:ALA:HB3	1:AB:53:LYS:HG3	1.86	0.57
1:AS:42:LYS:HG3	1:AS:44:SER:H	1.68	0.57
1:AV:102:LEU:HG	1:AW:50:SER:HB2	1.86	0.57
1:AW:32:ALA:HB3	1:AW:53:LYS:HG3	1.86	0.57
1:CA:39:LYS:HE2	1:CA:41:THR:HB	1.86	0.57
1:EX:74:ILE:HG21	1:EX:83:LYS:HD3	1.85	0.57
1:FE:75:ARG:NH2	1:FE:77:ASP:OD2	2.37	0.57
1:FU:12:TYR:HB2	1:FU:22:ARG:HG3	1.85	0.57
1:GM:104:THR:HG22	1:GN:83:LYS:HD2	1.87	0.57
1:AA:42:LYS:HG3	1:AA:44:SER:H	1.70	0.57
1:AD:12:TYR:HB2	1:AD:22:ARG:HG3	1.86	0.57
1:BZ:42:LYS:HG3	1:BZ:44:SER:H	1.70	0.57
1:EE:12:TYR:HB2	1:EE:22:ARG:HG3	1.86	0.57
1:EM:83:LYS:HD2	1:FT:104:THR:HG22	1.85	0.57
1:EN:42:LYS:HG3	1:EN:44:SER:H	1.68	0.57
1:FL:42:LYS:HG3	1:FL:44:SER:H	1.70	0.57
1:AG:42:LYS:HG3	1:AG:44:SER:H	1.69	0.57
1:AJ:42:LYS:HG3	1:AJ:44:SER:H	1.70	0.57
1:AX:103:VAL:O	1:AX:104:THR:OG1	2.16	0.57
1:BA:36:LEU:HB3	1:BA:49:LYS:HB2	1.87	0.57
1:BZ:50:SER:HB2	1:CA:102:LEU:HG	1.86	0.57
1:CI:12:TYR:HB2	1:CI:22:ARG:HG3	1.87	0.57
1:DG:50:SER:HB2	1:DH:102:LEU:HG	1.85	0.57
1:DM:34:LYS:HB3	1:DM:51:GLU:HB3	1.87	0.57
1:EJ:75:ARG:NH2	1:EJ:77:ASP:OD2	2.37	0.57
1:FF:99:TRP:CH2	1:FG:87:MET:HG2	2.40	0.57
1:AI:34:LYS:HB3	1:AI:51:GLU:HB3	1.86	0.57
1:AI:50:SER:HB2	1:EP:102:LEU:HG	1.85	0.57
1:BK:5:ASN:HD22	1:BL:89:ILE:HG13	1.70	0.57
1:CR:50:SER:HB2	1:CS:102:LEU:HG	1.85	0.57
1:DA:42:LYS:HG3	1:DA:44:SER:H	1.70	0.57
1:DX:15:GLU:HG3	1:DX:16:LYS:N	2.18	0.57
1:EO:36:LEU:HB3	1:EO:49:LYS:HB2	1.87	0.57
1:EW:99:TRP:CH2	1:EX:87:MET:HG2	2.40	0.57
1:FR:99:TRP:CH2	1:FS:87:MET:HG2	2.40	0.57
1:GA:42:LYS:HG3	1:GA:44:SER:H	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GJ:102:LEU:HG	1:GK:50:SER:HB2	1.87	0.57
1:AA:50:SER:HB2	1:AB:102:LEU:HG	1.86	0.57
1:AX:75:ARG:NH2	1:AX:77:ASP:OD2	2.37	0.57
1:BA:50:SER:HB2	1:GC:102:LEU:HG	1.85	0.57
1:BB:42:LYS:HG3	1:BB:44:SER:H	1.69	0.57
1:BG:35:ARG:NH1	1:GX:106:GLN:O	2.33	0.57
1:BW:12:TYR:HB2	1:BW:22:ARG:HG3	1.87	0.57
1:CO:42:LYS:HG3	1:CO:44:SER:H	1.70	0.57
1:CQ:75:ARG:NH2	1:CQ:77:ASP:OD2	2.38	0.57
1:DN:39:LYS:HE2	1:DN:41:THR:HB	1.86	0.57
1:DO:15:GLU:HG3	1:DO:16:LYS:N	2.18	0.57
1:DU:23:ASP:OD2	1:DU:26:ASN:ND2	2.38	0.57
1:DV:102:LEU:HG	1:DW:50:SER:HB2	1.86	0.57
1:EI:34:LYS:HB3	1:EI:51:GLU:HB3	1.87	0.57
1:FE:96:ASP:OD1	1:FN:1:SER:OG	2.20	0.57
1:FY:32:ALA:HB3	1:FY:53:LYS:HG2	1.87	0.57
1:CF:5:ASN:HD22	1:CG:89:ILE:HG13	1.70	0.57
1:CU:12:TYR:HB2	1:CU:22:ARG:HG3	1.86	0.57
1:DW:32:ALA:HB3	1:DW:53:LYS:HG3	1.86	0.57
1:EH:34:LYS:HB3	1:EH:51:GLU:HB3	1.87	0.57
1:EJ:103:VAL:O	1:EJ:104:THR:OG1	2.16	0.57
1:FD:80:ALA:HA	1:FD:83:LYS:HB2	1.87	0.57
1:GS:42:LYS:HG3	1:GS:44:SER:H	1.68	0.57
1:AL:75:ARG:NH2	1:AL:77:ASP:OD2	2.38	0.57
1:BM:36:LEU:HB3	1:BM:49:LYS:HB2	1.87	0.57
1:BR:74:ILE:HG21	1:BR:83:LYS:HD3	1.87	0.57
1:CK:23:ASP:OD2	1:CK:26:ASN:ND2	2.38	0.57
1:CR:102:LEU:HG	1:CS:50:SER:HB2	1.86	0.57
1:DE:61:THR:HA	1:GG:45:PRO:HB3	1.86	0.57
1:DL:36:LEU:HB3	1:DL:49:LYS:HB2	1.87	0.57
1:DP:102:LEU:HG	1:DQ:50:SER:HB2	1.86	0.57
1:EB:5:ASN:HD22	1:EC:89:ILE:HG13	1.70	0.57
1:ED:36:LEU:HB3	1:ED:49:LYS:HB2	1.87	0.57
1:EH:102:LEU:HG	1:EI:50:SER:HB2	1.87	0.57
1:GM:64:LEU:HD11	1:GM:67:ILE:HG13	1.87	0.57
1:AC:1:SER:OG	1:ES:96:ASP:OD1	2.21	0.57
1:AE:61:THR:HA	1:FU:45:PRO:HB3	1.87	0.57
1:AO:36:LEU:HB3	1:AO:49:LYS:HB2	1.87	0.57
1:AU:15:GLU:HG3	1:AU:16:LYS:N	2.20	0.57
1:BD:15:GLU:HG3	1:BD:16:LYS:N	2.20	0.57
1:BD:34:LYS:HB3	1:BD:51:GLU:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:54:ILE:HD13	1:GL:89:ILE:HG21	1.87	0.57
1:DG:102:LEU:HG	1:DH:50:SER:HB2	1.86	0.57
1:DM:50:SER:HB2	1:DN:102:LEU:HG	1.86	0.57
1:EJ:1:SER:OG	1:FQ:96:ASP:OD2	2.20	0.57
1:EL:74:ILE:HG21	1:EL:83:LYS:HD3	1.87	0.57
1:ES:75:ARG:NH2	1:ES:77:ASP:OD2	2.37	0.57
1:FD:32:ALA:HB3	1:FD:53:LYS:HG2	1.87	0.57
1:GA:64:LEU:HD11	1:GA:67:ILE:HG13	1.87	0.57
1:GF:23:ASP:OD2	1:GF:26:ASN:ND2	2.38	0.57
1:GK:32:ALA:HB3	1:GK:53:LYS:HG2	1.86	0.57
1:GM:47:MET:HB2	1:GM:49:LYS:HZ3	1.69	0.57
1:GU:23:ASP:OD2	1:GU:26:ASN:ND2	2.38	0.57
1:AR:96:ASP:OD2	1:EA:1:SER:OG	2.17	0.56
1:BF:74:ILE:HG21	1:BF:83:LYS:HD3	1.87	0.56
1:BL:15:GLU:HG2	1:BL:16:LYS:H	1.71	0.56
1:BN:102:LEU:HG	1:BO:50:SER:HB2	1.86	0.56
1:BV:36:LEU:HB3	1:BV:49:LYS:HB2	1.87	0.56
1:DM:42:LYS:HG3	1:DM:44:SER:H	1.70	0.56
1:AK:34:LYS:HB3	1:AK:51:GLU:HB3	1.86	0.56
1:AL:100:THR:HG23	1:ED:87:MET:HE1	1.86	0.56
1:CP:34:LYS:HB3	1:CP:51:GLU:HB3	1.86	0.56
1:DA:102:LEU:HG	1:DB:50:SER:HB2	1.87	0.56
1:DD:12:TYR:HB2	1:DD:22:ARG:HG3	1.86	0.56
1:DG:42:LYS:HG3	1:DG:44:SER:H	1.69	0.56
1:DV:42:LYS:HG3	1:DV:44:SER:H	1.70	0.56
1:GM:42:LYS:HG3	1:GM:44:SER:H	1.70	0.56
1:GV:99:TRP:CH2	1:GW:87:MET:HG2	2.40	0.56
1:AC:54:ILE:HD13	1:ES:89:ILE:HG21	1.87	0.56
1:AF:15:GLU:HG3	1:AF:16:LYS:N	2.21	0.56
1:AV:50:SER:HB2	1:AW:102:LEU:HG	1.86	0.56
1:AX:1:SER:OG	1:FZ:96:ASP:OD2	2.21	0.56
1:BA:87:MET:HE1	1:GC:100:THR:HG23	1.87	0.56
1:BG:96:ASP:OD2	1:GX:1:SER:OG	2.17	0.56
1:BJ:23:ASP:OD2	1:BJ:26:ASN:ND2	2.38	0.56
1:BP:15:GLU:HG3	1:BP:16:LYS:N	2.20	0.56
1:BV:89:ILE:HG21	1:GO:54:ILE:HD13	1.88	0.56
1:BY:23:ASP:OD2	1:BY:26:ASN:ND2	2.38	0.56
1:CW:23:ASP:OD2	1:CW:26:ASN:ND2	2.38	0.56
1:DA:35:ARG:NH1	1:DB:106:GLN:O	2.31	0.56
1:DB:34:LYS:HB3	1:DB:51:GLU:HB3	1.86	0.56
1:DM:102:LEU:HG	1:DN:50:SER:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DR:15:GLU:HG3	1:DR:16:LYS:N	2.20	0.56
1:DV:50:SER:HB2	1:DW:102:LEU:HG	1.87	0.56
1:DW:34:LYS:HB3	1:DW:51:GLU:HB3	1.87	0.56
1:EB:101:GLU:O	1:EB:105:ASP:HB2	2.06	0.56
1:EC:15:GLU:HG2	1:EC:16:LYS:H	1.70	0.56
1:EH:50:SER:HB2	1:EI:102:LEU:HG	1.86	0.56
1:EJ:15:GLU:HG3	1:EJ:16:LYS:H	1.70	0.56
1:FX:64:LEU:HD11	1:FX:67:ILE:HG13	1.86	0.56
1:GP:42:LYS:HG3	1:GP:44:SER:H	1.69	0.56
1:GX:96:ASP:OD1	1:GX:97:GLY:N	2.39	0.56
1:AB:39:LYS:HE2	1:AB:41:THR:HB	1.88	0.56
1:AX:15:GLU:HG3	1:AX:16:LYS:H	1.70	0.56
1:CD:74:ILE:HG21	1:CD:83:LYS:HD3	1.87	0.56
1:CM:74:ILE:HG21	1:CM:83:LYS:HD3	1.87	0.56
1:CY:74:ILE:HG21	1:CY:83:LYS:HD3	1.87	0.56
1:DC:15:GLU:HG3	1:DC:16:LYS:H	1.70	0.56
1:DF:23:ASP:OD2	1:DF:26:ASN:ND2	2.38	0.56
1:FZ:75:ARG:NH2	1:FZ:77:ASP:OD2	2.37	0.56
1:GE:36:LEU:HB3	1:GE:49:LYS:HB2	1.87	0.56
1:GT:36:LEU:HB3	1:GT:49:LYS:HB2	1.87	0.56
1:AS:45:PRO:HB3	1:EO:61:THR:HA	1.88	0.56
1:BA:89:ILE:HG21	1:GC:54:ILE:HD13	1.88	0.56
1:BO:34:LYS:HB3	1:BO:51:GLU:HB3	1.88	0.56
1:CB:1:SER:OG	1:GL:96:ASP:OD2	2.20	0.56
1:CR:42:LYS:HG3	1:CR:44:SER:H	1.69	0.56
1:DZ:74:ILE:HG21	1:DZ:83:LYS:HD3	1.87	0.56
1:EI:39:LYS:HE2	1:EI:41:THR:HB	1.86	0.56
1:GG:42:LYS:HG3	1:GG:44:SER:H	1.69	0.56
1:GO:75:ARG:NH2	1:GO:77:ASP:OD2	2.38	0.56
1:AF:23:ASP:OD2	1:AF:26:ASN:ND2	2.38	0.56
1:BA:75:ARG:NH2	1:BA:77:ASP:OD2	2.39	0.56
1:CV:61:THR:HA	1:GP:45:PRO:HB3	1.87	0.56
1:DC:75:ARG:NH2	1:DC:77:ASP:OD2	2.38	0.56
1:DQ:34:LYS:HB3	1:DQ:51:GLU:HB3	1.88	0.56
1:ER:80:ALA:HA	1:ER:83:LYS:HB2	1.87	0.56
1:EZ:83:LYS:HD2	1:FA:104:THR:HG22	1.87	0.56
1:FV:61:THR:HA	1:FX:45:PRO:HB3	1.88	0.56
1:FY:80:ALA:HA	1:FY:83:LYS:HB2	1.87	0.56
1:GI:15:GLU:HG3	1:GI:16:LYS:N	2.21	0.56
1:GJ:104:THR:HA	1:GK:83:LYS:HE3	1.88	0.56
1:GO:36:LEU:HB3	1:GO:49:LYS:HB2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GX:103:VAL:O	1:GX:104:THR:OG1	2.22	0.56
1:AA:34:LYS:HB3	1:AA:51:GLU:HB3	1.86	0.56
1:AK:39:LYS:HE2	1:AK:41:THR:HB	1.88	0.56
1:AM:45:PRO:HB3	1:AT:61:THR:HA	1.88	0.56
1:CS:34:LYS:HB3	1:CS:51:GLU:HB3	1.88	0.56
1:DA:34:LYS:HB3	1:DA:51:GLU:HB3	1.87	0.56
1:EO:57:VAL:HG12	1:EO:64:LEU:HA	1.88	0.56
1:EP:23:ASP:OD2	1:EP:26:ASN:ND2	2.38	0.56
1:EV:15:GLU:HG3	1:EV:16:LYS:N	2.21	0.56
1:GK:80:ALA:HA	1:GK:83:LYS:HB2	1.88	0.56
1:AA:102:LEU:HG	1:AB:50:SER:HB2	1.86	0.56
1:AH:61:THR:HA	1:FO:45:PRO:HB3	1.88	0.56
1:AR:103:VAL:O	1:AR:104:THR:OG1	2.23	0.56
1:BV:75:ARG:NH2	1:BV:77:ASP:OD2	2.39	0.56
1:CA:34:LYS:HB3	1:CA:51:GLU:HB3	1.87	0.56
1:CY:61:THR:O	1:GS:40:ARG:NE	2.35	0.56
1:DH:61:THR:HA	1:GJ:45:PRO:HB3	1.88	0.56
1:EG:15:GLU:HG3	1:EG:16:LYS:H	1.71	0.56
1:EG:23:ASP:OD2	1:EG:26:ASN:ND2	2.38	0.56
1:FE:50:SER:HB2	1:FN:102:LEU:HG	1.87	0.56
1:FO:64:LEU:HD11	1:FO:67:ILE:HG13	1.87	0.56
1:FU:40:ARG:NH1	1:FU:42:LYS:O	2.39	0.56
1:AB:34:LYS:HB3	1:AB:51:GLU:HB3	1.88	0.56
1:AD:42:LYS:HG3	1:AD:44:SER:H	1.71	0.56
1:AJ:64:LEU:HD11	1:AJ:67:ILE:HG13	1.88	0.56
1:BK:101:GLU:O	1:BK:105:ASP:HB2	2.06	0.56
1:BY:15:GLU:HG3	1:BY:16:LYS:N	2.21	0.56
1:CF:45:PRO:HB3	1:CS:61:THR:HA	1.88	0.56
1:CF:101:GLU:O	1:CF:105:ASP:HB2	2.06	0.56
1:CG:15:GLU:HG2	1:CG:16:LYS:H	1.71	0.56
1:DJ:5:ASN:HD22	1:DK:89:ILE:HG13	1.70	0.56
1:ER:32:ALA:HB3	1:ER:53:LYS:HG2	1.87	0.56
1:FB:23:ASP:OD2	1:FB:26:ASN:ND2	2.38	0.56
1:FF:102:LEU:HG	1:FG:50:SER:HB2	1.88	0.56
1:FS:61:THR:O	1:GD:40:ARG:NE	2.36	0.56
1:FT:103:VAL:O	1:FT:104:THR:OG1	2.22	0.56
1:GR:15:GLU:HG3	1:GR:16:LYS:N	2.21	0.56
1:AJ:34:LYS:HB3	1:AJ:51:GLU:HB3	1.87	0.56
1:AY:5:ASN:HD22	1:AZ:89:ILE:HG13	1.71	0.56
1:DB:39:LYS:HE2	1:DB:41:THR:HB	1.88	0.56
1:FA:36:LEU:HB3	1:FA:49:LYS:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FH:96:ASP:OD1	1:FH:97:GLY:N	2.40	0.56
1:FO:102:LEU:HG	1:FP:50:SER:HB2	1.87	0.56
1:BK:45:PRO:HB3	1:DQ:61:THR:HA	1.88	0.55
1:BZ:34:LYS:HB3	1:BZ:51:GLU:HB3	1.87	0.55
1:BZ:102:LEU:HG	1:CA:50:SER:HB2	1.87	0.55
1:EQ:64:LEU:HD11	1:EQ:67:ILE:HG13	1.87	0.55
1:EW:102:LEU:HG	1:EX:50:SER:HB2	1.88	0.55
1:FK:15:GLU:HG3	1:FK:16:LYS:N	2.21	0.55
1:FO:104:THR:HA	1:FP:83:LYS:HE3	1.88	0.55
1:FQ:75:ARG:NH2	1:FQ:77:ASP:OD2	2.38	0.55
1:FR:102:LEU:HG	1:FS:50:SER:HB2	1.88	0.55
1:FS:58:ASP:HB3	1:FS:65:ILE:HD11	1.88	0.55
1:AC:15:GLU:HG3	1:AC:16:LYS:H	1.71	0.55
1:AL:15:GLU:HG3	1:AL:16:LYS:H	1.70	0.55
1:BO:61:THR:HA	1:BT:45:PRO:HB3	1.88	0.55
1:CH:36:LEU:HB3	1:CH:49:LYS:HB2	1.87	0.55
1:CO:34:LYS:HB3	1:CO:51:GLU:HB3	1.87	0.55
1:CU:42:LYS:HG3	1:CU:44:SER:H	1.71	0.55
1:DS:42:LYS:HG3	1:DS:44:SER:H	1.71	0.55
1:DX:75:ARG:NH2	1:DX:77:ASP:OD2	2.38	0.55
1:EB:42:LYS:HG3	1:EB:44:SER:H	1.72	0.55
1:EJ:36:LEU:HB3	1:EJ:49:LYS:HB2	1.89	0.55
1:EM:96:ASP:OD1	1:EM:97:GLY:N	2.39	0.55
1:EQ:42:LYS:HG3	1:EQ:44:SER:H	1.72	0.55
1:EW:83:LYS:HE3	1:EX:104:THR:HA	1.89	0.55
1:FB:15:GLU:HG3	1:FB:16:LYS:H	1.71	0.55
1:FF:83:LYS:HE3	1:FG:104:THR:HA	1.89	0.55
1:FM:39:LYS:HE2	1:FM:41:THR:HB	1.88	0.55
1:GB:39:LYS:HE2	1:GB:41:THR:HB	1.88	0.55
1:GW:58:ASP:HB3	1:GW:65:ILE:HD11	1.88	0.55
1:BB:45:PRO:HB3	1:EF:61:THR:HA	1.88	0.55
1:BJ:15:GLU:HG3	1:BJ:16:LYS:H	1.72	0.55
1:BT:5:ASN:HD22	1:BU:89:ILE:HG13	1.71	0.55
1:CO:50:SER:HB2	1:CP:102:LEU:HG	1.88	0.55
1:CP:39:LYS:HE2	1:CP:41:THR:HB	1.88	0.55
1:DO:75:ARG:NH2	1:DO:77:ASP:OD2	2.38	0.55
1:DS:104:THR:HA	1:DT:83:LYS:HE3	1.89	0.55
1:FL:104:THR:HG22	1:FM:83:LYS:HD2	1.87	0.55
1:AV:42:LYS:HG3	1:AV:44:SER:H	1.70	0.55
1:AX:36:LEU:HB3	1:AX:49:LYS:HB2	1.89	0.55
1:BM:75:ARG:NH2	1:BM:77:ASP:OD2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EO:75:ARG:NH2	1:EO:77:ASP:OD2	2.35	0.55
1:FF:64:LEU:HD11	1:FF:67:ILE:HG13	1.89	0.55
1:FL:47:MET:HB2	1:FL:49:LYS:NZ	2.21	0.55
1:FN:75:ARG:NH2	1:FN:77:ASP:OD2	2.38	0.55
1:GA:104:THR:HG22	1:GB:83:LYS:HD2	1.87	0.55
1:AJ:102:LEU:HG	1:AK:50:SER:HB2	1.87	0.55
1:AS:40:ARG:NH1	1:AS:42:LYS:O	2.40	0.55
1:CO:102:LEU:HG	1:CP:50:SER:HB2	1.87	0.55
1:FC:64:LEU:HD11	1:FC:67:ILE:HG13	1.86	0.55
1:FW:15:GLU:HG3	1:FW:16:LYS:N	2.21	0.55
1:GA:47:MET:HB2	1:GA:49:LYS:NZ	2.21	0.55
1:GC:75:ARG:NH2	1:GC:77:ASP:OD2	2.38	0.55
1:GD:83:LYS:HD2	1:GE:104:THR:HG22	1.88	0.55
1:GG:50:SER:HB2	1:GH:102:LEU:HG	1.89	0.55
1:GN:39:LYS:HE2	1:GN:41:THR:HB	1.88	0.55
1:AJ:50:SER:HB2	1:AK:102:LEU:HG	1.88	0.55
1:BA:64:LEU:HD11	1:BA:67:ILE:HG13	1.89	0.55
1:BK:42:LYS:HG3	1:BK:44:SER:H	1.72	0.55
1:BM:64:LEU:HD11	1:BM:67:ILE:HG13	1.89	0.55
1:BT:42:LYS:HG3	1:BT:44:SER:H	1.72	0.55
1:CQ:15:GLU:HG3	1:CQ:16:LYS:H	1.70	0.55
1:CT:15:GLU:HG3	1:CT:16:LYS:N	2.21	0.55
1:CW:15:GLU:HG3	1:CW:16:LYS:H	1.70	0.55
1:DF:50:SER:HB2	1:DR:102:LEU:HG	1.88	0.55
1:DI:15:GLU:HG3	1:DI:16:LYS:N	2.21	0.55
1:DN:34:LYS:HB3	1:DN:51:GLU:HB3	1.87	0.55
1:EH:42:LYS:HG3	1:EH:44:SER:H	1.70	0.55
1:EN:83:LYS:HD2	1:EO:104:THR:HG22	1.88	0.55
1:EQ:104:THR:HA	1:ER:83:LYS:HE3	1.88	0.55
1:FB:104:THR:HA	1:FK:83:LYS:HE3	1.88	0.55
1:FD:15:GLU:HG2	1:FD:16:LYS:H	1.72	0.55
1:FO:42:LYS:HG3	1:FO:44:SER:H	1.72	0.55
1:FX:42:LYS:HG3	1:FX:44:SER:H	1.72	0.55
1:GL:75:ARG:NH2	1:GL:77:ASP:OD2	2.38	0.55
1:GP:40:ARG:NH1	1:GP:42:LYS:O	2.39	0.55
1:GS:83:LYS:HD2	1:GT:104:THR:HG22	1.88	0.55
1:AG:19:VAL:HG23	1:AH:108:LEU:HD13	1.89	0.55
1:AM:42:LYS:HG3	1:AM:44:SER:H	1.72	0.55
1:BH:42:LYS:HG3	1:BH:44:SER:H	1.71	0.55
1:BM:50:SER:HB2	1:DC:102:LEU:HG	1.89	0.55
1:BV:64:LEU:HD11	1:BV:67:ILE:HG13	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:50:SER:HB2	1:CQ:102:LEU:HG	1.89	0.55
1:DJ:42:LYS:HG3	1:DJ:44:SER:H	1.72	0.55
1:DU:15:GLU:HG3	1:DU:16:LYS:N	2.21	0.55
1:DW:39:LYS:HE2	1:DW:41:THR:HB	1.88	0.55
1:ET:45:PRO:HB3	1:GT:61:THR:HA	1.88	0.55
1:FX:104:THR:HA	1:FY:83:LYS:HE3	1.88	0.55
1:GG:40:ARG:NH1	1:GG:42:LYS:O	2.39	0.55
1:AI:15:GLU:HG3	1:AI:16:LYS:N	2.21	0.55
1:AO:50:SER:HB2	1:DX:102:LEU:HG	1.89	0.55
1:AY:42:LYS:HG3	1:AY:44:SER:H	1.71	0.55
1:CB:15:GLU:HG3	1:CB:16:LYS:H	1.70	0.55
1:DO:15:GLU:HG3	1:DO:16:LYS:H	1.70	0.55
1:ED:75:ARG:NH2	1:ED:77:ASP:OD2	2.39	0.55
1:GU:15:GLU:HG3	1:GU:16:LYS:H	1.72	0.55
1:GV:102:LEU:HG	1:GW:50:SER:HB2	1.88	0.55
1:AG:45:PRO:HB3	1:FA:61:THR:HA	1.88	0.55
1:AI:104:THR:HG22	1:EP:83:LYS:HB3	1.89	0.55
1:BP:102:LEU:HG	1:CW:50:SER:HB2	1.89	0.55
1:CE:15:GLU:HG3	1:CE:16:LYS:H	1.72	0.55
1:CJ:61:THR:HA	1:DP:45:PRO:HB3	1.89	0.55
1:DL:50:SER:HB2	1:DO:102:LEU:HG	1.89	0.55
1:DX:15:GLU:HG3	1:DX:16:LYS:H	1.71	0.55
1:FI:19:VAL:HG23	1:FJ:108:LEU:HD13	1.89	0.55
1:FI:45:PRO:HB3	1:GE:61:THR:HA	1.88	0.55
1:FT:96:ASP:OD1	1:FT:97:GLY:N	2.39	0.55
1:GM:19:VAL:HG23	1:GN:108:LEU:HD13	1.89	0.55
1:AH:61:THR:OG1	1:FO:40:ARG:NH2	2.40	0.55
1:CE:103:VAL:O	1:CE:104:THR:OG1	2.23	0.55
1:EB:34:LYS:HB3	1:EB:51:GLU:HB3	1.89	0.55
1:ET:19:VAL:HG23	1:EU:108:LEU:HD13	1.89	0.55
1:EW:64:LEU:HD11	1:EW:67:ILE:HG13	1.90	0.55
1:FC:102:LEU:HG	1:FD:50:SER:HB2	1.88	0.55
1:FP:80:ALA:HA	1:FP:83:LYS:HB2	1.88	0.55
1:AX:54:ILE:HD13	1:FZ:89:ILE:HG21	1.87	0.54
1:BD:15:GLU:HG3	1:BD:16:LYS:H	1.72	0.54
1:CO:64:LEU:HD11	1:CO:67:ILE:HG13	1.88	0.54
1:DO:64:LEU:HD11	1:DO:67:ILE:HG13	1.89	0.54
1:EE:42:LYS:HG3	1:EE:44:SER:H	1.71	0.54
1:ET:40:ARG:NH1	1:ET:42:LYS:O	2.40	0.54
1:FR:64:LEU:HD11	1:FR:67:ILE:HG13	1.89	0.54
1:FU:19:VAL:HG23	1:FV:108:LEU:HD13	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GJ:42:LYS:HG3	1:GJ:44:SER:H	1.72	0.54
1:GV:83:LYS:HE3	1:GW:104:THR:HA	1.89	0.54
1:AU:15:GLU:HG3	1:AU:16:LYS:H	1.72	0.54
1:AW:39:LYS:HE2	1:AW:41:THR:HB	1.88	0.54
1:CK:50:SER:HB2	1:CT:102:LEU:HG	1.89	0.54
1:CR:19:VAL:HG23	1:CS:108:LEU:HD13	1.89	0.54
1:DC:36:LEU:HB3	1:DC:49:LYS:HB2	1.89	0.54
1:DG:19:VAL:HG23	1:DH:108:LEU:HD13	1.89	0.54
1:DX:64:LEU:HD11	1:DX:67:ILE:HG13	1.89	0.54
1:FI:40:ARG:NH1	1:FI:42:LYS:O	2.40	0.54
1:FQ:36:LEU:HB3	1:FQ:49:LYS:HB2	1.89	0.54
1:AC:64:LEU:HD11	1:AC:67:ILE:HG13	1.89	0.54
1:AW:34:LYS:HB3	1:AW:51:GLU:HB3	1.88	0.54
1:BN:45:PRO:HB3	1:DT:61:THR:HA	1.89	0.54
1:BS:103:VAL:O	1:BS:104:THR:OG1	2.23	0.54
1:CZ:15:GLU:HG3	1:CZ:16:LYS:H	1.72	0.54
1:EJ:54:ILE:HD13	1:FQ:89:ILE:HG21	1.87	0.54
1:EQ:102:LEU:HG	1:ER:50:SER:HB2	1.88	0.54
1:EZ:40:ARG:NE	1:FG:61:THR:O	2.33	0.54
1:FC:42:LYS:HG3	1:FC:44:SER:H	1.72	0.54
1:BY:15:GLU:HG3	1:BY:16:LYS:H	1.72	0.54
1:CF:42:LYS:HG3	1:CF:44:SER:H	1.72	0.54
1:CN:28:LYS:HB3	1:CN:59:PRO:HD3	1.90	0.54
1:DL:75:ARG:NH2	1:DL:77:ASP:OD2	2.39	0.54
1:DT:97:GLY:O	1:DT:101:GLU:HG3	2.08	0.54
1:EI:32:ALA:HB3	1:EI:53:LYS:HG3	1.89	0.54
1:FC:104:THR:HA	1:FD:83:LYS:HE3	1.88	0.54
1:FR:83:LYS:HE3	1:FS:104:THR:HA	1.89	0.54
1:FX:102:LEU:HG	1:FY:50:SER:HB2	1.88	0.54
1:GL:36:LEU:HB3	1:GL:49:LYS:HB2	1.89	0.54
1:GM:47:MET:HB2	1:GM:49:LYS:NZ	2.22	0.54
1:AO:75:ARG:NH2	1:AO:77:ASP:OD2	2.39	0.54
1:BC:36:LEU:HB2	1:BC:49:LYS:HB2	1.89	0.54
1:CJ:97:GLY:O	1:CJ:101:GLU:HG3	2.08	0.54
1:CN:103:VAL:O	1:CN:104:THR:OG1	2.23	0.54
1:DA:64:LEU:HD11	1:DA:67:ILE:HG13	1.88	0.54
1:DB:32:ALA:HB3	1:DB:53:LYS:HG3	1.90	0.54
1:DC:64:LEU:HD11	1:DC:67:ILE:HG13	1.89	0.54
1:DH:61:THR:OG1	1:GJ:40:ARG:NH2	2.40	0.54
1:DI:102:LEU:HG	1:DU:50:SER:HB2	1.89	0.54
1:DK:64:LEU:HD11	1:DK:67:ILE:HG13	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DN:32:ALA:HB3	1:DN:53:LYS:HG3	1.89	0.54
1:EQ:45:PRO:HB3	1:GQ:61:THR:HA	1.88	0.54
1:FL:19:VAL:HG23	1:FM:108:LEU:HD13	1.89	0.54
1:FU:102:LEU:HG	1:FV:50:SER:HB2	1.90	0.54
1:GA:19:VAL:HG23	1:GB:108:LEU:HD13	1.89	0.54
1:GA:102:LEU:HG	1:GB:50:SER:HB2	1.90	0.54
1:GM:35:ARG:NH1	1:GN:106:GLN:O	2.35	0.54
1:GX:15:GLU:HG3	1:GX:16:LYS:H	1.73	0.54
1:AX:64:LEU:HD11	1:AX:67:ILE:HG13	1.89	0.54
1:BS:28:LYS:HB3	1:BS:59:PRO:HD3	1.90	0.54
1:ED:64:LEU:HD11	1:ED:67:ILE:HG13	1.89	0.54
1:FL:64:LEU:HD11	1:FL:67:ILE:HG13	1.89	0.54
1:GE:57:VAL:HG12	1:GE:64:LEU:HA	1.88	0.54
1:AF:15:GLU:HG3	1:AF:16:LYS:H	1.73	0.54
1:AL:102:LEU:HG	1:ED:50:SER:HB2	1.89	0.54
1:AM:5:ASN:HD22	1:AN:89:ILE:HG13	1.71	0.54
1:BC:61:THR:OG1	1:DJ:40:ARG:NH2	2.41	0.54
1:CB:36:LEU:HB3	1:CB:49:LYS:HB2	1.89	0.54
1:CG:64:LEU:HD11	1:CG:67:ILE:HG13	1.89	0.54
1:CH:75:ARG:NH2	1:CH:77:ASP:OD2	2.39	0.54
1:DA:50:SER:HB2	1:DB:102:LEU:HG	1.88	0.54
1:DO:36:LEU:HB3	1:DO:49:LYS:HB2	1.89	0.54
1:EN:40:ARG:NE	1:GW:61:THR:O	2.36	0.54
1:FI:102:LEU:HG	1:FJ:50:SER:HB2	1.90	0.54
1:GT:57:VAL:HG12	1:GT:64:LEU:HA	1.88	0.54
1:AK:32:ALA:HB3	1:AK:53:LYS:HG3	1.90	0.54
1:AL:64:LEU:HD11	1:AL:67:ILE:HG13	1.89	0.54
1:AO:64:LEU:HD11	1:AO:67:ILE:HG13	1.89	0.54
1:BI:61:THR:HA	1:DG:45:PRO:HB3	1.88	0.54
1:BP:15:GLU:HG3	1:BP:16:LYS:H	1.72	0.54
1:CX:42:LYS:HG3	1:CX:44:SER:H	1.73	0.54
1:DL:64:LEU:HD11	1:DL:67:ILE:HG13	1.89	0.54
1:FE:36:LEU:HB3	1:FE:49:LYS:HB2	1.89	0.54
1:FL:102:LEU:HG	1:FM:50:SER:HB2	1.90	0.54
1:GD:42:LYS:HG3	1:GD:44:SER:H	1.72	0.54
1:GO:74:ILE:HG21	1:GO:83:LYS:HD3	1.90	0.54
1:AR:28:LYS:HB3	1:AR:59:PRO:HD3	1.90	0.54
1:AS:19:VAL:HG23	1:AT:108:LEU:HD13	1.89	0.54
1:CH:64:LEU:HD11	1:CH:67:ILE:HG13	1.89	0.54
1:DR:15:GLU:HG3	1:DR:16:LYS:H	1.73	0.54
1:FR:42:LYS:HG3	1:FR:44:SER:H	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FS:36:LEU:HB3	1:FS:49:LYS:HB2	1.90	0.54
1:AM:40:ARG:NH2	1:AT:61:THR:OG1	2.41	0.54
1:AN:64:LEU:HD11	1:AN:67:ILE:HG13	1.89	0.54
1:AS:39:LYS:HD2	1:AS:41:THR:HB	1.90	0.54
1:AZ:64:LEU:HD11	1:AZ:67:ILE:HG13	1.90	0.54
1:BJ:15:GLU:HG3	1:BJ:16:LYS:N	2.23	0.54
1:BL:64:LEU:HD11	1:BL:67:ILE:HG13	1.89	0.54
1:DX:36:LEU:HB3	1:DX:49:LYS:HB2	1.89	0.54
1:EW:42:LYS:HG3	1:EW:44:SER:H	1.73	0.54
1:GP:102:LEU:HG	1:GQ:50:SER:HB2	1.90	0.54
1:GV:64:LEU:HD11	1:GV:67:ILE:HG13	1.89	0.54
1:AE:97:GLY:O	1:AE:101:GLU:HG3	2.08	0.53
1:AI:64:LEU:HD11	1:AI:67:ILE:HG13	1.90	0.53
1:BM:89:ILE:HG21	1:DC:54:ILE:HD13	1.90	0.53
1:BU:64:LEU:HD11	1:BU:67:ILE:HG13	1.89	0.53
1:BX:97:GLY:O	1:BX:101:GLU:HG3	2.08	0.53
1:CT:15:GLU:HG3	1:CT:16:LYS:H	1.73	0.53
1:DI:15:GLU:HG3	1:DI:16:LYS:H	1.73	0.53
1:EJ:64:LEU:HD11	1:EJ:67:ILE:HG13	1.89	0.53
1:EN:51:GLU:OE2	1:EN:53:LYS:NZ	2.24	0.53
1:AX:74:ILE:HG21	1:AX:83:LYS:HD3	1.91	0.53
1:BB:19:VAL:HG23	1:BC:108:LEU:HD13	1.89	0.53
1:BG:28:LYS:HB3	1:BG:59:PRO:HD3	1.90	0.53
1:BI:97:GLY:O	1:BI:101:GLU:HG3	2.08	0.53
1:CQ:36:LEU:HB3	1:CQ:49:LYS:HB2	1.89	0.53
1:DB:61:THR:HA	1:GV:45:PRO:HB3	1.91	0.53
1:FC:45:PRO:HB3	1:FJ:61:THR:HA	1.88	0.53
1:FE:35:ARG:NH1	1:FN:106:GLN:O	2.35	0.53
1:FF:42:LYS:HG3	1:FF:44:SER:H	1.73	0.53
1:FP:15:GLU:HG2	1:FP:16:LYS:H	1.73	0.53
1:GD:19:VAL:HG23	1:GE:108:LEU:HD13	1.91	0.53
1:AI:106:GLN:O	1:EP:35:ARG:NH1	2.36	0.53
1:CD:34:LYS:HB3	1:CD:51:GLU:HB3	1.90	0.53
1:CM:34:LYS:HB3	1:CM:51:GLU:HB3	1.90	0.53
1:CY:34:LYS:HB3	1:CY:51:GLU:HB3	1.90	0.53
1:DU:15:GLU:HG3	1:DU:16:LYS:H	1.73	0.53
1:DY:50:SER:HB2	1:DZ:102:LEU:HG	1.91	0.53
1:EJ:74:ILE:HG21	1:EJ:83:LYS:HD3	1.91	0.53
1:GG:54:ILE:HD13	1:GH:89:ILE:HG21	1.90	0.53
1:GS:19:VAL:HG23	1:GT:108:LEU:HD13	1.91	0.53
1:BH:104:THR:HA	1:BI:83:LYS:HE3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:64:LEU:HD11	1:BP:67:ILE:HG13	1.91	0.53
1:CR:47:MET:HB2	1:CR:49:LYS:HZ3	1.73	0.53
1:CV:97:GLY:O	1:CV:101:GLU:HG3	2.08	0.53
1:DE:97:GLY:O	1:DE:101:GLU:HG3	2.08	0.53
1:EB:45:PRO:HB3	1:GH:61:THR:HA	1.89	0.53
1:EX:58:ASP:HB3	1:EX:65:ILE:HD11	1.89	0.53
1:FB:102:LEU:HG	1:FK:50:SER:HB2	1.90	0.53
1:FG:36:LEU:HB3	1:FG:49:LYS:HB2	1.89	0.53
1:AB:61:THR:HA	1:FR:45:PRO:HB3	1.91	0.53
1:BE:50:SER:HB2	1:BF:102:LEU:HG	1.91	0.53
1:BH:57:VAL:HG22	1:BH:64:LEU:HA	1.91	0.53
1:CA:32:ALA:HB3	1:CA:53:LYS:HG3	1.89	0.53
1:CH:89:ILE:HG21	1:CQ:54:ILE:HD13	1.90	0.53
1:DH:36:LEU:HB2	1:DH:49:LYS:HB2	1.89	0.53
1:DZ:58:ASP:HB3	1:DZ:65:ILE:HD11	1.90	0.53
1:GP:35:ARG:NH1	1:GQ:106:GLN:O	2.34	0.53
1:AL:36:LEU:HB3	1:AL:49:LYS:HB2	1.89	0.53
1:BG:1:SER:OG	1:GX:96:ASP:OD2	2.18	0.53
1:BW:104:THR:HA	1:BX:83:LYS:HE3	1.91	0.53
1:BX:61:THR:HA	1:CR:45:PRO:HB3	1.89	0.53
1:CP:32:ALA:HB3	1:CP:53:LYS:HG3	1.90	0.53
1:DR:64:LEU:HD11	1:DR:67:ILE:HG13	1.91	0.53
1:EK:42:LYS:HG3	1:EK:44:SER:H	1.73	0.53
1:FB:50:SER:HB2	1:FK:102:LEU:HG	1.91	0.53
1:GK:15:GLU:HG2	1:GK:16:LYS:H	1.73	0.53
1:AH:36:LEU:HB2	1:AH:49:LYS:HB2	1.89	0.53
1:AP:50:SER:HB2	1:AQ:102:LEU:HG	1.91	0.53
1:BN:19:VAL:HG23	1:BO:108:LEU:HD13	1.89	0.53
1:BO:61:THR:OG1	1:BT:40:ARG:NH2	2.41	0.53
1:BW:57:VAL:HG22	1:BW:64:LEU:HA	1.91	0.53
1:CB:64:LEU:HD11	1:CB:67:ILE:HG13	1.89	0.53
1:CC:50:SER:HB2	1:CD:102:LEU:HG	1.90	0.53
1:CI:104:THR:HA	1:CJ:83:LYS:HE3	1.91	0.53
1:EG:64:LEU:HD11	1:EG:67:ILE:HG13	1.91	0.53
1:EX:36:LEU:HB3	1:EX:49:LYS:HB2	1.90	0.53
1:GM:102:LEU:HG	1:GN:50:SER:HB2	1.90	0.53
1:AY:45:PRO:HB3	1:EU:61:THR:HA	1.89	0.53
1:BQ:42:LYS:HG3	1:BQ:44:SER:H	1.73	0.53
1:CF:40:ARG:NH2	1:CS:61:THR:OG1	2.42	0.53
1:CQ:64:LEU:HD11	1:CQ:67:ILE:HG13	1.89	0.53
1:DL:89:ILE:HG21	1:DO:54:ILE:HD13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DY:45:PRO:HB3	1:GN:61:THR:HA	1.91	0.53
1:EC:64:LEU:HD11	1:EC:67:ILE:HG13	1.89	0.53
1:EF:97:GLY:O	1:EF:101:GLU:HG3	2.08	0.53
1:EZ:40:ARG:NH2	1:FG:61:THR:OG1	2.42	0.53
1:GG:102:LEU:HG	1:GH:50:SER:HB2	1.90	0.53
1:AV:19:VAL:HG23	1:AW:108:LEU:HD13	1.91	0.53
1:BJ:35:ARG:NH1	1:GR:106:GLN:O	2.38	0.53
1:BK:40:ARG:NH2	1:DQ:61:THR:OG1	2.42	0.53
1:DA:19:VAL:HG23	1:DB:108:LEU:HD13	1.91	0.53
1:DB:23:ASP:OD2	1:DB:26:ASN:ND2	2.42	0.53
1:DP:19:VAL:HG23	1:DQ:108:LEU:HD13	1.89	0.53
1:DY:42:LYS:HG3	1:DY:44:SER:H	1.73	0.53
1:EH:19:VAL:HG23	1:EI:108:LEU:HD13	1.91	0.53
1:ER:45:PRO:HB2	1:ER:76:ALA:HB3	1.91	0.53
1:EW:45:PRO:HB3	1:FM:61:THR:HA	1.91	0.53
1:FE:64:LEU:HD11	1:FE:67:ILE:HG13	1.91	0.53
1:FU:39:LYS:HD2	1:FU:41:THR:HB	1.91	0.53
1:FV:61:THR:OG1	1:FX:40:ARG:NH2	2.42	0.53
1:GG:19:VAL:HG23	1:GH:108:LEU:HD13	1.90	0.53
1:AA:19:VAL:HG23	1:AB:108:LEU:HD13	1.91	0.53
1:AF:64:LEU:HD11	1:AF:67:ILE:HG13	1.91	0.53
1:AJ:19:VAL:HG23	1:AK:108:LEU:HD13	1.91	0.53
1:AP:42:LYS:HG3	1:AP:44:SER:H	1.73	0.53
1:AU:104:THR:HG22	1:GF:83:LYS:HB3	1.89	0.53
1:BD:104:THR:HG22	1:GU:83:LYS:HB3	1.89	0.53
1:BE:42:LYS:HG3	1:BE:44:SER:H	1.73	0.53
1:CZ:103:VAL:O	1:CZ:104:THR:OG1	2.23	0.53
1:DP:47:MET:HB2	1:DP:49:LYS:HZ3	1.73	0.53
1:ET:102:LEU:HG	1:EU:50:SER:HB2	1.91	0.53
1:FF:45:PRO:HB3	1:GB:61:THR:HA	1.91	0.53
1:FU:35:ARG:NH1	1:FV:106:GLN:O	2.34	0.53
1:GP:19:VAL:HG23	1:GQ:108:LEU:HD13	1.89	0.53
1:AH:34:LYS:HB3	1:AH:51:GLU:HB3	1.91	0.52
1:CK:64:LEU:HD11	1:CK:67:ILE:HG13	1.91	0.52
1:CL:50:SER:HB2	1:CM:102:LEU:HG	1.91	0.52
1:CX:50:SER:HB2	1:CY:102:LEU:HG	1.90	0.52
1:DH:34:LYS:HB3	1:DH:51:GLU:HB3	1.91	0.52
1:ET:39:LYS:HD2	1:ET:41:THR:HB	1.91	0.52
1:FI:39:LYS:HD2	1:FI:41:THR:HB	1.91	0.52
1:GV:42:LYS:HG3	1:GV:44:SER:H	1.73	0.52
1:AC:50:SER:HB2	1:ES:102:LEU:HG	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:40:ARG:NE	1:EX:61:THR:O	2.36	0.52
1:AG:47:MET:HB2	1:AG:49:LYS:HZ3	1.74	0.52
1:AL:54:ILE:HD13	1:ED:89:ILE:HG21	1.90	0.52
1:AU:106:GLN:O	1:GF:35:ARG:NH1	2.36	0.52
1:AY:18:VAL:HG22	1:AY:34:LYS:HG3	1.92	0.52
1:BC:34:LYS:HB3	1:BC:51:GLU:HB3	1.91	0.52
1:CF:34:LYS:HB3	1:CF:51:GLU:HB3	1.90	0.52
1:FD:45:PRO:HB2	1:FD:76:ALA:HB3	1.91	0.52
1:GP:39:LYS:HD2	1:GP:41:THR:HB	1.91	0.52
1:GW:36:LEU:HB3	1:GW:49:LYS:HB2	1.90	0.52
1:BN:47:MET:HB2	1:BN:49:LYS:HZ3	1.74	0.52
1:BV:104:THR:HG22	1:GO:83:LYS:HE2	1.91	0.52
1:EE:104:THR:HA	1:EF:83:LYS:HE3	1.91	0.52
1:FC:34:LYS:HB3	1:FC:51:GLU:HB3	1.92	0.52
1:GG:39:LYS:HD2	1:GG:41:THR:HB	1.91	0.52
1:BK:34:LYS:HB3	1:BK:51:GLU:HB3	1.90	0.52
1:BR:34:LYS:HB3	1:BR:51:GLU:HB3	1.90	0.52
1:CD:61:THR:O	1:DS:40:ARG:NE	2.35	0.52
1:CL:39:LYS:HD2	1:CL:41:THR:HB	1.92	0.52
1:EV:15:GLU:HG3	1:EV:16:LYS:H	1.74	0.52
1:GM:1:SER:OG	1:GN:96:ASP:OD2	2.24	0.52
1:GO:15:GLU:HG3	1:GO:16:LYS:H	1.74	0.52
1:AQ:34:LYS:HB3	1:AQ:51:GLU:HB3	1.90	0.52
1:BF:34:LYS:HB3	1:BF:51:GLU:HB3	1.90	0.52
1:BT:18:VAL:HG22	1:BT:34:LYS:HG3	1.91	0.52
1:BY:35:ARG:NH1	1:GI:106:GLN:O	2.39	0.52
1:CB:102:LEU:HG	1:GL:50:SER:HB2	1.92	0.52
1:CI:57:VAL:HG22	1:CI:64:LEU:HA	1.91	0.52
1:CM:58:ASP:HB3	1:CM:65:ILE:HD11	1.91	0.52
1:CW:64:LEU:HD11	1:CW:67:ILE:HG13	1.91	0.52
1:DU:64:LEU:HD11	1:DU:67:ILE:HG13	1.91	0.52
1:AO:89:ILE:HG21	1:DX:54:ILE:HD13	1.91	0.52
1:BR:61:THR:OG1	1:BW:40:ARG:NH2	2.43	0.52
1:BY:64:LEU:HD11	1:BY:67:ILE:HG13	1.90	0.52
1:CR:47:MET:HB2	1:CR:49:LYS:NZ	2.25	0.52
1:CU:104:THR:HA	1:CV:83:LYS:HE3	1.90	0.52
1:DF:64:LEU:HD11	1:DF:67:ILE:HG13	1.91	0.52
1:DG:47:MET:HB2	1:DG:49:LYS:NZ	2.25	0.52
1:DN:74:ILE:HG21	1:DN:83:LYS:HD3	1.92	0.52
1:EL:34:LYS:HB3	1:EL:51:GLU:HB3	1.90	0.52
1:EQ:40:ARG:NH2	1:GQ:61:THR:OG1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FA:57:VAL:HG12	1:FA:64:LEU:HA	1.91	0.52
1:AI:15:GLU:HG3	1:AI:16:LYS:H	1.73	0.52
1:AP:99:TRP:CH2	1:AQ:87:MET:HG2	2.44	0.52
1:AY:40:ARG:NH2	1:EU:61:THR:OG1	2.42	0.52
1:BH:18:VAL:HG22	1:BH:34:LYS:HG3	1.92	0.52
1:BQ:50:SER:HB2	1:BR:102:LEU:HG	1.91	0.52
1:CB:50:SER:HB2	1:GL:102:LEU:HG	1.92	0.52
1:DY:40:ARG:NE	1:GN:61:THR:O	2.26	0.52
1:EK:50:SER:HB2	1:EL:102:LEU:HG	1.91	0.52
1:ET:35:ARG:NH1	1:EU:106:GLN:O	2.34	0.52
1:FF:39:LYS:HD2	1:FF:41:THR:HB	1.92	0.52
1:FN:15:GLU:HG3	1:FN:16:LYS:H	1.74	0.52
1:FX:34:LYS:HB3	1:FX:51:GLU:HB3	1.91	0.52
1:AD:18:VAL:HG22	1:AD:34:LYS:HG3	1.92	0.52
1:BW:18:VAL:HG22	1:BW:34:LYS:HG3	1.92	0.52
1:BZ:19:VAL:HG23	1:CA:108:LEU:HD13	1.91	0.52
1:CL:42:LYS:HG3	1:CL:44:SER:H	1.73	0.52
1:DG:47:MET:HB2	1:DG:49:LYS:HZ3	1.75	0.52
1:DI:106:GLN:O	1:DU:35:ARG:NH1	2.36	0.52
1:DP:64:LEU:HD11	1:DP:67:ILE:HG13	1.92	0.52
1:EQ:34:LYS:HB3	1:EQ:51:GLU:HB3	1.91	0.52
1:EZ:19:VAL:HG23	1:FA:108:LEU:HD13	1.91	0.52
1:FC:40:ARG:NH2	1:FJ:61:THR:OG1	2.42	0.52
1:FZ:64:LEU:HD11	1:FZ:67:ILE:HG13	1.91	0.52
1:AM:18:VAL:HG22	1:AM:34:LYS:HG3	1.91	0.52
1:AT:34:LYS:HB3	1:AT:51:GLU:HB3	1.92	0.52
1:BA:104:THR:HG22	1:GC:83:LYS:HE2	1.91	0.52
1:BP:106:GLN:O	1:CW:35:ARG:NH1	2.36	0.52
1:BR:61:THR:O	1:BW:40:ARG:NE	2.35	0.52
1:CA:74:ILE:HG21	1:CA:83:LYS:HD3	1.92	0.52
1:CC:42:LYS:HG3	1:CC:44:SER:H	1.73	0.52
1:CI:18:VAL:HG22	1:CI:34:LYS:HG3	1.92	0.52
1:CO:19:VAL:HG23	1:CP:108:LEU:HD13	1.91	0.52
1:CY:45:PRO:HB2	1:CY:76:ALA:HB3	1.92	0.52
1:DS:19:VAL:HG23	1:DT:108:LEU:HD13	1.92	0.52
1:DZ:2:LYS:HA	1:DZ:2:LYS:HE3	1.92	0.52
1:EB:40:ARG:NH2	1:GH:61:THR:OG1	2.42	0.52
1:EK:39:LYS:HD2	1:EK:41:THR:HB	1.92	0.52
1:ES:64:LEU:HD11	1:ES:67:ILE:HG13	1.91	0.52
1:FQ:64:LEU:HD11	1:FQ:67:ILE:HG13	1.92	0.52
1:FY:45:PRO:HB2	1:FY:76:ALA:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GC:74:ILE:HG21	1:GC:83:LYS:HD3	1.90	0.52
1:GG:35:ARG:NH1	1:GH:106:GLN:O	2.35	0.52
1:AQ:61:THR:OG1	1:CU:40:ARG:NH2	2.42	0.52
1:BB:39:LYS:HD2	1:BB:41:THR:HB	1.92	0.52
1:BJ:64:LEU:HD11	1:BJ:67:ILE:HG13	1.91	0.52
1:CD:45:PRO:HB2	1:CD:76:ALA:HB3	1.92	0.52
1:CK:35:ARG:NH1	1:CT:106:GLN:O	2.36	0.52
1:CK:83:LYS:HD2	1:CT:104:THR:HG22	1.92	0.52
1:DI:64:LEU:HD11	1:DI:67:ILE:HG13	1.91	0.52
1:DW:35:ARG:O	1:DW:36:LEU:HD12	2.10	0.52
1:DZ:34:LYS:HB3	1:DZ:51:GLU:HB3	1.90	0.52
1:EL:45:PRO:HB2	1:EL:76:ALA:HB3	1.92	0.52
1:FK:15:GLU:HG3	1:FK:16:LYS:H	1.74	0.52
1:GA:47:MET:HB2	1:GA:49:LYS:HZ3	1.75	0.52
1:AD:57:VAL:HG22	1:AD:64:LEU:HA	1.91	0.51
1:BD:64:LEU:HD11	1:BD:67:ILE:HG13	1.91	0.51
1:BF:2:LYS:HE3	1:BF:2:LYS:HA	1.92	0.51
1:BQ:39:LYS:HD2	1:BQ:41:THR:HB	1.92	0.51
1:CT:64:LEU:HD11	1:CT:67:ILE:HG13	1.91	0.51
1:CY:2:LYS:HA	1:CY:2:LYS:HE3	1.92	0.51
1:DI:104:THR:HG22	1:DU:83:LYS:HD2	1.92	0.51
1:DM:19:VAL:HG23	1:DN:108:LEU:HD13	1.91	0.51
1:DV:19:VAL:HG23	1:DW:108:LEU:HD13	1.91	0.51
1:EN:45:PRO:HB3	1:GW:61:THR:HA	1.93	0.51
1:EQ:58:ASP:HB3	1:EQ:65:ILE:HD11	1.92	0.51
1:EW:39:LYS:HD2	1:EW:41:THR:HB	1.92	0.51
1:GC:15:GLU:HG3	1:GC:16:LYS:H	1.74	0.51
1:AB:35:ARG:O	1:AB:36:LEU:HD12	2.10	0.51
1:AU:64:LEU:HD11	1:AU:67:ILE:HG13	1.91	0.51
1:BD:106:GLN:O	1:GU:35:ARG:NH1	2.37	0.51
1:CB:74:ILE:HG21	1:CB:83:LYS:HD3	1.91	0.51
1:CI:19:VAL:HG23	1:CJ:108:LEU:HD13	1.93	0.51
1:EM:103:VAL:O	1:EM:104:THR:OG1	2.22	0.51
1:EN:19:VAL:HG23	1:EO:108:LEU:HD13	1.91	0.51
1:EZ:39:LYS:HD2	1:EZ:41:THR:HB	1.93	0.51
1:FS:2:LYS:HA	1:FS:2:LYS:HE3	1.92	0.51
1:GL:64:LEU:HD11	1:GL:67:ILE:HG13	1.92	0.51
1:GP:50:SER:HB2	1:GQ:102:LEU:HG	1.92	0.51
1:GW:2:LYS:HA	1:GW:2:LYS:HE3	1.92	0.51
1:AQ:2:LYS:HA	1:AQ:2:LYS:HE3	1.92	0.51
1:AX:50:SER:HB2	1:FZ:102:LEU:HG	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:61:THR:OG1	1:DD:40:ARG:NH2	2.43	0.51
1:BP:104:THR:HG22	1:CW:83:LYS:HD2	1.92	0.51
1:DD:104:THR:HA	1:DE:83:LYS:HE3	1.91	0.51
1:DF:35:ARG:NH1	1:DR:106:GLN:O	2.36	0.51
1:EJ:50:SER:HB2	1:FQ:102:LEU:HG	1.92	0.51
1:FU:50:SER:HB2	1:FV:102:LEU:HG	1.92	0.51
1:AG:39:LYS:HD2	1:AG:41:THR:HB	1.93	0.51
1:AP:45:PRO:HB3	1:AW:61:THR:HA	1.91	0.51
1:DW:74:ILE:HG21	1:DW:83:LYS:HD3	1.92	0.51
1:EE:57:VAL:HG22	1:EE:64:LEU:HA	1.91	0.51
1:FE:102:LEU:HG	1:FN:50:SER:HB2	1.93	0.51
1:FI:35:ARG:NH1	1:FJ:106:GLN:O	2.34	0.51
1:AB:74:ILE:HG21	1:AB:83:LYS:HD3	1.92	0.51
1:AP:83:LYS:HD2	1:AQ:104:THR:HG22	1.93	0.51
1:BE:83:LYS:HD2	1:BF:104:THR:HG22	1.93	0.51
1:BJ:104:THR:HA	1:GR:83:LYS:HE3	1.92	0.51
1:CL:83:LYS:HD2	1:CM:104:THR:HG22	1.93	0.51
1:CX:83:LYS:HD2	1:CY:104:THR:HG22	1.93	0.51
1:CY:61:THR:OG1	1:GS:40:ARG:NH2	2.44	0.51
1:DF:83:LYS:HD2	1:DR:104:THR:HG22	1.92	0.51
1:ET:50:SER:HB2	1:EU:102:LEU:HG	1.93	0.51
1:FI:50:SER:HB2	1:FJ:102:LEU:HG	1.93	0.51
1:FL:35:ARG:NH1	1:FM:106:GLN:O	2.34	0.51
1:AK:74:ILE:HG21	1:AK:83:LYS:HD3	1.93	0.51
1:AY:64:LEU:HD11	1:AY:67:ILE:HG13	1.93	0.51
1:BB:47:MET:HB2	1:BB:49:LYS:HZ3	1.76	0.51
1:BN:47:MET:HB2	1:BN:49:LYS:NZ	2.25	0.51
1:BR:45:PRO:HB2	1:BR:76:ALA:HB3	1.93	0.51
1:BY:104:THR:HA	1:GI:83:LYS:HE3	1.92	0.51
1:CP:74:ILE:HG21	1:CP:83:LYS:HD3	1.93	0.51
1:DD:19:VAL:HG23	1:DE:108:LEU:HD13	1.92	0.51
1:DS:18:VAL:HG22	1:DS:34:LYS:HG3	1.92	0.51
1:DS:35:ARG:NH1	1:DT:106:GLN:O	2.39	0.51
1:EI:74:ILE:HG21	1:EI:83:LYS:HD3	1.92	0.51
1:FM:51:GLU:OE2	1:FM:53:LYS:NZ	2.34	0.51
1:AG:64:LEU:HD11	1:AG:67:ILE:HG13	1.93	0.51
1:AJ:18:VAL:HG22	1:AJ:34:LYS:HG3	1.93	0.51
1:AS:47:MET:HB2	1:AS:49:LYS:NZ	2.25	0.51
1:BB:47:MET:HB2	1:BB:49:LYS:NZ	2.25	0.51
1:BC:2:LYS:HA	1:BC:2:LYS:HE3	1.93	0.51
1:BJ:102:LEU:HG	1:GR:50:SER:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:64:LEU:HD11	1:BT:67:ILE:HG13	1.93	0.51
1:BU:26:ASN:HB2	1:BU:28:LYS:HD2	1.92	0.51
1:CC:39:LYS:HD2	1:CC:41:THR:HB	1.93	0.51
1:CM:45:PRO:HB2	1:CM:76:ALA:HB3	1.93	0.51
1:CR:64:LEU:HD11	1:CR:67:ILE:HG13	1.92	0.51
1:CU:19:VAL:HG23	1:CV:108:LEU:HD13	1.92	0.51
1:CU:57:VAL:HG22	1:CU:64:LEU:HA	1.91	0.51
1:DF:15:GLU:HG3	1:DF:16:LYS:N	2.25	0.51
1:DP:47:MET:HB2	1:DP:49:LYS:NZ	2.25	0.51
1:DY:39:LYS:HD2	1:DY:41:THR:HB	1.91	0.51
1:EX:2:LYS:HA	1:EX:2:LYS:HE3	1.92	0.51
1:FW:15:GLU:HG3	1:FW:16:LYS:H	1.74	0.51
1:GB:45:PRO:HB2	1:GB:76:ALA:HB3	1.93	0.51
1:GJ:58:ASP:HB3	1:GJ:65:ILE:HD11	1.92	0.51
1:AA:18:VAL:HG22	1:AA:34:LYS:HG3	1.93	0.51
1:AG:47:MET:HB2	1:AG:49:LYS:NZ	2.25	0.51
1:AL:87:MET:HG2	1:ED:99:TRP:CH2	2.46	0.51
1:AS:47:MET:HB2	1:AS:49:LYS:HZ3	1.76	0.51
1:BH:34:LYS:HB3	1:BH:51:GLU:HB3	1.93	0.51
1:BM:102:LEU:HG	1:DC:50:SER:HB2	1.93	0.51
1:BT:49:LYS:HE3	1:BT:73:SER:OG	2.11	0.51
1:BY:102:LEU:HG	1:GI:50:SER:HB2	1.93	0.51
1:CC:83:LYS:HD2	1:CD:104:THR:HG22	1.93	0.51
1:ER:26:ASN:HB2	1:ER:28:LYS:HD2	1.92	0.51
1:FB:15:GLU:HG3	1:FB:16:LYS:N	2.26	0.51
1:GA:35:ARG:NH1	1:GB:106:GLN:O	2.34	0.51
1:GV:19:VAL:HG23	1:GW:108:LEU:HD13	1.93	0.51
1:AT:2:LYS:HA	1:AT:2:LYS:HE3	1.93	0.51
1:AW:35:ARG:O	1:AW:36:LEU:HD12	2.10	0.51
1:AW:74:ILE:HG21	1:AW:83:LYS:HD3	1.92	0.51
1:BB:64:LEU:HD11	1:BB:67:ILE:HG13	1.93	0.51
1:BK:49:LYS:HE3	1:BK:73:SER:OG	2.11	0.51
1:CG:39:LYS:HE2	1:CG:41:THR:HB	1.93	0.51
1:DD:18:VAL:HG22	1:DD:34:LYS:HG3	1.92	0.51
1:DD:57:VAL:HG22	1:DD:64:LEU:HA	1.91	0.51
1:DS:39:LYS:HD2	1:DS:41:THR:HB	1.93	0.51
1:EJ:102:LEU:HG	1:FQ:50:SER:HB2	1.92	0.51
1:FC:58:ASP:HB3	1:FC:65:ILE:HD11	1.92	0.51
1:FF:19:VAL:HG23	1:FG:108:LEU:HD13	1.93	0.51
1:FG:2:LYS:HA	1:FG:2:LYS:HE3	1.93	0.51
1:GN:45:PRO:HB2	1:GN:76:ALA:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GR:15:GLU:HG3	1:GR:16:LYS:H	1.74	0.51
1:AE:57:VAL:HG12	1:AE:64:LEU:HA	1.93	0.51
1:AF:54:ILE:HD13	1:EV:89:ILE:HG21	1.93	0.51
1:AP:47:MET:HB2	1:AP:49:LYS:NZ	2.26	0.51
1:AR:64:LEU:HD11	1:AR:67:ILE:HG13	1.93	0.51
1:AS:64:LEU:HD11	1:AS:67:ILE:HG13	1.93	0.51
1:BG:64:LEU:HD11	1:BG:67:ILE:HG13	1.93	0.51
1:BK:64:LEU:HD11	1:BK:67:ILE:HG13	1.93	0.51
1:BL:26:ASN:HB2	1:BL:28:LYS:HD2	1.93	0.51
1:BN:34:LYS:HB3	1:BN:51:GLU:HB3	1.93	0.51
1:BN:64:LEU:HD11	1:BN:67:ILE:HG13	1.93	0.51
1:BW:34:LYS:HB3	1:BW:51:GLU:HB3	1.93	0.51
1:CH:102:LEU:HG	1:CQ:50:SER:HB2	1.93	0.51
1:CI:40:ARG:NE	1:CM:61:THR:O	2.38	0.51
1:CX:47:MET:HB2	1:CX:49:LYS:NZ	2.26	0.51
1:DB:61:THR:O	1:GV:40:ARG:NE	2.27	0.51
1:FY:26:ASN:HB2	1:FY:28:LYS:HD2	1.93	0.51
1:AN:26:ASN:HB2	1:AN:28:LYS:HD2	1.93	0.50
1:AS:34:LYS:HB3	1:AS:51:GLU:HB3	1.93	0.50
1:CI:35:ARG:NH1	1:CJ:106:GLN:O	2.40	0.50
1:DS:23:ASP:OD2	1:DS:26:ASN:ND2	2.44	0.50
1:DW:45:PRO:HB2	1:DW:76:ALA:HB3	1.93	0.50
1:FM:34:LYS:HZ1	1:FM:36:LEU:HD13	1.75	0.50
1:FX:58:ASP:HB3	1:FX:65:ILE:HD11	1.92	0.50
1:GQ:2:LYS:HA	1:GQ:2:LYS:HE3	1.93	0.50
1:GS:39:LYS:HD2	1:GS:41:THR:HB	1.93	0.50
1:AD:23:ASP:OD2	1:AD:26:ASN:ND2	2.44	0.50
1:AF:102:LEU:HG	1:EV:50:SER:HB2	1.93	0.50
1:AF:104:THR:HA	1:EV:83:LYS:HE3	1.93	0.50
1:AK:51:GLU:HG3	1:AK:69:ASN:HD21	1.77	0.50
1:AO:99:TRP:CH2	1:DX:87:MET:HG2	2.46	0.50
1:AQ:45:PRO:HB2	1:AQ:76:ALA:HB3	1.92	0.50
1:BH:40:ARG:NE	1:EL:61:THR:O	2.35	0.50
1:BM:99:TRP:CH2	1:DC:87:MET:HG2	2.46	0.50
1:CU:18:VAL:HG22	1:CU:34:LYS:HG3	1.92	0.50
1:CU:23:ASP:OD2	1:CU:26:ASN:ND2	2.44	0.50
1:CX:39:LYS:HD2	1:CX:41:THR:HB	1.93	0.50
1:CZ:64:LEU:HD11	1:CZ:67:ILE:HG13	1.93	0.50
1:EB:49:LYS:HE3	1:EB:73:SER:OG	2.11	0.50
1:EG:104:THR:HA	1:FW:83:LYS:HE3	1.92	0.50
1:FP:26:ASN:HB2	1:FP:28:LYS:HD2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FR:39:LYS:HD2	1:FR:41:THR:HB	1.93	0.50
1:GI:15:GLU:HG3	1:GI:16:LYS:H	1.74	0.50
1:BL:39:LYS:HE2	1:BL:41:THR:HB	1.93	0.50
1:CE:64:LEU:HD11	1:CE:67:ILE:HG13	1.93	0.50
1:CH:99:TRP:CH2	1:CQ:87:MET:HG2	2.46	0.50
1:CI:34:LYS:HB3	1:CI:51:GLU:HB3	1.93	0.50
1:CN:64:LEU:HD11	1:CN:67:ILE:HG13	1.93	0.50
1:CS:2:LYS:HE3	1:CS:2:LYS:HA	1.93	0.50
1:CU:39:LYS:HD2	1:CU:41:THR:HB	1.94	0.50
1:DH:2:LYS:HA	1:DH:2:LYS:HE3	1.93	0.50
1:DZ:61:THR:O	1:EE:40:ARG:NE	2.38	0.50
1:EC:26:ASN:HB2	1:EC:28:LYS:HD2	1.93	0.50
1:EN:12:TYR:HB2	1:EN:22:ARG:HG3	1.93	0.50
1:FD:26:ASN:HB2	1:FD:28:LYS:HD2	1.92	0.50
1:FO:58:ASP:HB3	1:FO:65:ILE:HD11	1.92	0.50
1:AD:39:LYS:HD2	1:AD:41:THR:HB	1.94	0.50
1:AZ:26:ASN:HB2	1:AZ:28:LYS:HD2	1.92	0.50
1:BH:39:LYS:HD2	1:BH:41:THR:HB	1.93	0.50
1:BR:2:LYS:HA	1:BR:2:LYS:HE3	1.92	0.50
1:DG:64:LEU:HD11	1:DG:67:ILE:HG13	1.93	0.50
1:DL:99:TRP:CH2	1:DO:87:MET:HG2	2.46	0.50
1:DV:18:VAL:HG22	1:DV:34:LYS:HG3	1.93	0.50
1:DV:47:MET:HB2	1:DV:49:LYS:NZ	2.27	0.50
1:DZ:61:THR:HA	1:EE:45:PRO:HB3	1.94	0.50
1:EA:64:LEU:HD11	1:EA:67:ILE:HG13	1.93	0.50
1:EL:2:LYS:HA	1:EL:2:LYS:HE3	1.92	0.50
1:EW:83:LYS:HD2	1:EX:104:THR:HG22	1.94	0.50
1:GH:2:LYS:HA	1:GH:2:LYS:HE3	1.93	0.50
1:AO:102:LEU:HG	1:DX:50:SER:HB2	1.93	0.50
1:BH:19:VAL:HG23	1:BI:108:LEU:HD13	1.93	0.50
1:BU:39:LYS:HE2	1:BU:41:THR:HB	1.94	0.50
1:BW:19:VAL:HG23	1:BX:108:LEU:HD13	1.93	0.50
1:CO:18:VAL:HG22	1:CO:34:LYS:HG3	1.93	0.50
1:DD:39:LYS:HD2	1:DD:41:THR:HB	1.94	0.50
1:DE:57:VAL:HG12	1:DE:64:LEU:HA	1.93	0.50
1:DK:39:LYS:HE2	1:DK:41:THR:HB	1.93	0.50
1:DP:39:LYS:HD2	1:DP:41:THR:HB	1.92	0.50
1:DY:19:VAL:HG23	1:DZ:108:LEU:HD13	1.94	0.50
1:EP:64:LEU:HD11	1:EP:67:ILE:HG13	1.93	0.50
1:FS:61:THR:HA	1:GD:45:PRO:HB3	1.92	0.50
1:AD:19:VAL:HG23	1:AE:108:LEU:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:39:LYS:HE2	1:AN:41:THR:HB	1.93	0.50
1:AP:19:VAL:HG23	1:AQ:108:LEU:HD13	1.94	0.50
1:AY:49:LYS:HE3	1:AY:73:SER:OG	2.11	0.50
1:BE:19:VAL:HG23	1:BF:108:LEU:HD13	1.94	0.50
1:BE:39:LYS:HD2	1:BE:41:THR:HB	1.92	0.50
1:BF:45:PRO:HB2	1:BF:76:ALA:HB3	1.93	0.50
1:CV:57:VAL:HG12	1:CV:64:LEU:HA	1.93	0.50
1:DA:18:VAL:HG22	1:DA:34:LYS:HG3	1.93	0.50
1:DB:74:ILE:HG21	1:DB:83:LYS:HD3	1.93	0.50
1:DD:23:ASP:OD2	1:DD:26:ASN:ND2	2.45	0.50
1:DG:39:LYS:HD2	1:DG:41:THR:HB	1.92	0.50
1:DL:102:LEU:HG	1:DO:50:SER:HB2	1.93	0.50
1:EH:54:ILE:HG22	1:EI:90:ILE:HD13	1.93	0.50
1:EY:64:LEU:HD11	1:EY:67:ILE:HG13	1.94	0.50
1:FF:83:LYS:HD2	1:FG:104:THR:HG22	1.94	0.50
1:FS:49:LYS:HE3	1:FS:73:SER:OG	2.12	0.50
1:AC:87:MET:HG2	1:ES:99:TRP:CH2	2.47	0.50
1:AV:18:VAL:HG22	1:AV:34:LYS:HG3	1.93	0.50
1:BU:15:GLU:HG2	1:BU:16:LYS:N	2.27	0.50
1:BZ:54:ILE:HG22	1:CA:90:ILE:HD13	1.93	0.50
1:CI:23:ASP:OD2	1:CI:26:ASN:ND2	2.45	0.50
1:DB:49:LYS:HE3	1:DB:73:SER:OG	2.12	0.50
1:DZ:45:PRO:HB2	1:DZ:76:ALA:HB3	1.92	0.50
1:EC:58:ASP:OD2	1:EC:63:VAL:HG12	2.12	0.50
1:EE:18:VAL:HG22	1:EE:34:LYS:HG3	1.92	0.50
1:EG:15:GLU:HB3	1:EG:18:VAL:HB	1.94	0.50
1:EW:19:VAL:HG23	1:EX:108:LEU:HD13	1.93	0.50
1:EW:54:ILE:HD13	1:EX:89:ILE:HG21	1.94	0.50
1:FB:64:LEU:HD11	1:FB:67:ILE:HG13	1.93	0.50
1:FM:45:PRO:HB2	1:FM:76:ALA:HB3	1.94	0.50
1:FR:54:ILE:HD13	1:FS:89:ILE:HG21	1.94	0.50
1:FS:45:PRO:HB2	1:FS:76:ALA:HB3	1.94	0.50
1:GK:26:ASN:HB2	1:GK:28:LYS:HD2	1.92	0.50
1:AD:104:THR:HA	1:AE:83:LYS:HE3	1.94	0.50
1:AP:39:LYS:HD2	1:AP:41:THR:HB	1.93	0.50
1:BW:39:LYS:HD2	1:BW:41:THR:HB	1.94	0.50
1:BX:57:VAL:HG12	1:BX:64:LEU:HA	1.94	0.50
1:BY:54:ILE:HD13	1:GI:89:ILE:HG21	1.93	0.50
1:BZ:64:LEU:HD11	1:BZ:67:ILE:HG13	1.94	0.50
1:CB:104:THR:HG22	1:GL:83:LYS:HB3	1.94	0.50
1:CF:49:LYS:HE3	1:CF:73:SER:OG	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:58:ASP:OD2	1:CG:63:VAL:HG12	2.12	0.50
1:CR:39:LYS:HD2	1:CR:41:THR:HB	1.92	0.50
1:DK:26:ASN:HB2	1:DK:28:LYS:HD2	1.93	0.50
1:DQ:2:LYS:HA	1:DQ:2:LYS:HE3	1.93	0.50
1:DT:57:VAL:HG12	1:DT:64:LEU:HA	1.94	0.50
1:EB:64:LEU:HD11	1:EB:67:ILE:HG13	1.93	0.50
1:EG:35:ARG:NH1	1:FW:106:GLN:O	2.39	0.50
1:EZ:12:TYR:HB2	1:EZ:22:ARG:HG3	1.93	0.50
1:FL:1:SER:OG	1:FM:96:ASP:OD2	2.24	0.50
1:FR:19:VAL:HG23	1:FS:108:LEU:HD13	1.93	0.50
1:FT:64:LEU:HD11	1:FT:67:ILE:HG13	1.94	0.50
1:GA:1:SER:OG	1:GB:96:ASP:OD2	2.24	0.50
1:GG:34:LYS:HB3	1:GG:51:GLU:HB3	1.94	0.50
1:GK:45:PRO:HB2	1:GK:76:ALA:HB3	1.94	0.50
1:AM:64:LEU:HD11	1:AM:67:ILE:HG13	1.93	0.50
1:BH:23:ASP:OD2	1:BH:26:ASN:ND2	2.44	0.50
