Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 04:38 AM UTC

PDB ID	:	4WIZ / pdb_00004wiz
Title	:	Crystal structure of Grouper nervous necrosis virus-like particle at 3.6A
Authors	:	Chen, N.C.; Chen, C.J.; Yoshimura, M.; Guan, H.H.; Chen, T.Y.
Deposited on	:	2014-09-28
Resolution	:	3.60 Å(reported)

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

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

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

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

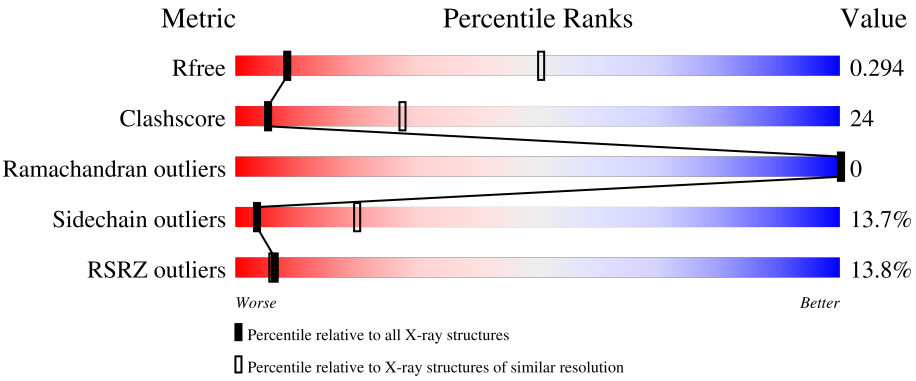
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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

Mol	Chain	Length	Quality of chain
1	AA	338	8% 48% 31% • • 15%
1	AB	338	13% 49% 29% 6% • 15%
1	AC	338	19% 46% 34% • • 15%
1	AD	338	5% 48% 31% 5% • 15%
1	AE	338	8% 48% 30% 6% • 15%

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Mol	Chain	Length	Quality of chain
1	AF	338	6% 48% 31% 5% 15%
1	AG	338	8% 46% 33% 5% 15%
1	AH	338	14% 47% 32% 5% 15%
1	AI	338	18% 45% 33% 6% 15%
1	AJ	338	5% 49% 30% 5% 15%
1	AK	338	5% 49% 30% 5% 15%
1	AL	338	5% 47% 33% 15%
1	AM	338	14% 46% 33% 5% 15%
1	AN	338	8% 46% 32% 6% 15%
1	AO	338	8% 46% 33% 5% 15%
1	AP	338	8% 47% 32% 5% 15%
1	AQ	338	8% 48% 32% 15%
1	AR	338	4% 48% 30% 6% 15%
1	AS	338	6% 47% 32% 5% 15%
1	AT	338	5% 46% 35% 15%
1	AU	338	10% 46% 32% 6% 15%
1	AV	338	10% 48% 32% 15%
1	AW	338	4% 48% 33% 15%
1	AX	338	9% 49% 31% 5% 15%
1	AY	338	4% 49% 30% 15%
1	AZ	338	4% 47% 32% 6% 15%
1	Aa	338	7% 47% 32% 5% 15%
1	Ab	338	16% 47% 31% 6% 15%
1	Ac	338	12% 48% 31% 5% 15%
1	Ad	338	7% 47% 33% 15%

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Mol	Chain	Length	Quality of chain
1	BA	338	10% 51% 27% 6% • 15%
1	BB	338	24% 50% 28% 7% • 15%
1	BC	338	14% 52% 25% 7% • 15%
1	BD	338	7% 51% 27% 6% 15%
1	BE	338	11% 53% 24% 7% • 15%
1	BF	338	12% 54% 24% 7% 15%
1	BG	338	17% 51% 27% 7% • 15%
1	BH	338	25% 51% 27% 6% • 15%
1	BI	338	24% 53% 25% 6% • 15%
1	BJ	338	7% 54% 24% 7% 15%
1	BK	338	7% 51% 27% 5% • 15%
1	BL	338	5% 52% 25% 7% • 15%
1	BM	338	26% 52% 25% 7% • 15%
1	BN	338	13% 54% 25% 6% • 15%
1	BO	338	23% 52% 25% 7% 15%
1	BP	338	16% 52% 25% 6% • 15%
1	BQ	338	9% 51% 28% 5% • 15%
1	BR	338	3% 55% 23% 6% • 15%
1	BS	338	12% 51% 26% 6% • 15%
1	BT	338	6% 53% 25% 6% • 15%
1	BU	338	24% 52% 25% 6% • 15%
1	BV	338	8% 53% 25% 6% • 15%
1	BW	338	3% 52% 26% 6% • 15%
1	BX	338	12% 54% 24% 6% • 15%
1	BY	338	4% 54% 25% 6% 15%

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Mol	Chain	Length	Quality of chain
1	BZ	338	4% 54% 24% 6% • 15%
1	Ba	338	7% 52% 26% 5% • 15%
1	Bb	338	26% 53% 25% 6% • 15%
1	Bc	338	26% 53% 25% 7% • 15%
1	Bd	338	10% 55% 24% 5% • 15%
1	CA	338	12% 58% 25% 7% • 10%
1	CB	338	22% 58% 25% 7% 10%
1	CC	338	22% 57% 26% 7% • 10%
1	CD	338	8% 57% 26% 6% 10%
1	CE	338	14% 59% 23% 7% • 10%
1	CF	338	16% 59% 23% 7% 10%
1	CG	338	20% 59% 25% 6% 10%
1	CH	338	22% 58% 25% 6% 10%
1	CI	338	20% 59% 25% 5% 10%
1	CJ	338	14% 60% 23% 7% 10%
1	CK	338	9% 56% 26% 7% • 10%
1	CL	338	3% 57% 27% 6% 10%
1	CM	338	23% 58% 25% 6% • 10%
1	CN	338	15% 61% 23% 5% • 10%
1	CO	338	18% 58% 26% 6% • 10%
1	CP	338	9% 58% 25% 6% 10%
1	CQ	338	10% 58% 27% 5% 10%
1	CR	338	3% 59% 25% 5% • 10%
1	CS	338	14% 60% 23% 7% • 10%
1	CT	338	7% 58% 25% 6% • 10%