1:CF:64:LEU:HD11	1:CF:67:ILE:HG13	1.93	0.50
1:CG:26:ASN:HB2	1:CG:28:LYS:HD2	1.93	0.50
1:CI:45:PRO:HB3	1:CM:61:THR:HA	1.94	0.50
1:CJ:57:VAL:HG12	1:CJ:64:LEU:HA	1.94	0.50
1:CO:54:ILE:HG22	1:CP:90:ILE:HD13	1.93	0.50
1:EW:12:TYR:HB2	1:EW:22:ARG:HG3	1.94	0.50
1:FR:83:LYS:HD2	1:FS:104:THR:HG22	1.94	0.50
1:GD:39:LYS:HD2	1:GD:41:THR:HB	1.94	0.50
1:AB:45:PRO:HB2	1:AB:76:ALA:HB3	1.93	0.49
1:AK:61:THR:HA	1:CX:45:PRO:HB3	1.94	0.49
1:AW:45:PRO:HB2	1:AW:76:ALA:HB3	1.93	0.49
1:AX:87:MET:HG2	1:FZ:99:TRP:CH2	2.47	0.49
1:AY:32:ALA:HB3	1:AY:53:LYS:HG2	1.94	0.49
1:AZ:15:GLU:HG2	1:AZ:16:LYS:N	2.27	0.49
1:AZ:58:ASP:OD2	1:AZ:63:VAL:HG12	2.12	0.49
1:DF:106:GLN:HB3	1:DR:35:ARG:HD3	1.93	0.49
1:EE:35:ARG:NH1	1:EF:106:GLN:O	2.39	0.49
1:EJ:87:MET:HG2	1:FQ:99:TRP:CH2	2.47	0.49
1:EU:2:LYS:HA	1:EU:2:LYS:HE3	1.93	0.49
1:FD:15:GLU:HG2	1:FD:16:LYS:N	2.27	0.49
1:FF:12:TYR:HB2	1:FF:22:ARG:HG3	1.94	0.49
1:FJ:2:LYS:HA	1:FJ:2:LYS:HE3	1.93	0.49
1:GV:39:LYS:HD2	1:GV:41:THR:HB	1.93	0.49
1:GX:64:LEU:HD11	1:GX:67:ILE:HG13	1.94	0.49
1:AV:54:ILE:HG22	1:AW:90:ILE:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:102:LEU:HG	1:FZ:50:SER:HB2	1.94	0.49
1:AY:40:ARG:NE	1:EU:61:THR:O	2.37	0.49
1:BO:2:LYS:HA	1:BO:2:LYS:HE3	1.93	0.49
1:BW:23:ASP:OD2	1:BW:26:ASN:ND2	2.45	0.49
1:CJ:1:SER:O	1:CJ:2:LYS:HD2	2.13	0.49
1:CP:49:LYS:HE3	1:CP:73:SER:OG	2.12	0.49
1:DE:1:SER:O	1:DE:2:LYS:HD2	2.13	0.49
1:DF:15:GLU:HB3	1:DF:18:VAL:HB	1.94	0.49
1:DM:64:LEU:HD11	1:DM:67:ILE:HG13	1.94	0.49
1:EC:45:PRO:HB2	1:EC:76:ALA:HB3	1.94	0.49
1:EW:40:ARG:NE	1:FM:61:THR:O	2.26	0.49
1:EZ:23:ASP:OD2	1:EZ:26:ASN:ND2	2.45	0.49
1:FL:57:VAL:HG22	1:FL:64:LEU:HA	1.94	0.49
1:GA:57:VAL:HG22	1:GA:64:LEU:HA	1.93	0.49
1:GJ:90:ILE:HD13	1:GK:54:ILE:HG22	1.94	0.49
1:AN:58:ASP:OD2	1:AN:63:VAL:HG12	2.12	0.49
1:BL:58:ASP:OD2	1:BL:63:VAL:HG12	2.12	0.49
1:BN:39:LYS:HD2	1:BN:41:THR:HB	1.93	0.49
1:BO:61:THR:O	1:BT:40:ARG:NE	2.38	0.49
1:BP:35:ARG:HD3	1:CW:106:GLN:HB3	1.93	0.49
1:BQ:19:VAL:HG23	1:BR:108:LEU:HD13	1.94	0.49
1:BQ:83:LYS:HD2	1:BR:104:THR:HG22	1.93	0.49
1:CA:49:LYS:HE3	1:CA:73:SER:OG	2.12	0.49
1:CI:39:LYS:HD2	1:CI:41:THR:HB	1.94	0.49
1:CV:1:SER:O	1:CV:2:LYS:HD2	2.13	0.49
1:DD:34:LYS:HB3	1:DD:51:GLU:HB3	1.93	0.49
1:DM:18:VAL:HG22	1:DM:34:LYS:HG3	1.94	0.49
1:EA:103:VAL:O	1:EA:104:THR:OG1	2.23	0.49
1:EK:83:LYS:HD2	1:EL:104:THR:HG22	1.93	0.49
1:EQ:40:ARG:NE	1:GQ:61:THR:O	2.37	0.49
1:FF:54:ILE:HD13	1:FG:89:ILE:HG21	1.95	0.49
1:FP:64:LEU:HD11	1:FP:67:ILE:HG13	1.93	0.49
1:FV:2:LYS:HA	1:FV:2:LYS:HE3	1.93	0.49
1:FW:64:LEU:HD11	1:FW:67:ILE:HG13	1.95	0.49
1:GM:57:VAL:HG22	1:GM:64:LEU:HA	1.93	0.49
1:GW:49:LYS:HE3	1:GW:73:SER:OG	2.12	0.49
1:AM:49:LYS:HE3	1:AM:73:SER:OG	2.11	0.49
1:BH:40:ARG:NH2	1:EL:61:THR:OG1	2.45	0.49
1:BU:58:ASP:OD2	1:BU:63:VAL:HG12	2.12	0.49
1:CD:61:THR:OG1	1:DS:40:ARG:NH2	2.45	0.49
1:CX:19:VAL:HG23	1:CY:108:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DY:83:LYS:HD2	1:DZ:104:THR:HG22	1.93	0.49
1:EE:19:VAL:HG23	1:EF:108:LEU:HD13	1.93	0.49
1:EX:45:PRO:HB2	1:EX:76:ALA:HB3	1.94	0.49
1:EX:49:LYS:HE3	1:EX:73:SER:OG	2.12	0.49
1:FC:40:ARG:NE	1:FJ:61:THR:O	2.37	0.49
1:FD:64:LEU:HD11	1:FD:67:ILE:HG13	1.94	0.49
1:FG:45:PRO:HB2	1:FG:76:ALA:HB3	1.94	0.49
1:FO:3:VAL:HG12	1:FO:8:THR:HG23	1.94	0.49
1:FU:34:LYS:HB3	1:FU:51:GLU:HB3	1.95	0.49
1:GD:12:TYR:HB2	1:GD:22:ARG:HG3	1.93	0.49
1:AB:1:SER:O	1:AB:2:LYS:HD2	2.12	0.49
1:AG:34:LYS:HB3	1:AG:51:GLU:HB3	1.93	0.49
1:AK:49:LYS:HE3	1:AK:73:SER:OG	2.12	0.49
1:AL:51:GLU:OE2	1:AL:53:LYS:HD3	2.12	0.49
1:AM:90:ILE:HD13	1:AN:54:ILE:HG22	1.95	0.49
1:AV:32:ALA:HB3	1:AV:53:LYS:HG2	1.95	0.49
1:BK:40:ARG:NE	1:DQ:61:THR:O	2.38	0.49
1:BQ:45:PRO:HB3	1:DN:61:THR:HA	1.94	0.49
1:BT:32:ALA:HB3	1:BT:53:LYS:HG2	1.94	0.49
1:CB:87:MET:HG2	1:GL:99:TRP:CH2	2.47	0.49
1:CD:2:LYS:HA	1:CD:2:LYS:HE3	1.92	0.49
1:CY:61:THR:HA	1:GS:45:PRO:HB3	1.94	0.49
1:DJ:64:LEU:HD11	1:DJ:67:ILE:HG13	1.93	0.49
1:DJ:90:ILE:HD13	1:DK:54:ILE:HG22	1.95	0.49
1:DK:58:ASP:OD2	1:DK:63:VAL:HG12	2.12	0.49
1:DS:57:VAL:HG22	1:DS:64:LEU:HA	1.93	0.49
1:DW:61:THR:HA	1:EK:45:PRO:HB3	1.94	0.49
1:EG:102:LEU:HG	1:FW:50:SER:HB2	1.93	0.49
1:EI:49:LYS:HE3	1:EI:73:SER:OG	2.12	0.49
1:EZ:45:PRO:HB3	1:FG:61:THR:HA	1.94	0.49
1:GK:39:LYS:HE2	1:GK:41:THR:HB	1.94	0.49
1:GK:64:LEU:HD11	1:GK:67:ILE:HG13	1.93	0.49
1:GS:12:TYR:HB2	1:GS:22:ARG:HG3	1.93	0.49
1:AH:2:LYS:HA	1:AH:2:LYS:HE3	1.93	0.49
1:CM:2:LYS:HA	1:CM:2:LYS:HE3	1.92	0.49
1:CP:45:PRO:HB2	1:CP:76:ALA:HB3	1.95	0.49
1:EC:39:LYS:HE2	1:EC:41:THR:HB	1.93	0.49
1:EE:23:ASP:OD2	1:EE:26:ASN:ND2	2.45	0.49
1:EE:34:LYS:HB3	1:EE:51:GLU:HB3	1.93	0.49
1:EH:32:ALA:HB3	1:EH:53:LYS:HG2	1.95	0.49
1:EK:19:VAL:HG23	1:EL:108:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ET:34:LYS:HB3	1:ET:51:GLU:HB3	1.94	0.49
1:FG:49:LYS:HE3	1:FG:73:SER:OG	2.12	0.49
1:FP:45:PRO:HB2	1:FP:76:ALA:HB3	1.94	0.49
1:GC:64:LEU:HD11	1:GC:67:ILE:HG13	1.94	0.49
1:GJ:3:VAL:HG12	1:GJ:8:THR:HG23	1.95	0.49
1:AC:102:LEU:HG	1:ES:50:SER:HB2	1.94	0.49
1:CC:45:PRO:HB3	1:CP:61:THR:HA	1.94	0.49
1:DA:54:ILE:HG22	1:DB:90:ILE:HD13	1.93	0.49
1:DM:54:ILE:HG22	1:DN:90:ILE:HD13	1.93	0.49
1:DN:49:LYS:HE3	1:DN:73:SER:OG	2.12	0.49
1:DV:54:ILE:HG22	1:DW:90:ILE:HD13	1.94	0.49
1:EH:18:VAL:HG22	1:EH:34:LYS:HG3	1.94	0.49
1:EN:39:LYS:HD2	1:EN:41:THR:HB	1.94	0.49
1:EV:64:LEU:HD11	1:EV:67:ILE:HG13	1.94	0.49
1:FF:40:ARG:NE	1:GB:61:THR:O	2.26	0.49
1:GD:23:ASP:OD2	1:GD:26:ASN:ND2	2.45	0.49
1:GS:23:ASP:OD2	1:GS:26:ASN:ND2	2.45	0.49
1:GV:12:TYR:HB2	1:GV:22:ARG:HG3	1.95	0.49
1:GV:47:MET:HB2	1:GV:49:LYS:NZ	2.27	0.49
1:AI:102:LEU:HG	1:EP:50:SER:HB2	1.95	0.49
1:AJ:54:ILE:HG22	1:AK:90:ILE:HD13	1.93	0.49
1:AZ:39:LYS:HE2	1:AZ:41:THR:HB	1.94	0.49
1:AZ:45:PRO:HB2	1:AZ:76:ALA:HB3	1.94	0.49
1:BZ:1:SER:OG	1:CA:96:ASP:OD2	2.27	0.49
1:CF:90:ILE:HD13	1:CG:54:ILE:HG22	1.95	0.49
1:DC:51:GLU:OE2	1:DC:53:LYS:HD3	2.13	0.49
1:EB:40:ARG:NE	1:GH:61:THR:O	2.37	0.49
1:EN:23:ASP:OD2	1:EN:26:ASN:ND2	2.45	0.49
1:FB:35:ARG:NH1	1:FK:106:GLN:O	2.39	0.49
1:FC:90:ILE:HD13	1:FD:54:ILE:HG22	1.95	0.49
1:FI:34:LYS:HB3	1:FI:51:GLU:HB3	1.95	0.49
1:FN:64:LEU:HD11	1:FN:67:ILE:HG13	1.94	0.49
1:AB:53:LYS:HB3	1:AB:69:ASN:ND2	2.28	0.49
1:AE:1:SER:O	1:AE:2:LYS:HD2	2.13	0.49
1:AW:34:LYS:HZ1	1:AW:36:LEU:HD13	1.77	0.49
1:AW:49:LYS:HE3	1:AW:73:SER:OG	2.13	0.49
1:AY:90:ILE:HD13	1:AZ:54:ILE:HG22	1.95	0.49
1:BX:1:SER:O	1:BX:2:LYS:HD2	2.13	0.49
1:DI:35:ARG:HD3	1:DU:106:GLN:HB3	1.93	0.49
1:DX:51:GLU:OE2	1:DX:53:LYS:HD3	2.12	0.49
1:EF:1:SER:O	1:EF:2:LYS:HD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FK:64:LEU:HD11	1:FK:67:ILE:HG13	1.95	0.49
1:FO:90:ILE:HD13	1:FP:54:ILE:HG22	1.95	0.49
1:AA:54:ILE:HG22	1:AB:90:ILE:HD13	1.94	0.49
1:AL:50:SER:HB2	1:ED:102:LEU:HG	1.93	0.49
1:AM:40:ARG:NE	1:AT:61:THR:O	2.38	0.49
1:AW:53:LYS:HB3	1:AW:69:ASN:ND2	2.28	0.49
1:AY:34:LYS:HB3	1:AY:51:GLU:HB3	1.95	0.49
1:BZ:18:VAL:HG22	1:BZ:34:LYS:HG3	1.94	0.49
1:CA:61:THR:HA	1:CL:45:PRO:HB3	1.94	0.49
1:CB:51:GLU:OE2	1:CB:53:LYS:HD3	2.13	0.49
1:CO:1:SER:OG	1:CP:96:ASP:OD2	2.27	0.49
1:DW:1:SER:O	1:DW:2:LYS:HD2	2.12	0.49
1:EJ:51:GLU:OE2	1:EJ:53:LYS:HD3	2.13	0.49
1:EM:64:LEU:HD11	1:EM:67:ILE:HG13	1.93	0.49
1:EQ:57:VAL:HG22	1:EQ:64:LEU:HA	1.95	0.49
1:FD:35:ARG:O	1:FD:36:LEU:HD12	2.13	0.49
1:GP:34:LYS:HB3	1:GP:51:GLU:HB3	1.95	0.49
1:AB:49:LYS:HE3	1:AB:73:SER:OG	2.13	0.48
1:AC:104:THR:HG22	1:ES:83:LYS:HB3	1.94	0.48
1:AP:51:GLU:OE2	1:AP:69:ASN:ND2	2.46	0.48
1:AU:102:LEU:HG	1:GF:50:SER:HB2	1.95	0.48
1:AX:51:GLU:OE2	1:AX:53:LYS:HD3	2.13	0.48
1:BI:1:SER:O	1:BI:2:LYS:HD2	2.13	0.48
1:CC:64:LEU:HD11	1:CC:67:ILE:HG13	1.95	0.48
1:CP:23:ASP:OD2	1:CP:26:ASN:ND2	2.46	0.48
1:CX:3:VAL:HG12	1:CX:8:THR:HG23	1.95	0.48
1:DW:49:LYS:HE3	1:DW:73:SER:OG	2.13	0.48
1:ER:35:ARG:O	1:ER:36:LEU:HD12	2.13	0.48
1:FC:3:VAL:HG12	1:FC:8:THR:HG23	1.94	0.48
1:FR:47:MET:HB2	1:FR:49:LYS:NZ	2.27	0.48
1:FY:64:LEU:HD11	1:FY:67:ILE:HG13	1.93	0.48
1:AF:106:GLN:HB3	1:EV:35:ARG:HD3	1.95	0.48
1:AW:1:SER:O	1:AW:2:LYS:HD2	2.12	0.48
1:BE:64:LEU:HD11	1:BE:67:ILE:HG13	1.95	0.48
1:BQ:64:LEU:HD11	1:BQ:67:ILE:HG13	1.95	0.48
1:CI:47:MET:HB2	1:CI:49:LYS:NZ	2.29	0.48
1:CL:64:LEU:HD11	1:CL:67:ILE:HG13	1.95	0.48
1:CP:51:GLU:HG3	1:CP:69:ASN:HD21	1.77	0.48
1:DB:51:GLU:HG3	1:DB:69:ASN:HD21	1.77	0.48
1:DH:61:THR:O	1:GJ:40:ARG:NE	2.37	0.48
1:DN:1:SER:O	1:DN:2:LYS:HD2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DQ:97:GLY:O	1:DQ:101:GLU:HG3	2.13	0.48
1:EK:64:LEU:HD11	1:EK:67:ILE:HG13	1.95	0.48
1:EQ:90:ILE:HD13	1:ER:54:ILE:HG22	1.95	0.48
1:ER:64:LEU:HD11	1:ER:67:ILE:HG13	1.93	0.48
1:FX:90:ILE:HD13	1:FY:54:ILE:HG22	1.95	0.48
1:FY:35:ARG:O	1:FY:36:LEU:HD12	2.13	0.48
1:GV:83:LYS:HD2	1:GW:104:THR:HG22	1.94	0.48
1:AP:64:LEU:HD11	1:AP:67:ILE:HG13	1.95	0.48
1:AX:104:THR:HG22	1:FZ:83:LYS:HB3	1.94	0.48
1:BO:97:GLY:O	1:BO:101:GLU:HG3	2.13	0.48
1:BQ:51:GLU:OE2	1:BQ:69:ASN:ND2	2.47	0.48
1:BS:64:LEU:HD11	1:BS:67:ILE:HG13	1.93	0.48
1:CQ:51:GLU:OE2	1:CQ:53:LYS:HD3	2.13	0.48
1:DE:36:LEU:HB3	1:DE:49:LYS:HB2	1.95	0.48
1:EE:47:MET:HB2	1:EE:49:LYS:NZ	2.28	0.48
1:EN:50:SER:HB2	1:EO:102:LEU:HG	1.95	0.48
1:FL:34:LYS:HB3	1:FL:51:GLU:HB3	1.94	0.48
1:GB:1:SER:O	1:GB:2:LYS:HD2	2.13	0.48
1:GF:64:LEU:HD11	1:GF:67:ILE:HG13	1.93	0.48
1:GN:1:SER:O	1:GN:2:LYS:HD2	2.13	0.48
1:GS:47:MET:HB2	1:GS:49:LYS:NZ	2.28	0.48
1:AD:45:PRO:HB3	1:EX:61:THR:HA	1.95	0.48
1:BC:97:GLY:O	1:BC:101:GLU:HG3	2.13	0.48
1:BD:102:LEU:HG	1:GU:50:SER:HB2	1.95	0.48
1:CG:45:PRO:HB2	1:CG:76:ALA:HB3	1.94	0.48
1:CL:19:VAL:HG23	1:CM:108:LEU:HD13	1.94	0.48
1:DB:45:PRO:HB2	1:DB:76:ALA:HB3	1.95	0.48
1:DD:47:MET:HB2	1:DD:49:LYS:NZ	2.29	0.48
1:DO:51:GLU:OE2	1:DO:53:LYS:HD3	2.13	0.48
1:EE:39:LYS:HD2	1:EE:41:THR:HB	1.94	0.48
1:EI:1:SER:O	1:EI:2:LYS:HD2	2.12	0.48
1:EK:51:GLU:OE2	1:EK:69:ASN:ND2	2.47	0.48
1:EL:49:LYS:HE3	1:EL:73:SER:OG	2.13	0.48
1:EN:47:MET:HB2	1:EN:49:LYS:NZ	2.28	0.48
1:EO:1:SER:O	1:EO:2:LYS:HD2	2.13	0.48
1:EY:89:ILE:HG21	1:FH:54:ILE:HD13	1.96	0.48
1:EZ:47:MET:HB2	1:EZ:49:LYS:NZ	2.28	0.48
1:FM:1:SER:O	1:FM:2:LYS:HD2	2.13	0.48
1:GD:47:MET:HB2	1:GD:49:LYS:NZ	2.28	0.48
1:AE:36:LEU:HB3	1:AE:49:LYS:HB2	1.96	0.48
1:AF:15:GLU:HB3	1:AF:18:VAL:HB	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:97:GLY:O	1:AH:101:GLU:HG3	2.13	0.48
1:AK:28:LYS:HB2	1:AK:57:VAL:O	2.14	0.48
1:AK:45:PRO:HB2	1:AK:76:ALA:HB3	1.95	0.48
1:AT:97:GLY:O	1:AT:101:GLU:HG3	2.13	0.48
1:BA:74:ILE:HG21	1:BA:83:LYS:HD3	1.95	0.48
1:BH:47:MET:HB2	1:BH:49:LYS:NZ	2.28	0.48
1:BW:47:MET:HB2	1:BW:49:LYS:NZ	2.29	0.48
1:BZ:47:MET:HB2	1:BZ:49:LYS:NZ	2.27	0.48
1:CV:36:LEU:HB3	1:CV:49:LYS:HB2	1.96	0.48
1:DW:53:LYS:HB3	1:DW:69:ASN:ND2	2.29	0.48
1:DZ:35:ARG:O	1:DZ:36:LEU:HD12	2.13	0.48
1:EH:64:LEU:HD11	1:EH:67:ILE:HG13	1.94	0.48
1:EJ:104:THR:HG22	1:FQ:83:LYS:HB3	1.94	0.48
1:GJ:57:VAL:HG22	1:GJ:64:LEU:HA	1.96	0.48
1:GU:64:LEU:HD11	1:GU:67:ILE:HG13	1.94	0.48
1:AK:35:ARG:O	1:AK:36:LEU:HD12	2.14	0.48
1:BE:51:GLU:OE2	1:BE:69:ASN:ND2	2.47	0.48
1:BN:104:THR:HG22	1:BO:83:LYS:HB3	1.96	0.48
1:BR:49:LYS:HE3	1:BR:73:SER:OG	2.14	0.48
1:BV:74:ILE:HG21	1:BV:83:LYS:HD3	1.95	0.48
1:CA:1:SER:O	1:CA:2:LYS:HD2	2.12	0.48
1:CO:32:ALA:HB3	1:CO:53:LYS:HG2	1.95	0.48
1:DC:103:VAL:C	1:DC:104:THR:HG1	2.12	0.48
1:DP:104:THR:HG22	1:DQ:83:LYS:HB3	1.96	0.48
1:DY:64:LEU:HD11	1:DY:67:ILE:HG13	1.95	0.48
1:FL:47:MET:HB2	1:FL:49:LYS:HZ3	1.77	0.48
1:FP:39:LYS:HE2	1:FP:41:THR:HB	1.94	0.48
1:GA:34:LYS:HB3	1:GA:51:GLU:HB3	1.94	0.48
1:GE:1:SER:O	1:GE:2:LYS:HD2	2.13	0.48
1:GH:49:LYS:HE3	1:GH:73:SER:OG	2.13	0.48
1:GT:1:SER:O	1:GT:2:LYS:HD2	2.13	0.48
1:GW:45:PRO:HB2	1:GW:76:ALA:HB3	1.94	0.48
1:AA:32:ALA:HB3	1:AA:53:LYS:HG2	1.95	0.48
1:AA:39:LYS:HD2	1:AA:41:THR:HB	1.96	0.48
1:BY:106:GLN:HB3	1:GI:35:ARG:HD3	1.96	0.48
1:BZ:32:ALA:HB3	1:BZ:53:LYS:HG2	1.95	0.48
1:CC:19:VAL:HG23	1:CD:108:LEU:HD13	1.94	0.48
1:CD:35:ARG:O	1:CD:36:LEU:HD12	2.13	0.48
1:CD:61:THR:HA	1:DS:45:PRO:HB3	1.96	0.48
1:CS:97:GLY:O	1:CS:101:GLU:HG3	2.13	0.48
1:DD:101:GLU:O	1:DD:105:ASP:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DM:32:ALA:HB3	1:DM:53:LYS:HG2	1.95	0.48
1:DS:47:MET:HB2	1:DS:49:LYS:NZ	2.29	0.48
1:EB:90:ILE:HD13	1:EC:54:ILE:HG22	1.95	0.48
1:EI:51:GLU:HG3	1:EI:69:ASN:HD21	1.79	0.48
1:EL:35:ARG:O	1:EL:36:LEU:HD12	2.13	0.48
1:FB:89:ILE:HG21	1:FK:54:ILE:HD13	1.96	0.48
1:FX:57:VAL:HG22	1:FX:64:LEU:HA	1.95	0.48
1:GO:64:LEU:HD11	1:GO:67:ILE:HG13	1.94	0.48
1:AJ:32:ALA:HB3	1:AJ:53:LYS:HG2	1.95	0.48
1:AK:61:THR:O	1:CX:40:ARG:NE	2.27	0.48
1:AM:32:ALA:HB3	1:AM:53:LYS:HG2	1.94	0.48
1:AN:45:PRO:HB2	1:AN:76:ALA:HB3	1.94	0.48
1:AP:54:ILE:HD13	1:AQ:89:ILE:HG21	1.96	0.48
1:BE:45:PRO:HB3	1:EI:61:THR:HA	1.94	0.48
1:BK:32:ALA:HB3	1:BK:53:LYS:HG2	1.96	0.48
1:BL:45:PRO:HB2	1:BL:76:ALA:HB3	1.94	0.48
1:BT:90:ILE:HD13	1:BU:54:ILE:HG22	1.95	0.48
1:CA:45:PRO:HB2	1:CA:76:ALA:HB3	1.96	0.48
1:CF:40:ARG:NE	1:CS:61:THR:O	2.38	0.48
1:CY:35:ARG:O	1:CY:36:LEU:HD12	2.13	0.48
1:DH:97:GLY:O	1:DH:101:GLU:HG3	2.13	0.48
1:FC:57:VAL:HG22	1:FC:64:LEU:HA	1.95	0.48
1:GV:3:VAL:HG12	1:GV:8:THR:HG23	1.96	0.48
1:GV:54:ILE:HD13	1:GW:89:ILE:HG21	1.95	0.48
1:AB:61:THR:O	1:FR:40:ARG:NE	2.27	0.48
1:AK:23:ASP:OD2	1:AK:26:ASN:ND2	2.46	0.48
1:AV:110:LEU:HD13	1:FZ:11:ILE:HG22	1.96	0.48
1:BB:3:VAL:HA	1:BB:7:GLN:O	2.14	0.48
1:BB:104:THR:HG22	1:BC:83:LYS:HB3	1.96	0.48
1:BK:90:ILE:HD13	1:BL:54:ILE:HG22	1.95	0.48
1:BM:74:ILE:HG21	1:BM:83:LYS:HD3	1.95	0.48
1:BU:45:PRO:HB2	1:BU:76:ALA:HB3	1.94	0.48
1:CH:74:ILE:HG21	1:CH:83:LYS:HD3	1.95	0.48
1:CK:106:GLN:HB3	1:CT:35:ARG:HD3	1.94	0.48
1:CM:35:ARG:O	1:CM:36:LEU:HD12	2.13	0.48
1:CP:28:LYS:HB2	1:CP:57:VAL:O	2.14	0.48
1:CR:90:ILE:HD13	1:CS:54:ILE:HG22	1.96	0.48
1:DN:28:LYS:HB2	1:DN:57:VAL:O	2.14	0.48
1:DY:51:GLU:OE2	1:DY:69:ASN:ND2	2.47	0.48
1:EU:49:LYS:HE3	1:EU:73:SER:OG	2.14	0.48
1:GG:47:MET:HB2	1:GG:49:LYS:NZ	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:35:ARG:NH1	1:EV:106:GLN:O	2.39	0.48
1:AS:3:VAL:HA	1:AS:7:GLN:O	2.14	0.48
1:AS:104:THR:HG22	1:AT:83:LYS:HB3	1.96	0.48
1:BF:35:ARG:O	1:BF:36:LEU:HD12	2.13	0.48
1:BJ:106:GLN:HB3	1:GR:35:ARG:HD3	1.96	0.48
1:CU:47:MET:HB2	1:CU:49:LYS:NZ	2.29	0.48
1:DA:32:ALA:HB3	1:DA:53:LYS:HG2	1.95	0.48
1:DC:45:PRO:HB2	1:DC:76:ALA:HB3	1.95	0.48
1:DK:45:PRO:HB2	1:DK:76:ALA:HB3	1.94	0.48
1:DV:64:LEU:HD11	1:DV:67:ILE:HG13	1.96	0.48
1:DW:28:LYS:HB2	1:DW:57:VAL:O	2.14	0.48
1:DZ:49:LYS:HE3	1:DZ:73:SER:OG	2.14	0.48
1:EW:47:MET:HB2	1:EW:49:LYS:NZ	2.27	0.48
1:FH:64:LEU:HD11	1:FH:67:ILE:HG13	1.96	0.48
1:FJ:15:GLU:HG3	1:FJ:16:LYS:N	2.29	0.48
1:FR:12:TYR:HB2	1:FR:22:ARG:HG3	1.95	0.48
1:FU:90:ILE:HD13	1:FV:54:ILE:HG22	1.96	0.48
1:GI:64:LEU:HD11	1:GI:67:ILE:HG13	1.94	0.48
1:GM:34:LYS:HB3	1:GM:51:GLU:HB3	1.95	0.48
1:AJ:39:LYS:HD2	1:AJ:41:THR:HB	1.96	0.47
1:BF:49:LYS:HE3	1:BF:73:SER:OG	2.14	0.47
1:BR:35:ARG:O	1:BR:36:LEU:HD12	2.13	0.47
1:BX:36:LEU:HB3	1:BX:49:LYS:HB2	1.95	0.47
1:CC:12:TYR:HB2	1:CC:22:ARG:HG3	1.96	0.47
1:CL:51:GLU:OE2	1:CL:69:ASN:ND2	2.47	0.47
1:DV:39:LYS:HD2	1:DV:41:THR:HB	1.96	0.47
1:ED:74:ILE:HG21	1:ED:83:LYS:HD3	1.95	0.47
1:EI:28:LYS:HB2	1:EI:57:VAL:O	2.14	0.47
1:EI:35:ARG:O	1:EI:36:LEU:HD12	2.14	0.47
1:FA:1:SER:O	1:FA:2:LYS:HD2	2.13	0.47
1:FC:49:LYS:HE3	1:FC:73:SER:OG	2.14	0.47
1:FP:49:LYS:HE3	1:FP:73:SER:OG	2.14	0.47
1:FU:3:VAL:HA	1:FU:7:GLN:O	2.14	0.47
1:GM:54:ILE:HG22	1:GN:90:ILE:HD13	1.96	0.47
1:GR:64:LEU:HD11	1:GR:67:ILE:HG13	1.95	0.47
1:AA:64:LEU:HD11	1:AA:67:ILE:HG13	1.96	0.47
1:AQ:35:ARG:O	1:AQ:36:LEU:HD12	2.13	0.47
1:AW:80:ALA:O	1:AW:84:THR:OG1	2.31	0.47
1:BC:61:THR:O	1:DJ:40:ARG:NE	2.37	0.47
1:BE:54:ILE:HD13	1:BF:89:ILE:HG21	1.97	0.47
1:BH:45:PRO:HB3	1:EL:61:THR:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:12:TYR:HB2	1:CL:22:ARG:HG3	1.96	0.47
1:CP:35:ARG:O	1:CP:36:LEU:HD12	2.14	0.47
1:CX:64:LEU:HD11	1:CX:67:ILE:HG13	1.95	0.47
1:DJ:32:ALA:HB3	1:DJ:53:LYS:HG2	1.95	0.47
1:DP:90:ILE:HD13	1:DQ:54:ILE:HG22	1.96	0.47
1:EE:101:GLU:O	1:EE:105:ASP:HB3	2.14	0.47
1:ER:39:LYS:HE2	1:ER:41:THR:HB	1.95	0.47
1:FD:39:LYS:HE2	1:FD:41:THR:HB	1.95	0.47
1:FO:57:VAL:HG22	1:FO:64:LEU:HA	1.95	0.47
1:GX:28:LYS:HB3	1:GX:59:PRO:HD3	1.96	0.47
1:AD:101:GLU:O	1:AD:105:ASP:HB3	2.15	0.47
1:AM:34:LYS:HB3	1:AM:51:GLU:HB3	1.95	0.47
1:AQ:61:THR:HA	1:CU:45:PRO:HB3	1.96	0.47
1:AT:74:ILE:HG21	1:AT:83:LYS:HD3	1.96	0.47
1:AU:54:ILE:HD13	1:GF:89:ILE:HG21	1.96	0.47
1:AW:28:LYS:HB2	1:AW:57:VAL:O	2.14	0.47
1:BF:61:THR:HA	1:DD:45:PRO:HB3	1.96	0.47
1:BG:103:VAL:O	1:BG:104:THR:OG1	2.24	0.47
1:BR:61:THR:HA	1:BW:45:PRO:HB3	1.96	0.47
1:CA:28:LYS:HB2	1:CA:57:VAL:O	2.14	0.47
1:CI:101:GLU:O	1:CI:105:ASP:HB3	2.14	0.47
1:CJ:36:LEU:HB3	1:CJ:49:LYS:HB2	1.95	0.47
1:DA:39:LYS:HD2	1:DA:41:THR:HB	1.96	0.47
1:DG:3:VAL:HA	1:DG:7:GLN:O	2.14	0.47
1:DG:90:ILE:HD13	1:DH:54:ILE:HG22	1.96	0.47
1:DN:51:GLU:HG3	1:DN:69:ASN:HD21	1.79	0.47
1:FF:47:MET:HB2	1:FF:49:LYS:NZ	2.27	0.47
1:FG:53:LYS:HZ3	1:FG:53:LYS:HB2	1.79	0.47
1:FP:58:ASP:OD2	1:FP:63:VAL:HG12	2.14	0.47
1:AD:50:SER:HB2	1:AE:102:LEU:HG	1.96	0.47
1:AG:90:ILE:HD13	1:AH:54:ILE:HG22	1.96	0.47
1:AH:61:THR:O	1:FO:40:ARG:NE	2.37	0.47
1:BO:74:ILE:HG21	1:BO:83:LYS:HD3	1.96	0.47
1:BT:34:LYS:HB3	1:BT:51:GLU:HB3	1.95	0.47
1:CD:17:ASP:OD1	1:CD:35:ARG:NE	2.33	0.47
1:CR:3:VAL:HA	1:CR:7:GLN:O	2.14	0.47
1:DM:39:LYS:HD2	1:DM:41:THR:HB	1.96	0.47
1:DW:51:GLU:HG3	1:DW:69:ASN:OD1	2.15	0.47
1:EH:47:MET:HB2	1:EH:49:LYS:NZ	2.27	0.47
1:EQ:49:LYS:HE3	1:EQ:73:SER:OG	2.14	0.47
1:GA:39:LYS:HD2	1:GA:41:THR:HB	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GM:39:LYS:HD2	1:GM:41:THR:HB	1.97	0.47
1:GS:50:SER:HB2	1:GT:102:LEU:HG	1.95	0.47
1:AA:47:MET:HB2	1:AA:49:LYS:NZ	2.27	0.47
1:AG:3:VAL:HA	1:AG:7:GLN:O	2.14	0.47
1:AQ:49:LYS:HE3	1:AQ:73:SER:OG	2.15	0.47
1:AS:90:ILE:HD13	1:AT:54:ILE:HG22	1.96	0.47
1:AV:39:LYS:HD2	1:AV:41:THR:HB	1.96	0.47
1:BE:47:MET:HB2	1:BE:49:LYS:NZ	2.27	0.47
1:BN:90:ILE:HD13	1:BO:54:ILE:HG22	1.96	0.47
1:CU:101:GLU:O	1:CU:105:ASP:HB3	2.15	0.47
1:DB:35:ARG:O	1:DB:36:LEU:HD12	2.14	0.47
1:DJ:99:TRP:CH2	1:DK:87:MET:HG2	2.50	0.47
1:DT:1:SER:O	1:DT:2:LYS:HD2	2.14	0.47
1:DY:12:TYR:HB2	1:DY:22:ARG:HG3	1.96	0.47
1:EH:39:LYS:HD2	1:EH:41:THR:HB	1.96	0.47
1:ET:90:ILE:HD13	1:EU:54:ILE:HG22	1.96	0.47
1:EY:103:VAL:O	1:EY:104:THR:OG1	2.21	0.47
1:FL:39:LYS:HD2	1:FL:41:THR:HB	1.97	0.47
1:GL:45:PRO:HB2	1:GL:76:ALA:HB3	1.97	0.47
1:AL:45:PRO:HB2	1:AL:76:ALA:HB3	1.95	0.47
1:AW:42:LYS:HG3	1:AW:44:SER:HB3	1.97	0.47
1:BC:74:ILE:HG21	1:BC:83:LYS:HD3	1.97	0.47
1:BE:40:ARG:NE	1:EI:61:THR:O	2.27	0.47
1:DN:45:PRO:HB2	1:DN:76:ALA:HB3	1.96	0.47
1:DT:45:PRO:HB2	1:DT:76:ALA:HB3	1.96	0.47
1:EM:51:GLU:OE2	1:EM:53:LYS:HD3	2.15	0.47
1:FX:49:LYS:HE3	1:FX:73:SER:OG	2.14	0.47
1:AB:42:LYS:HG3	1:AB:44:SER:HB3	1.97	0.47
1:AG:104:THR:HG22	1:AH:83:LYS:HB3	1.96	0.47
1:AK:42:LYS:HG3	1:AK:44:SER:HB3	1.97	0.47
1:AO:74:ILE:HG21	1:AO:83:LYS:HD3	1.95	0.47
1:AV:47:MET:HB2	1:AV:49:LYS:NZ	2.27	0.47
1:AY:108:LEU:HD13	1:AZ:19:VAL:HG23	1.96	0.47
1:BA:83:LYS:HE3	1:GC:104:THR:HA	1.96	0.47
1:BB:90:ILE:HD13	1:BC:54:ILE:HG22	1.96	0.47
1:BH:101:GLU:O	1:BH:105:ASP:HB3	2.14	0.47
1:BN:3:VAL:HA	1:BN:7:GLN:O	2.14	0.47
1:BU:16:LYS:HD2	1:GO:13:SER:HB2	1.97	0.47
1:BW:101:GLU:O	1:BW:105:ASP:HB3	2.14	0.47
1:CA:23:ASP:OD2	1:CA:26:ASN:ND2	2.48	0.47
1:CA:35:ARG:O	1:CA:36:LEU:HD12	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:49:LYS:HE3	1:CD:73:SER:OG	2.14	0.47
1:CM:17:ASP:OD1	1:CM:35:ARG:NE	2.34	0.47
1:CM:36:LEU:HB2	1:CM:49:LYS:HB2	1.97	0.47
1:CN:96:ASP:OD1	1:CN:97:GLY:N	2.48	0.47
1:CQ:45:PRO:HB2	1:CQ:76:ALA:HB3	1.95	0.47
1:CX:54:ILE:HD13	1:CY:89:ILE:HG21	1.97	0.47
1:DB:1:SER:O	1:DB:2:LYS:HD2	2.15	0.47
1:DJ:83:LYS:HE3	1:DK:104:THR:HA	1.97	0.47
1:DL:74:ILE:HG21	1:DL:83:LYS:HD3	1.95	0.47
1:DN:23:ASP:OD2	1:DN:26:ASN:ND2	2.48	0.47
1:DX:45:PRO:HB2	1:DX:76:ALA:HB3	1.96	0.47
1:EI:42:LYS:HG3	1:EI:44:SER:HB3	1.97	0.47
1:EI:45:PRO:HB2	1:EI:76:ALA:HB3	1.96	0.47
1:FH:28:LYS:HB3	1:FH:59:PRO:HD3	1.96	0.47
1:FH:103:VAL:O	1:FH:104:THR:OG1	2.22	0.47
1:FI:90:ILE:HD13	1:FJ:54:ILE:HG22	1.96	0.47
1:FN:45:PRO:HB2	1:FN:76:ALA:HB3	1.96	0.47
1:FO:45:PRO:HB2	1:FO:76:ALA:HB3	1.97	0.47
1:FT:28:LYS:HB3	1:FT:59:PRO:HD3	1.96	0.47
1:FX:45:PRO:HB2	1:FX:76:ALA:HB3	1.97	0.47
1:FY:39:LYS:HE2	1:FY:41:THR:HB	1.95	0.47
1:FY:58:ASP:OD2	1:FY:63:VAL:HG12	2.14	0.47
1:GA:54:ILE:HG22	1:GB:90:ILE:HD13	1.96	0.47
1:GC:45:PRO:HB2	1:GC:76:ALA:HB3	1.96	0.47
1:GH:15:GLU:HG3	1:GH:16:LYS:N	2.30	0.47
1:GJ:45:PRO:HB2	1:GJ:76:ALA:HB3	1.97	0.47
1:GK:49:LYS:HE3	1:GK:73:SER:OG	2.14	0.47
1:AG:40:ARG:NH1	1:AG:42:LYS:O	2.48	0.47
1:AM:83:LYS:HE3	1:AN:104:THR:HA	1.97	0.47
1:CC:51:GLU:OE2	1:CC:69:ASN:ND2	2.47	0.47
1:CM:49:LYS:HE3	1:CM:73:SER:OG	2.14	0.47
1:CX:51:GLU:OE2	1:CX:69:ASN:ND2	2.47	0.47
1:DJ:45:PRO:HB2	1:DJ:76:ALA:HB3	1.96	0.47
1:DN:42:LYS:HG3	1:DN:44:SER:HB3	1.97	0.47
1:DP:3:VAL:HA	1:DP:7:GLN:O	2.14	0.47
1:EB:32:ALA:HB3	1:EB:53:LYS:HG2	1.96	0.47
1:FL:54:ILE:HG22	1:FM:90:ILE:HD13	1.96	0.47
1:FV:61:THR:O	1:FX:40:ARG:NE	2.37	0.47
1:GD:22:ARG:HG2	1:GD:30:THR:HG23	1.97	0.47
1:GD:50:SER:HB2	1:GE:102:LEU:HG	1.95	0.47
1:GJ:80:ALA:O	1:GJ:84:THR:OG1	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GP:90:ILE:HD13	1:GQ:54:ILE:HG22	1.96	0.47
1:GQ:15:GLU:HG3	1:GQ:16:LYS:N	2.30	0.47
1:BE:12:TYR:HB2	1:BE:22:ARG:HG3	1.96	0.47
1:BI:36:LEU:HB3	1:BI:49:LYS:HB2	1.96	0.47
1:CD:36:LEU:HB2	1:CD:49:LYS:HB2	1.97	0.47
1:CJ:45:PRO:HB2	1:CJ:76:ALA:HB3	1.97	0.47
1:CL:54:ILE:HD13	1:CM:89:ILE:HG21	1.97	0.47
1:CY:23:ASP:OD2	1:CY:26:ASN:ND2	2.48	0.47
1:CY:36:LEU:HB2	1:CY:49:LYS:HB2	1.97	0.47
1:CY:49:LYS:HE3	1:CY:73:SER:OG	2.14	0.47
1:DN:35:ARG:O	1:DN:36:LEU:HD12	2.14	0.47
1:DS:50:SER:HB2	1:DT:102:LEU:HG	1.96	0.47
1:DW:42:LYS:HG3	1:DW:44:SER:HB3	1.97	0.47
1:ER:58:ASP:OD2	1:ER:63:VAL:HG12	2.15	0.47
1:FD:58:ASP:OD2	1:FD:63:VAL:HG12	2.15	0.47
1:FE:45:PRO:HB2	1:FE:76:ALA:HB3	1.97	0.47
1:FS:23:ASP:OD2	1:FS:26:ASN:ND2	2.48	0.47
1:GA:90:ILE:HD13	1:GB:54:ILE:HG22	1.97	0.47
1:GG:3:VAL:HA	1:GG:7:GLN:O	2.14	0.47
1:GG:90:ILE:HD13	1:GH:54:ILE:HG22	1.96	0.47
1:GM:90:ILE:HD13	1:GN:54:ILE:HG22	1.97	0.47
1:GO:45:PRO:HB2	1:GO:76:ALA:HB3	1.96	0.47
1:GP:3:VAL:HA	1:GP:7:GLN:O	2.14	0.47
1:AB:51:GLU:HG3	1:AB:69:ASN:OD1	2.15	0.47
1:AE:45:PRO:HB2	1:AE:76:ALA:HB3	1.97	0.47
1:AM:99:TRP:CH2	1:AN:87:MET:HG2	2.50	0.47
1:AP:12:TYR:HB2	1:AP:22:ARG:HG3	1.96	0.47
1:BG:68:VAL:HG11	1:GX:90:ILE:HG21	1.97	0.47
1:CC:3:VAL:HG12	1:CC:8:THR:HG23	1.95	0.47
1:CN:32:ALA:HB3	1:CN:53:LYS:HG3	1.97	0.47
1:CX:12:TYR:HB2	1:CX:22:ARG:HG3	1.96	0.47
1:CY:17:ASP:OD1	1:CY:35:ARG:NE	2.34	0.47
1:DG:104:THR:HG22	1:DH:83:LYS:HB3	1.96	0.47
1:DO:45:PRO:HB2	1:DO:76:ALA:HB3	1.97	0.47
1:DQ:74:ILE:HG21	1:DQ:83:LYS:HD3	1.97	0.47
1:DT:36:LEU:HB3	1:DT:49:LYS:HB2	1.97	0.47
1:ED:45:PRO:HB2	1:ED:76:ALA:HB3	1.97	0.47
1:EH:110:LEU:HD13	1:FQ:11:ILE:HG22	1.97	0.47
1:EM:32:ALA:HB3	1:EM:53:LYS:HG3	1.97	0.47
1:EM:68:VAL:HG11	1:FT:90:ILE:HG21	1.97	0.47
1:EY:28:LYS:HB3	1:EY:59:PRO:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GO:103:VAL:C	1:GO:104:THR:HG1	2.14	0.47
1:AR:68:VAL:HG11	1:EA:90:ILE:HG21	1.97	0.46
1:AV:64:LEU:HD11	1:AV:67:ILE:HG13	1.96	0.46
1:AW:51:GLU:HG3	1:AW:69:ASN:OD1	2.15	0.46
1:BG:51:GLU:OE2	1:BG:53:LYS:HD3	2.14	0.46
1:BS:32:ALA:HB3	1:BS:53:LYS:HG3	1.97	0.46
1:BV:83:LYS:HE3	1:GO:104:THR:HA	1.96	0.46
1:CE:32:ALA:HB3	1:CE:53:LYS:HG3	1.97	0.46
1:DV:32:ALA:HB3	1:DV:53:LYS:HG2	1.96	0.46
1:EA:96:ASP:OD1	1:EA:97:GLY:N	2.48	0.46
1:EB:108:LEU:HD13	1:EC:19:VAL:HG23	1.98	0.46
1:EI:53:LYS:HB3	1:EI:69:ASN:OD1	2.15	0.46
1:EM:90:ILE:HG21	1:FT:68:VAL:HG11	1.97	0.46
1:EX:23:ASP:OD2	1:EX:26:ASN:ND2	2.48	0.46
1:GH:26:ASN:HB2	1:GH:28:LYS:HD2	1.97	0.46
1:GN:34:LYS:HZ1	1:GN:36:LEU:HD13	1.79	0.46
1:GS:22:ARG:HG2	1:GS:30:THR:HG23	1.98	0.46
1:AA:110:LEU:HD13	1:ES:11:ILE:HG22	1.96	0.46
1:AD:47:MET:HB2	1:AD:49:LYS:NZ	2.29	0.46
1:AR:32:ALA:HB3	1:AR:53:LYS:HG3	1.97	0.46
1:BT:99:TRP:CH2	1:BU:87:MET:HG2	2.50	0.46
1:BZ:39:LYS:HD2	1:BZ:41:THR:HB	1.96	0.46
1:CA:51:GLU:HG3	1:CA:69:ASN:HD21	1.79	0.46
1:CC:47:MET:HB2	1:CC:49:LYS:NZ	2.26	0.46
1:CC:54:ILE:HD13	1:CD:89:ILE:HG21	1.97	0.46
1:CF:32:ALA:HB3	1:CF:53:LYS:HG2	1.96	0.46
1:CR:104:THR:HG22	1:CS:83:LYS:HB3	1.96	0.46
1:CU:50:SER:HB2	1:CV:102:LEU:HG	1.96	0.46
1:CZ:32:ALA:HB3	1:CZ:53:LYS:HG3	1.97	0.46
1:DB:53:LYS:HB3	1:DB:69:ASN:OD1	2.15	0.46
1:DG:34:LYS:HB3	1:DG:51:GLU:HB3	1.97	0.46
1:DM:1:SER:OG	1:DN:96:ASP:OD2	2.27	0.46
1:EF:45:PRO:HB2	1:EF:76:ALA:HB3	1.97	0.46
1:EM:54:ILE:HD13	1:FT:89:ILE:HG21	1.97	0.46
1:EN:3:VAL:HA	1:EN:7:GLN:O	2.16	0.46
1:EU:26:ASN:HB2	1:EU:28:LYS:HD2	1.97	0.46
1:FC:80:ALA:O	1:FC:84:THR:OG1	2.30	0.46
1:FH:26:ASN:CG	1:FH:28:LYS:HG2	2.36	0.46
1:FR:2:LYS:HD3	1:FR:2:LYS:HA	1.85	0.46
1:GW:23:ASP:OD2	1:GW:26:ASN:ND2	2.48	0.46
1:BA:45:PRO:HB2	1:BA:76:ALA:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:102:LEU:HG	1:GC:50:SER:HB2	1.97	0.46
1:BG:32:ALA:HB3	1:BG:53:LYS:HG3	1.96	0.46
1:BZ:110:LEU:HD13	1:GL:11:ILE:HG22	1.97	0.46
1:CC:54:ILE:HG22	1:CD:90:ILE:HD13	1.98	0.46
1:CF:45:PRO:HB2	1:CF:76:ALA:HB3	1.97	0.46
1:CG:49:LYS:HE3	1:CG:73:SER:OG	2.16	0.46
1:CL:54:ILE:HG22	1:CM:90:ILE:HD13	1.98	0.46
1:CR:34:LYS:HB3	1:CR:51:GLU:HB3	1.97	0.46
1:DN:53:LYS:HB3	1:DN:69:ASN:OD1	2.15	0.46
1:DP:34:LYS:HB3	1:DP:51:GLU:HB3	1.97	0.46
1:DV:1:SER:OG	1:DW:96:ASP:OD2	2.27	0.46
1:EF:36:LEU:HB3	1:EF:49:LYS:HB2	1.96	0.46
1:EU:15:GLU:HG3	1:EU:16:LYS:N	2.31	0.46
1:EX:64:LEU:HD11	1:EX:67:ILE:HG13	1.98	0.46
1:EZ:3:VAL:HA	1:EZ:7:GLN:O	2.16	0.46
1:FD:101:GLU:O	1:FD:105:ASP:HB2	2.16	0.46
1:FI:3:VAL:HA	1:FI:7:GLN:O	2.14	0.46
1:FV:15:GLU:HG3	1:FV:16:LYS:N	2.30	0.46
1:GU:15:GLU:HB3	1:GU:18:VAL:HB	1.97	0.46
1:AM:108:LEU:HD13	1:AN:19:VAL:HG23	1.96	0.46
1:BB:34:LYS:HB3	1:BB:51:GLU:HB3	1.97	0.46
1:BB:40:ARG:NH1	1:BB:42:LYS:O	2.48	0.46
1:CA:61:THR:O	1:CL:40:ARG:NE	2.27	0.46
1:CH:45:PRO:HB2	1:CH:76:ALA:HB3	1.97	0.46
1:CO:39:LYS:HD2	1:CO:41:THR:HB	1.96	0.46
1:DH:74:ILE:HG21	1:DH:83:LYS:HD3	1.97	0.46
1:DJ:18:VAL:HG22	1:DJ:34:LYS:HG3	1.97	0.46
1:DM:47:MET:HB2	1:DM:49:LYS:NZ	2.27	0.46
1:DY:74:ILE:HD13	1:DY:83:LYS:HG2	1.98	0.46
1:EB:83:LYS:HE3	1:EC:104:THR:HA	1.97	0.46
1:EK:54:ILE:HD13	1:EL:89:ILE:HG21	1.97	0.46
1:ET:3:VAL:HA	1:ET:7:GLN:O	2.14	0.46
1:EY:54:ILE:HD13	1:FH:89:ILE:HG21	1.98	0.46
1:FG:23:ASP:OD2	1:FG:26:ASN:ND2	2.48	0.46
1:GI:103:VAL:C	1:GI:104:THR:HG1	2.13	0.46
1:GK:58:ASP:OD2	1:GK:63:VAL:HG12	2.15	0.46
1:GW:64:LEU:HD11	1:GW:67:ILE:HG13	1.98	0.46
1:AK:1:SER:O	1:AK:2:LYS:HD2	2.15	0.46
1:AY:45:PRO:HB2	1:AY:76:ALA:HB3	1.97	0.46
1:BE:54:ILE:HG22	1:BF:90:ILE:HD13	1.98	0.46
1:BF:23:ASP:OD2	1:BF:26:ASN:ND2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:45:PRO:HB2	1:BI:76:ALA:HB3	1.96	0.46
1:BT:45:PRO:HB2	1:BT:76:ALA:HB3	1.97	0.46
1:CL:47:MET:HB2	1:CL:49:LYS:NZ	2.27	0.46
1:DY:54:ILE:HD13	1:DZ:89:ILE:HG21	1.97	0.46
1:EE:3:VAL:HA	1:EE:7:GLN:O	2.16	0.46
1:ES:45:PRO:HB2	1:ES:76:ALA:HB3	1.98	0.46
1:FC:45:PRO:HB2	1:FC:76:ALA:HB3	1.97	0.46
1:FM:42:LYS:HG3	1:FM:44:SER:HB3	1.97	0.46
1:GH:74:ILE:HD13	1:GH:83:LYS:HG3	1.97	0.46
1:GM:17:ASP:OD1	1:GM:35:ARG:NE	2.34	0.46
1:AD:3:VAL:HA	1:AD:7:GLN:O	2.16	0.46
1:AQ:23:ASP:OD2	1:AQ:26:ASN:ND2	2.49	0.46
1:AY:83:LYS:HE3	1:AZ:104:THR:HA	1.98	0.46
1:BG:96:ASP:OD1	1:BG:97:GLY:N	2.48	0.46
1:BN:40:ARG:NH1	1:BN:42:LYS:O	2.49	0.46
1:BQ:54:ILE:HD13	1:BR:89:ILE:HG21	1.97	0.46
1:BV:102:LEU:HG	1:GO:50:SER:HB2	1.97	0.46
1:CP:1:SER:O	1:CP:2:LYS:HD2	2.15	0.46
1:CU:3:VAL:HA	1:CU:7:GLN:O	2.16	0.46
1:DE:45:PRO:HB2	1:DE:76:ALA:HB3	1.97	0.46
1:DP:40:ARG:NH1	1:DP:42:LYS:O	2.49	0.46
1:DY:54:ILE:HG22	1:DZ:90:ILE:HD13	1.98	0.46
1:EG:89:ILE:HG21	1:FW:54:ILE:HD13	1.98	0.46
1:EG:106:GLN:HB3	1:FW:35:ARG:HD3	1.96	0.46
1:EI:23:ASP:OD2	1:EI:26:ASN:ND2	2.48	0.46
1:FF:90:ILE:HD13	1:FG:54:ILE:HG22	1.98	0.46
1:FO:80:ALA:O	1:FO:84:THR:OG1	2.29	0.46
1:GA:17:ASP:OD1	1:GA:35:ARG:NE	2.35	0.46
1:GJ:34:LYS:HB3	1:GJ:51:GLU:HB3	1.98	0.46
1:GR:103:VAL:C	1:GR:104:THR:HG1	2.13	0.46
1:GV:108:LEU:HD13	1:GW:19:VAL:HG23	1.98	0.46
1:AF:45:PRO:HB2	1:AF:76:ALA:HB3	1.98	0.46
1:AK:53:LYS:HB3	1:AK:69:ASN:OD1	2.15	0.46
1:BQ:12:TYR:HB2	1:BQ:22:ARG:HG3	1.96	0.46
1:BS:87:MET:HE1	1:CZ:100:THR:HG23	1.98	0.46
1:BX:45:PRO:HB2	1:BX:76:ALA:HB3	1.97	0.46
1:CA:53:LYS:HB3	1:CA:69:ASN:OD1	2.15	0.46
1:CE:90:ILE:HG21	1:CN:68:VAL:HG11	1.98	0.46
1:CI:54:ILE:HG22	1:CJ:90:ILE:HD13	1.98	0.46
1:DS:3:VAL:HA	1:DS:7:GLN:O	2.16	0.46
1:DZ:17:ASP:OD1	1:DZ:35:ARG:NE	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:32:ALA:HB3	1:EA:53:LYS:HG3	1.97	0.46
1:EJ:45:PRO:HB2	1:EJ:76:ALA:HB3	1.98	0.46
1:EK:12:TYR:HB2	1:EK:22:ARG:HG3	1.96	0.46
1:EK:108:LEU:HD13	1:EL:19:VAL:HG23	1.97	0.46
1:EQ:45:PRO:HB2	1:EQ:76:ALA:HB3	1.97	0.46
1:FK:74:ILE:HG21	1:FK:83:LYS:HD3	1.97	0.46
1:FQ:45:PRO:HB2	1:FQ:76:ALA:HB3	1.97	0.46
1:GB:42:LYS:HG3	1:GB:44:SER:HB3	1.98	0.46
1:GU:15:GLU:HG3	1:GU:16:LYS:N	2.30	0.46
1:AP:54:ILE:HG22	1:AQ:90:ILE:HD13	1.98	0.46
1:AU:35:ARG:HD3	1:GF:106:GLN:HB3	1.97	0.46
1:AZ:16:LYS:HD2	1:GC:13:SER:HB2	1.97	0.46
1:BK:45:PRO:HB2	1:BK:76:ALA:HB3	1.97	0.46
1:BS:90:ILE:HG21	1:CZ:68:VAL:HG11	1.98	0.46
1:BT:108:LEU:HD13	1:BU:19:VAL:HG23	1.96	0.46
1:CE:68:VAL:HG11	1:CN:90:ILE:HG21	1.98	0.46
1:CF:108:LEU:HD13	1:CG:19:VAL:HG23	1.98	0.46
1:CI:3:VAL:HA	1:CI:7:GLN:O	2.16	0.46
1:CX:108:LEU:HD13	1:CY:19:VAL:HG23	1.98	0.46
1:DD:3:VAL:HA	1:DD:7:GLN:O	2.16	0.46
1:DG:40:ARG:NH1	1:DG:42:LYS:O	2.48	0.46
1:DJ:108:LEU:HD13	1:DK:19:VAL:HG23	1.97	0.46
1:EC:61:THR:HA	1:EH:45:PRO:HB3	1.98	0.46
1:EG:2:LYS:HD3	1:EG:2:LYS:HA	1.76	0.46
1:EY:90:ILE:HG21	1:FH:68:VAL:HG11	1.96	0.46
1:FB:45:PRO:HB2	1:FB:76:ALA:HB3	1.98	0.46
1:FB:106:GLN:HB3	1:FK:35:ARG:HD3	1.98	0.46
1:FD:16:LYS:HD2	1:FN:13:SER:HB2	1.97	0.46
1:FL:90:ILE:HD13	1:FM:54:ILE:HG22	1.98	0.46
1:FY:49:LYS:HE3	1:FY:73:SER:OG	2.16	0.46
1:GN:74:ILE:HG21	1:GN:83:LYS:HD3	1.97	0.46
1:AC:51:GLU:OE2	1:AC:53:LYS:HD3	2.16	0.46
1:AF:89:ILE:HG21	1:EV:54:ILE:HD13	1.98	0.46
1:AH:74:ILE:HG21	1:AH:83:LYS:HD3	1.97	0.46
1:AM:45:PRO:HB2	1:AM:76:ALA:HB3	1.97	0.46
1:AY:99:TRP:CH2	1:AZ:87:MET:HG2	2.50	0.46
1:BF:36:LEU:HB2	1:BF:49:LYS:HB2	1.97	0.46
1:BR:23:ASP:OD2	1:BR:26:ASN:ND2	2.48	0.46
1:CK:15:GLU:HG3	1:CK:16:LYS:N	2.29	0.46
1:CK:45:PRO:HB2	1:CK:76:ALA:HB3	1.98	0.46
1:CP:53:LYS:HB3	1:CP:69:ASN:OD1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:45:PRO:HB2	1:CV:76:ALA:HB3	1.97	0.46
1:CW:45:PRO:HB2	1:CW:76:ALA:HB3	1.98	0.46
1:DF:45:PRO:HB2	1:DF:76:ALA:HB3	1.98	0.46
1:DJ:34:LYS:HB3	1:DJ:51:GLU:HB3	1.97	0.46
1:DY:108:LEU:HD13	1:DZ:19:VAL:HG23	1.98	0.46
1:EB:50:SER:HB2	1:EC:102:LEU:HG	1.98	0.46
1:EM:26:ASN:CG	1:EM:28:LYS:HG2	2.36	0.46
1:ES:103:VAL:C	1:ES:104:THR:HG1	2.15	0.46
1:EY:26:ASN:CG	1:EY:28:LYS:HG2	2.36	0.46
1:FB:13:SER:HB2	1:FJ:16:LYS:HD2	1.98	0.46
1:FD:49:LYS:HE3	1:FD:73:SER:OG	2.16	0.46
1:FR:108:LEU:HD13	1:FS:19:VAL:HG23	1.98	0.46
1:GA:3:VAL:HA	1:GA:7:GLN:O	2.16	0.46
1:GB:74:ILE:HG21	1:GB:83:LYS:HD3	1.97	0.46
1:GK:101:GLU:O	1:GK:105:ASP:HB2	2.16	0.46
1:AC:45:PRO:HB2	1:AC:76:ALA:HB3	1.97	0.46
1:AN:49:LYS:HE3	1:AN:73:SER:OG	2.16	0.46
1:AU:2:LYS:HG3	1:AU:3:VAL:H	1.81	0.46
1:AX:45:PRO:HB2	1:AX:76:ALA:HB3	1.98	0.46
1:BD:2:LYS:HG3	1:BD:3:VAL:H	1.81	0.46
1:BJ:36:LEU:HD12	1:BJ:36:LEU:HA	1.84	0.46
1:BS:96:ASP:OD1	1:BS:97:GLY:N	2.48	0.46
1:BT:54:ILE:HG22	1:BU:90:ILE:HD13	1.98	0.46
1:CC:74:ILE:HD13	1:CC:83:LYS:HG2	1.98	0.46
1:CE:96:ASP:OD1	1:CE:97:GLY:N	2.49	0.46
1:EA:26:ASN:CG	1:EA:28:LYS:HG2	2.36	0.46
1:EE:2:LYS:HD3	1:EE:2:LYS:HA	1.88	0.46
1:EP:2:LYS:HD3	1:EP:2:LYS:HA	1.77	0.46
1:ER:101:GLU:O	1:ER:105:ASP:HB2	2.16	0.46
1:EU:34:LYS:NZ	1:EU:36:LEU:HD13	2.31	0.46
1:FK:2:LYS:HG3	1:FK:3:VAL:H	1.81	0.46
1:FY:101:GLU:O	1:FY:105:ASP:HB2	2.16	0.46
1:GN:97:GLY:O	1:GN:101:GLU:HG3	2.16	0.46
1:GW:17:ASP:OD1	1:GW:35:ARG:NE	2.36	0.46
1:AT:15:GLU:HG3	1:AT:16:LYS:N	2.31	0.45
1:AY:50:SER:HB2	1:AZ:102:LEU:HG	1.98	0.45
1:BD:35:ARG:HD3	1:GU:106:GLN:HB3	1.97	0.45
1:BO:15:GLU:HG3	1:BO:16:LYS:N	2.31	0.45
1:BQ:34:LYS:HB3	1:BQ:51:GLU:HB3	1.98	0.45
1:BS:45:PRO:HB2	1:BS:76:ALA:HB3	1.98	0.45
1:CC:40:ARG:NE	1:CP:61:THR:O	2.27	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:26:ASN:HB2	1:CS:28:LYS:HD2	1.98	0.45
1:DB:42:LYS:HG3	1:DB:44:SER:HB3	1.97	0.45
1:DD:47:MET:HB2	1:DD:49:LYS:HZ1	1.81	0.45
1:DD:54:ILE:HG22	1:DE:90:ILE:HD13	1.98	0.45
1:DU:45:PRO:HB2	1:DU:76:ALA:HB3	1.98	0.45
1:DZ:36:LEU:HB2	1:DZ:49:LYS:HB2	1.97	0.45
1:EB:45:PRO:HB2	1:EB:76:ALA:HB3	1.97	0.45
1:EC:49:LYS:HE3	1:EC:73:SER:OG	2.16	0.45
1:ET:87:MET:HE1	1:EU:100:THR:HG23	1.99	0.45
1:EV:2:LYS:HG3	1:EV:3:VAL:H	1.81	0.45
1:FI:87:MET:HE1	1:FJ:100:THR:HG23	1.99	0.45
1:FK:80:ALA:O	1:FK:84:THR:OG1	2.31	0.45
1:FX:80:ALA:O	1:FX:84:THR:OG1	2.29	0.45
1:GD:3:VAL:HA	1:GD:7:GLN:O	2.16	0.45
1:GP:47:MET:HB2	1:GP:49:LYS:NZ	2.32	0.45
1:GX:45:PRO:HB2	1:GX:76:ALA:HB3	1.98	0.45
1:AT:56:ARG:HG2	1:AT:65:ILE:HD12	1.99	0.45
1:BC:26:ASN:HB2	1:BC:28:LYS:HD2	1.97	0.45
1:BL:61:THR:HA	1:BZ:45:PRO:HB3	1.98	0.45
1:BP:2:LYS:HG3	1:BP:3:VAL:H	1.81	0.45
1:BQ:108:LEU:HD13	1:BR:19:VAL:HG23	1.98	0.45
1:BY:45:PRO:HB2	1:BY:76:ALA:HB3	1.98	0.45
1:CG:61:THR:HA	1:DM:45:PRO:HB3	1.98	0.45
1:CL:74:ILE:HD13	1:CL:83:LYS:HG2	1.98	0.45
1:CP:42:LYS:HG3	1:CP:44:SER:HB3	1.97	0.45
1:CU:54:ILE:HG22	1:CV:90:ILE:HD13	1.98	0.45
1:DJ:49:LYS:HE3	1:DJ:73:SER:OG	2.16	0.45
1:DQ:15:GLU:HG3	1:DQ:16:LYS:N	2.31	0.45
1:EL:36:LEU:HB2	1:EL:49:LYS:HB2	1.97	0.45
1:ER:49:LYS:HE3	1:ER:73:SER:OG	2.16	0.45
1:EW:90:ILE:HD13	1:EX:54:ILE:HG22	1.99	0.45
1:FH:45:PRO:HB2	1:FH:76:ALA:HB3	1.98	0.45
1:FL:3:VAL:HA	1:FL:7:GLN:O	2.16	0.45
1:FM:74:ILE:HG21	1:FM:83:LYS:HD3	1.98	0.45
1:GF:45:PRO:HB2	1:GF:76:ALA:HB3	1.98	0.45
1:GI:26:ASN:ND2	1:GI:29:ASP:OD2	2.45	0.45
1:GS:3:VAL:HA	1:GS:7:GLN:O	2.15	0.45
1:AB:34:LYS:HZ1	1:AB:36:LEU:HD13	1.80	0.45
1:BE:74:ILE:HD13	1:BE:83:LYS:HG2	1.98	0.45
1:BH:3:VAL:HA	1:BH:7:GLN:O	2.16	0.45
1:BJ:45:PRO:HB2	1:BJ:76:ALA:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:45:PRO:HB2	1:BM:76:ALA:HB3	1.97	0.45
1:BR:36:LEU:HB2	1:BR:49:LYS:HB2	1.97	0.45
1:CA:42:LYS:HG3	1:CA:44:SER:HB3	1.97	0.45
1:CH:11:ILE:HG22	1:CO:110:LEU:HD13	1.99	0.45
1:CS:74:ILE:HG21	1:CS:83:LYS:HD3	1.97	0.45
1:DV:2:LYS:HD3	1:DV:2:LYS:HA	1.87	0.45
1:DV:3:VAL:HA	1:DV:7:GLN:O	2.17	0.45
1:EK:34:LYS:HB3	1:EK:51:GLU:HB3	1.99	0.45
1:EN:2:LYS:HD3	1:EN:2:LYS:HA	1.88	0.45
1:EP:45:PRO:HB2	1:EP:76:ALA:HB3	1.98	0.45
1:ET:47:MET:HB2	1:ET:49:LYS:NZ	2.32	0.45
1:EV:80:ALA:O	1:EV:84:THR:OG1	2.32	0.45
1:FO:34:LYS:HB3	1:FO:51:GLU:HB3	1.98	0.45
1:FP:101:GLU:O	1:FP:105:ASP:HB2	2.16	0.45
1:GG:32:ALA:HB3	1:GG:53:LYS:HG2	1.99	0.45
1:GU:45:PRO:HB2	1:GU:76:ALA:HB3	1.98	0.45
1:GX:26:ASN:CG	1:GX:28:LYS:HG2	2.36	0.45
1:AH:15:GLU:HG3	1:AH:16:LYS:N	2.31	0.45
1:AM:50:SER:HB2	1:AN:102:LEU:HG	1.98	0.45
1:AP:74:ILE:HD13	1:AP:83:LYS:HG2	1.98	0.45
1:AR:45:PRO:HB2	1:AR:76:ALA:HB3	1.98	0.45
1:AT:36:LEU:HB2	1:AT:49:LYS:HB2	1.98	0.45
1:BA:26:ASN:CG	1:BA:28:LYS:HG2	2.37	0.45
1:BC:18:VAL:HG22	1:BC:34:LYS:HG3	1.99	0.45
1:BK:83:LYS:HE3	1:BL:104:THR:HA	1.97	0.45
1:BV:45:PRO:HB2	1:BV:76:ALA:HB3	1.97	0.45
1:CC:108:LEU:HD13	1:CD:19:VAL:HG23	1.98	0.45
1:CL:108:LEU:HD13	1:CM:19:VAL:HG23	1.98	0.45
1:CM:23:ASP:OD2	1:CM:26:ASN:ND2	2.48	0.45
1:CZ:26:ASN:CG	1:CZ:28:LYS:HG2	2.36	0.45
1:DK:49:LYS:HE3	1:DK:73:SER:OG	2.16	0.45
1:DL:26:ASN:CG	1:DL:28:LYS:HG2	2.37	0.45
1:DM:3:VAL:HA	1:DM:7:GLN:O	2.17	0.45
1:DR:2:LYS:HG3	1:DR:3:VAL:H	1.81	0.45
1:DY:34:LYS:HB3	1:DY:51:GLU:HB3	1.99	0.45
1:DZ:23:ASP:OD2	1:DZ:26:ASN:ND2	2.49	0.45
1:EY:45:PRO:HB2	1:EY:76:ALA:HB3	1.99	0.45
1:FI:47:MET:HB2	1:FI:49:LYS:NZ	2.32	0.45
1:GO:57:VAL:HG22	1:GO:64:LEU:HA	1.99	0.45
1:AA:3:VAL:HA	1:AA:7:GLN:O	2.16	0.45
1:AO:26:ASN:CG	1:AO:28:LYS:HG2	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:45:PRO:HB2	1:AO:76:ALA:HB3	1.98	0.45
1:AT:26:ASN:HB2	1:AT:28:LYS:HD2	1.97	0.45
1:BC:15:GLU:HG3	1:BC:16:LYS:N	2.31	0.45
1:BC:56:ARG:HG2	1:BC:65:ILE:HD12	1.99	0.45
1:BH:54:ILE:HG22	1:BI:90:ILE:HD13	1.98	0.45
1:BQ:54:ILE:HG22	1:BR:90:ILE:HD13	1.98	0.45
1:BT:19:VAL:HG23	1:BU:108:LEU:HD13	1.99	0.45
1:BV:26:ASN:CG	1:BV:28:LYS:HG2	2.37	0.45
1:BW:54:ILE:HG22	1:BX:90:ILE:HD13	1.98	0.45
1:CF:83:LYS:HE3	1:CG:104:THR:HA	1.97	0.45
1:CL:34:LYS:HB3	1:CL:51:GLU:HB3	1.98	0.45
1:CN:45:PRO:HB2	1:CN:76:ALA:HB3	1.98	0.45
1:CZ:96:ASP:OD1	1:CZ:97:GLY:N	2.49	0.45
1:DL:45:PRO:HB2	1:DL:76:ALA:HB3	1.98	0.45
1:DM:2:LYS:HD3	1:DM:2:LYS:HA	1.87	0.45
1:DW:34:LYS:HZ3	1:DW:36:LEU:HD13	1.82	0.45
1:EE:50:SER:HB2	1:EF:102:LEU:HG	1.99	0.45
1:EF:39:LYS:HE2	1:EF:41:THR:HB	1.99	0.45
1:EG:45:PRO:HB2	1:EG:76:ALA:HB3	1.98	0.45
1:EM:45:PRO:HB2	1:EM:76:ALA:HB3	1.99	0.45
1:EQ:87:MET:HG2	1:ER:99:TRP:CH2	2.51	0.45
1:EU:74:ILE:HD13	1:EU:83:LYS:HG3	1.97	0.45
1:EX:17:ASP:OD1	1:EX:35:ARG:NE	2.36	0.45
1:EY:68:VAL:HG11	1:FH:90:ILE:HG21	1.97	0.45
1:FR:90:ILE:HD13	1:FS:54:ILE:HG22	1.98	0.45
1:FT:51:GLU:OE2	1:FT:53:LYS:HD3	2.16	0.45
1:GE:36:LEU:HD12	1:GE:36:LEU:HA	1.89	0.45
1:GN:23:ASP:OD2	1:GN:26:ASN:ND2	2.49	0.45
1:GN:42:LYS:HG3	1:GN:44:SER:HB3	1.98	0.45
1:GV:90:ILE:HD13	1:GW:54:ILE:HG22	1.98	0.45
1:GW:53:LYS:HB2	1:GW:53:LYS:HZ3	1.82	0.45
1:AN:61:THR:HA	1:DA:45:PRO:HB3	1.99	0.45
1:BB:74:ILE:HD13	1:BB:83:LYS:HG2	1.99	0.45
1:BK:54:ILE:HG22	1:BL:90:ILE:HD13	1.99	0.45
1:BM:26:ASN:CG	1:BM:28:LYS:HG2	2.37	0.45
1:BT:50:SER:HB2	1:BU:102:LEU:HG	1.98	0.45
1:BU:61:THR:HA	1:CO:45:PRO:HB3	1.99	0.45
1:CE:26:ASN:CG	1:CE:28:LYS:HG2	2.36	0.45
1:CH:26:ASN:CG	1:CH:28:LYS:HG2	2.37	0.45
1:CR:40:ARG:NH1	1:CR:42:LYS:O	2.49	0.45
1:DJ:50:SER:HB2	1:DK:102:LEU:HG	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DS:58:ASP:OD2	1:DS:63:VAL:HG12	2.16	0.45
1:EG:36:LEU:HD12	1:EG:36:LEU:HA	1.84	0.45
1:EK:54:ILE:HG22	1:EL:90:ILE:HD13	1.98	0.45
1:EL:23:ASP:OD2	1:EL:26:ASN:ND2	2.49	0.45
1:EM:89:ILE:HG21	1:FT:54:ILE:HD13	1.98	0.45
1:EN:22:ARG:HG2	1:EN:30:THR:HG23	1.97	0.45
1:EQ:99:TRP:CH2	1:ER:87:MET:HG2	2.52	0.45
1:EZ:22:ARG:HG2	1:EZ:30:THR:HG23	1.97	0.45
1:FG:80:ALA:HA	1:FG:83:LYS:HB2	1.99	0.45
1:FM:23:ASP:OD2	1:FM:26:ASN:ND2	2.50	0.45
1:FS:64:LEU:HD11	1:FS:67:ILE:HG13	1.98	0.45
1:FT:26:ASN:CG	1:FT:28:LYS:HG2	2.36	0.45
1:FV:34:LYS:NZ	1:FV:36:LEU:HD13	2.32	0.45
1:FW:74:ILE:HG21	1:FW:83:LYS:HD3	1.99	0.45
1:FZ:45:PRO:HB2	1:FZ:76:ALA:HB3	1.98	0.45
1:GB:23:ASP:OD2	1:GB:26:ASN:ND2	2.50	0.45
1:GE:11:ILE:HD11	1:GE:14:THR:OG1	2.17	0.45
1:GW:80:ALA:HA	1:GW:83:LYS:HB2	1.99	0.45
1:AB:58:ASP:HB2	1:AB:65:ILE:HD11	1.99	0.45
1:AJ:3:VAL:HA	1:AJ:7:GLN:O	2.17	0.45
1:AJ:45:PRO:HB3	1:AZ:61:THR:HA	1.99	0.45
1:AM:19:VAL:HG23	1:AN:108:LEU:HD13	1.99	0.45
1:AR:96:ASP:OD1	1:AR:97:GLY:N	2.49	0.45
1:AS:74:ILE:HD13	1:AS:83:LYS:HG2	1.99	0.45
1:AZ:49:LYS:HE3	1:AZ:73:SER:OG	2.16	0.45
1:BI:39:LYS:HE2	1:BI:41:THR:HB	1.99	0.45
1:BK:50:SER:HB2	1:BL:102:LEU:HG	1.98	0.45
1:BT:83:LYS:HE3	1:BU:104:THR:HA	1.97	0.45
1:BW:3:VAL:HA	1:BW:7:GLN:O	2.16	0.45
1:CD:23:ASP:OD2	1:CD:26:ASN:ND2	2.49	0.45
1:CL:3:VAL:HA	1:CL:7:GLN:O	2.17	0.45
1:DK:61:THR:HA	1:GM:45:PRO:HB3	1.99	0.45
1:DS:54:ILE:HG22	1:DT:90:ILE:HD13	1.99	0.45
1:DY:3:VAL:HA	1:DY:7:GLN:O	2.17	0.45
1:FJ:34:LYS:NZ	1:FJ:36:LEU:HD13	2.32	0.45
1:FO:3:VAL:HA	1:FO:7:GLN:O	2.17	0.45
1:AI:35:ARG:HD3	1:EP:106:GLN:HB3	1.98	0.45
1:AR:90:ILE:HG21	1:EA:68:VAL:HG11	1.97	0.45
1:AY:19:VAL:HG23	1:AZ:108:LEU:HD13	1.99	0.45
1:BG:45:PRO:HB2	1:BG:76:ALA:HB3	1.99	0.45
1:BJ:89:ILE:HG21	1:GR:54:ILE:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:15:GLU:HG2	1:BL:16:LYS:N	2.32	0.45
1:BO:26:ASN:HB2	1:BO:28:LYS:HD2	1.97	0.45
1:BQ:74:ILE:HD13	1:BQ:83:LYS:HG2	1.98	0.45
1:BS:68:VAL:HG11	1:CZ:90:ILE:HG21	1.98	0.45
1:BY:36:LEU:HD12	1:BY:36:LEU:HA	1.84	0.45
1:CC:34:LYS:HB3	1:CC:51:GLU:HB3	1.99	0.45
1:CS:15:GLU:HG3	1:CS:16:LYS:N	2.31	0.45
1:DD:50:SER:HB2	1:DE:102:LEU:HG	1.99	0.45
1:DI:2:LYS:HG3	1:DI:3:VAL:H	1.81	0.45
1:DO:74:ILE:HG21	1:DO:83:LYS:HD3	1.99	0.45
1:DQ:26:ASN:HB2	1:DQ:28:LYS:HD2	1.98	0.45
1:EF:57:VAL:HG12	1:EF:64:LEU:HA	1.99	0.45
1:EK:74:ILE:HD13	1:EK:83:LYS:HG2	1.98	0.45
1:EV:26:ASN:ND2	1:EV:29:ASP:OD2	2.45	0.45
1:GD:2:LYS:HD3	1:GD:2:LYS:HA	1.88	0.45
1:GE:26:ASN:HB2	1:GE:28:LYS:HD2	1.99	0.45
1:GH:34:LYS:NZ	1:GH:36:LEU:HD13	2.31	0.45
1:GI:74:ILE:HG21	1:GI:83:LYS:HD3	1.99	0.45
1:AJ:47:MET:HB2	1:AJ:49:LYS:NZ	2.30	0.45
1:BE:108:LEU:HD13	1:BF:19:VAL:HG23	1.98	0.45
1:BI:57:VAL:HG12	1:BI:64:LEU:HA	1.99	0.45
1:BO:56:ARG:HG2	1:BO:65:ILE:HD12	1.99	0.45
1:CO:3:VAL:HA	1:CO:7:GLN:O	2.17	0.45
1:ED:26:ASN:CG	1:ED:28:LYS:HG2	2.37	0.45
1:EL:17:ASP:OD1	1:EL:35:ARG:NE	2.34	0.45
1:EW:108:LEU:HD13	1:EX:19:VAL:HG23	1.98	0.45
1:FA:11:ILE:HD11	1:FA:14:THR:OG1	2.17	0.45
1:FF:108:LEU:HD13	1:FG:19:VAL:HG23	1.98	0.45
1:FU:47:MET:HB2	1:FU:49:LYS:NZ	2.32	0.45
1:GB:97:GLY:O	1:GB:101:GLU:HG3	2.16	0.45
1:GE:45:PRO:HB2	1:GE:76:ALA:HB3	1.99	0.45
1:GP:87:MET:HE1	1:GQ:100:THR:HA	1.98	0.45
1:GR:26:ASN:ND2	1:GR:29:ASP:OD2	2.45	0.45
1:GT:26:ASN:HB2	1:GT:28:LYS:HD2	1.99	0.45
1:GT:45:PRO:HB2	1:GT:76:ALA:HB3	1.99	0.45
1:AO:11:ILE:HG22	1:DV:110:LEU:HD13	1.99	0.45
1:AP:40:ARG:NE	1:AW:61:THR:O	2.27	0.45
1:AV:3:VAL:HA	1:AV:7:GLN:O	2.16	0.45
1:BG:90:ILE:HG21	1:GX:68:VAL:HG11	1.97	0.45
1:BK:108:LEU:HD13	1:BL:19:VAL:HG23	1.98	0.45
1:BN:108:LEU:HD13	1:BO:19:VAL:HG23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BU:49:LYS:HE3	1:BU:73:SER:OG	2.16	0.45
1:BZ:3:VAL:HA	1:BZ:7:GLN:O	2.17	0.45
1:CC:3:VAL:HA	1:CC:7:GLN:O	2.17	0.45
1:CE:45:PRO:HB2	1:CE:76:ALA:HB3	1.99	0.45
1:CF:50:SER:HB2	1:CG:102:LEU:HG	1.98	0.45
1:CT:2:LYS:HG3	1:CT:3:VAL:H	1.81	0.45
1:CZ:28:LYS:HB3	1:CZ:59:PRO:HD3	1.99	0.45
1:DD:35:ARG:NH1	1:DE:106:GLN:O	2.39	0.45
1:DH:15:GLU:HG3	1:DH:16:LYS:N	2.31	0.45
1:DQ:56:ARG:HG2	1:DQ:65:ILE:HD12	1.99	0.45
1:DW:61:THR:O	1:EK:40:ARG:NE	2.27	0.45
1:EG:51:GLU:OE2	1:EG:53:LYS:HD3	2.17	0.45
1:EH:3:VAL:HA	1:EH:7:GLN:O	2.17	0.45
1:EX:80:ALA:HA	1:EX:83:LYS:HB2	1.99	0.45
1:FC:99:TRP:CH2	1:FD:87:MET:HG2	2.52	0.45
1:FE:26:ASN:CG	1:FE:28:LYS:HG2	2.38	0.45
1:FX:99:TRP:CH2	1:FY:87:MET:HG2	2.52	0.45
1:GF:36:LEU:HD12	1:GF:36:LEU:HA	1.88	0.45
1:GM:3:VAL:HA	1:GM:7:GLN:O	2.16	0.45
1:GQ:97:GLY:O	1:GQ:101:GLU:HG3	2.18	0.45
1:GR:74:ILE:HG21	1:GR:83:LYS:HD3	1.99	0.45
1:GS:2:LYS:HD3	1:GS:2:LYS:HA	1.88	0.45
1:AD:35:ARG:NH1	1:AE:106:GLN:O	2.39	0.44
1:AF:51:GLU:OE2	1:AF:53:LYS:HD3	2.17	0.44
1:AP:108:LEU:HD13	1:AQ:19:VAL:HG23	1.98	0.44
1:AQ:36:LEU:HB2	1:AQ:49:LYS:HB2	1.98	0.44
1:AR:54:ILE:HD13	1:EA:89:ILE:HG21	1.99	0.44
1:BA:103:VAL:C	1:BA:104:THR:HG1	2.15	0.44
1:BL:49:LYS:HE3	1:BL:73:SER:OG	2.16	0.44
1:BX:39:LYS:HE2	1:BX:41:THR:HB	1.99	0.44
1:CG:15:GLU:HG2	1:CG:16:LYS:N	2.32	0.44
1:CI:50:SER:HB2	1:CJ:102:LEU:HG	1.99	0.44
1:CU:35:ARG:NH1	1:CV:106:GLN:O	2.39	0.44
1:DA:1:SER:OG	1:DB:96:ASP:OD2	2.27	0.44
1:DB:58:ASP:HB2	1:DB:65:ILE:HD11	1.99	0.44
1:EE:54:ILE:HG22	1:EF:90:ILE:HD13	1.98	0.44
1:EK:90:ILE:HD13	1:EL:54:ILE:HG22	1.99	0.44
1:FA:103:VAL:O	1:FA:104:THR:OG1	2.35	0.44
1:FG:64:LEU:HD11	1:FG:67:ILE:HG13	1.99	0.44
1:GH:97:GLY:O	1:GH:101:GLU:HG3	2.18	0.44
1:GJ:47:MET:HB2	1:GJ:49:LYS:NZ	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GK:53:LYS:HE2	1:GK:69:ASN:ND2	2.32	0.44
1:GN:58:ASP:HB2	1:GN:65:ILE:HD11	1.99	0.44
1:GQ:34:LYS:NZ	1:GQ:36:LEU:HD13	2.32	0.44
1:GV:3:VAL:HA	1:GV:7:GLN:O	2.17	0.44
1:AP:34:LYS:HB3	1:AP:51:GLU:HB3	1.98	0.44
1:BC:16:LYS:HD2	1:GU:13:SER:HB2	1.98	0.44
1:BE:90:ILE:HD13	1:BF:54:ILE:HG22	2.00	0.44
1:BQ:90:ILE:HD13	1:BR:54:ILE:HG22	1.99	0.44
1:CC:35:ARG:O	1:CC:36:LEU:HD12	2.17	0.44
1:CU:47:MET:HB2	1:CU:49:LYS:HZ1	1.81	0.44
1:CX:74:ILE:HD13	1:CX:83:LYS:HG2	1.98	0.44
1:DB:28:LYS:HB3	1:DB:59:PRO:HD3	1.99	0.44
1:DL:11:ILE:HG22	1:DM:110:LEU:HD13	1.99	0.44
1:DM:57:VAL:HG22	1:DM:64:LEU:HA	1.99	0.44
1:DP:34:LYS:NZ	1:DP:36:LEU:HD11	2.33	0.44
1:EA:28:LYS:HB3	1:EA:59:PRO:HD3	2.00	0.44
1:EB:54:ILE:HG22	1:EC:90:ILE:HD13	1.99	0.44
1:ER:58:ASP:HB3	1:ER:65:ILE:HD11	2.00	0.44
1:FC:87:MET:HG2	1:FD:99:TRP:CH2	2.51	0.44
1:FO:99:TRP:CH2	1:FP:87:MET:HG2	2.52	0.44
1:FU:101:GLU:O	1:FU:105:ASP:HB2	2.17	0.44
1:FW:2:LYS:HG3	1:FW:3:VAL:H	1.81	0.44
1:GG:87:MET:HE1	1:GH:100:THR:HA	1.99	0.44
1:GJ:99:TRP:CH2	1:GK:87:MET:HG2	2.52	0.44
1:GL:26:ASN:CG	1:GL:28:LYS:HG2	2.38	0.44
1:GX:51:GLU:OE2	1:GX:53:LYS:HD3	2.16	0.44
1:AD:54:ILE:HG22	1:AE:90:ILE:HD13	1.99	0.44
1:AI:2:LYS:HG3	1:AI:3:VAL:H	1.81	0.44
1:AV:90:ILE:HD13	1:AW:54:ILE:HG22	2.00	0.44
1:AV:108:LEU:HD13	1:AW:19:VAL:HG23	2.00	0.44
1:BR:17:ASP:OD1	1:BR:35:ARG:NE	2.34	0.44
1:CB:45:PRO:HB2	1:CB:76:ALA:HB3	1.98	0.44
1:CI:103:VAL:O	1:CI:104:THR:OG1	2.28	0.44
1:CL:35:ARG:O	1:CL:36:LEU:HD12	2.17	0.44
1:CO:23:ASP:OD2	1:CO:26:ASN:ND2	2.51	0.44
1:CX:34:LYS:HB3	1:CX:51:GLU:HB3	1.99	0.44
1:DH:18:VAL:HG22	1:DH:34:LYS:HG3	1.99	0.44
1:DM:23:ASP:OD2	1:DM:26:ASN:ND2	2.51	0.44
1:DV:23:ASP:OD2	1:DV:26:ASN:ND2	2.51	0.44
1:DY:35:ARG:O	1:DY:36:LEU:HD12	2.17	0.44
1:EO:26:ASN:HB2	1:EO:28:LYS:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EO:45:PRO:HB2	1:EO:76:ALA:HB3	1.99	0.44
1:ES:26:ASN:CG	1:ES:28:LYS:HG2	2.38	0.44
1:EU:97:GLY:O	1:EU:101:GLU:HG3	2.18	0.44
1:FA:45:PRO:HB2	1:FA:76:ALA:HB3	1.99	0.44
1:FJ:49:LYS:HE3	1:FJ:73:SER:OG	2.18	0.44
1:FK:26:ASN:ND2	1:FK:29:ASP:OD2	2.45	0.44
1:FR:3:VAL:HA	1:FR:7:GLN:O	2.16	0.44
1:GJ:87:MET:HG2	1:GK:99:TRP:CH2	2.51	0.44
1:GR:2:LYS:HG3	1:GR:3:VAL:H	1.81	0.44
1:AG:108:LEU:HD13	1:AH:19:VAL:HG23	1.99	0.44
1:AP:3:VAL:HA	1:AP:7:GLN:O	2.17	0.44
1:AV:23:ASP:OD2	1:AV:26:ASN:ND2	2.51	0.44
1:AY:54:ILE:HG22	1:AZ:90:ILE:HD13	1.98	0.44
1:BB:34:LYS:NZ	1:BB:36:LEU:HD11	2.33	0.44
1:BH:50:SER:HB2	1:BI:102:LEU:HG	1.99	0.44
1:BW:50:SER:HB2	1:BX:102:LEU:HG	1.99	0.44
1:BZ:23:ASP:OD2	1:BZ:26:ASN:ND2	2.51	0.44
1:CP:26:ASN:HB2	1:CP:28:LYS:HD2	2.00	0.44
1:CX:54:ILE:HG22	1:CY:90:ILE:HD13	1.98	0.44
1:CY:56:ARG:HG2	1:CY:65:ILE:HD12	1.99	0.44
1:DV:57:VAL:HG22	1:DV:64:LEU:HA	1.99	0.44
1:DV:90:ILE:HD13	1:DW:54:ILE:HG22	2.00	0.44
1:EA:45:PRO:HB2	1:EA:76:ALA:HB3	1.99	0.44
1:EF:26:ASN:HB2	1:EF:28:LYS:HD2	2.00	0.44
1:EK:3:VAL:HA	1:EK:7:GLN:O	2.17	0.44
1:EP:36:LEU:HD12	1:EP:36:LEU:HA	1.88	0.44
1:EZ:50:SER:HB2	1:FA:102:LEU:HG	1.98	0.44
1:FC:3:VAL:HA	1:FC:7:GLN:O	2.17	0.44
1:FI:32:ALA:HB3	1:FI:53:LYS:HG2	2.00	0.44
1:FJ:97:GLY:O	1:FJ:101:GLU:HG3	2.18	0.44
1:FM:97:GLY:O	1:FM:101:GLU:HG3	2.17	0.44
1:FO:47:MET:HB2	1:FO:49:LYS:NZ	2.32	0.44
1:FO:87:MET:HG2	1:FP:99:TRP:CH2	2.51	0.44
1:GF:56:ARG:HG2	1:GF:65:ILE:HB	2.00	0.44
1:GJ:3:VAL:HA	1:GJ:7:GLN:O	2.17	0.44
1:GK:15:GLU:HG2	1:GK:16:LYS:N	2.32	0.44
1:GP:32:ALA:HB3	1:GP:53:LYS:HG2	2.00	0.44
1:GP:101:GLU:O	1:GP:105:ASP:HB2	2.17	0.44
1:GU:56:ARG:HG2	1:GU:65:ILE:HB	1.99	0.44
1:GX:2:LYS:HD3	1:GX:2:LYS:HA	1.83	0.44
1:AB:23:ASP:OD2	1:AB:26:ASN:ND2	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:99:TRP:CH2	1:ED:87:MET:HG2	2.53	0.44
1:AT:45:PRO:HB2	1:AT:76:ALA:HB3	2.00	0.44
1:BC:45:PRO:HB2	1:BC:76:ALA:HB3	2.00	0.44
1:BN:74:ILE:HD13	1:BN:83:LYS:HG2	1.98	0.44
1:BQ:3:VAL:HA	1:BQ:7:GLN:O	2.17	0.44
1:CC:90:ILE:HD13	1:CD:54:ILE:HG22	1.99	0.44
1:DP:108:LEU:HD13	1:DQ:19:VAL:HG23	1.99	0.44
1:DW:34:LYS:HZ1	1:DW:36:LEU:HD13	1.81	0.44
1:EH:23:ASP:OD2	1:EH:26:ASN:ND2	2.51	0.44
1:FD:53:LYS:HE2	1:FD:69:ASN:ND2	2.33	0.44
1:FD:58:ASP:HB3	1:FD:65:ILE:HD11	2.00	0.44
1:FI:101:GLU:O	1:FI:105:ASP:HB2	2.17	0.44
1:FI:103:VAL:O	1:FI:104:THR:OG1	2.34	0.44
1:FL:103:VAL:O	1:FL:104:THR:OG1	2.32	0.44
1:FT:45:PRO:HB2	1:FT:76:ALA:HB3	1.98	0.44
1:GI:2:LYS:HG3	1:GI:3:VAL:H	1.81	0.44
1:GT:39:LYS:HE2	1:GT:41:THR:HB	2.00	0.44
1:AC:74:ILE:HG21	1:AC:83:LYS:HD3	1.99	0.44
1:AK:26:ASN:HB2	1:AK:28:LYS:HD2	2.00	0.44
1:AL:104:THR:HA	1:ED:83:LYS:HE3	1.99	0.44
1:AS:34:LYS:NZ	1:AS:36:LEU:HD11	2.33	0.44
1:AY:80:ALA:O	1:AY:84:THR:OG1	2.36	0.44
1:BE:3:VAL:HA	1:BE:7:GLN:O	2.17	0.44
1:BM:11:ILE:HG22	1:DA:110:LEU:HD13	1.99	0.44
1:BP:54:ILE:HD13	1:CW:89:ILE:HG21	1.99	0.44
1:BY:51:GLU:OE2	1:BY:53:LYS:HD3	2.17	0.44
1:CJ:39:LYS:HE2	1:CJ:41:THR:HB	1.99	0.44
1:DA:3:VAL:HA	1:DA:7:GLN:O	2.17	0.44
1:DJ:47:MET:HB2	1:DJ:49:LYS:NZ	2.33	0.44
1:DX:74:ILE:HG21	1:DX:83:LYS:HD3	2.00	0.44
1:EA:2:LYS:HD3	1:EA:2:LYS:HA	1.82	0.44
1:EH:90:ILE:HD13	1:EI:54:ILE:HG22	2.00	0.44
1:EK:2:LYS:HD3	1:EK:2:LYS:HA	1.85	0.44
1:ET:101:GLU:O	1:ET:105:ASP:HB2	2.18	0.44
1:ET:103:VAL:O	1:ET:104:THR:OG1	2.34	0.44
1:EY:51:GLU:OE2	1:EY:53:LYS:HD3	2.16	0.44
1:FN:57:VAL:HG22	1:FN:64:LEU:HA	1.99	0.44
1:GC:57:VAL:HG22	1:GC:64:LEU:HA	1.99	0.44
1:GE:39:LYS:HE2	1:GE:41:THR:HB	2.00	0.44
1:GW:34:LYS:NZ	1:GW:36:LEU:HD13	2.33	0.44
1:AG:74:ILE:HD13	1:AG:83:LYS:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:89:ILE:HG21	1:EA:54:ILE:HD13	1.99	0.44
1:AS:108:LEU:HD13	1:AT:19:VAL:HG23	1.99	0.44
1:BG:54:ILE:HD13	1:GX:89:ILE:HG21	1.98	0.44
1:BH:35:ARG:NH1	1:BI:106:GLN:O	2.39	0.44
1:BN:34:LYS:NZ	1:BN:36:LEU:HD11	2.33	0.44
1:CF:54:ILE:HG22	1:CG:90:ILE:HD13	1.99	0.44
1:CX:3:VAL:HA	1:CX:7:GLN:O	2.17	0.44
1:DA:90:ILE:HD13	1:DB:54:ILE:HG22	2.00	0.44
1:DE:26:ASN:HB2	1:DE:28:LYS:HD2	1.99	0.44
1:DP:74:ILE:HD13	1:DP:83:LYS:HG2	1.99	0.44
1:DT:39:LYS:HE2	1:DT:41:THR:HB	1.99	0.44
1:EO:80:ALA:HA	1:EO:83:LYS:HB2	2.00	0.44
1:ER:53:LYS:HE2	1:ER:69:ASN:ND2	2.33	0.44
1:FC:26:ASN:HB2	1:FC:28:LYS:HD2	2.00	0.44
1:FJ:26:ASN:HB2	1:FJ:28:LYS:HD2	2.00	0.44
1:FK:12:TYR:HD2	1:FK:24:PHE:CZ	2.36	0.44
1:FP:53:LYS:HE2	1:FP:69:ASN:ND2	2.32	0.44
1:FV:97:GLY:O	1:FV:101:GLU:HG3	2.18	0.44
1:FX:87:MET:HG2	1:FY:99:TRP:CH2	2.51	0.44
1:AF:13:SER:HB2	1:EU:16:LYS:HD2	2.00	0.44
1:AH:18:VAL:HG22	1:AH:34:LYS:HG3	1.99	0.44
1:AO:32:ALA:HB3	1:AO:53:LYS:HG3	2.00	0.44
1:AV:45:PRO:HB3	1:ER:61:THR:HA	2.00	0.44
1:BB:108:LEU:HD13	1:BC:19:VAL:HG23	1.99	0.44
1:BE:34:LYS:HB3	1:BE:51:GLU:HB3	1.98	0.44
1:BE:35:ARG:O	1:BE:36:LEU:HD12	2.17	0.44
1:BG:26:ASN:ND2	1:BG:29:ASP:OD2	2.42	0.44
1:BM:87:MET:HG2	1:DC:99:TRP:CH2	2.53	0.44
1:BQ:47:MET:HB2	1:BQ:49:LYS:NZ	2.27	0.44
1:CK:36:LEU:HD12	1:CK:36:LEU:HA	1.85	0.44
1:CV:26:ASN:HB2	1:CV:28:LYS:HD2	1.99	0.44
1:CV:39:LYS:HE2	1:CV:41:THR:HB	1.99	0.44
1:CX:90:ILE:HD13	1:CY:54:ILE:HG22	1.99	0.44
1:EL:53:LYS:HE2	1:EL:69:ASN:ND2	2.33	0.44
1:EQ:19:VAL:HG23	1:ER:108:LEU:HD13	2.00	0.44
1:EW:3:VAL:HA	1:EW:7:GLN:O	2.16	0.44
1:FF:3:VAL:HA	1:FF:7:GLN:O	2.16	0.44
1:FH:51:GLU:OE2	1:FH:53:LYS:HD3	2.17	0.44
1:FV:49:LYS:HE3	1:FV:73:SER:OG	2.17	0.44
1:FX:3:VAL:HA	1:FX:7:GLN:O	2.17	0.44
1:GM:38:PRO:HD3	1:GM:48:ALA:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GN:28:LYS:HB3	1:GN:59:PRO:HD3	2.00	0.44
1:GQ:45:PRO:HB2	1:GQ:76:ALA:HB3	2.00	0.44
1:AA:45:PRO:HB3	1:FD:61:THR:HA	2.00	0.44
1:AA:57:VAL:HG22	1:AA:64:LEU:HA	2.00	0.44
1:AE:39:LYS:HE2	1:AE:41:THR:HB	1.99	0.44
1:AO:83:LYS:HE3	1:DX:104:THR:HA	2.00	0.44
1:AO:87:MET:HG2	1:DX:99:TRP:CH2	2.53	0.44
1:AP:90:ILE:HD13	1:AQ:54:ILE:HG22	2.00	0.44
1:BM:28:LYS:O	1:BM:56:ARG:HA	2.18	0.44
1:BQ:40:ARG:NE	1:DN:61:THR:O	2.27	0.44
1:BS:56:ARG:HG2	1:BS:65:ILE:HD12	2.00	0.44
1:CO:108:LEU:HD13	1:CP:19:VAL:HG23	2.00	0.44
1:CS:56:ARG:HG2	1:CS:65:ILE:HD12	1.99	0.44
1:DL:87:MET:HG2	1:DO:99:TRP:CH2	2.53	0.44
1:DM:90:ILE:HD13	1:DN:54:ILE:HG22	2.00	0.44
1:DT:26:ASN:HB2	1:DT:28:LYS:HD2	2.00	0.44
1:EK:103:VAL:HB	1:EL:87:MET:HE1	2.00	0.44
1:EO:39:LYS:HE2	1:EO:41:THR:HB	2.00	0.44
1:EV:74:ILE:HG21	1:EV:83:LYS:HD3	1.99	0.44
1:EY:100:THR:HG23	1:FH:87:MET:HE1	1.99	0.44
1:FS:34:LYS:NZ	1:FS:36:LEU:HD13	2.33	0.44
1:GA:68:VAL:HG11	1:GB:90:ILE:HG21	1.99	0.44
1:GG:101:GLU:O	1:GG:105:ASP:HB2	2.18	0.44
1:GH:58:ASP:OD1	1:GH:60:THR:HG22	2.18	0.44
1:GO:51:GLU:OE2	1:GO:53:LYS:HD3	2.18	0.44
1:AG:34:LYS:NZ	1:AG:36:LEU:HD11	2.33	0.43
1:AM:54:ILE:HG22	1:AN:90:ILE:HD13	1.98	0.43
1:AP:35:ARG:O	1:AP:36:LEU:HD12	2.17	0.43
1:AR:26:ASN:ND2	1:AR:29:ASP:OD2	2.42	0.43
1:AT:16:LYS:HD2	1:GF:13:SER:HB2	1.99	0.43
1:BG:89:ILE:HG21	1:GX:54:ILE:HD13	1.99	0.43
1:BQ:103:VAL:HB	1:BR:87:MET:HE1	2.00	0.43
1:BR:53:LYS:HE2	1:BR:69:ASN:ND2	2.33	0.43
1:BR:64:LEU:HD11	1:BR:67:ILE:HG13	2.00	0.43
1:BV:28:LYS:O	1:BV:56:ARG:HA	2.18	0.43
1:CD:56:ARG:HG2	1:CD:65:ILE:HD12	1.99	0.43
1:CH:28:LYS:O	1:CH:56:ARG:HA	2.18	0.43
1:CJ:26:ASN:HB2	1:CJ:28:LYS:HD2	2.00	0.43
1:DA:23:ASP:OD2	1:DA:26:ASN:ND2	2.51	0.43
1:DH:16:LYS:HD2	1:DU:13:SER:HB2	2.01	0.43
1:DL:83:LYS:HE3	1:DO:104:THR:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DV:45:PRO:HB3	1:GK:61:THR:HA	2.00	0.43
1:EK:47:MET:HB2	1:EK:49:LYS:NZ	2.27	0.43
1:EX:34:LYS:NZ	1:EX:36:LEU:HD13	2.33	0.43
1:FC:19:VAL:HG23	1:FD:108:LEU:HD13	2.00	0.43
1:GM:68:VAL:HG11	1:GN:90:ILE:HG21	1.99	0.43
1:AJ:57:VAL:HG22	1:AJ:64:LEU:HA	2.00	0.43
1:AK:58:ASP:HB2	1:AK:65:ILE:HD11	2.00	0.43
1:AW:58:ASP:HB2	1:AW:65:ILE:HD11	1.99	0.43
1:BA:12:TYR:HD2	1:BA:24:PHE:CZ	2.36	0.43
1:BH:103:VAL:O	1:BH:104:THR:OG1	2.28	0.43
1:BQ:2:LYS:HD3	1:BQ:2:LYS:HA	1.86	0.43
1:CD:53:LYS:HE2	1:CD:69:ASN:ND2	2.33	0.43
1:CM:64:LEU:HD11	1:CM:67:ILE:HG13	1.99	0.43
1:CX:35:ARG:O	1:CX:36:LEU:HD12	2.17	0.43
1:CZ:56:ARG:HG2	1:CZ:65:ILE:HD12	2.00	0.43
1:DU:36:LEU:HD12	1:DU:36:LEU:HA	1.84	0.43
1:ED:32:ALA:HB3	1:ED:53:LYS:HG3	2.00	0.43
1:FG:34:LYS:NZ	1:FG:36:LEU:HD13	2.33	0.43
1:FO:50:SER:HB2	1:FP:102:LEU:HG	2.00	0.43
1:FZ:26:ASN:CG	1:FZ:28:LYS:HG2	2.38	0.43
1:GC:51:GLU:OE2	1:GC:53:LYS:HD3	2.18	0.43
1:GQ:26:ASN:HB2	1:GQ:28:LYS:HD2	2.00	0.43
1:GQ:58:ASP:OD1	1:GQ:60:THR:HG22	2.19	0.43
1:AI:26:ASN:ND2	1:AI:29:ASP:OD2	2.46	0.43
1:BA:28:LYS:O	1:BA:56:ARG:HA	2.18	0.43
1:BE:103:VAL:HB	1:BF:87:MET:HE1	2.00	0.43
1:BG:104:THR:HG22	1:GX:83:LYS:HB3	2.00	0.43
1:BU:1:SER:O	1:BU:2:LYS:HD2	2.18	0.43
1:BZ:108:LEU:HD13	1:CA:19:VAL:HG23	2.00	0.43
1:CA:26:ASN:HB2	1:CA:28:LYS:HD2	2.01	0.43
1:CH:83:LYS:HE3	1:CQ:104:THR:HA	2.00	0.43
1:CK:13:SER:HB2	1:CS:16:LYS:HD2	2.01	0.43
1:CR:74:ILE:HD13	1:CR:83:LYS:HG2	1.98	0.43
1:DE:39:LYS:HE2	1:DE:41:THR:HB	1.99	0.43
1:DL:32:ALA:HB3	1:DL:53:LYS:HG3	2.00	0.43
1:EB:2:LYS:HD3	1:EB:2:LYS:HA	1.87	0.43
1:EC:15:GLU:HG2	1:EC:16:LYS:N	2.32	0.43
1:EE:96:ASP:OD1	1:EE:97:GLY:N	2.52	0.43
1:EP:56:ARG:HG2	1:EP:65:ILE:HB	2.00	0.43
1:EQ:26:ASN:HB2	1:EQ:28:LYS:HD2	2.00	0.43
1:EU:11:ILE:HD11	1:EU:14:THR:OG1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FA:80:ALA:HA	1:FA:83:LYS:HB2	2.00	0.43
1:FP:15:GLU:HG2	1:FP:16:LYS:N	2.32	0.43
1:FQ:26:ASN:CG	1:FQ:28:LYS:HG2	2.38	0.43
1:FS:80:ALA:HA	1:FS:83:LYS:HB2	1.99	0.43
1:GA:51:GLU:OE1	1:GA:69:ASN:ND2	2.51	0.43
1:GB:28:LYS:HB3	1:GB:59:PRO:HD3	2.00	0.43
1:AA:90:ILE:HD13	1:AB:54:ILE:HG22	2.00	0.43
1:AJ:23:ASP:OD2	1:AJ:26:ASN:ND2	2.51	0.43
1:AJ:90:ILE:HD13	1:AK:54:ILE:HG22	2.00	0.43
1:AK:80:ALA:O	1:AK:84:THR:OG1	2.31	0.43
1:BK:2:LYS:HD3	1:BK:2:LYS:HA	1.87	0.43
1:BV:87:MET:HG2	1:GO:99:TRP:CH2	2.53	0.43
1:BW:2:LYS:HD3	1:BW:2:LYS:HA	1.88	0.43
1:CM:53:LYS:HE2	1:CM:69:ASN:ND2	2.33	0.43
1:CP:58:ASP:HB2	1:CP:65:ILE:HD11	2.00	0.43
1:CZ:45:PRO:HB2	1:CZ:76:ALA:HB3	1.99	0.43
1:DA:57:VAL:HG22	1:DA:64:LEU:HA	2.00	0.43
1:DH:56:ARG:HG2	1:DH:65:ILE:HD12	1.99	0.43
1:DJ:54:ILE:HG22	1:DK:90:ILE:HD13	1.99	0.43
1:DK:1:SER:O	1:DK:2:LYS:HD2	2.18	0.43
1:DS:96:ASP:OD1	1:DS:97:GLY:N	2.52	0.43
1:DZ:53:LYS:HE2	1:DZ:69:ASN:ND2	2.33	0.43
1:EH:108:LEU:HD13	1:EI:19:VAL:HG23	2.00	0.43
1:EO:36:LEU:HD12	1:EO:36:LEU:HA	1.89	0.43
1:ET:32:ALA:HB3	1:ET:53:LYS:HG2	2.00	0.43
1:FD:1:SER:O	1:FD:2:LYS:HD2	2.18	0.43
1:FM:28:LYS:HB3	1:FM:59:PRO:HD3	2.00	0.43
1:FP:1:SER:O	1:FP:2:LYS:HD2	2.18	0.43
1:FU:32:ALA:HB3	1:FU:53:LYS:HG2	2.00	0.43
1:FW:26:ASN:ND2	1:FW:29:ASP:OD2	2.45	0.43
1:FY:1:SER:O	1:FY:2:LYS:HD2	2.18	0.43
1:GD:54:ILE:HD13	1:GE:89:ILE:HG21	2.01	0.43
1:GQ:49:LYS:HE3	1:GQ:73:SER:OG	2.17	0.43
1:GS:47:MET:HB2	1:GS:49:LYS:HZ1	1.84	0.43
1:AA:23:ASP:OD2	1:AA:26:ASN:ND2	2.51	0.43
1:AL:74:ILE:HG21	1:AL:83:LYS:HD3	2.00	0.43
1:AN:1:SER:O	1:AN:2:LYS:HD2	2.18	0.43
1:AY:2:LYS:HD3	1:AY:2:LYS:HA	1.87	0.43
1:AZ:1:SER:O	1:AZ:2:LYS:HD2	2.18	0.43
1:BL:1:SER:O	1:BL:2:LYS:HD2	2.19	0.43
1:BW:35:ARG:NH1	1:BX:106:GLN:O	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:96:ASP:OD1	1:CI:97:GLY:N	2.52	0.43
1:CQ:74:ILE:HG21	1:CQ:83:LYS:HD3	1.99	0.43
1:CR:108:LEU:HD13	1:CS:19:VAL:HG23	1.99	0.43
1:DF:13:SER:HB2	1:DQ:16:LYS:HD2	2.00	0.43
1:DG:34:LYS:NZ	1:DG:36:LEU:HD11	2.33	0.43
1:DG:108:LEU:HD13	1:DH:19:VAL:HG23	1.99	0.43
1:DV:108:LEU:HD13	1:DW:19:VAL:HG23	2.00	0.43
1:EM:28:LYS:HB3	1:EM:59:PRO:HD3	1.99	0.43
1:EQ:3:VAL:HA	1:EQ:7:GLN:O	2.17	0.43
1:EU:23:ASP:OD2	1:EU:26:ASN:ND2	2.52	0.43
1:FE:12:TYR:HD2	1:FE:24:PHE:CZ	2.37	0.43
1:FL:51:GLU:OE1	1:FL:69:ASN:ND2	2.51	0.43
1:FM:58:ASP:HB2	1:FM:65:ILE:HD11	1.99	0.43
1:FN:51:GLU:OE2	1:FN:53:LYS:HD3	2.18	0.43
1:FY:53:LYS:HE2	1:FY:69:ASN:ND2	2.33	0.43
1:GJ:19:VAL:HG23	1:GK:108:LEU:HD13	2.00	0.43
1:AA:108:LEU:HD13	1:AB:19:VAL:HG23	2.00	0.43
1:AQ:56:ARG:HG2	1:AQ:65:ILE:HD12	1.99	0.43
1:AU:12:TYR:HD2	1:AU:24:PHE:CZ	2.37	0.43
1:AW:26:ASN:HB2	1:AW:28:LYS:HD2	2.00	0.43
1:BF:53:LYS:HE2	1:BF:69:ASN:ND2	2.33	0.43
1:BF:56:ARG:HG2	1:BF:65:ILE:HD12	1.99	0.43
1:BK:104:THR:HG22	1:BL:83:LYS:HB3	2.00	0.43
1:BL:74:ILE:HG21	1:BL:83:LYS:HG2	2.00	0.43
1:BQ:35:ARG:O	1:BQ:36:LEU:HD12	2.17	0.43
1:BR:56:ARG:HG2	1:BR:65:ILE:HD12	1.99	0.43
1:BZ:57:VAL:HG22	1:BZ:64:LEU:HA	1.99	0.43
1:CR:34:LYS:NZ	1:CR:36:LEU:HD11	2.33	0.43
1:CY:64:LEU:HD11	1:CY:67:ILE:HG13	2.01	0.43
1:DC:74:ILE:HG21	1:DC:83:LYS:HD3	1.99	0.43
1:DH:45:PRO:HB2	1:DH:76:ALA:HB3	2.00	0.43
1:DK:53:LYS:HE2	1:DK:69:ASN:ND2	2.34	0.43
1:DZ:56:ARG:HG2	1:DZ:65:ILE:HD12	2.01	0.43
1:EK:35:ARG:O	1:EK:36:LEU:HD12	2.18	0.43
1:EL:56:ARG:HG2	1:EL:65:ILE:HD12	1.99	0.43
1:EL:64:LEU:HD11	1:EL:67:ILE:HG13	2.01	0.43
1:EM:56:ARG:HG2	1:EM:65:ILE:HD12	2.00	0.43
1:FA:39:LYS:HE2	1:FA:41:THR:HB	2.00	0.43
1:FL:45:PRO:HB3	1:FY:61:THR:HA	2.00	0.43
1:FL:68:VAL:HG11	1:FM:90:ILE:HG21	2.00	0.43
1:FP:61:THR:HA	1:GA:45:PRO:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FQ:28:LYS:O	1:FQ:56:ARG:HA	2.19	0.43
1:FR:103:VAL:O	1:FR:104:THR:OG1	2.31	0.43
1:GD:45:PRO:HB2	1:GD:76:ALA:HB3	2.01	0.43
1:GJ:50:SER:HB2	1:GK:102:LEU:HG	2.00	0.43
1:GM:51:GLU:OE1	1:GM:69:ASN:ND2	2.51	0.43
1:GS:54:ILE:HD13	1:GT:89:ILE:HG21	2.01	0.43
1:AJ:110:LEU:HD13	1:ED:11:ILE:HG22	1.99	0.43
1:BA:87:MET:HG2	1:GC:99:TRP:CH2	2.53	0.43
1:BD:12:TYR:HD2	1:BD:24:PHE:CZ	2.37	0.43
1:BD:74:ILE:HG21	1:BD:83:LYS:HD3	2.01	0.43
1:BI:26:ASN:HB2	1:BI:28:LYS:HD2	2.00	0.43
1:BJ:51:GLU:OE2	1:BJ:53:LYS:HD3	2.18	0.43
1:BV:12:TYR:HD2	1:BV:24:PHE:CZ	2.36	0.43
1:CG:53:LYS:HE2	1:CG:69:ASN:ND2	2.34	0.43
1:CH:32:ALA:HB3	1:CH:53:LYS:HG3	2.00	0.43
1:CH:87:MET:HG2	1:CQ:99:TRP:CH2	2.53	0.43
1:DG:28:LYS:HB3	1:DG:28:LYS:HE2	1.82	0.43
1:EC:53:LYS:HE2	1:EC:69:ASN:ND2	2.34	0.43
1:EG:13:SER:HB2	1:FV:16:LYS:HD2	2.00	0.43
1:ER:78:ALA:O	1:ER:83:LYS:NZ	2.52	0.43
1:FJ:58:ASP:OD1	1:FJ:60:THR:HG22	2.18	0.43
1:FZ:2:LYS:HD2	1:FZ:2:LYS:HA	1.65	0.43
1:FZ:28:LYS:O	1:FZ:56:ARG:HA	2.19	0.43
1:GD:47:MET:HB2	1:GD:49:LYS:HZ1	1.84	0.43
1:GH:23:ASP:OD2	1:GH:26:ASN:ND2	2.52	0.43
1:GJ:26:ASN:HB2	1:GJ:28:LYS:HD2	2.00	0.43
1:GK:1:SER:O	1:GK:2:LYS:HD2	2.18	0.43
1:GK:58:ASP:HB3	1:GK:65:ILE:HD11	2.01	0.43
1:GN:35:ARG:O	1:GN:36:LEU:HD12	2.19	0.43
1:AI:12:TYR:HD2	1:AI:24:PHE:CZ	2.37	0.43
1:AI:74:ILE:HG21	1:AI:83:LYS:HD3	2.01	0.43
1:BH:2:LYS:HD3	1:BH:2:LYS:HA	1.88	0.43
1:BO:16:LYS:HD2	1:CW:13:SER:HB2	2.01	0.43
1:BS:54:ILE:HD13	1:CZ:89:ILE:HG21	2.00	0.43
1:BT:2:LYS:HD3	1:BT:2:LYS:HA	1.87	0.43
1:CB:2:LYS:HE2	1:GJ:112:THR:OG1	2.19	0.43
1:CE:28:LYS:HB3	1:CE:59:PRO:HD3	1.99	0.43
1:CE:54:ILE:HD13	1:CN:89:ILE:HG21	2.00	0.43
1:CE:89:ILE:HG21	1:CN:54:ILE:HD13	2.00	0.43
1:CF:39:LYS:HD2	1:CF:41:THR:HB	2.01	0.43
1:CL:90:ILE:HD13	1:CM:54:ILE:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DF:36:LEU:HD12	1:DF:36:LEU:HA	1.84	0.43
1:DG:74:ILE:HD13	1:DG:83:LYS:HG2	1.99	0.43
1:DK:74:ILE:HG21	1:DK:83:LYS:HG2	2.01	0.43
1:DM:108:LEU:HD13	1:DN:19:VAL:HG23	2.00	0.43
1:DY:103:VAL:O	1:DY:104:THR:OG1	2.32	0.43
1:DZ:26:ASN:OD1	1:DZ:28:LYS:HG2	2.18	0.43
1:DZ:64:LEU:HD11	1:DZ:67:ILE:HG13	2.00	0.43
1:EN:54:ILE:HD13	1:EO:89:ILE:HG21	2.01	0.43
1:EV:12:TYR:HD2	1:EV:24:PHE:CZ	2.37	0.43
1:EZ:54:ILE:HD13	1:FA:89:ILE:HG21	2.00	0.43
1:FL:23:ASP:OD2	1:FL:26:ASN:ND2	2.51	0.43
1:FZ:12:TYR:HD2	1:FZ:24:PHE:CZ	2.37	0.43
1:GB:58:ASP:HB2	1:GB:65:ILE:HD11	1.99	0.43
1:GT:11:ILE:HD11	1:GT:14:THR:OG1	2.19	0.43
1:AA:1:SER:OG	1:AB:96:ASP:OD2	2.27	0.43
1:AD:96:ASP:OD1	1:AD:97:GLY:N	2.52	0.43
1:AH:45:PRO:HB2	1:AH:76:ALA:HB3	2.00	0.43
1:AP:45:PRO:HB2	1:AP:76:ALA:HB3	2.01	0.43
1:AQ:53:LYS:HE2	1:AQ:69:ASN:ND2	2.34	0.43
1:AZ:53:LYS:HE2	1:AZ:69:ASN:ND2	2.34	0.43
1:BL:53:LYS:HE2	1:BL:69:ASN:ND2	2.34	0.43
1:CG:74:ILE:HG21	1:CG:83:LYS:HG2	2.00	0.43
1:DH:26:ASN:HB2	1:DH:28:LYS:HD2	2.01	0.43
1:DO:36:LEU:HD12	1:DO:36:LEU:HA	1.87	0.43
1:DY:90:ILE:HD13	1:DZ:54:ILE:HG22	1.99	0.43
1:EH:57:VAL:HG22	1:EH:64:LEU:HA	1.99	0.43
1:EO:11:ILE:HD11	1:EO:14:THR:OG1	2.19	0.43
1:EU:58:ASP:OD1	1:EU:60:THR:HG22	2.19	0.43
1:EW:50:SER:HB2	1:EX:102:LEU:HG	2.01	0.43
1:EY:87:MET:HE1	1:FH:100:THR:HG23	1.99	0.43
1:FF:34:LYS:HB3	1:FF:51:GLU:HB3	2.01	0.43
1:FF:50:SER:HB2	1:FG:102:LEU:HG	2.01	0.43
1:FJ:23:ASP:OD2	1:FJ:26:ASN:ND2	2.52	0.43
1:FJ:45:PRO:HB2	1:FJ:76:ALA:HB3	2.00	0.43
1:FV:26:ASN:HB2	1:FV:28:LYS:HD2	2.00	0.43
1:FX:104:THR:HG22	1:FY:83:LYS:HD2	2.01	0.43
1:FY:58:ASP:HB3	1:FY:65:ILE:HD11	2.00	0.43
1:GA:23:ASP:OD2	1:GA:26:ASN:ND2	2.52	0.43
1:GI:12:TYR:HD2	1:GI:24:PHE:CZ	2.37	0.43
1:GR:12:TYR:HD2	1:GR:24:PHE:CZ	2.37	0.43
1:GU:36:LEU:HD12	1:GU:36:LEU:HA	1.90	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:28:LYS:HB3	1:AB:59:PRO:HD3	2.00	0.43
1:AE:26:ASN:HB2	1:AE:28:LYS:HD2	1.99	0.43
1:AJ:1:SER:OG	1:AK:96:ASP:OD2	2.27	0.43
1:AJ:2:LYS:HD3	1:AJ:2:LYS:HA	1.87	0.43
1:AN:58:ASP:HB3	1:AN:65:ILE:HD11	2.01	0.43
1:BX:26:ASN:HB2	1:BX:28:LYS:HD2	2.00	0.43
1:CF:104:THR:HG22	1:CG:83:LYS:HB3	2.00	0.43
1:CG:1:SER:O	1:CG:2:LYS:HD2	2.19	0.43
1:DW:26:ASN:HB2	1:DW:28:LYS:HD2	2.00	0.43
1:DW:58:ASP:HB2	1:DW:65:ILE:HD11	2.00	0.43
1:EB:104:THR:HG22	1:EC:83:LYS:HB3	2.00	0.43
1:EC:74:ILE:HG21	1:EC:83:LYS:HG2	2.00	0.43
1:ED:28:LYS:O	1:ED:56:ARG:HA	2.18	0.43
1:EL:26:ASN:OD1	1:EL:28:LYS:HG2	2.18	0.43
1:EN:101:GLU:O	1:EN:105:ASP:HB2	2.19	0.43
1:ER:23:ASP:OD2	1:ER:26:ASN:ND2	2.52	0.43
1:EW:34:LYS:HB3	1:EW:51:GLU:HB3	2.01	0.43
1:FC:104:THR:HG22	1:FD:83:LYS:HD2	2.01	0.43
1:GE:80:ALA:HA	1:GE:83:LYS:HB2	2.00	0.43
1:GH:45:PRO:HB2	1:GH:76:ALA:HB3	2.01	0.43
1:GM:23:ASP:OD2	1:GM:26:ASN:ND2	2.52	0.43
1:AA:2:LYS:HD3	1:AA:2:LYS:HA	1.87	0.42
1:AA:17:ASP:OD1	1:AA:35:ARG:NE	2.35	0.42
1:AN:74:ILE:HG21	1:AN:83:LYS:HG2	2.01	0.42
1:AT:53:LYS:HB3	1:AT:69:ASN:ND2	2.34	0.42
1:BD:54:ILE:HD13	1:GU:89:ILE:HG21	2.01	0.42
1:BH:96:ASP:OD1	1:BH:97:GLY:N	2.52	0.42
1:BI:53:LYS:HB3	1:BI:69:ASN:ND2	2.34	0.42
1:BO:45:PRO:HB2	1:BO:76:ALA:HB3	2.00	0.42
1:BY:13:SER:HB2	1:GH:16:LYS:HD2	2.00	0.42
1:CN:56:ARG:HG2	1:CN:65:ILE:HD12	2.00	0.42
1:CT:26:ASN:ND2	1:CT:29:ASP:OD2	2.46	0.42
1:CY:53:LYS:HE2	1:CY:69:ASN:ND2	2.33	0.42
1:DL:28:LYS:O	1:DL:56:ARG:HA	2.18	0.42
1:EM:26:ASN:ND2	1:EM:29:ASP:OD2	2.46	0.42
1:ES:36:LEU:HB3	1:ES:49:LYS:HB2	2.01	0.42
1:FB:56:ARG:HG2	1:FB:65:ILE:HB	1.99	0.42
1:FM:35:ARG:O	1:FM:36:LEU:HD12	2.19	0.42
1:FT:26:ASN:ND2	1:FT:29:ASP:OD2	2.44	0.42
1:FU:87:MET:HE1	1:FV:100:THR:HA	2.01	0.42
1:FV:45:PRO:HB2	1:FV:76:ALA:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FY:78:ALA:O	1:FY:83:LYS:NZ	2.52	0.42
1:GA:2:LYS:HD3	1:GA:2:LYS:HA	1.87	0.42
1:GB:35:ARG:O	1:GB:36:LEU:HD12	2.19	0.42
1:GL:28:LYS:O	1:GL:56:ARG:HA	2.19	0.42
1:GQ:23:ASP:OD2	1:GQ:26:ASN:ND2	2.52	0.42
1:GQ:74:ILE:HD13	1:GQ:83:LYS:HG3	2.00	0.42
1:GS:45:PRO:HB2	1:GS:76:ALA:HB3	2.01	0.42
1:AE:11:ILE:HD11	1:AE:14:THR:OG1	2.20	0.42
1:AE:53:LYS:HB3	1:AE:69:ASN:ND2	2.34	0.42
1:AO:28:LYS:O	1:AO:56:ARG:HA	2.18	0.42
1:AP:83:LYS:HB2	1:AP:83:LYS:HE2	1.93	0.42
1:AQ:17:ASP:OD1	1:AQ:35:ARG:NE	2.34	0.42
1:BG:87:MET:HE3	1:BG:87:MET:HB3	1.82	0.42
1:BS:26:ASN:ND2	1:BS:29:ASP:OD2	2.42	0.42
1:BU:53:LYS:HE2	1:BU:69:ASN:ND2	2.34	0.42
1:BX:53:LYS:HB3	1:BX:69:ASN:ND2	2.34	0.42
1:BZ:90:ILE:HD13	1:CA:54:ILE:HG22	2.00	0.42
1:CA:58:ASP:HB2	1:CA:65:ILE:HD11	2.01	0.42
1:CO:90:ILE:HD13	1:CP:54:ILE:HG22	2.00	0.42
1:EC:58:ASP:HB3	1:EC:65:ILE:HD11	2.01	0.42
1:EH:17:ASP:OD1	1:EH:35:ARG:NE	2.35	0.42
1:EJ:2:LYS:HE2	1:FO:112:THR:OG1	2.19	0.42
1:FC:51:GLU:HG3	1:FC:69:ASN:OD1	2.19	0.42
1:FE:28:LYS:O	1:FE:56:ARG:HA	2.19	0.42
1:FQ:2:LYS:HD2	1:FQ:2:LYS:HA	1.65	0.42
1:FQ:12:TYR:HD2	1:FQ:24:PHE:CZ	2.38	0.42
1:FX:39:LYS:HD2	1:FX:41:THR:HB	2.01	0.42
1:FX:51:GLU:HG3	1:FX:69:ASN:OD1	2.19	0.42
1:FX:68:VAL:HG11	1:FY:90:ILE:HG21	2.01	0.42
1:GT:80:ALA:HA	1:GT:83:LYS:HB2	2.00	0.42
1:AD:110:LEU:HD23	1:AE:19:VAL:HG21	2.02	0.42
1:BI:32:ALA:HB3	1:BI:53:LYS:HG3	2.02	0.42
1:BJ:13:SER:HB2	1:GQ:16:LYS:HD2	2.01	0.42
1:BW:96:ASP:OD1	1:BW:97:GLY:N	2.52	0.42
1:CD:26:ASN:OD1	1:CD:28:LYS:HG2	2.19	0.42
1:CE:56:ARG:HG2	1:CE:65:ILE:HD12	2.00	0.42
1:CN:28:LYS:O	1:CN:56:ARG:HA	2.19	0.42
1:CR:28:LYS:HB3	1:CR:28:LYS:HE2	1.82	0.42
1:CS:103:VAL:O	1:CS:104:THR:OG1	2.31	0.42
1:CW:36:LEU:HD12	1:CW:36:LEU:HA	1.84	0.42
1:EV:2:LYS:HD3	1:EV:2:LYS:HA	1.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FR:45:PRO:HB2	1:FR:76:ALA:HB3	2.02	0.42
1:FV:23:ASP:OD2	1:FV:26:ASN:ND2	2.52	0.42
1:FX:26:ASN:HB2	1:FX:28:LYS:HD2	2.00	0.42
1:GA:22:ARG:HG3	1:GA:30:THR:HG23	2.00	0.42
1:AH:16:LYS:HD2	1:EP:13:SER:HB2	2.00	0.42
1:AH:26:ASN:HB2	1:AH:28:LYS:HD2	2.00	0.42
1:AN:53:LYS:HE2	1:AN:69:ASN:ND2	2.34	0.42
1:AX:2:LYS:HE2	1:FX:112:THR:OG1	2.19	0.42
1:AY:39:LYS:HD2	1:AY:41:THR:HB	2.01	0.42
1:AZ:58:ASP:HB3	1:AZ:65:ILE:HD11	2.01	0.42
1:BE:45:PRO:HB2	1:BE:76:ALA:HB3	2.02	0.42
1:BM:32:ALA:HB3	1:BM:53:LYS:HG3	2.00	0.42
1:BM:83:LYS:HE3	1:DC:104:THR:HA	1.99	0.42
1:BN:32:ALA:HB3	1:BN:53:LYS:HG2	2.01	0.42
1:BO:35:ARG:O	1:BO:36:LEU:HD12	2.19	0.42
1:BS:89:ILE:HG21	1:CZ:54:ILE:HD13	2.00	0.42
1:CG:58:ASP:HB3	1:CG:65:ILE:HD11	2.01	0.42
1:CL:103:VAL:HB	1:CM:87:MET:HE1	2.00	0.42
1:CU:96:ASP:OD1	1:CU:97:GLY:N	2.52	0.42
1:DE:11:ILE:HD11	1:DE:14:THR:OG1	2.19	0.42
1:DE:53:LYS:HB3	1:DE:69:ASN:ND2	2.34	0.42
1:DM:103:VAL:O	1:DM:104:THR:OG1	2.30	0.42
1:DN:26:ASN:HB2	1:DN:28:LYS:HD2	2.01	0.42
1:DQ:53:LYS:HB3	1:DQ:69:ASN:ND2	2.34	0.42
1:EB:39:LYS:HD2	1:EB:41:THR:HB	2.01	0.42
1:EE:49:LYS:HE3	1:EE:73:SER:OG	2.20	0.42
1:EH:1:SER:OG	1:EI:96:ASP:OD2	2.27	0.42
1:EN:103:VAL:O	1:EN:104:THR:OG1	2.30	0.42
1:EQ:51:GLU:HG3	1:EQ:69:ASN:OD1	2.19	0.42
1:ER:1:SER:O	1:ER:2:LYS:HD2	2.18	0.42
1:ES:12:TYR:HD2	1:ES:24:PHE:CZ	2.37	0.42
1:EU:45:PRO:HB2	1:EU:76:ALA:HB3	2.00	0.42
1:EW:101:GLU:O	1:EW:105:ASP:HB2	2.20	0.42
1:FA:53:LYS:HB3	1:FA:69:ASN:ND2	2.35	0.42
1:FF:101:GLU:O	1:FF:105:ASP:HB2	2.20	0.42
1:FV:58:ASP:OD1	1:FV:60:THR:HG22	2.19	0.42
1:FW:12:TYR:HD2	1:FW:24:PHE:CZ	2.37	0.42
1:GB:103:VAL:O	1:GB:104:THR:OG1	2.35	0.42
1:GM:40:ARG:HG3	1:GM:40:ARG:HH11	1.84	0.42
1:GX:87:MET:HE3	1:GX:87:MET:HB3	1.83	0.42
1:AC:2:LYS:HE2	1:EQ:112:THR:OG1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:26:ASN:HB2	1:AF:28:LYS:HD2	2.02	0.42
1:AH:56:ARG:HG2	1:AH:65:ILE:HD12	1.99	0.42
1:AJ:17:ASP:OD1	1:AJ:35:ARG:NE	2.35	0.42
1:AJ:108:LEU:HD13	1:AK:19:VAL:HG23	2.00	0.42
1:AV:1:SER:OG	1:AW:96:ASP:OD2	2.27	0.42
1:AV:57:VAL:HG22	1:AV:64:LEU:HA	2.00	0.42
1:BK:39:LYS:HD2	1:BK:41:THR:HB	2.01	0.42
1:BQ:45:PRO:HB2	1:BQ:76:ALA:HB3	2.02	0.42
1:BX:32:ALA:HB3	1:BX:53:LYS:HG3	2.02	0.42
1:CC:103:VAL:HB	1:CD:87:MET:HE1	2.00	0.42
1:CD:64:LEU:HD11	1:CD:67:ILE:HG13	2.01	0.42
1:CJ:11:ILE:HD11	1:CJ:14:THR:OG1	2.20	0.42
1:CS:45:PRO:HB2	1:CS:76:ALA:HB3	2.01	0.42
1:CV:53:LYS:HB3	1:CV:69:ASN:ND2	2.35	0.42
1:DD:96:ASP:OD1	1:DD:97:GLY:N	2.52	0.42
1:DI:74:ILE:HG21	1:DI:83:LYS:HD3	2.02	0.42
1:DR:12:TYR:HD2	1:DR:24:PHE:CZ	2.37	0.42
1:EF:11:ILE:HD11	1:EF:14:THR:OG1	2.20	0.42
1:EY:26:ASN:ND2	1:EY:29:ASP:OD2	2.44	0.42
1:FL:28:LYS:HB3	1:FL:28:LYS:HE2	1.82	0.42
1:FS:17:ASP:OD1	1:FS:35:ARG:NE	2.36	0.42
1:GA:108:LEU:HD13	1:GB:19:VAL:HG23	2.01	0.42
1:GS:108:LEU:HD13	1:GT:19:VAL:HG23	2.02	0.42
1:AQ:64:LEU:HD11	1:AQ:67:ILE:HG13	2.00	0.42
1:AU:74:ILE:HG21	1:AU:83:LYS:HD3	2.01	0.42
1:BP:12:TYR:HD2	1:BP:24:PHE:CZ	2.38	0.42
1:BS:28:LYS:O	1:BS:56:ARG:HA	2.19	0.42
1:BT:39:LYS:HD2	1:BT:41:THR:HB	2.01	0.42
1:CF:58:ASP:HB3	1:CF:65:ILE:HD11	2.01	0.42
1:CS:53:LYS:HB3	1:CS:69:ASN:ND2	2.34	0.42
1:CX:45:PRO:HB2	1:CX:76:ALA:HB3	2.02	0.42
1:DC:36:LEU:HD12	1:DC:36:LEU:HA	1.87	0.42
1:DN:2:LYS:HD2	1:DN:2:LYS:HA	1.82	0.42
1:DP:32:ALA:HB3	1:DP:53:LYS:HG2	2.02	0.42
1:DS:2:LYS:HD3	1:DS:2:LYS:HA	1.88	0.42
1:DX:36:LEU:HD12	1:DX:36:LEU:HA	1.87	0.42
1:EC:1:SER:O	1:EC:2:LYS:HD2	2.19	0.42
1:EG:26:ASN:HB2	1:EG:28:LYS:HD2	2.02	0.42
1:EI:26:ASN:HB2	1:EI:28:LYS:HD2	2.01	0.42
1:ES:28:LYS:O	1:ES:56:ARG:HA	2.19	0.42
1:FD:23:ASP:OD2	1:FD:26:ASN:ND2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FO:19:VAL:HG23	1:FP:108:LEU:HD13	2.00	0.42
1:FO:39:LYS:HD2	1:FO:41:THR:HB	2.02	0.42
1:FS:53:LYS:HB2	1:FS:53:LYS:HZ3	1.84	0.42
1:FU:26:ASN:HB2	1:FU:28:LYS:HD2	2.02	0.42
1:FX:19:VAL:HG23	1:FY:108:LEU:HD13	2.00	0.42
1:GA:101:GLU:O	1:GA:105:ASP:HB2	2.20	0.42
1:GH:56:ARG:HG2	1:GH:65:ILE:HD12	2.02	0.42
1:GK:23:ASP:OD2	1:GK:26:ASN:ND2	2.52	0.42
1:GM:108:LEU:HD13	1:GN:19:VAL:HG23	2.01	0.42
1:GN:34:LYS:HZ3	1:GN:36:LEU:HD13	1.82	0.42
1:GS:101:GLU:O	1:GS:105:ASP:HB2	2.19	0.42
1:AI:104:THR:HG22	1:EP:83:LYS:HD2	2.02	0.42
1:AK:1:SER:N	1:AK:33:TYR:OH	2.53	0.42
1:AU:45:PRO:HB2	1:AU:76:ALA:HB3	2.01	0.42
1:BD:100:THR:HG23	1:GU:87:MET:HE1	2.02	0.42
1:BF:26:ASN:OD1	1:BF:28:LYS:HG2	2.19	0.42
1:BP:45:PRO:HB2	1:BP:76:ALA:HB3	2.01	0.42
1:BQ:7:GLN:NE2	1:BR:89:ILE:HD11	2.35	0.42
1:BW:49:LYS:HE3	1:BW:73:SER:OG	2.20	0.42
1:CM:26:ASN:OD1	1:CM:28:LYS:HG2	2.19	0.42
1:CX:103:VAL:HB	1:CY:87:MET:HE1	2.00	0.42
1:DQ:45:PRO:HB2	1:DQ:76:ALA:HB3	2.01	0.42
1:EB:47:MET:HB2	1:EB:49:LYS:NZ	2.34	0.42
1:EQ:68:VAL:HG11	1:ER:90:ILE:HG21	2.01	0.42
1:EQ:104:THR:HG22	1:ER:83:LYS:HD2	2.01	0.42
1:FB:90:ILE:HG21	1:FK:68:VAL:HG11	2.02	0.42
1:FC:68:VAL:HG11	1:FD:90:ILE:HG21	2.01	0.42
1:FD:78:ALA:O	1:FD:83:LYS:NZ	2.52	0.42
1:FL:101:GLU:O	1:FL:105:ASP:HB2	2.20	0.42
1:FO:104:THR:HG22	1:FP:83:LYS:HD2	2.01	0.42
1:FV:74:ILE:HD13	1:FV:83:LYS:HG3	2.00	0.42
1:GD:101:GLU:O	1:GD:105:ASP:HB2	2.19	0.42
1:GI:45:PRO:HB2	1:GI:76:ALA:HB3	2.01	0.42
1:GJ:39:LYS:HD2	1:GJ:41:THR:HB	2.02	0.42
1:GM:101:GLU:O	1:GM:105:ASP:HB2	2.20	0.42
1:GV:50:SER:HB2	1:GW:102:LEU:HG	2.01	0.42
1:AD:49:LYS:HE3	1:AD:73:SER:OG	2.20	0.42
1:AG:26:ASN:HB2	1:AG:28:LYS:HD2	2.02	0.42
1:AM:39:LYS:HD2	1:AM:41:THR:HB	2.01	0.42
1:AR:56:ARG:HG2	1:AR:65:ILE:HD12	2.00	0.42
1:AY:58:ASP:HB3	1:AY:65:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:112:THR:OG1	1:GC:2:LYS:HE2	2.20	0.42
1:BD:104:THR:HG22	1:GU:83:LYS:HD2	2.01	0.42
1:BF:17:ASP:OD1	1:BF:35:ARG:NE	2.34	0.42
1:BK:23:ASP:OD2	1:BK:26:ASN:ND2	2.53	0.42
1:BR:26:ASN:OD1	1:BR:28:LYS:HG2	2.20	0.42
1:CO:57:VAL:HG22	1:CO:64:LEU:HA	2.00	0.42
1:CV:11:ILE:HD11	1:CV:14:THR:OG1	2.20	0.42
1:CV:32:ALA:HB3	1:CV:53:LYS:HG3	2.01	0.42
1:CV:36:LEU:HD12	1:CV:36:LEU:HA	1.92	0.42
1:CY:26:ASN:OD1	1:CY:28:LYS:HG2	2.19	0.42
1:DA:108:LEU:HD13	1:DB:19:VAL:HG23	2.00	0.42
1:DD:49:LYS:HE3	1:DD:73:SER:OG	2.20	0.42
1:DE:36:LEU:HD12	1:DE:36:LEU:HA	1.91	0.42
1:DH:103:VAL:O	1:DH:104:THR:OG1	2.31	0.42
1:DI:26:ASN:ND2	1:DI:29:ASP:OD2	2.46	0.42
1:DM:28:LYS:HB3	1:DM:28:LYS:HE2	1.81	0.42
1:DR:45:PRO:HB2	1:DR:76:ALA:HB3	2.01	0.42
1:EA:87:MET:HB3	1:EA:87:MET:HE3	1.77	0.42
1:ED:2:LYS:HD2	1:ED:2:LYS:HA	1.64	0.42
1:EE:110:LEU:HD23	1:EF:19:VAL:HG21	2.02	0.42
1:EK:7:GLN:NE2	1:EL:89:ILE:HD11	2.35	0.42
1:EP:17:ASP:HB3	1:EP:35:ARG:HB3	2.02	0.42
1:EQ:103:VAL:O	1:EQ:104:THR:OG1	2.32	0.42
1:ES:36:LEU:HD12	1:ES:36:LEU:HA	1.88	0.42
1:EZ:45:PRO:HB2	1:EZ:76:ALA:HB3	2.01	0.42
1:FE:36:LEU:HD12	1:FE:36:LEU:HA	1.88	0.42
1:FJ:74:ILE:HD13	1:FJ:83:LYS:HG3	2.00	0.42
1:FL:22:ARG:HG3	1:FL:30:THR:HG23	2.01	0.42
1:GD:108:LEU:HD13	1:GE:19:VAL:HG23	2.02	0.42
1:GM:104:THR:HG22	1:GN:83:LYS:HB3	2.02	0.42
1:GV:34:LYS:HB3	1:GV:51:GLU:HB3	2.01	0.42
1:GX:26:ASN:ND2	1:GX:29:ASP:OD2	2.44	0.42
1:AD:58:ASP:HB3	1:AD:65:ILE:HD11	2.02	0.42
1:AI:54:ILE:HD13	1:EP:89:ILE:HG21	2.01	0.42
1:AR:87:MET:HE3	1:AR:87:MET:HB3	1.78	0.42
1:AS:26:ASN:HB2	1:AS:28:LYS:HD2	2.02	0.42
1:BB:26:ASN:HB2	1:BB:28:LYS:HD2	2.02	0.42
1:BC:53:LYS:HB3	1:BC:69:ASN:ND2	2.35	0.42
1:BD:26:ASN:ND2	1:BD:29:ASP:OD2	2.46	0.42
1:BF:64:LEU:HD11	1:BF:67:ILE:HG13	2.00	0.42
1:BH:49:LYS:HE3	1:BH:73:SER:OG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:53:LYS:HB3	1:BO:69:ASN:ND2	2.35	0.42
1:BU:58:ASP:HB3	1:BU:65:ILE:HD11	2.01	0.42
1:BV:32:ALA:HB3	1:BV:53:LYS:HG3	2.01	0.42
1:CP:1:SER:N	1:CP:33:TYR:OH	2.53	0.42
1:CU:49:LYS:HE3	1:CU:73:SER:OG	2.20	0.42
1:DB:1:SER:N	1:DB:33:TYR:OH	2.53	0.42
1:DD:45:PRO:HB2	1:DD:76:ALA:HB3	2.02	0.42
1:DQ:35:ARG:O	1:DQ:36:LEU:HD12	2.20	0.42
1:DY:47:MET:HB2	1:DY:49:LYS:NZ	2.26	0.42
1:EB:58:ASP:HB3	1:EB:65:ILE:HD11	2.02	0.42
1:EK:45:PRO:HB2	1:EK:76:ALA:HB3	2.02	0.42
1:EL:1:SER:N	1:EL:33:TYR:OH	2.53	0.42
1:EQ:39:LYS:HD2	1:EQ:41:THR:HB	2.01	0.42
1:ET:26:ASN:HB2	1:ET:28:LYS:HD2	2.02	0.42
1:FJ:56:ARG:HG2	1:FJ:65:ILE:HD12	2.02	0.42
1:FO:26:ASN:HB2	1:FO:28:LYS:HD2	2.01	0.42
1:FP:58:ASP:HB3	1:FP:65:ILE:HD11	2.00	0.42
1:FR:50:SER:HB2	1:FS:102:LEU:HG	2.01	0.42
1:GA:28:LYS:HB3	1:GA:28:LYS:HE2	1.82	0.42
1:GL:12:TYR:HD2	1:GL:24:PHE:CZ	2.38	0.42
1:GM:22:ARG:HG3	1:GM:30:THR:HG23	2.00	0.42
1:GM:40:ARG:HH12	1:GM:43:ASP:C	2.23	0.42
1:AE:32:ALA:HB3	1:AE:53:LYS:HG3	2.01	0.42
1:AR:28:LYS:O	1:AR:56:ARG:HA	2.19	0.42
1:BG:28:LYS:O	1:BG:56:ARG:HA	2.19	0.42
1:BG:56:ARG:HG2	1:BG:65:ILE:HD12	2.00	0.42
1:BH:110:LEU:HD23	1:BI:19:VAL:HG21	2.02	0.42
1:BL:58:ASP:HB3	1:BL:65:ILE:HD11	2.01	0.42
1:BR:15:GLU:HG2	1:BR:16:LYS:H	1.85	0.42
1:BU:74:ILE:HG21	1:BU:83:LYS:HG2	2.01	0.42
1:BZ:45:PRO:HB2	1:BZ:76:ALA:HB3	2.02	0.42
1:CF:47:MET:HB2	1:CF:49:LYS:NZ	2.34	0.42
1:CM:56:ARG:HG2	1:CM:65:ILE:HD12	2.01	0.42
1:CW:26:ASN:HB2	1:CW:28:LYS:HD2	2.02	0.42
1:DI:12:TYR:HD2	1:DI:24:PHE:CZ	2.37	0.42
1:DR:2:LYS:HD3	1:DR:2:LYS:HA	1.93	0.42
1:DV:28:LYS:HB3	1:DV:28:LYS:HE2	1.82	0.42
1:EA:56:ARG:HG2	1:EA:65:ILE:HD12	2.00	0.42
1:EL:15:GLU:HG2	1:EL:16:LYS:H	1.85	0.42
1:EP:26:ASN:HB2	1:EP:28:LYS:HD2	2.02	0.42
1:EU:56:ARG:HG2	1:EU:65:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FA:26:ASN:HB2	1:FA:28:LYS:HD2	2.00	0.42
1:FF:45:PRO:HB2	1:FF:76:ALA:HB3	2.01	0.42
1:FY:23:ASP:OD2	1:FY:26:ASN:ND2	2.52	0.42
1:GM:45:PRO:HB2	1:GM:76:ALA:HB3	2.02	0.42
1:AA:40:ARG:HH12	1:AA:43:ASP:C	2.23	0.41
1:AB:1:SER:N	1:AB:33:TYR:OH	2.53	0.41
1:AJ:74:ILE:HD13	1:AJ:83:LYS:HG2	2.02	0.41
1:AU:104:THR:HG22	1:GF:83:LYS:HD2	2.02	0.41
1:BA:32:ALA:HB3	1:BA:53:LYS:HG3	2.01	0.41
1:BE:7:GLN:NE2	1:BF:89:ILE:HD11	2.35	0.41
1:BH:90:ILE:HD13	1:BI:54:ILE:HG22	2.03	0.41
1:BZ:40:ARG:HH12	1:BZ:43:ASP:C	2.23	0.41
1:CA:1:SER:N	1:CA:33:TYR:OH	2.53	0.41
1:CE:2:LYS:HD3	1:CE:2:LYS:HA	1.83	0.41
1:CI:45:PRO:HB2	1:CI:76:ALA:HB3	2.02	0.41
1:CJ:53:LYS:HB3	1:CJ:69:ASN:ND2	2.34	0.41
1:CO:40:ARG:HH12	1:CO:43:ASP:C	2.23	0.41
1:CU:45:PRO:HB2	1:CU:76:ALA:HB3	2.02	0.41
1:CU:110:LEU:HD23	1:CV:19:VAL:HG21	2.02	0.41
1:CX:68:VAL:HG11	1:CY:90:ILE:HG21	2.02	0.41
1:DE:32:ALA:HB3	1:DE:53:LYS:HG3	2.02	0.41
1:DF:26:ASN:HB2	1:DF:28:LYS:HD2	2.02	0.41
1:DK:58:ASP:HB3	1:DK:65:ILE:HD11	2.02	0.41
1:DV:74:ILE:HD13	1:DV:83:LYS:HG2	2.02	0.41
1:ED:12:TYR:HD2	1:ED:24:PHE:CZ	2.38	0.41
1:EQ:80:ALA:O	1:EQ:84:THR:OG1	2.30	0.41
1:EY:47:MET:HB2	1:EY:49:LYS:NZ	2.35	0.41
1:FB:26:ASN:HB2	1:FB:28:LYS:HD2	2.02	0.41
1:FD:34:LYS:NZ	1:FD:36:LEU:HD13	2.35	0.41
1:FI:26:ASN:HB2	1:FI:28:LYS:HD2	2.02	0.41
1:FL:38:PRO:HD3	1:FL:48:ALA:HB2	2.01	0.41
1:FN:74:ILE:HG21	1:FN:83:LYS:HD3	2.02	0.41
1:FO:68:VAL:HG11	1:FP:90:ILE:HG21	2.02	0.41
1:GA:38:PRO:HD3	1:GA:48:ALA:HB2	2.01	0.41
1:GC:15:GLU:HB3	1:GC:18:VAL:HB	2.02	0.41
1:GQ:56:ARG:HG2	1:GQ:65:ILE:HD12	2.02	0.41
1:GT:53:LYS:HB3	1:GT:69:ASN:ND2	2.35	0.41
1:AA:74:ILE:HD13	1:AA:83:LYS:HG2	2.02	0.41
1:AJ:40:ARG:HH12	1:AJ:43:ASP:C	2.23	0.41
1:AV:17:ASP:OD1	1:AV:35:ARG:NE	2.35	0.41
1:BD:26:ASN:HB2	1:BD:28:LYS:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:106:GLN:HB3	1:GX:35:ARG:HD3	2.02	0.41
1:BK:47:MET:HB2	1:BK:49:LYS:NZ	2.34	0.41
1:BP:2:LYS:HD3	1:BP:2:LYS:HA	1.92	0.41
1:BR:1:SER:N	1:BR:33:TYR:OH	2.53	0.41
1:BW:110:LEU:HD23	1:BX:19:VAL:HG21	2.02	0.41
1:CF:23:ASP:OD2	1:CF:26:ASN:ND2	2.53	0.41
1:CH:12:TYR:HD2	1:CH:24:PHE:CZ	2.38	0.41
1:CI:2:LYS:HD3	1:CI:2:LYS:HA	1.88	0.41
1:CO:45:PRO:HB2	1:CO:76:ALA:HB3	2.02	0.41
1:CT:45:PRO:HB2	1:CT:76:ALA:HB3	2.01	0.41
1:CY:53:LYS:NZ	1:CY:55:THR:OG1	2.54	0.41
1:DD:110:LEU:HD23	1:DE:19:VAL:HG21	2.02	0.41
1:DJ:39:LYS:HD2	1:DJ:41:THR:HB	2.01	0.41
1:DM:40:ARG:NH1	1:DM:40:ARG:HG3	2.36	0.41
1:DV:40:ARG:NH1	1:DV:40:ARG:HG3	2.36	0.41
1:EN:45:PRO:HB2	1:EN:76:ALA:HB3	2.00	0.41
1:FC:112:THR:OG1	1:FN:2:LYS:HE2	2.20	0.41
1:FH:26:ASN:ND2	1:FH:29:ASP:OD2	2.45	0.41
1:FH:47:MET:HB2	1:FH:49:LYS:NZ	2.35	0.41
1:FN:15:GLU:HB3	1:FN:18:VAL:HB	2.02	0.41
1:AP:7:GLN:NE2	1:AQ:89:ILE:HD11	2.35	0.41
1:AS:32:ALA:HB3	1:AS:53:LYS:HG2	2.02	0.41
1:BF:15:GLU:HG2	1:BF:16:LYS:H	1.85	0.41
1:BI:11:ILE:HD11	1:BI:14:THR:OG1	2.20	0.41
1:BK:58:ASP:HB3	1:BK:65:ILE:HD11	2.01	0.41
1:BX:11:ILE:HD11	1:BX:14:THR:OG1	2.20	0.41
1:CC:45:PRO:HB2	1:CC:76:ALA:HB3	2.02	0.41
1:CI:49:LYS:HE3	1:CI:73:SER:OG	2.20	0.41
1:CN:87:MET:HE3	1:CN:87:MET:HB3	1.87	0.41
1:DA:17:ASP:OD1	1:DA:35:ARG:NE	2.35	0.41
1:DH:53:LYS:HB3	1:DH:69:ASN:ND2	2.35	0.41
1:DI:2:LYS:HD3	1:DI:2:LYS:HA	1.92	0.41
1:DJ:58:ASP:HB3	1:DJ:65:ILE:HD11	2.01	0.41
1:DN:58:ASP:HB2	1:DN:65:ILE:HD11	2.01	0.41
1:DS:49:LYS:HE3	1:DS:73:SER:OG	2.19	0.41
1:DY:68:VAL:HG11	1:DZ:90:ILE:HG21	2.03	0.41
1:EF:36:LEU:HD12	1:EF:36:LEU:HA	1.92	0.41
1:EI:58:ASP:HB2	1:EI:65:ILE:HD11	2.01	0.41
1:EQ:108:LEU:HD13	1:ER:19:VAL:HG23	2.03	0.41
1:EV:45:PRO:HB2	1:EV:76:ALA:HB3	2.01	0.41
1:EZ:90:ILE:HD13	1:FA:54:ILE:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:2:LYS:HD3	1:FB:2:LYS:HA	1.76	0.41
1:FC:39:LYS:HD2	1:FC:41:THR:HB	2.02	0.41
1:FL:40:ARG:HH12	1:FL:43:ASP:C	2.24	0.41
1:FL:108:LEU:HD13	1:FM:19:VAL:HG23	2.02	0.41
1:GG:28:LYS:HB3	1:GG:28:LYS:HE2	1.83	0.41
1:GM:40:ARG:NH1	1:GM:40:ARG:HG3	2.35	0.41
1:AH:53:LYS:HB3	1:AH:69:ASN:ND2	2.35	0.41
1:AI:68:VAL:HG11	1:EP:90:ILE:HG21	2.03	0.41
1:AJ:40:ARG:NH1	1:AJ:40:ARG:HG3	2.36	0.41
1:AN:97:GLY:O	1:AN:101:GLU:HG3	2.21	0.41
1:AQ:26:ASN:OD1	1:AQ:28:LYS:HG2	2.20	0.41
1:AU:100:THR:HG23	1:GF:87:MET:HE1	2.02	0.41
1:BM:12:TYR:HD2	1:BM:24:PHE:CZ	2.38	0.41
1:BP:26:ASN:HB2	1:BP:28:LYS:HD2	2.02	0.41
1:BS:51:GLU:OE2	1:BS:53:LYS:HD3	2.21	0.41
1:BW:90:ILE:HD13	1:BX:54:ILE:HG22	2.03	0.41
1:CF:112:THR:OG1	1:CQ:2:LYS:HE2	2.21	0.41
1:CL:7:GLN:NE2	1:CM:89:ILE:HD11	2.35	0.41
1:CN:51:GLU:OE2	1:CN:53:LYS:HD3	2.21	0.41
1:CU:2:LYS:HD3	1:CU:2:LYS:HA	1.88	0.41
1:CY:1:SER:N	1:CY:33:TYR:OH	2.53	0.41
1:DK:97:GLY:O	1:DK:101:GLU:HG3	2.21	0.41
1:DR:26:ASN:HB2	1:DR:28:LYS:HD2	2.02	0.41
1:DZ:15:GLU:HG2	1:DZ:16:LYS:H	1.85	0.41
1:EH:40:ARG:NH1	1:EH:40:ARG:HG3	2.36	0.41
1:ES:2:LYS:HD2	1:ES:2:LYS:HA	1.65	0.41
1:FC:50:SER:HB2	1:FD:102:LEU:HG	2.02	0.41
1:FH:56:ARG:HG2	1:FH:65:ILE:HB	2.02	0.41
1:FP:23:ASP:OD2	1:FP:26:ASN:ND2	2.53	0.41
1:GA:40:ARG:HH12	1:GA:43:ASP:C	2.24	0.41
1:GV:45:PRO:HB2	1:GV:76:ALA:HB3	2.02	0.41
1:AA:40:ARG:NH1	1:AA:40:ARG:HG3	2.36	0.41
1:AC:13:SER:HB2	1:ER:16:LYS:HD2	2.02	0.41
1:AI:26:ASN:HB2	1:AI:28:LYS:HD2	2.02	0.41
1:AM:58:ASP:HB3	1:AM:65:ILE:HD11	2.01	0.41
1:AR:106:GLN:HB3	1:EA:35:ARG:HD3	2.03	0.41
1:AU:26:ASN:HB2	1:AU:28:LYS:HD2	2.02	0.41
1:AV:74:ILE:HD13	1:AV:83:LYS:HG2	2.02	0.41
1:AZ:74:ILE:HG21	1:AZ:83:LYS:HG2	2.01	0.41
1:BA:10:ASP:HB3	1:GA:111:ALA:HB1	2.03	0.41
1:BB:32:ALA:HB3	1:BB:53:LYS:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:2:LYS:HD2	1:BM:2:LYS:HA	1.65	0.41
1:BT:23:ASP:OD2	1:BT:26:ASN:ND2	2.53	0.41
1:CR:26:ASN:HB2	1:CR:28:LYS:HD2	2.02	0.41
1:CT:12:TYR:HD2	1:CT:24:PHE:CZ	2.37	0.41
1:DD:2:LYS:HD3	1:DD:2:LYS:HA	1.88	0.41
1:DK:90:ILE:HD12	1:DK:90:ILE:HA	1.96	0.41
1:DM:74:ILE:HD13	1:DM:83:LYS:HG2	2.02	0.41
1:DP:26:ASN:HB2	1:DP:28:LYS:HD2	2.02	0.41
1:DT:53:LYS:HB3	1:DT:69:ASN:ND2	2.35	0.41
1:DU:26:ASN:HB2	1:DU:28:LYS:HD2	2.02	0.41
1:EG:90:ILE:HG21	1:FW:68:VAL:HG11	2.02	0.41
1:EN:68:VAL:HG11	1:EO:90:ILE:HG21	2.03	0.41
1:EZ:101:GLU:O	1:EZ:105:ASP:HB2	2.20	0.41
1:FT:47:MET:HB2	1:FT:49:LYS:NZ	2.35	0.41
1:GE:53:LYS:HB3	1:GE:69:ASN:ND2	2.35	0.41
1:GG:26:ASN:HB2	1:GG:28:LYS:HD2	2.02	0.41
1:GN:51:GLU:HG3	1:GN:69:ASN:OD1	2.21	0.41
1:GO:15:GLU:HB3	1:GO:18:VAL:HB	2.02	0.41
1:GP:28:LYS:HB3	1:GP:28:LYS:HE2	1.83	0.41
1:AA:45:PRO:HB2	1:AA:76:ALA:HB3	2.02	0.41
1:AD:99:TRP:CH2	1:AE:87:MET:HG2	2.56	0.41
1:AE:36:LEU:HD12	1:AE:36:LEU:HA	1.92	0.41
1:AF:2:LYS:HD3	1:AF:2:LYS:HA	1.76	0.41
1:AJ:45:PRO:HB2	1:AJ:76:ALA:HB3	2.02	0.41
1:AM:23:ASP:OD2	1:AM:26:ASN:ND2	2.53	0.41
1:AM:57:VAL:HG22	1:AM:64:LEU:HA	2.03	0.41
1:AQ:15:GLU:HG2	1:AQ:16:LYS:H	1.85	0.41
1:AU:26:ASN:ND2	1:AU:29:ASP:OD2	2.46	0.41
1:AV:40:ARG:NH1	1:AV:40:ARG:HG3	2.36	0.41
1:AX:13:SER:HB2	1:FY:16:LYS:HD2	2.02	0.41
1:BJ:26:ASN:HB2	1:BJ:28:LYS:HD2	2.02	0.41
1:BT:58:ASP:HB3	1:BT:65:ILE:HD11	2.01	0.41
1:BW:45:PRO:HB2	1:BW:76:ALA:HB3	2.02	0.41
1:BY:26:ASN:HB2	1:BY:28:LYS:HD2	2.02	0.41
1:CE:51:GLU:OE2	1:CE:53:LYS:HD3	2.21	0.41
1:CJ:32:ALA:HB3	1:CJ:53:LYS:HG3	2.02	0.41
1:CK:26:ASN:HB2	1:CK:28:LYS:HD2	2.02	0.41
1:CN:2:LYS:HD3	1:CN:2:LYS:HA	1.82	0.41
1:CT:2:LYS:HD3	1:CT:2:LYS:HA	1.92	0.41
1:CZ:28:LYS:O	1:CZ:56:ARG:HA	2.21	0.41
1:DG:26:ASN:HB2	1:DG:28:LYS:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DN:1:SER:N	1:DN:33:TYR:OH	2.53	0.41
1:DY:45:PRO:HB2	1:DY:76:ALA:HB3	2.02	0.41
1:EB:23:ASP:OD2	1:EB:26:ASN:ND2	2.53	0.41
1:EC:97:GLY:O	1:EC:101:GLU:HG3	2.21	0.41
1:EW:45:PRO:HB2	1:EW:76:ALA:HB3	2.02	0.41
1:EY:83:LYS:HB3	1:FH:104:THR:HG22	2.01	0.41
1:FL:2:LYS:HD3	1:FL:2:LYS:HA	1.87	0.41
1:FX:47:MET:HB2	1:FX:49:LYS:NZ	2.36	0.41
1:GG:104:THR:HG22	1:GH:83:LYS:CG	2.43	0.41
1:GR:26:ASN:HB2	1:GR:28:LYS:HD2	2.03	0.41
1:AL:2:LYS:HE2	1:EB:112:THR:OG1	2.21	0.41
1:AM:47:MET:HB2	1:AM:49:LYS:NZ	2.36	0.41
1:AN:90:ILE:HD12	1:AN:90:ILE:HA	1.96	0.41
1:AU:68:VAL:HG11	1:GF:90:ILE:HG21	2.02	0.41
1:BD:45:PRO:HB2	1:BD:76:ALA:HB3	2.03	0.41
1:BN:28:LYS:HB3	1:BN:28:LYS:HE2	1.82	0.41
1:BT:112:THR:OG1	1:GO:2:LYS:HE2	2.20	0.41
1:CD:1:SER:N	1:CD:33:TYR:OH	2.53	0.41
1:CD:53:LYS:NZ	1:CD:55:THR:OG1	2.54	0.41
1:CE:87:MET:HE3	1:CE:87:MET:HB3	1.86	0.41
1:CE:106:GLN:HB3	1:CN:35:ARG:HD3	2.03	0.41
1:CK:90:ILE:HG21	1:CT:68:VAL:HG11	2.03	0.41
1:CL:45:PRO:HB2	1:CL:76:ALA:HB3	2.02	0.41
1:CS:35:ARG:O	1:CS:36:LEU:HD12	2.20	0.41
1:CX:83:LYS:HB2	1:CX:83:LYS:HE2	1.93	0.41
1:CY:15:GLU:HG2	1:CY:16:LYS:H	1.85	0.41
1:DA:68:VAL:HG11	1:DB:90:ILE:HG21	2.03	0.41
1:DJ:23:ASP:OD2	1:DJ:26:ASN:ND2	2.54	0.41
1:DY:7:GLN:NE2	1:DZ:89:ILE:HD11	2.35	0.41
1:DZ:1:SER:N	1:DZ:33:TYR:OH	2.53	0.41
1:EH:40:ARG:HH12	1:EH:43:ASP:C	2.23	0.41
1:EH:74:ILE:HD13	1:EH:83:LYS:HG2	2.02	0.41
1:EN:47:MET:HB2	1:EN:49:LYS:HZ2	1.84	0.41
1:EQ:47:MET:HB2	1:EQ:49:LYS:NZ	2.36	0.41
1:ER:15:GLU:HG2	1:ER:17:ASP:H	1.86	0.41
1:FC:47:MET:HB2	1:FC:49:LYS:NZ	2.36	0.41
1:FC:108:LEU:HD13	1:FD:19:VAL:HG23	2.03	0.41
1:FH:12:TYR:HD2	1:FH:24:PHE:CZ	2.39	0.41
1:FI:28:LYS:HB3	1:FI:28:LYS:HE2	1.83	0.41
1:FM:53:LYS:HB3	1:FM:69:ASN:OD1	2.21	0.41
1:FR:101:GLU:O	1:FR:105:ASP:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FV:56:ARG:HG2	1:FV:65:ILE:HD12	2.02	0.41
1:GA:83:LYS:HE3	1:GB:104:THR:HA	2.03	0.41
1:GQ:103:VAL:O	1:GQ:104:THR:OG1	2.34	0.41
1:AA:40:ARG:HG3	1:AA:40:ARG:HH11	1.86	0.41
1:AD:45:PRO:HB2	1:AD:76:ALA:HB3	2.02	0.41
1:AD:90:ILE:HD13	1:AE:54:ILE:HG22	2.03	0.41
1:AI:108:LEU:HD13	1:EP:19:VAL:HG23	2.03	0.41
1:AZ:97:GLY:O	1:AZ:101:GLU:HG3	2.21	0.41
1:BK:112:THR:OG1	1:DC:2:LYS:HE2	2.21	0.41
1:BQ:103:VAL:O	1:BQ:104:THR:OG1	2.32	0.41
1:BT:57:VAL:HG22	1:BT:64:LEU:HA	2.03	0.41
1:CB:108:LEU:HD13	1:GL:19:VAL:HG23	2.03	0.41
1:CE:35:ARG:HD3	1:CN:106:GLN:HB3	2.03	0.41
1:CE:100:THR:HG23	1:CN:87:MET:HE1	2.03	0.41
1:CF:57:VAL:HG22	1:CF:64:LEU:HA	2.03	0.41
1:CM:1:SER:N	1:CM:33:TYR:OH	2.53	0.41
1:CM:15:GLU:HG2	1:CM:16:LYS:H	1.85	0.41
1:CR:32:ALA:HB3	1:CR:53:LYS:HG2	2.02	0.41
1:DL:12:TYR:HD2	1:DL:24:PHE:CZ	2.38	0.41
1:DM:40:ARG:HH12	1:DM:43:ASP:C	2.23	0.41
1:DZ:74:ILE:HG21	1:DZ:83:LYS:CD	2.51	0.41
1:EA:28:LYS:O	1:EA:56:ARG:HA	2.20	0.41
1:EF:53:LYS:HB3	1:EF:69:ASN:ND2	2.34	0.41
1:EO:53:LYS:HB3	1:EO:69:ASN:ND2	2.35	0.41
1:FE:108:LEU:HD13	1:FN:19:VAL:HG23	2.03	0.41
1:FL:83:LYS:HE3	1:FM:104:THR:HA	2.03	0.41
1:GI:26:ASN:HB2	1:GI:28:LYS:HD2	2.03	0.41
1:GS:90:ILE:HD13	1:GT:54:ILE:HG22	2.02	0.41
1:GW:26:ASN:OD1	1:GW:28:LYS:HG2	2.21	0.41
1:AC:108:LEU:HD13	1:ES:19:VAL:HG23	2.03	0.41
1:AF:90:ILE:HG21	1:EV:68:VAL:HG11	2.02	0.41
1:AJ:40:ARG:HG3	1:AJ:40:ARG:HH11	1.86	0.41
1:AM:112:THR:OG1	1:DX:2:LYS:HE2	2.21	0.41
1:AO:12:TYR:HD2	1:AO:24:PHE:CZ	2.38	0.41
1:AQ:1:SER:N	1:AQ:33:TYR:OH	2.53	0.41
1:AR:51:GLU:OE2	1:AR:53:LYS:HD3	2.21	0.41
1:AS:54:ILE:HG22	1:AT:90:ILE:HD13	2.03	0.41
1:AU:28:LYS:O	1:AU:56:ARG:HA	2.21	0.41
1:AV:40:ARG:HH12	1:AV:43:ASP:C	2.23	0.41
1:AV:45:PRO:HB2	1:AV:76:ALA:HB3	2.02	0.41
1:AV:90:ILE:HD12	1:AV:90:ILE:HA	1.98	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:23:ASP:OD2	1:AY:26:ASN:ND2	2.53	0.41
1:BA:108:LEU:HD13	1:GC:19:VAL:HG23	2.03	0.41
1:BB:54:ILE:HG22	1:BC:90:ILE:HD13	2.03	0.41
1:BD:28:LYS:O	1:BD:56:ARG:HA	2.21	0.41
1:BG:12:TYR:HD2	1:BG:24:PHE:CZ	2.39	0.41
1:BH:99:TRP:CH2	1:BI:87:MET:HG2	2.56	0.41
1:BN:26:ASN:HB2	1:BN:28:LYS:HD2	2.02	0.41
1:BV:19:VAL:HG23	1:GO:108:LEU:HD13	2.03	0.41
1:BV:108:LEU:HD13	1:GO:19:VAL:HG23	2.03	0.41
1:BW:99:TRP:CH2	1:BX:87:MET:HG2	2.56	0.41
1:CB:35:ARG:HD3	1:GL:106:GLN:HB3	2.03	0.41
1:CC:2:LYS:HD3	1:CC:2:LYS:HA	1.81	0.41
1:CD:15:GLU:HG2	1:CD:16:LYS:H	1.85	0.41
1:CH:36:LEU:HD12	1:CH:36:LEU:HA	1.84	0.41
1:CN:26:ASN:ND2	1:CN:29:ASP:OD2	2.42	0.41
1:CO:40:ARG:NH1	1:CO:40:ARG:HG3	2.36	0.41
1:CU:12:TYR:CB	1:CU:22:ARG:HG3	2.51	0.41
1:CY:74:ILE:HG21	1:CY:83:LYS:CD	2.51	0.41
1:DA:40:ARG:HH12	1:DA:43:ASP:C	2.23	0.41
1:DA:40:ARG:HH11	1:DA:40:ARG:HG3	1.86	0.41
1:DA:74:ILE:HD13	1:DA:83:LYS:HG2	2.02	0.41
1:DD:28:LYS:HB3	1:DD:28:LYS:HE2	1.83	0.41
1:DG:32:ALA:HB3	1:DG:53:LYS:HG2	2.02	0.41
1:DH:23:ASP:OD2	1:DH:26:ASN:ND2	2.54	0.41
1:DJ:112:THR:OG1	1:DO:2:LYS:HE2	2.21	0.41
1:DP:54:ILE:HG22	1:DQ:90:ILE:HD13	2.03	0.41
1:DS:45:PRO:HB2	1:DS:76:ALA:HB3	2.03	0.41
1:DT:11:ILE:HD11	1:DT:14:THR:OG1	2.21	0.41
1:DV:40:ARG:HH12	1:DV:43:ASP:C	2.23	0.41
1:DW:1:SER:N	1:DW:33:TYR:OH	2.53	0.41
1:DW:17:ASP:HB3	1:DW:35:ARG:O	2.21	0.41
1:DW:23:ASP:OD2	1:DW:26:ASN:ND2	2.54	0.41
1:EA:26:ASN:ND2	1:EA:29:ASP:OD2	2.46	0.41
1:EB:57:VAL:HG22	1:EB:64:LEU:HA	2.03	0.41
1:EC:23:ASP:OD2	1:EC:26:ASN:ND2	2.54	0.41
1:EE:28:LYS:HB3	1:EE:28:LYS:HE2	1.83	0.41
1:EF:32:ALA:HB3	1:EF:53:LYS:HG3	2.01	0.41
1:EH:40:ARG:HG3	1:EH:40:ARG:HH11	1.86	0.41
1:EH:45:PRO:HB2	1:EH:76:ALA:HB3	2.02	0.41
1:EI:1:SER:N	1:EI:33:TYR:OH	2.53	0.41
1:EK:103:VAL:O	1:EK:104:THR:OG1	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EM:11:ILE:HG22	1:FR:110:LEU:HD13	2.03	0.41
1:EN:108:LEU:HD13	1:EO:19:VAL:HG23	2.02	0.41
1:EQ:2:LYS:HD3	1:EQ:2:LYS:HA	1.88	0.41
1:ER:34:LYS:NZ	1:ER:36:LEU:HD13	2.35	0.41
1:ET:28:LYS:HB3	1:ET:28:LYS:HE2	1.83	0.41
1:ET:104:THR:HG22	1:EU:83:LYS:CG	2.43	0.41
1:EY:12:TYR:HD2	1:EY:24:PHE:CZ	2.39	0.41
1:FC:2:LYS:HD3	1:FC:2:LYS:HA	1.88	0.41
1:FL:40:ARG:HH11	1:FL:40:ARG:HG3	1.86	0.41
1:FU:87:MET:HE1	1:FV:100:THR:HG23	2.03	0.41
1:FX:50:SER:HB2	1:FY:102:LEU:HG	2.02	0.41
1:GA:40:ARG:HH11	1:GA:40:ARG:HG3	1.86	0.41
1:GA:104:THR:HG22	1:GB:83:LYS:HB3	2.02	0.41
1:GB:51:GLU:HG3	1:GB:69:ASN:OD1	2.21	0.41
1:GH:103:VAL:O	1:GH:104:THR:OG1	2.34	0.41
1:GJ:49:LYS:HE3	1:GJ:73:SER:OG	2.21	0.41
1:GJ:104:THR:HG22	1:GK:83:LYS:HD2	2.01	0.41
1:GJ:108:LEU:HD13	1:GK:19:VAL:HG23	2.03	0.41
1:GL:51:GLU:CD	1:GL:69:ASN:HD21	2.25	0.41
1:GO:17:ASP:HB3	1:GO:35:ARG:HB3	2.03	0.41
1:GP:26:ASN:HB2	1:GP:28:LYS:HD2	2.02	0.41
1:GV:101:GLU:O	1:GV:105:ASP:HB2	2.20	0.41
1:GW:53:LYS:HB2	1:GW:53:LYS:NZ	2.35	0.41
1:AV:40:ARG:HG3	1:AV:40:ARG:HH11	1.86	0.41
1:AW:1:SER:N	1:AW:33:TYR:OH	2.53	0.41
1:AY:47:MET:HB2	1:AY:49:LYS:NZ	2.35	0.41
1:BF:1:SER:N	1:BF:33:TYR:OH	2.53	0.41
1:BJ:90:ILE:HG21	1:GR:68:VAL:HG11	2.02	0.41
1:BN:35:ARG:O	1:BN:36:LEU:HD12	2.21	0.41
1:BS:35:ARG:HD3	1:CZ:106:GLN:HB3	2.03	0.41
1:BZ:40:ARG:NH1	1:BZ:40:ARG:HG3	2.36	0.41
1:BZ:40:ARG:HG3	1:BZ:40:ARG:HH11	1.86	0.41
1:CL:68:VAL:HG11	1:CM:90:ILE:HG21	2.03	0.41
1:CR:1:SER:O	1:CR:2:LYS:HE2	2.21	0.41
1:CZ:51:GLU:OE2	1:CZ:53:LYS:HD3	2.21	0.41
1:DD:12:TYR:CB	1:DD:22:ARG:HG3	2.51	0.41
1:DG:1:SER:O	1:DG:2:LYS:HE2	2.21	0.41
1:DJ:19:VAL:HG23	1:DK:108:LEU:HD13	2.03	0.41
1:DJ:57:VAL:HG22	1:DJ:64:LEU:HA	2.03	0.41
1:DS:90:ILE:HD12	1:DS:90:ILE:HA	1.97	0.41
1:DT:1:SER:N	1:DT:33:TYR:OH	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EE:26:ASN:HB2	1:EE:28:LYS:HD2	2.03	0.41
1:EE:99:TRP:CH2	1:EF:87:MET:HG2	2.56	0.41
1:EM:83:LYS:HB3	1:FT:104:THR:HG22	2.02	0.41
1:EM:104:THR:HG22	1:FT:83:LYS:HB3	2.02	0.41
1:EW:68:VAL:HG11	1:EX:90:ILE:HG21	2.03	0.41
1:FA:74:ILE:HG21	1:FA:83:LYS:HG2	2.03	0.41
1:FG:56:ARG:HG2	1:FG:65:ILE:HD12	2.02	0.41
1:FI:87:MET:HE1	1:FJ:100:THR:HA	2.03	0.41
1:FI:104:THR:HG22	1:FJ:83:LYS:CG	2.44	0.41
1:FL:104:THR:HG22	1:FM:83:LYS:HB3	2.02	0.41
1:FR:34:LYS:HB3	1:FR:51:GLU:HB3	2.02	0.41
1:GN:51:GLU:OE2	1:GN:53:LYS:NZ	2.35	0.41
1:GP:104:THR:HG22	1:GQ:83:LYS:CG	2.44	0.41
1:AC:87:MET:HE3	1:ES:100:THR:HA	2.03	0.40
1:AD:12:TYR:CB	1:AD:22:ARG:HG3	2.51	0.40
1:AG:1:SER:O	1:AG:2:LYS:HE2	2.21	0.40
1:AG:32:ALA:HB3	1:AG:53:LYS:HG2	2.02	0.40
1:AN:23:ASP:OD2	1:AN:26:ASN:ND2	2.54	0.40
1:AO:90:ILE:HG21	1:DX:68:VAL:HG11	2.03	0.40
1:AR:12:TYR:HD2	1:AR:24:PHE:CZ	2.39	0.40
1:BB:35:ARG:O	1:BB:36:LEU:HD12	2.21	0.40
1:BE:68:VAL:HG11	1:BF:90:ILE:HG21	2.03	0.40
1:BK:19:VAL:HG23	1:BL:108:LEU:HD13	2.03	0.40
1:BK:57:VAL:HG22	1:BK:64:LEU:HA	2.03	0.40
1:BL:97:GLY:O	1:BL:101:GLU:HG3	2.21	0.40
1:CC:68:VAL:HG11	1:CD:90:ILE:HG21	2.02	0.40
1:CO:40:ARG:HG3	1:CO:40:ARG:HH11	1.86	0.40
1:CT:28:LYS:O	1:CT:56:ARG:HA	2.21	0.40
1:DI:28:LYS:O	1:DI:56:ARG:HA	2.21	0.40
1:DL:90:ILE:HG21	1:DO:68:VAL:HG11	2.03	0.40
1:DP:1:SER:O	1:DP:2:LYS:HE2	2.21	0.40
1:DP:35:ARG:O	1:DP:36:LEU:HD12	2.21	0.40
1:DQ:23:ASP:OD2	1:DQ:26:ASN:ND2	2.54	0.40
1:DR:28:LYS:O	1:DR:56:ARG:HA	2.21	0.40
1:EA:51:GLU:OE2	1:EA:53:LYS:HD3	2.21	0.40
1:ET:87:MET:HE1	1:EU:100:THR:HA	2.03	0.40
1:FL:45:PRO:HB2	1:FL:76:ALA:HB3	2.02	0.40
1:FN:31:LEU:HD12	1:FN:53:LYS:O	2.21	0.40
1:FV:18:VAL:HG22	1:FV:34:LYS:HG3	2.04	0.40
1:FW:26:ASN:HB2	1:FW:28:LYS:HD2	2.03	0.40
1:FY:15:GLU:HG2	1:FY:17:ASP:H	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GD:90:ILE:HD13	1:GE:54:ILE:HG22	2.03	0.40
1:GM:83:LYS:HE3	1:GN:104:THR:HA	2.03	0.40
1:AC:106:GLN:HB3	1:ES:35:ARG:HD3	2.03	0.40
1:AR:35:ARG:HD3	1:EA:106:GLN:HB3	2.03	0.40
1:AS:35:ARG:O	1:AS:36:LEU:HD12	2.22	0.40
1:AW:34:LYS:HZ3	1:AW:36:LEU:HD13	1.86	0.40
1:AZ:23:ASP:OD2	1:AZ:26:ASN:ND2	2.54	0.40
1:BH:45:PRO:HB2	1:BH:76:ALA:HB3	2.03	0.40
1:BU:97:GLY:O	1:BU:101:GLU:HG3	2.21	0.40
1:BY:89:ILE:HG21	1:GI:54:ILE:HD13	2.03	0.40
1:CS:23:ASP:OD2	1:CS:26:ASN:ND2	2.54	0.40
1:DA:45:PRO:HB2	1:DA:76:ALA:HB3	2.02	0.40
1:DI:68:VAL:HG11	1:DU:90:ILE:HG21	2.03	0.40
1:DM:40:ARG:HG3	1:DM:40:ARG:HH11	1.86	0.40
1:DM:45:PRO:HB2	1:DM:76:ALA:HB3	2.02	0.40
1:DS:110:LEU:HD23	1:DT:19:VAL:HG21	2.02	0.40
1:EL:53:LYS:NZ	1:EL:55:THR:OG1	2.54	0.40
1:EN:28:LYS:HB3	1:EN:28:LYS:HE2	1.83	0.40
1:EX:53:LYS:NZ	1:EX:53:LYS:HB2	2.36	0.40
1:EY:104:THR:HG22	1:FH:83:LYS:HB3	2.02	0.40
1:EZ:68:VAL:HG11	1:FA:90:ILE:HG21	2.02	0.40
1:FH:2:LYS:HD3	1:FH:2:LYS:HA	1.83	0.40
1:FK:45:PRO:HB2	1:FK:76:ALA:HB3	2.02	0.40
1:FO:49:LYS:HE3	1:FO:73:SER:OG	2.21	0.40
1:GB:49:LYS:HE3	1:GB:73:SER:OG	2.21	0.40
1:GC:31:LEU:HD12	1:GC:53:LYS:O	2.21	0.40
1:GF:26:ASN:HB2	1:GF:28:LYS:HD2	2.02	0.40
1:GN:32:ALA:HB3	1:GN:53:LYS:HG3	2.03	0.40
1:AC:19:VAL:HG23	1:ES:108:LEU:HD13	2.04	0.40
1:AH:90:ILE:HD12	1:AH:90:ILE:HA	1.96	0.40
1:AO:19:VAL:HG23	1:DX:108:LEU:HD13	2.04	0.40
1:BN:54:ILE:HG22	1:BO:90:ILE:HD13	2.03	0.40
1:BO:23:ASP:OD2	1:BO:26:ASN:ND2	2.55	0.40
1:BQ:68:VAL:HG11	1:BR:90:ILE:HG21	2.03	0.40
1:BS:100:THR:HG23	1:CZ:87:MET:HE1	2.02	0.40
1:BV:2:LYS:HD2	1:BV:2:LYS:HA	1.65	0.40
1:CE:28:LYS:O	1:CE:56:ARG:HA	2.21	0.40
1:CE:87:MET:HE1	1:CN:100:THR:HG23	2.04	0.40
1:CF:2:LYS:HD3	1:CF:2:LYS:HA	1.87	0.40
1:CF:19:VAL:HG23	1:CG:108:LEU:HD13	2.03	0.40
1:CI:90:ILE:HD12	1:CI:90:ILE:HA	1.97	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:99:TRP:CH2	1:CJ:87:MET:HG2	2.56	0.40
1:CM:53:LYS:NZ	1:CM:55:THR:OG1	2.55	0.40
1:CO:68:VAL:HG11	1:CP:90:ILE:HG21	2.03	0.40
1:CO:74:ILE:HD13	1:CO:83:LYS:HG2	2.02	0.40
1:CU:28:LYS:HB3	1:CU:28:LYS:HE2	1.83	0.40
1:CW:47:MET:HB2	1:CW:49:LYS:HE2	2.04	0.40
1:CY:90:ILE:HD12	1:CY:90:ILE:HA	1.98	0.40
1:DA:40:ARG:NH1	1:DA:40:ARG:HG3	2.36	0.40
1:DI:45:PRO:HB2	1:DI:76:ALA:HB3	2.02	0.40
1:DV:40:ARG:HG3	1:DV:40:ARG:HH11	1.86	0.40
1:EM:28:LYS:O	1:EM:56:ARG:HA	2.21	0.40
1:EN:110:LEU:HD23	1:EO:19:VAL:HG21	2.03	0.40
1:EQ:50:SER:HB2	1:ER:102:LEU:HG	2.02	0.40
1:FE:56:ARG:HG2	1:FE:65:ILE:HB	2.04	0.40
1:FY:34:LYS:NZ	1:FY:36:LEU:HD13	2.35	0.40
1:GH:11:ILE:HD11	1:GH:14:THR:OG1	2.22	0.40
1:GJ:68:VAL:HG11	1:GK:90:ILE:HG21	2.02	0.40
1:GX:47:MET:HB2	1:GX:49:LYS:NZ	2.35	0.40
1:AE:47:MET:HB2	1:AE:49:LYS:NZ	2.37	0.40
1:AM:2:LYS:HD3	1:AM:2:LYS:HA	1.87	0.40
1:AT:23:ASP:OD2	1:AT:26:ASN:ND2	2.55	0.40
1:AT:49:LYS:HE3	1:AT:73:SER:OG	2.22	0.40
1:AX:106:GLN:HB3	1:FZ:35:ARG:HD3	2.03	0.40
1:BC:23:ASP:OD2	1:BC:26:ASN:ND2	2.55	0.40
1:BD:68:VAL:HG11	1:GU:90:ILE:HG21	2.02	0.40
1:BE:2:LYS:HD3	1:BE:2:LYS:HA	1.86	0.40
1:BJ:47:MET:HB2	1:BJ:49:LYS:HE2	2.03	0.40
1:BT:47:MET:HB2	1:BT:49:LYS:NZ	2.35	0.40
1:BU:23:ASP:OD2	1:BU:26:ASN:ND2	2.54	0.40
1:CB:15:GLU:HB3	1:CB:18:VAL:HB	2.04	0.40
1:CG:97:GLY:O	1:CG:101:GLU:HG3	2.21	0.40
1:CI:35:ARG:O	1:CI:36:LEU:HD12	2.22	0.40
1:DM:54:ILE:HD13	1:DN:89:ILE:HG21	2.03	0.40
1:DP:28:LYS:HB3	1:DP:28:LYS:HE2	1.82	0.40
1:DS:35:ARG:O	1:DS:36:LEU:HD12	2.22	0.40
1:DS:101:GLU:O	1:DS:105:ASP:HB3	2.20	0.40
1:DZ:53:LYS:NZ	1:DZ:55:THR:OG1	2.54	0.40
1:EH:90:ILE:HD12	1:EH:90:ILE:HA	1.98	0.40
1:EX:26:ASN:OD1	1:EX:28:LYS:HG2	2.20	0.40
1:FF:68:VAL:HG11	1:FG:90:ILE:HG21	2.04	0.40
1:FM:49:LYS:HE3	1:FM:73:SER:OG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FQ:51:GLU:CD	1:FQ:69:ASN:HD21	2.25	0.40
1:FV:11:ILE:HD11	1:FV:14:THR:OG1	2.22	0.40
1:GA:45:PRO:HB2	1:GA:76:ALA:HB3	2.02	0.40
1:GR:45:PRO:HB2	1:GR:76:ALA:HB3	2.03	0.40
1:GV:2:LYS:HD3	1:GV:2:LYS:HA	1.81	0.40
1:GW:15:GLU:HG2	1:GW:16:LYS:H	1.86	0.40
1:AI:28:LYS:O	1:AI:56:ARG:HA	2.21	0.40
1:AI:39:LYS:O	1:AI:39:LYS:HG3	2.21	0.40
1:AI:90:ILE:HG21	1:EP:68:VAL:HG11	2.04	0.40
1:AJ:68:VAL:HG11	1:AK:90:ILE:HG21	2.03	0.40
1:AS:18:VAL:HG22	1:AS:34:LYS:HG3	2.04	0.40
1:BL:23:ASP:OD2	1:BL:26:ASN:ND2	2.54	0.40
1:BP:28:LYS:O	1:BP:56:ARG:HA	2.21	0.40
1:BZ:74:ILE:HD13	1:BZ:83:LYS:HG2	2.02	0.40
1:CB:13:SER:HB2	1:GK:16:LYS:HD2	2.04	0.40
1:CF:18:VAL:HG22	1:CF:34:LYS:HG3	2.04	0.40
1:CN:12:TYR:HD2	1:CN:24:PHE:CZ	2.39	0.40
1:CV:47:MET:HB2	1:CV:49:LYS:NZ	2.37	0.40
1:CW:15:GLU:HG2	1:CW:18:VAL:HG23	2.04	0.40
1:DF:51:GLU:OE1	1:DF:53:LYS:HD3	2.20	0.40
1:DV:45:PRO:HB2	1:DV:76:ALA:HB3	2.02	0.40
1:EE:35:ARG:O	1:EE:36:LEU:HD12	2.22	0.40
1:EF:58:ASP:OD2	1:EF:61:THR:HG22	2.22	0.40
1:EJ:106:GLN:HB3	1:FQ:35:ARG:HD3	2.03	0.40
1:EK:68:VAL:HG11	1:EL:90:ILE:HG21	2.03	0.40
1:EY:2:LYS:HD3	1:EY:2:LYS:HA	1.83	0.40
1:FE:74:ILE:HG21	1:FE:83:LYS:HD3	2.03	0.40
1:FP:36:LEU:HB2	1:FP:49:LYS:CB	2.51	0.40
1:FS:101:GLU:O	1:FS:105:ASP:HB2	2.22	0.40
1:FU:68:VAL:HG11	1:FV:90:ILE:HG21	2.04	0.40
1:GN:49:LYS:HE3	1:GN:73:SER:OG	2.21	0.40
1:GQ:11:ILE:HD11	1:GQ:14:THR:OG1	2.22	0.40
1:GU:26:ASN:HB2	1:GU:28:LYS:HD2	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	AB	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	AC	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	AD	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	AE	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	AF	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	AG	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	AH	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	AI	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	AJ	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	AK	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	AL	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	AM	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	AN	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	AO	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	AP	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	AQ	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	AR	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	AS	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	AT	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	AU	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	AV	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	AW	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	AX	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	AY	111/113 (98%)	104 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AZ	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	BA	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	BB	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	BC	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	BD	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	BE	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	BF	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	BG	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	BH	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	BI	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	BJ	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	BK	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	BL	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	BM	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	BN	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	BO	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	BP	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	BQ	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	BR	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	BS	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	BT	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	BU	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	BV	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	BW	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	BX	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	BY	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	BZ	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	CA	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	CB	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	CC	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	CD	111/113 (98%)	101 (91%)	10 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CE	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	CF	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	CG	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	CH	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	CI	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	CJ	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	CK	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	CL	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	CM	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	CN	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	CO	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	CP	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	CQ	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	CR	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	CS	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	CT	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	CU	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	CV	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	CW	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	CX	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	CY	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	CZ	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	DA	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	DB	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	DC	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	DD	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	DE	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	DF	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	DG	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	DH	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	DI	111/113 (98%)	103 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DJ	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	DK	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	DL	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	DM	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	DN	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	DO	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	DP	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	DQ	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	DR	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	DS	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	DT	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	DU	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	DV	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	DW	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	DX	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	DY	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	DZ	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	EA	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	EB	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	EC	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	ED	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	EE	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	EF	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	EG	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	EH	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	EI	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	EJ	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	EK	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	EL	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	EM	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	EN	111/113 (98%)	105 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EO	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	EP	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	EQ	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
1	ER	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	ES	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	ET	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	EU	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	EV	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	EW	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	EX	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	EY	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	EZ	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	FA	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	FB	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	FC	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
1	FD	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	FE	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	FF	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	FG	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	FH	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	FI	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	FJ	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	FK	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	FL	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	FM	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	FN	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	FO	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
1	FP	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	FQ	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	FR	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	FS	111/113 (98%)	101 (91%)	10 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	FT	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	FU	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	FV	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	FW	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	FX	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
1	FY	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	FZ	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	GA	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	GB	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	GC	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	GD	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
1	GE	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	GF	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	GG	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	GH	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	GI	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	GJ	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
1	GK	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	GL	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	GM	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	GN	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	GO	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	GP	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	GQ	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
1	GR	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	GS	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
1	GT	111/113 (98%)	100 (90%)	11 (10%)	0	100	100
1	GU	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
1	GV	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
1	GW	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
1	GX	111/113 (98%)	104 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	19980/20340 (98%)	18429 (92%)	1551 (8%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	AA	94/94 (100%)	86 (92%)	8 (8%)	8 34
1	AB	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	AC	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	AD	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	AE	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	AF	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	AG	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	AH	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	AI	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	AJ	94/94 (100%)	87 (93%)	7 (7%)	11 40
1	AK	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	AL	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	AM	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	AN	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	AO	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	AP	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	AQ	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	AR	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	AS	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	AT	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	AU	94/94 (100%)	93 (99%)	1 (1%)	70 86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	AV	94/94 (100%)	86 (92%)	8 (8%)	8 34
1	AW	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	AX	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	AY	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	AZ	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	BA	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	BB	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	BC	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	BD	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	BE	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	BF	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	BG	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	BH	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	BI	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	BJ	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	BK	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	BL	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	BM	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	BN	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	BO	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	BP	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	BQ	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	BR	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	BS	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	BT	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	BU	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	BV	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	BW	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	BX	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	BY	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	BZ	94/94 (100%)	86 (92%)	8 (8%)	8 34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	CA	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CB	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	CC	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	CD	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CE	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CF	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CG	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	CH	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	CI	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	CJ	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CK	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	CL	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	CM	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CN	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CO	94/94 (100%)	87 (93%)	7 (7%)	11 40
1	CP	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CQ	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	CR	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	CS	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	CT	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	CU	94/94 (100%)	88 (94%)	6 (6%)	14 46
1	CV	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CW	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	CX	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	CY	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	CZ	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	DA	94/94 (100%)	87 (93%)	7 (7%)	11 40
1	DB	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	DC	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	DD	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	DE	94/94 (100%)	92 (98%)	2 (2%)	48 74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	DF	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	DG	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	DH	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	DI	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	DJ	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	DK	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	DL	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	DM	94/94 (100%)	86 (92%)	8 (8%)	8 34
1	DN	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	DO	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	DP	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	DQ	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	DR	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	DS	94/94 (100%)	88 (94%)	6 (6%)	14 46
1	DT	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	DU	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	DV	94/94 (100%)	87 (93%)	7 (7%)	11 40
1	DW	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	DX	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	DY	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	DZ	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	EA	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	EB	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	EC	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	ED	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	EE	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	EF	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	EG	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	EH	94/94 (100%)	86 (92%)	8 (8%)	8 34
1	EI	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	EJ	94/94 (100%)	90 (96%)	4 (4%)	25 57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	EK	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	EL	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	EM	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	EN	94/94 (100%)	88 (94%)	6 (6%)	14 46
1	EO	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	EP	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	EQ	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	ER	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	ES	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	ET	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	EU	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	EV	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	EW	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	EX	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	EY	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	EZ	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	FA	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	FB	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	FC	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	FD	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	FE	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	FF	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	FG	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	FH	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	FI	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	FJ	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	FK	94/94 (100%)	92 (98%)	2 (2%)	48 74
1	FL	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	FM	94/94 (100%)	93 (99%)	1 (1%)	70 86
1	FN	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	FO	94/94 (100%)	90 (96%)	4 (4%)	25 57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	FP	94/94 (100%)	90 (96%)	4 (4%)	25	57
1	FQ	94/94 (100%)	91 (97%)	3 (3%)	34	65
1	FR	94/94 (100%)	90 (96%)	4 (4%)	25	57
1	FS	94/94 (100%)	91 (97%)	3 (3%)	34	65
1	FT	94/94 (100%)	92 (98%)	2 (2%)	48	74
1	FU	94/94 (100%)	89 (95%)	5 (5%)	19	52
1	FV	94/94 (100%)	90 (96%)	4 (4%)	25	57
1	FW	94/94 (100%)	93 (99%)	1 (1%)	70	86
1	FX	94/94 (100%)	89 (95%)	5 (5%)	19	52
1	FY	94/94 (100%)	91 (97%)	3 (3%)	34	65
1	FZ	94/94 (100%)	91 (97%)	3 (3%)	34	65
1	GA	94/94 (100%)	89 (95%)	5 (5%)	19	52
1	GB	94/94 (100%)	93 (99%)	1 (1%)	70	86
1	GC	94/94 (100%)	91 (97%)	3 (3%)	34	65
1	GD	94/94 (100%)	88 (94%)	6 (6%)	14	46
1	GE	94/94 (100%)	91 (97%)	3 (3%)	34	65
1	GF	94/94 (100%)	90 (96%)	4 (4%)	25	57
1	GG	94/94 (100%)	89 (95%)	5 (5%)	19	52
1	GH	94/94 (100%)	91 (97%)	3 (3%)	34	65
1	GI	94/94 (100%)	93 (99%)	1 (1%)	70	86
1	GJ	94/94 (100%)	89 (95%)	5 (5%)	19	52
1	GK	94/94 (100%)	89 (95%)	5 (5%)	19	52
1	GL	94/94 (100%)	91 (97%)	3 (3%)	34	65
1	GM	94/94 (100%)	89 (95%)	5 (5%)	19	52
1	GN	94/94 (100%)	94 (100%)	0	100	100
1	GO	94/94 (100%)	91 (97%)	3 (3%)	34	65
1	GP	94/94 (100%)	89 (95%)	5 (5%)	19	52
1	GQ	94/94 (100%)	90 (96%)	4 (4%)	25	57
1	GR	94/94 (100%)	93 (99%)	1 (1%)	70	86
1	GS	94/94 (100%)	88 (94%)	6 (6%)	14	46
1	GT	94/94 (100%)	91 (97%)	3 (3%)	34	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	GU	94/94 (100%)	90 (96%)	4 (4%)	25 57
1	GV	94/94 (100%)	89 (95%)	5 (5%)	19 52
1	GW	94/94 (100%)	91 (97%)	3 (3%)	34 65
1	GX	94/94 (100%)	92 (98%)	2 (2%)	48 74
All	All	16920/16920 (100%)	16297 (96%)	623 (4%)	31 62

All (623) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AA	13	SER
1	AA	27	ASP
1	AA	28	LYS
1	AA	39	LYS
1	AA	49	LYS
1	AA	50	SER
1	AA	71	SER
1	AA	110	LEU
1	AB	27	ASP
1	AC	13	SER
1	AC	35	ARG
1	AC	58	ASP
1	AC	71	SER
1	AD	27	ASP
1	AD	28	LYS
1	AD	39	LYS
1	AD	49	LYS
1	AD	50	SER
1	AE	28	LYS
1	AE	35	ARG
1	AF	13	SER
1	AF	35	ARG
1	AF	39	LYS
1	AF	71	SER
1	AG	20	SER
1	AG	27	ASP
1	AG	28	LYS
1	AG	39	LYS
1	AG	71	SER
1	AH	28	LYS
1	AH	39	LYS
1	AH	50	SER

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Mol	Chain	Res	Type
1	AH	53	LYS
1	AI	35	ARG
1	AJ	13	SER
1	AJ	27	ASP
1	AJ	28	LYS
1	AJ	39	LYS
1	AJ	50	SER
1	AJ	71	SER
1	AJ	110	LEU
1	AK	28	LYS
1	AK	34	LYS
1	AL	13	SER
1	AL	35	ARG
1	AL	58	ASP
1	AL	71	SER
1	AM	2	LYS
1	AM	10	ASP
1	AM	13	SER
1	AM	39	LYS
1	AM	110	LEU
1	AN	28	LYS
1	AN	50	SER
1	AN	58	ASP
1	AN	75	ARG
1	AO	2	LYS
1	AP	2	LYS
1	AP	28	LYS
1	AP	39	LYS
1	AP	44	SER
1	AP	53	LYS
1	AQ	35	ARG
1	AQ	58	ASP
1	AR	13	SER
1	AR	105	ASP
1	AS	20	SER
1	AS	27	ASP
1	AS	28	LYS
1	AS	39	LYS
1	AS	71	SER
1	AT	28	LYS
1	AT	39	LYS
1	AT	50	SER

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Mol	Chain	Res	Type
1	AU	35	ARG
1	AV	13	SER
1	AV	27	ASP
1	AV	28	LYS
1	AV	39	LYS
1	AV	49	LYS
1	AV	50	SER
1	AV	71	SER
1	AV	110	LEU
1	AW	28	LYS
1	AX	13	SER
1	AX	35	ARG
1	AX	58	ASP
1	AX	71	SER
1	AY	2	LYS
1	AY	10	ASP
1	AY	13	SER
1	AY	39	LYS
1	AZ	28	LYS
1	AZ	50	SER
1	AZ	58	ASP
1	AZ	75	ARG
1	BA	2	LYS
1	BB	20	SER
1	BB	27	ASP
1	BB	28	LYS
1	BB	39	LYS
1	BB	71	SER
1	BC	28	LYS
1	BC	39	LYS
1	BC	50	SER
1	BC	53	LYS
1	BC	58	ASP
1	BD	35	ARG
1	BE	2	LYS
1	BE	28	LYS
1	BE	39	LYS
1	BE	44	SER
1	BE	53	LYS
1	BF	35	ARG
1	BF	58	ASP
1	BG	13	SER

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Mol	Chain	Res	Type
1	BG	105	ASP
1	BH	27	ASP
1	BH	28	LYS
1	BH	39	LYS
1	BH	49	LYS
1	BI	28	LYS
1	BI	35	ARG
1	BJ	13	SER
1	BJ	35	ARG
1	BJ	39	LYS
1	BJ	71	SER
1	BK	2	LYS
1	BK	39	LYS
1	BL	28	LYS
1	BL	50	SER
1	BL	58	ASP
1	BL	75	ARG
1	BM	2	LYS
1	BN	20	SER
1	BN	27	ASP
1	BN	28	LYS
1	BN	39	LYS
1	BN	71	SER
1	BO	28	LYS
1	BO	39	LYS
1	BO	50	SER
1	BP	35	ARG
1	BQ	2	LYS
1	BQ	28	LYS
1	BQ	39	LYS
1	BQ	44	SER
1	BQ	53	LYS
1	BR	35	ARG
1	BR	58	ASP
1	BS	13	SER
1	BS	105	ASP
1	BT	2	LYS
1	BT	10	ASP
1	BT	13	SER
1	BT	39	LYS
1	BU	28	LYS
1	BU	50	SER

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Mol	Chain	Res	Type
1	BU	58	ASP
1	BU	75	ARG
1	BV	2	LYS
1	BW	27	ASP
1	BW	28	LYS
1	BW	39	LYS
1	BW	49	LYS
1	BX	28	LYS
1	BX	35	ARG
1	BY	13	SER
1	BY	35	ARG
1	BY	39	LYS
1	BY	71	SER
1	BZ	13	SER
1	BZ	27	ASP
1	BZ	28	LYS
1	BZ	39	LYS
1	BZ	49	LYS
1	BZ	50	SER
1	BZ	71	SER
1	BZ	110	LEU
1	CA	28	LYS
1	CA	34	LYS
1	CB	13	SER
1	CB	35	ARG
1	CB	58	ASP
1	CB	71	SER
1	CC	2	LYS
1	CC	28	LYS
1	CC	39	LYS
1	CC	44	SER
1	CC	53	LYS
1	CD	35	ARG
1	CD	58	ASP
1	CE	13	SER
1	CE	105	ASP
1	CF	2	LYS
1	CF	39	LYS
1	CG	28	LYS
1	CG	50	SER
1	CG	58	ASP
1	CG	75	ARG

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Mol	Chain	Res	Type
1	CH	2	LYS
1	CI	27	ASP
1	CI	28	LYS
1	CI	39	LYS
1	CI	49	LYS
1	CJ	28	LYS
1	CJ	35	ARG
1	CK	13	SER
1	CK	15	GLU
1	CK	35	ARG
1	CK	39	LYS
1	CK	71	SER
1	CL	2	LYS
1	CL	28	LYS
1	CL	39	LYS
1	CL	44	SER
1	CL	53	LYS
1	CM	35	ARG
1	CM	58	ASP
1	CN	13	SER
1	CN	105	ASP
1	CO	13	SER
1	CO	27	ASP
1	CO	28	LYS
1	CO	39	LYS
1	CO	50	SER
1	CO	71	SER
1	CO	110	LEU
1	CP	28	LYS
1	CP	34	LYS
1	CQ	13	SER
1	CQ	35	ARG
1	CQ	58	ASP
1	CQ	71	SER
1	CR	20	SER
1	CR	27	ASP
1	CR	28	LYS
1	CR	39	LYS
1	CR	71	SER
1	CS	28	LYS
1	CS	39	LYS
1	CS	50	SER

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Mol	Chain	Res	Type
1	CT	35	ARG
1	CU	10	ASP
1	CU	27	ASP
1	CU	28	LYS
1	CU	39	LYS
1	CU	49	LYS
1	CU	50	SER
1	CV	28	LYS
1	CV	35	ARG
1	CW	13	SER
1	CW	35	ARG
1	CW	39	LYS
1	CW	71	SER
1	CX	2	LYS
1	CX	28	LYS
1	CX	39	LYS
1	CX	44	SER
1	CX	53	LYS
1	CY	35	ARG
1	CY	58	ASP
1	CZ	13	SER
1	CZ	105	ASP
1	DA	13	SER
1	DA	27	ASP
1	DA	28	LYS
1	DA	39	LYS
1	DA	50	SER
1	DA	71	SER
1	DA	110	LEU
1	DB	27	ASP
1	DB	34	LYS
1	DC	13	SER
1	DC	35	ARG
1	DC	58	ASP
1	DC	71	SER
1	DD	27	ASP
1	DD	28	LYS
1	DD	39	LYS
1	DD	49	LYS
1	DE	28	LYS
1	DE	35	ARG
1	DF	13	SER

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Mol	Chain	Res	Type
1	DF	35	ARG
1	DF	39	LYS
1	DF	71	SER
1	DG	20	SER
1	DG	27	ASP
1	DG	28	LYS
1	DG	39	LYS
1	DG	71	SER
1	DH	28	LYS
1	DH	39	LYS
1	DH	50	SER
1	DH	53	LYS
1	DI	35	ARG
1	DJ	2	LYS
1	DJ	13	SER
1	DJ	39	LYS
1	DK	28	LYS
1	DK	50	SER
1	DK	58	ASP
1	DK	75	ARG
1	DL	2	LYS
1	DM	13	SER
1	DM	27	ASP
1	DM	28	LYS
1	DM	39	LYS
1	DM	49	LYS
1	DM	50	SER
1	DM	71	SER
1	DM	110	LEU
1	DN	28	LYS
1	DN	34	LYS
1	DO	13	SER
1	DO	35	ARG
1	DO	58	ASP
1	DP	20	SER
1	DP	27	ASP
1	DP	28	LYS
1	DP	39	LYS
1	DP	71	SER
1	DQ	28	LYS
1	DQ	39	LYS
1	DQ	50	SER

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Mol	Chain	Res	Type
1	DR	35	ARG
1	DS	10	ASP
1	DS	27	ASP
1	DS	28	LYS
1	DS	39	LYS
1	DS	49	LYS
1	DS	50	SER
1	DT	28	LYS
1	DT	35	ARG
1	DU	13	SER
1	DU	35	ARG
1	DU	39	LYS
1	DU	71	SER
1	DV	13	SER
1	DV	27	ASP
1	DV	28	LYS
1	DV	39	LYS
1	DV	50	SER
1	DV	71	SER
1	DV	110	LEU
1	DW	28	LYS
1	DX	13	SER
1	DX	35	ARG
1	DX	58	ASP
1	DX	71	SER
1	DY	2	LYS
1	DY	28	LYS
1	DY	39	LYS
1	DY	44	SER
1	DY	53	LYS
1	DZ	35	ARG
1	DZ	58	ASP
1	EA	13	SER
1	EA	105	ASP
1	EB	2	LYS
1	EB	39	LYS
1	EC	28	LYS
1	EC	43	ASP
1	EC	50	SER
1	EC	58	ASP
1	EC	75	ARG
1	ED	2	LYS

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Mol	Chain	Res	Type
1	EE	10	ASP
1	EE	27	ASP
1	EE	28	LYS
1	EE	39	LYS
1	EE	49	LYS
1	EF	28	LYS
1	EF	35	ARG
1	EG	13	SER
1	EG	35	ARG
1	EG	39	LYS
1	EG	71	SER
1	EH	13	SER
1	EH	27	ASP
1	EH	28	LYS
1	EH	39	LYS
1	EH	49	LYS
1	EH	50	SER
1	EH	71	SER
1	EH	110	LEU
1	EI	28	LYS
1	EI	34	LYS
1	EJ	13	SER
1	EJ	35	ARG
1	EJ	58	ASP
1	EJ	71	SER
1	EK	2	LYS
1	EK	28	LYS
1	EK	39	LYS
1	EK	44	SER
1	EK	53	LYS
1	EL	35	ARG
1	EL	58	ASP
1	EM	7	GLN
1	EM	13	SER
1	EM	105	ASP
1	EN	10	ASP
1	EN	27	ASP
1	EN	28	LYS
1	EN	39	LYS
1	EN	50	SER
1	EN	53	LYS
1	EO	21	LEU

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Mol	Chain	Res	Type
1	EO	28	LYS
1	EO	35	ARG
1	EP	13	SER
1	EP	35	ARG
1	EP	39	LYS
1	EQ	2	LYS
1	EQ	13	SER
1	EQ	28	LYS
1	EQ	39	LYS
1	EQ	110	LEU
1	ER	28	LYS
1	ER	50	SER
1	ER	58	ASP
1	ES	2	LYS
1	ES	21	LEU
1	ES	35	ARG
1	ET	13	SER
1	ET	27	ASP
1	ET	28	LYS
1	ET	39	LYS
1	ET	58	ASP
1	EU	28	LYS
1	EU	39	LYS
1	EU	96	ASP
1	EV	35	ARG
1	EW	2	LYS
1	EW	28	LYS
1	EW	39	LYS
1	EW	44	SER
1	EW	50	SER
1	EX	20	SER
1	EX	35	ARG
1	EX	58	ASP
1	EY	35	ARG
1	EY	105	ASP
1	EZ	10	ASP
1	EZ	27	ASP
1	EZ	28	LYS
1	EZ	39	LYS
1	FA	21	LEU
1	FA	28	LYS
1	FA	35	ARG

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Mol	Chain	Res	Type
1	FB	13	SER
1	FB	21	LEU
1	FB	35	ARG
1	FB	39	LYS
1	FC	2	LYS
1	FC	13	SER
1	FC	28	LYS
1	FC	39	LYS
1	FD	28	LYS
1	FD	50	SER
1	FD	58	ASP
1	FE	2	LYS
1	FE	21	LEU
1	FE	35	ARG
1	FF	2	LYS
1	FF	28	LYS
1	FF	39	LYS
1	FF	44	SER
1	FF	50	SER
1	FG	20	SER
1	FG	35	ARG
1	FG	58	ASP
1	FH	7	GLN
1	FH	35	ARG
1	FH	105	ASP
1	FI	13	SER
1	FI	27	ASP
1	FI	28	LYS
1	FI	39	LYS
1	FI	58	ASP
1	FJ	28	LYS
1	FJ	39	LYS
1	FJ	50	SER
1	FJ	96	ASP
1	FK	27	ASP
1	FK	35	ARG
1	FL	13	SER
1	FL	27	ASP
1	FL	28	LYS
1	FL	39	LYS
1	FL	58	ASP
1	FM	27	ASP

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Mol	Chain	Res	Type
1	FN	13	SER
1	FN	35	ARG
1	FN	71	SER
1	FO	2	LYS
1	FO	28	LYS
1	FO	39	LYS
1	FO	110	LEU
1	FP	28	LYS
1	FP	50	SER
1	FP	58	ASP
1	FP	75	ARG
1	FQ	2	LYS
1	FQ	21	LEU
1	FQ	35	ARG
1	FR	28	LYS
1	FR	39	LYS
1	FR	44	SER
1	FR	50	SER
1	FS	20	SER
1	FS	35	ARG
1	FS	58	ASP
1	FT	35	ARG
1	FT	105	ASP
1	FU	13	SER
1	FU	27	ASP
1	FU	28	LYS
1	FU	39	LYS
1	FU	58	ASP
1	FV	28	LYS
1	FV	39	LYS
1	FV	50	SER
1	FV	96	ASP
1	FW	35	ARG
1	FX	2	LYS
1	FX	13	SER
1	FX	28	LYS
1	FX	39	LYS
1	FX	110	LEU
1	FY	28	LYS
1	FY	50	SER
1	FY	58	ASP
1	FZ	2	LYS

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Mol	Chain	Res	Type
1	FZ	21	LEU
1	FZ	35	ARG
1	GA	13	SER
1	GA	27	ASP
1	GA	28	LYS
1	GA	39	LYS
1	GA	58	ASP
1	GB	27	ASP
1	GC	13	SER
1	GC	35	ARG
1	GC	71	SER
1	GD	10	ASP
1	GD	27	ASP
1	GD	28	LYS
1	GD	39	LYS
1	GD	50	SER
1	GD	53	LYS
1	GE	21	LEU
1	GE	28	LYS
1	GE	35	ARG
1	GF	13	SER
1	GF	15	GLU
1	GF	35	ARG
1	GF	39	LYS
1	GG	13	SER
1	GG	27	ASP
1	GG	28	LYS
1	GG	39	LYS
1	GG	58	ASP
1	GH	28	LYS
1	GH	39	LYS
1	GH	96	ASP
1	GI	35	ARG
1	GJ	2	LYS
1	GJ	13	SER
1	GJ	28	LYS
1	GJ	39	LYS
1	GJ	110	LEU
1	GK	28	LYS
1	GK	36	LEU
1	GK	50	SER
1	GK	58	ASP

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Mol	Chain	Res	Type
1	GK	75	ARG
1	GL	2	LYS
1	GL	21	LEU
1	GL	35	ARG
1	GM	13	SER
1	GM	27	ASP
1	GM	28	LYS
1	GM	39	LYS
1	GM	58	ASP
1	GO	13	SER
1	GO	35	ARG
1	GO	71	SER
1	GP	13	SER
1	GP	27	ASP
1	GP	28	LYS
1	GP	39	LYS
1	GP	58	ASP
1	GQ	28	LYS
1	GQ	39	LYS
1	GQ	50	SER
1	GQ	96	ASP
1	GR	35	ARG
1	GS	10	ASP
1	GS	27	ASP
1	GS	28	LYS
1	GS	39	LYS
1	GS	50	SER
1	GS	53	LYS
1	GT	21	LEU
1	GT	28	LYS
1	GT	35	ARG
1	GU	13	SER
1	GU	15	GLU
1	GU	35	ARG
1	GU	39	LYS
1	GV	2	LYS
1	GV	28	LYS
1	GV	39	LYS
1	GV	44	SER
1	GV	50	SER
1	GW	20	SER
1	GW	35	ARG

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Mol	Chain	Res	Type
1	GW	58	ASP
1	GX	35	ARG
1	GX	105	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	AK	69	ASN
1	AM	5	ASN
1	AY	5	ASN
1	BK	5	ASN
1	BT	5	ASN
1	CA	69	ASN
1	CF	5	ASN
1	CP	69	ASN
1	DB	69	ASN
1	DJ	5	ASN
1	DN	69	ASN
1	EB	5	ASN
1	EI	69	ASN
1	FM	69	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

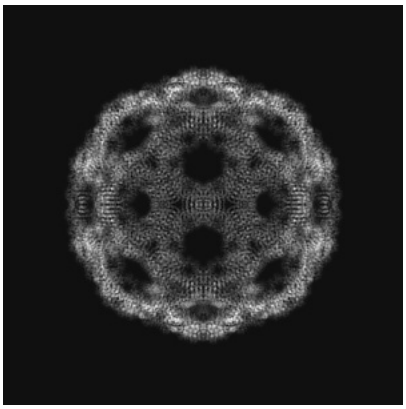
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-52005. These allow visual inspection of the internal detail of the map and identification of artifacts.

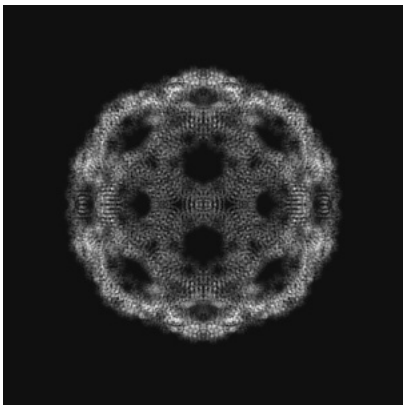
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

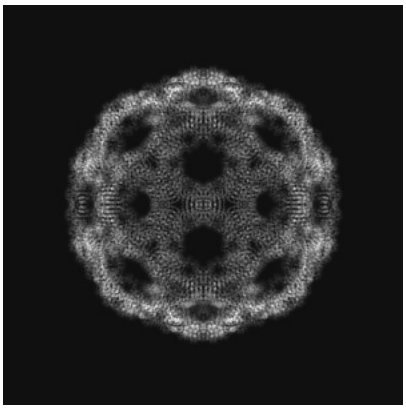
6.1.1 Primary map



X

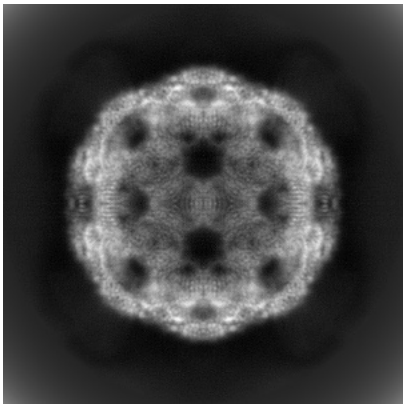


Y

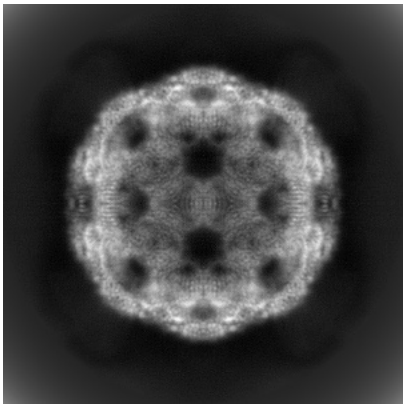


Z

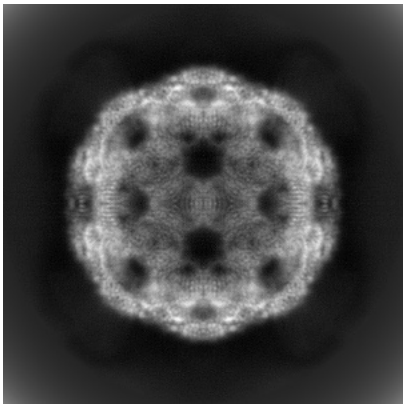
6.1.2 Raw map



X



Y

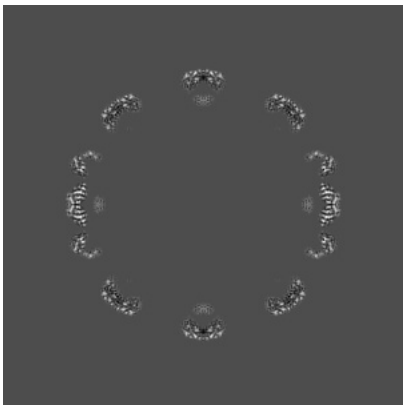


Z

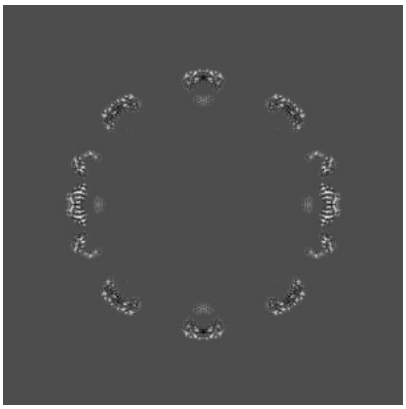
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

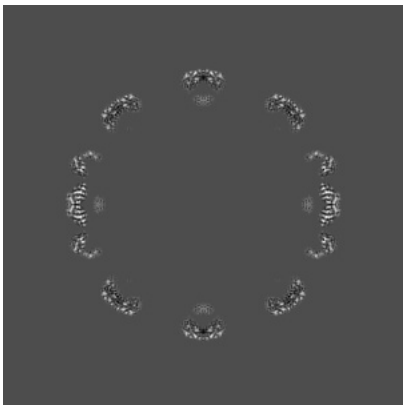
6.2.1 Primary map



X Index: 256

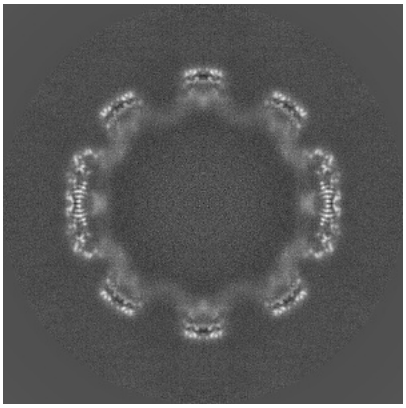


Y Index: 256

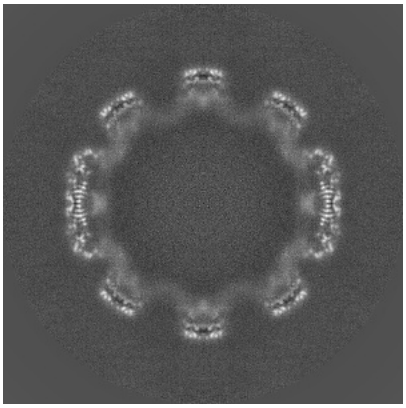


Z Index: 256

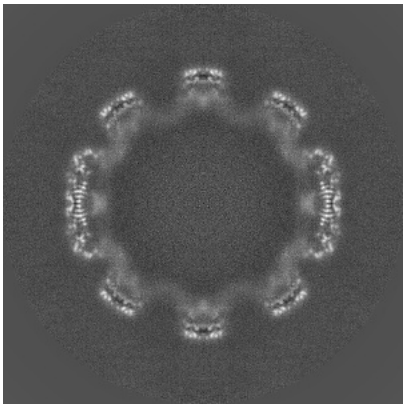
6.2.2 Raw map



X Index: 256



Y Index: 256

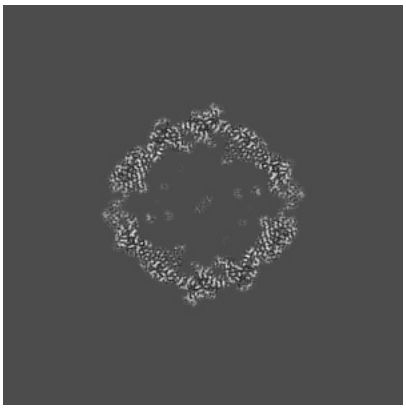


Z Index: 256

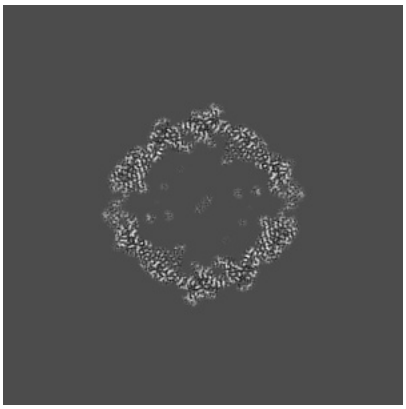
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

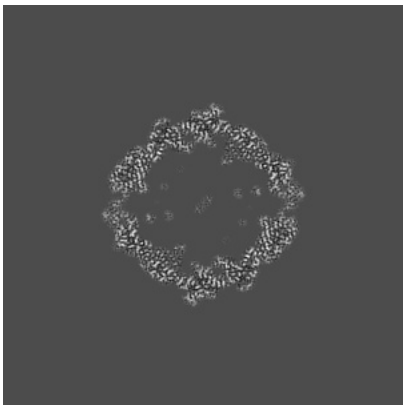
6.3.1 Primary map



X Index: 128

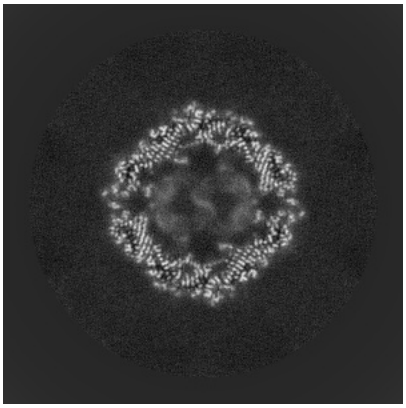


Y Index: 128

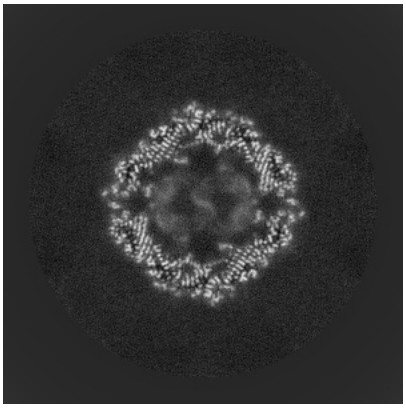


Z Index: 128

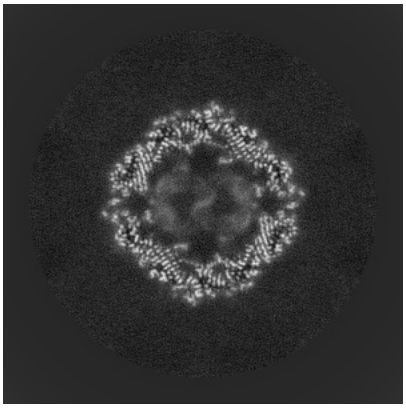
6.3.2 Raw map



X Index: 127



Y Index: 127

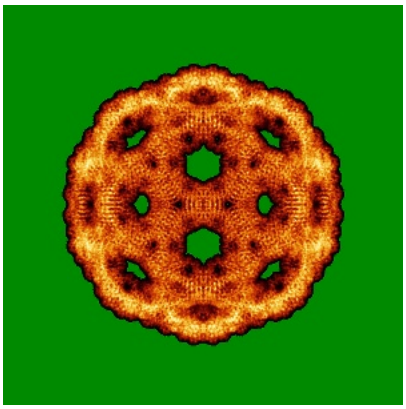


Z Index: 385

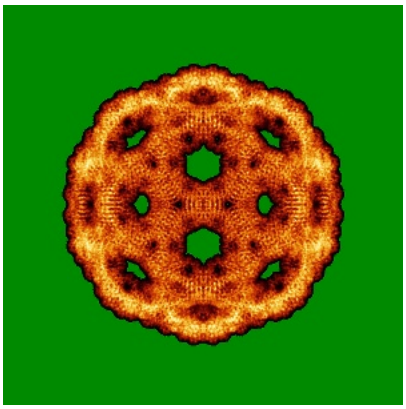
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

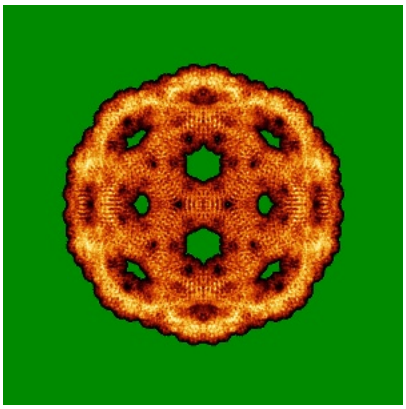
6.4.1 Primary map



X

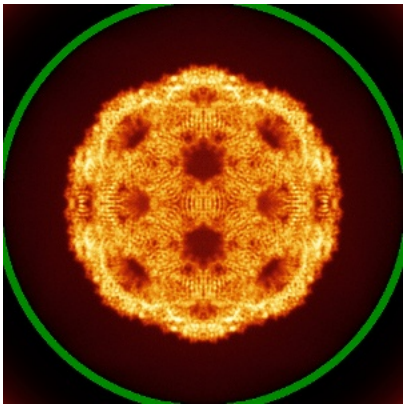


Y

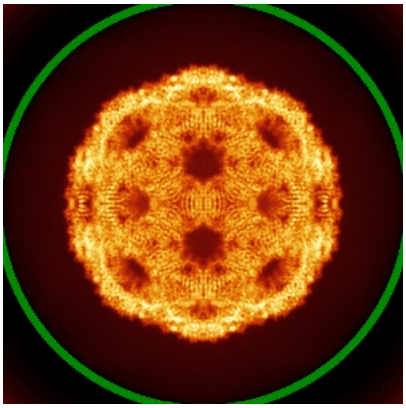


Z

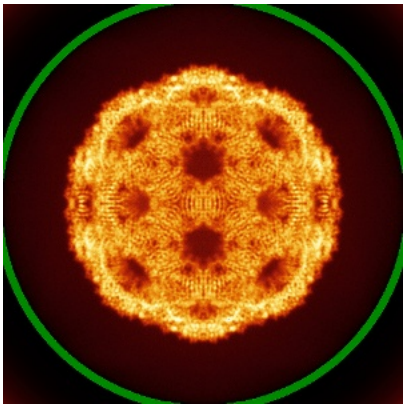
6.4.2 Raw map



X



Y

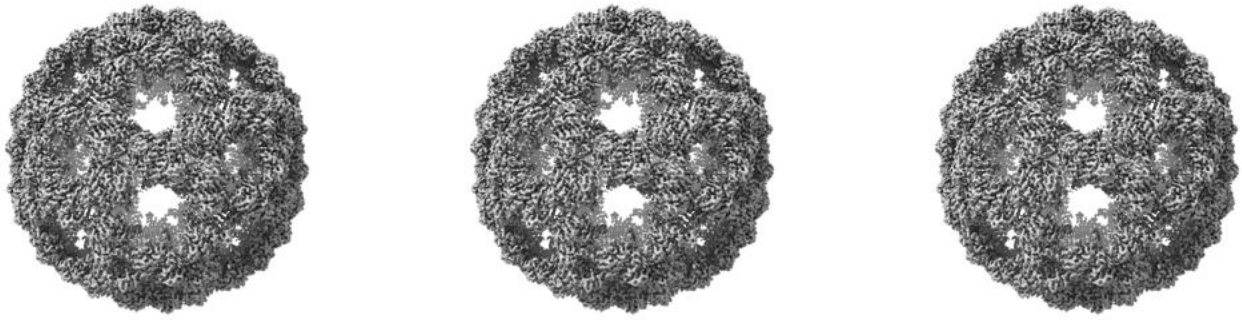


Z

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

6.5 Orthogonal surface views (i)

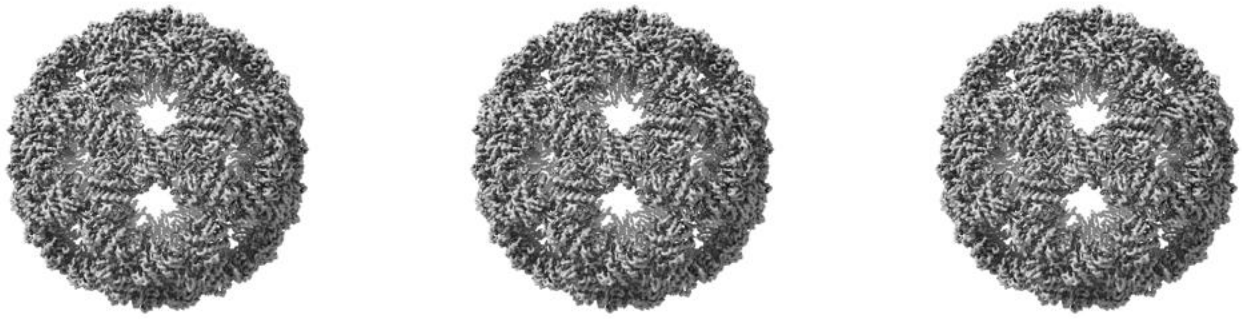
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0095. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

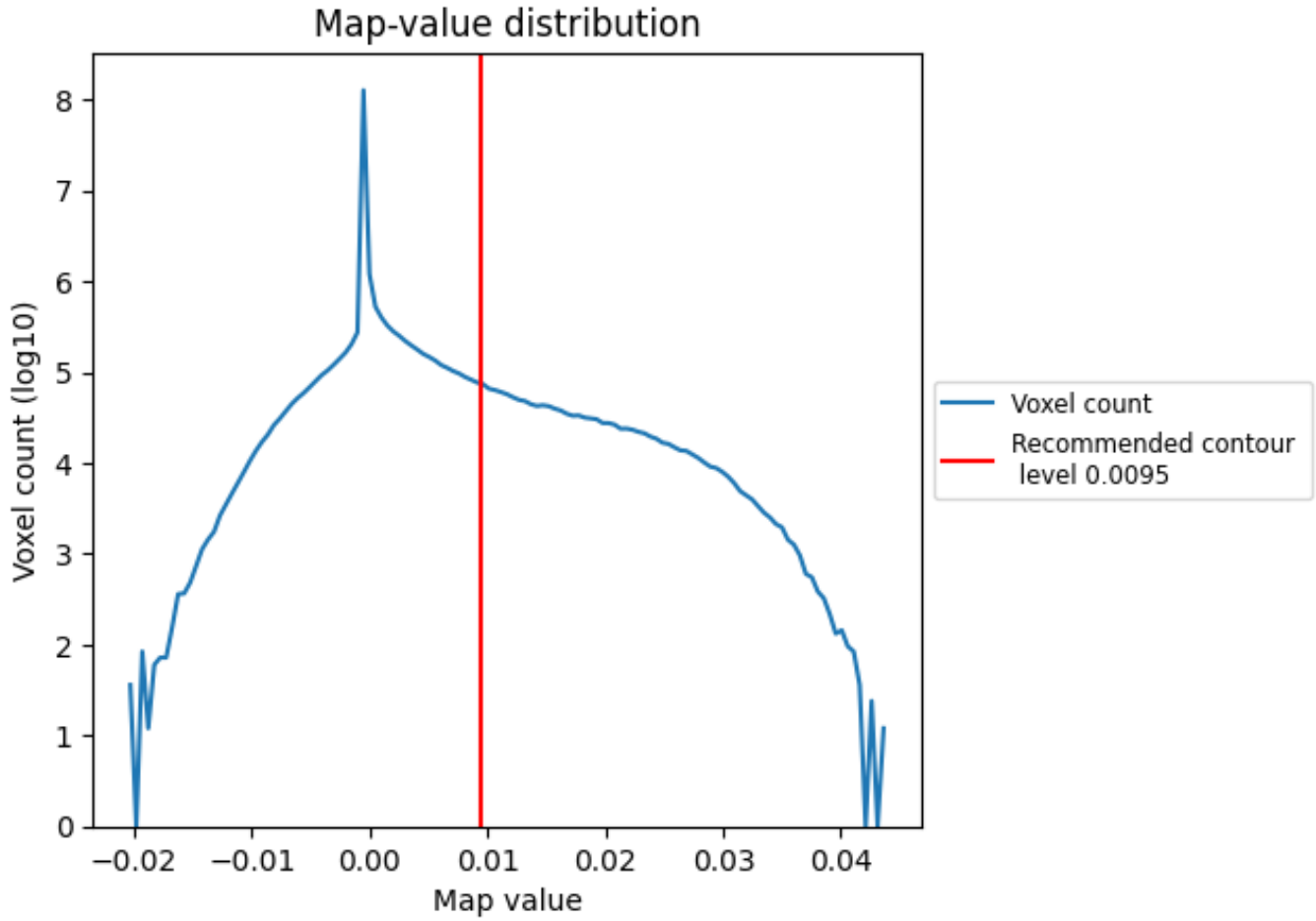
6.6 Mask visualisation (i)

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

7 Map analysis

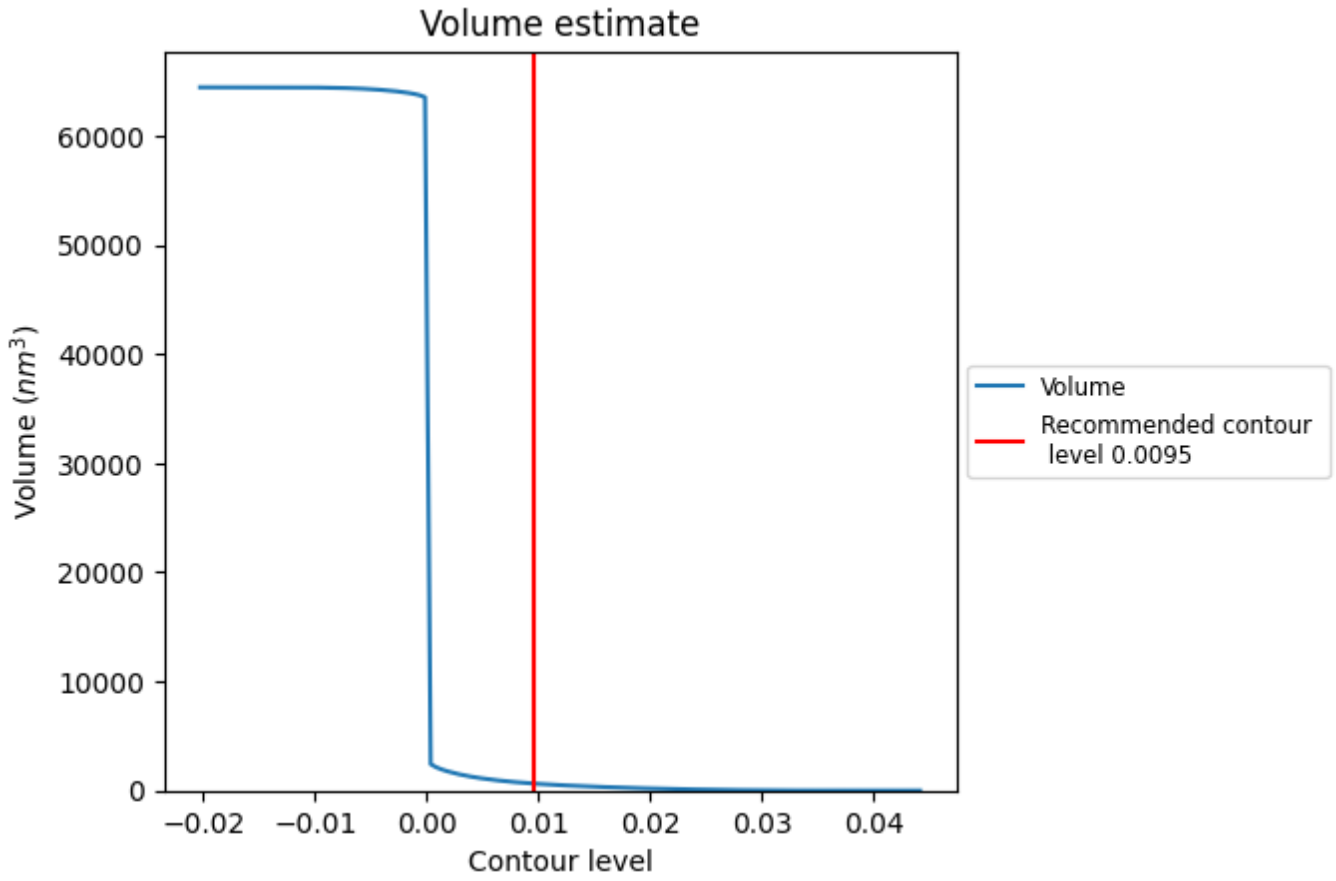
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

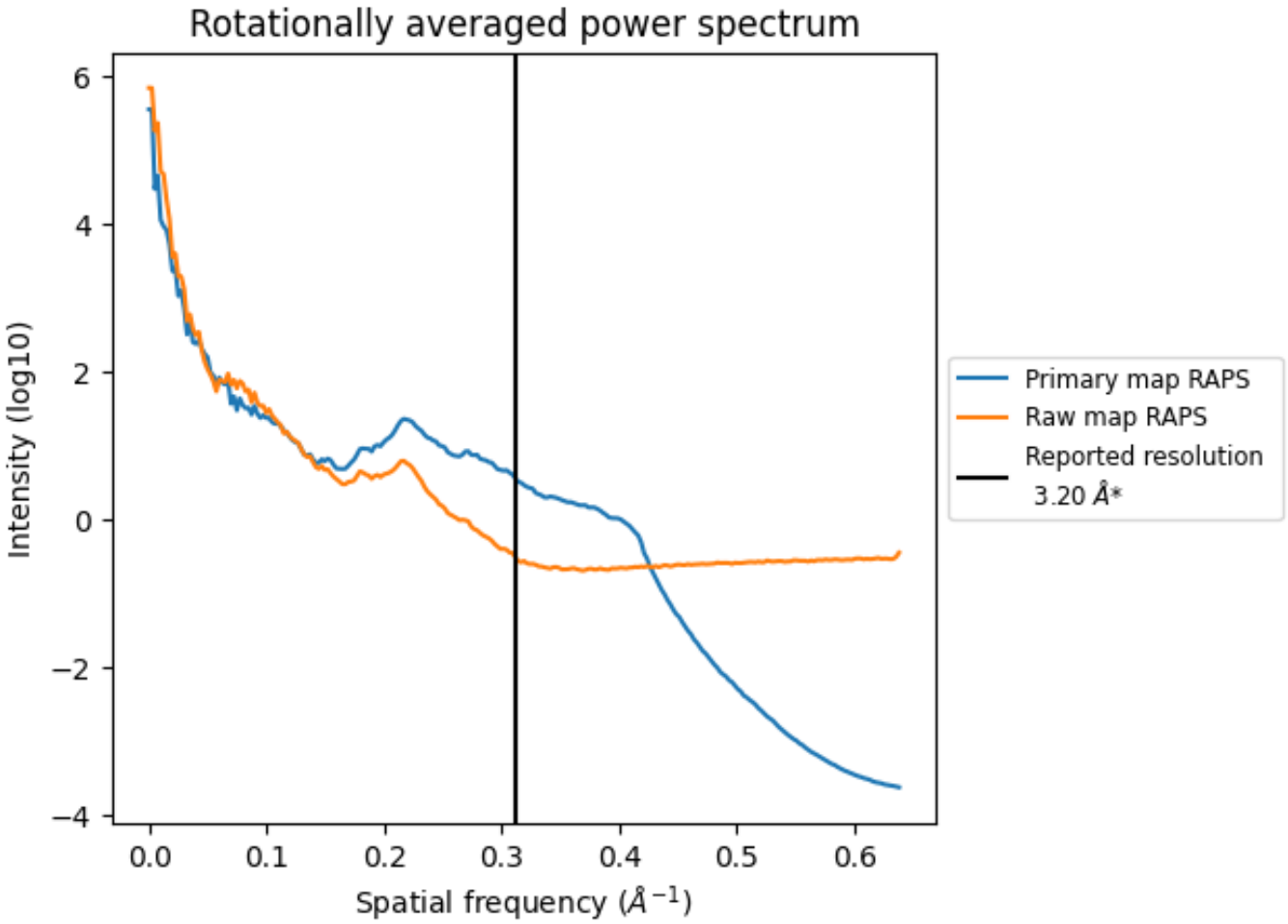
7.2 Volume estimate



The volume at the recommended contour level is 647 nm^3; this corresponds to an approximate mass of 584 kDa.

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

7.3 Rotationally averaged power spectrum (i)

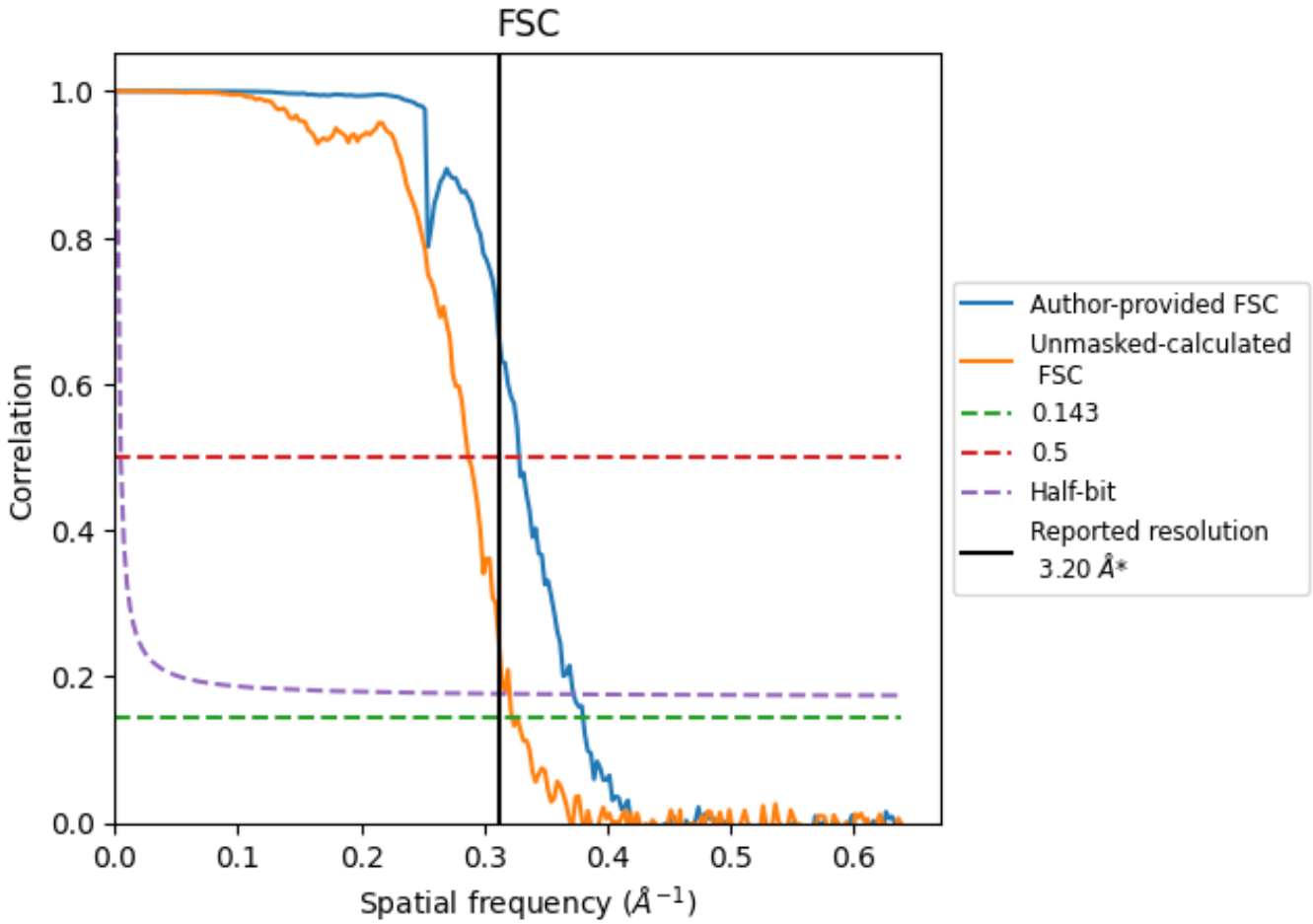


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8.2 Resolution estimates (i)

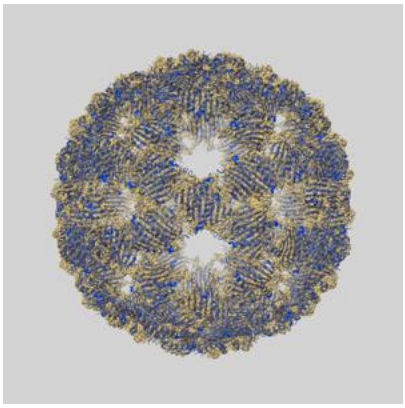
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	2.63	3.05	2.68
Unmasked-calculated*	3.10	3.49	3.12

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.63 differs from the reported value 3.2 by more than 10 %

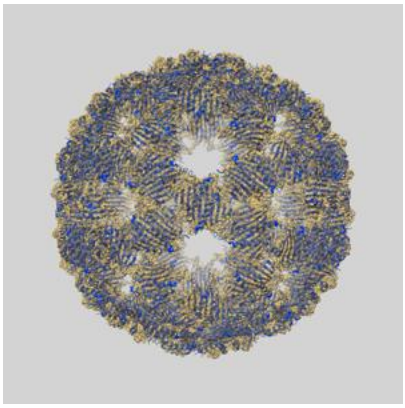
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-52005 and PDB model 9HAS. Per-residue inclusion information can be found in section 3 on page 19.

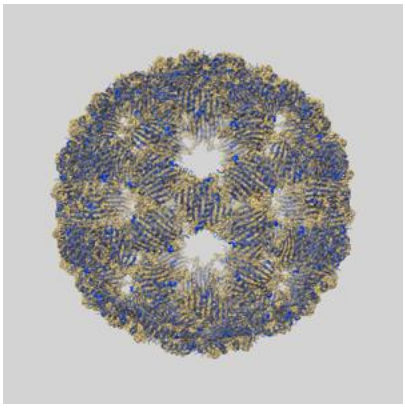
9.1 Map-model overlay



X



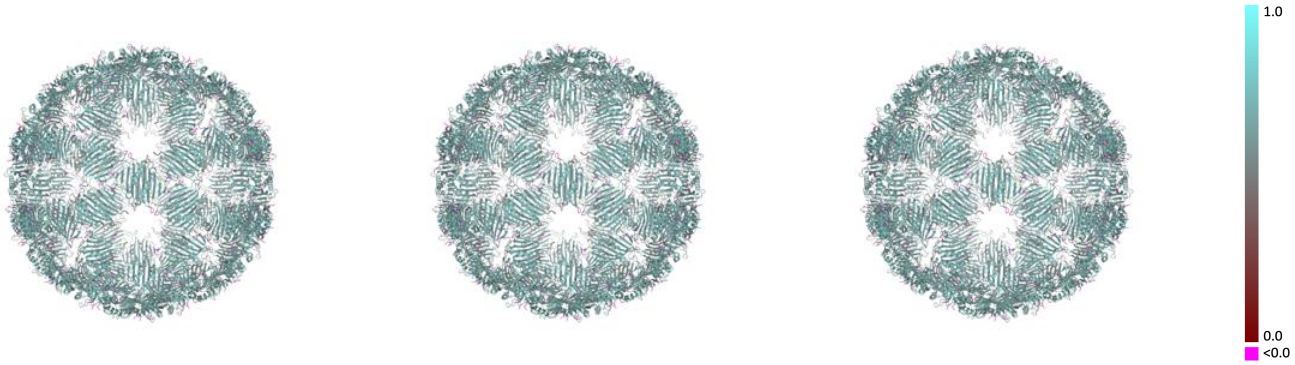
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0095 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

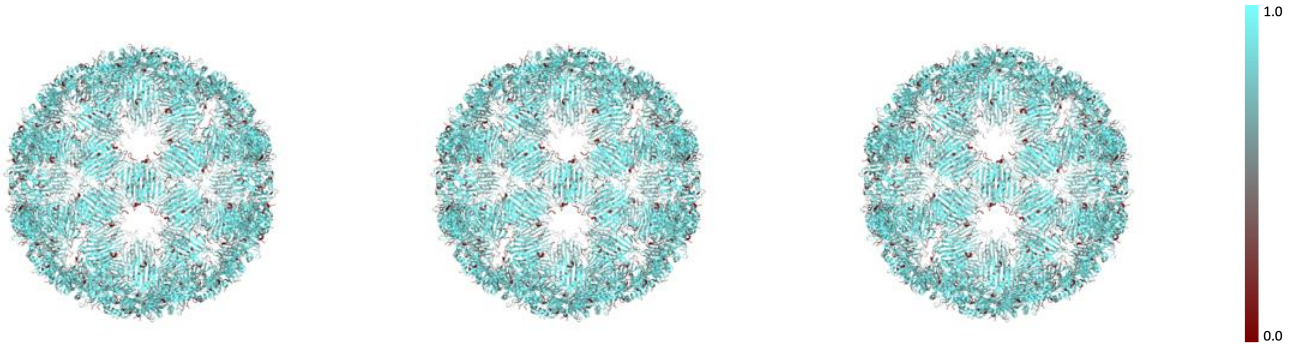
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

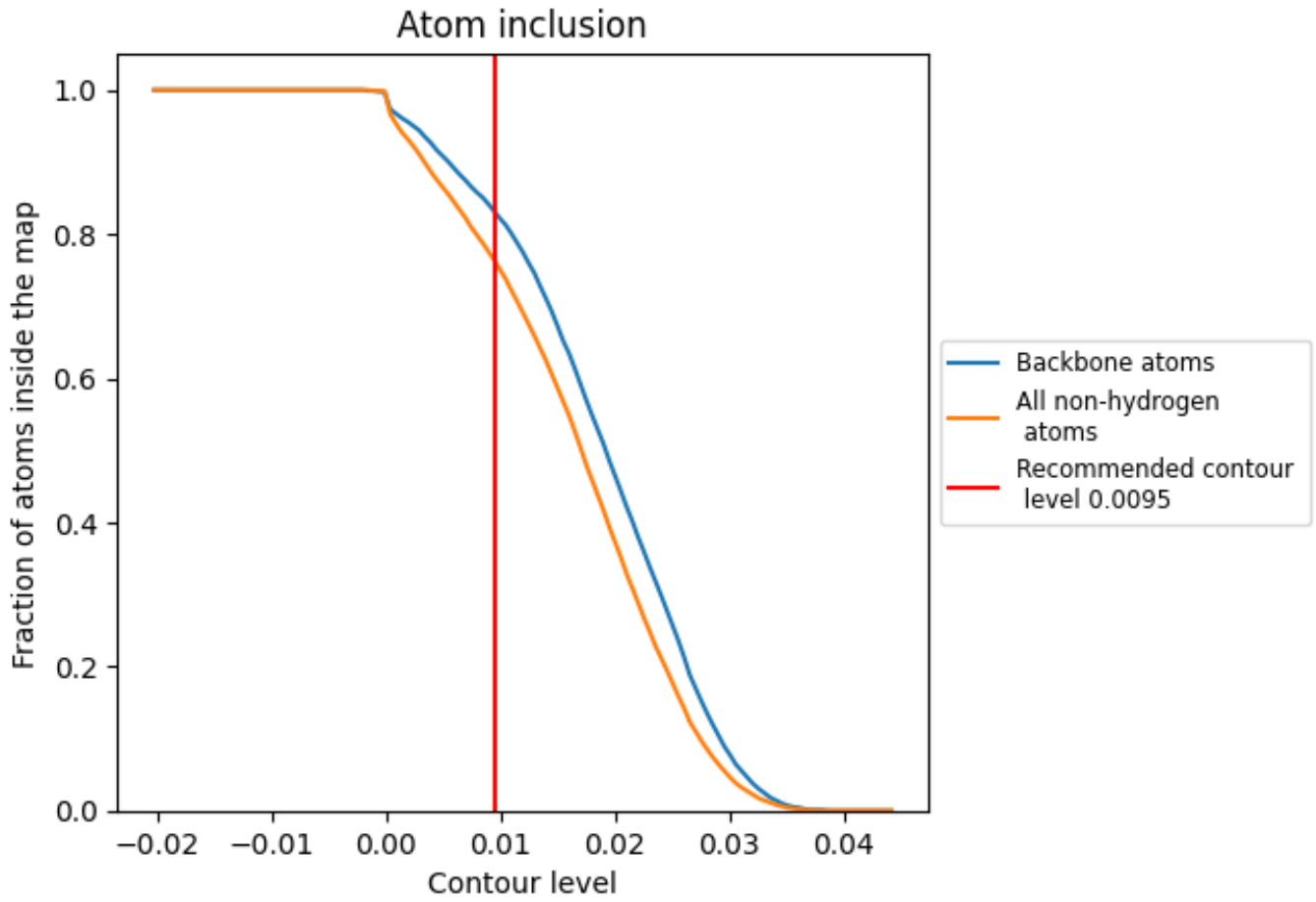
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0095).

9.4 Atom inclusion (i)



At the recommended contour level, 83% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0095) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7620	0.5880
AA	0.7560	0.5860
AB	0.7640	0.5920
AC	0.7440	0.5770
AD	0.7580	0.5890
AE	0.7670	0.6020
AF	0.7530	0.5790
AG	0.7530	0.5830
AH	0.7750	0.5980
AI	0.7550	0.5770
AJ	0.7580	0.5860
AK	0.7660	0.5950
AL	0.7440	0.5760
AM	0.7800	0.5940
AN	0.7920	0.6030
AO	0.7530	0.5770
AP	0.7660	0.5930
AQ	0.7680	0.5950
AR	0.7280	0.5720
AS	0.7540	0.5830
AT	0.7770	0.5980
AU	0.7550	0.5760
AV	0.7560	0.5870
AW	0.7650	0.5940
AX	0.7460	0.5760
AY	0.7800	0.5920
AZ	0.7930	0.6060
BA	0.7540	0.5780
BB	0.7530	0.5820
BC	0.7770	0.6000
BD	0.7550	0.5770
BE	0.7660	0.5890
BF	0.7710	0.5910
BG	0.7290	0.5700
BH	0.7580	0.5880

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Chain	Atom inclusion	Q-score
BI	0.7700	0.5970
BJ	0.7540	0.5800
BK	0.7790	0.5940
BL	0.7910	0.6060
BM	0.7530	0.5790
BN	0.7540	0.5820
BO	0.7780	0.5990
BP	0.7560	0.5800
BQ	0.7660	0.5910
BR	0.7710	0.5940
BS	0.7270	0.5700
BT	0.7800	0.5940
BU	0.7920	0.6060
BV	0.7540	0.5750
BW	0.7580	0.5890
BX	0.7700	0.5950
BY	0.7540	0.5780
BZ	0.7560	0.5880
CA	0.7650	0.5960
CB	0.7460	0.5790
CC	0.7670	0.5920
CD	0.7710	0.5950
CE	0.7270	0.5700
CF	0.7790	0.5950
CG	0.7910	0.6030
CH	0.7530	0.5790
CI	0.7580	0.5880
CJ	0.7700	0.5990
CK	0.7560	0.5810
CL	0.7660	0.5940
CM	0.7710	0.5970
CN	0.7270	0.5730
CO	0.7580	0.5870
CP	0.7660	0.5960
CQ	0.7440	0.5750
CR	0.7530	0.5820
CS	0.7780	0.5970
CT	0.7560	0.5790
CU	0.7580	0.5870
CV	0.7700	0.5960
CW	0.7560	0.5800
CX	0.7670	0.5900

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Chain	Atom inclusion	Q-score
CY	0.7710	0.5930
CZ	0.7270	0.5710
DA	0.7580	0.5890
DB	0.7650	0.5960
DC	0.7440	0.5790
DD	0.7580	0.5880
DE	0.7700	0.5960
DF	0.7550	0.5770
DG	0.7530	0.5840
DH	0.7780	0.5950
DI	0.7560	0.5800
DJ	0.7800	0.5930
DK	0.7900	0.6050
DL	0.7540	0.5780
DM	0.7560	0.5870
DN	0.7650	0.5950
DO	0.7440	0.5750
DP	0.7530	0.5820
DQ	0.7780	0.6010
DR	0.7560	0.5770
DS	0.7600	0.5900
DT	0.7700	0.6000
DU	0.7550	0.5820
DV	0.7580	0.5880
DW	0.7660	0.5950
DX	0.7440	0.5770
DY	0.7660	0.5920
DZ	0.7710	0.5930
EA	0.7270	0.5730
EB	0.7790	0.5940
EC	0.7910	0.6050
ED	0.7530	0.5790
EE	0.7580	0.5890
EF	0.7700	0.5960
EG	0.7530	0.5770
EH	0.7560	0.5890
EI	0.7650	0.5980
EJ	0.7460	0.5780
EK	0.7660	0.5930
EL	0.7710	0.5920
EM	0.7270	0.5680
EN	0.7560	0.5890

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Chain	Atom inclusion	Q-score
EO	0.7660	0.5980
EP	0.7550	0.5760
EQ	0.7840	0.5940
ER	0.7860	0.6040
ES	0.7580	0.5800
ET	0.7600	0.5840
EU	0.7750	0.5990
EV	0.7540	0.5810
EW	0.7640	0.5950
EX	0.7700	0.5980
EY	0.7300	0.5690
EZ	0.7580	0.5880
FA	0.7660	0.5980
FB	0.7530	0.5800
FC	0.7840	0.5920
FD	0.7860	0.6070
FE	0.7580	0.5820
FF	0.7640	0.5960
FG	0.7680	0.5970
FH	0.7290	0.5710
FI	0.7610	0.5810
FJ	0.7770	0.5950
FK	0.7540	0.5750
FL	0.7580	0.5880
FM	0.7670	0.5960
FN	0.7460	0.5800
FO	0.7810	0.5960
FP	0.7860	0.6060
FQ	0.7580	0.5810
FR	0.7640	0.5900
FS	0.7710	0.5940
FT	0.7300	0.5710
FU	0.7610	0.5840
FV	0.7770	0.5990
FW	0.7540	0.5810
FX	0.7840	0.5960
FY	0.7860	0.6060
FZ	0.7580	0.5780
GA	0.7590	0.5880
GB	0.7660	0.5950
GC	0.7450	0.5800
GD	0.7560	0.5830

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Chain	Atom inclusion	Q-score
GE	0.7660	0.5970
GF	0.7540	0.5760
GG	0.7610	0.5830
GH	0.7770	0.6000
GI	0.7530	0.5780
GJ	0.7810	0.5950
GK	0.7860	0.6050
GL	0.7580	0.5820
GM	0.7580	0.5870
GN	0.7670	0.5950
GO	0.7450	0.5800
GP	0.7600	0.5860
GQ	0.7770	0.6010
GR	0.7540	0.5780
GS	0.7560	0.5850
GT	0.7660	0.5990
GU	0.7540	0.5780
GV	0.7650	0.5910
GW	0.7710	0.5960
GX	0.7290	0.5730