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Mol	Chain	Length	Quality of chain
1	CU	338	22% 58% 24% 7% • 10%
1	CV	338	7% 59% 25% 6% 10%
1	CW	338	4% 60% 24% 6% 10%
1	CX	338	11% 58% 25% 7% 10%
1	CY	338	11% 58% 26% 5% • 10%
1	CZ	338	7% 58% 25% 7% • 10%
1	Ca	338	15% 59% 25% 5% 10%
1	Cb	338	26% 58% 25% 6% • 10%
1	Cc	338	22% 61% 23% 6% 10%
1	Cd	338	11% 56% 28% 6% • 10%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 203250 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Coat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BA	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AA	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CA	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BB	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AB	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CB	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BC	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AC	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CC	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BD	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AD	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CD	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BE	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AE	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CE	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BF	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AF	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CF	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BG	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AG	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CG	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BH	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AH	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CH	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BI	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AI	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CI	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BJ	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AJ	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CJ	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BK	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AK	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CK	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BL	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AL	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CL	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BM	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AM	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CM	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BN	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AN	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CN	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BO	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AO	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CO	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BP	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AP	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CP	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BQ	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AQ	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CQ	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BR	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AR	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CR	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BS	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AS	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CS	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BT	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AT	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CT	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BU	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AU	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CU	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BV	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AV	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CV	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BW	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AW	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CW	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BX	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AX	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CX	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BY	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AY	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CY	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BZ	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AZ	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CZ	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	Ba	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Aa	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	Ca	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	Bb	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	Ab	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	Cb	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	Bc	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	Ac	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	Cc	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	Bd	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	Ad	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	Cd	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			

There are 90 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	214	ASN	THR	engineered mutation	UNP Q8JNX5
AA	214	ASN	THR	engineered mutation	UNP Q8JNX5
CA	214	ASN	THR	engineered mutation	UNP Q8JNX5
BB	214	ASN	THR	engineered mutation	UNP Q8JNX5
AB	214	ASN	THR	engineered mutation	UNP Q8JNX5
CB	214	ASN	THR	engineered mutation	UNP Q8JNX5
BC	214	ASN	THR	engineered mutation	UNP Q8JNX5
AC	214	ASN	THR	engineered mutation	UNP Q8JNX5
CC	214	ASN	THR	engineered mutation	UNP Q8JNX5
BD	214	ASN	THR	engineered mutation	UNP Q8JNX5
AD	214	ASN	THR	engineered mutation	UNP Q8JNX5
CD	214	ASN	THR	engineered mutation	UNP Q8JNX5
BE	214	ASN	THR	engineered mutation	UNP Q8JNX5
AE	214	ASN	THR	engineered mutation	UNP Q8JNX5
CE	214	ASN	THR	engineered mutation	UNP Q8JNX5
BF	214	ASN	THR	engineered mutation	UNP Q8JNX5
AF	214	ASN	THR	engineered mutation	UNP Q8JNX5

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Chain	Residue	Modelled	Actual	Comment	Reference
CF	214	ASN	THR	engineered mutation	UNP Q8JNX5
BG	214	ASN	THR	engineered mutation	UNP Q8JNX5
AG	214	ASN	THR	engineered mutation	UNP Q8JNX5
CG	214	ASN	THR	engineered mutation	UNP Q8JNX5
BH	214	ASN	THR	engineered mutation	UNP Q8JNX5
AH	214	ASN	THR	engineered mutation	UNP Q8JNX5
CH	214	ASN	THR	engineered mutation	UNP Q8JNX5
BI	214	ASN	THR	engineered mutation	UNP Q8JNX5
AI	214	ASN	THR	engineered mutation	UNP Q8JNX5
CI	214	ASN	THR	engineered mutation	UNP Q8JNX5
BJ	214	ASN	THR	engineered mutation	UNP Q8JNX5
AJ	214	ASN	THR	engineered mutation	UNP Q8JNX5
CJ	214	ASN	THR	engineered mutation	UNP Q8JNX5
BK	214	ASN	THR	engineered mutation	UNP Q8JNX5
AK	214	ASN	THR	engineered mutation	UNP Q8JNX5
CK	214	ASN	THR	engineered mutation	UNP Q8JNX5
BL	214	ASN	THR	engineered mutation	UNP Q8JNX5
AL	214	ASN	THR	engineered mutation	UNP Q8JNX5
CL	214	ASN	THR	engineered mutation	UNP Q8JNX5
BM	214	ASN	THR	engineered mutation	UNP Q8JNX5
AM	214	ASN	THR	engineered mutation	UNP Q8JNX5
CM	214	ASN	THR	engineered mutation	UNP Q8JNX5
BN	214	ASN	THR	engineered mutation	UNP Q8JNX5
AN	214	ASN	THR	engineered mutation	UNP Q8JNX5
CN	214	ASN	THR	engineered mutation	UNP Q8JNX5
BO	214	ASN	THR	engineered mutation	UNP Q8JNX5
AO	214	ASN	THR	engineered mutation	UNP Q8JNX5
CO	214	ASN	THR	engineered mutation	UNP Q8JNX5
BP	214	ASN	THR	engineered mutation	UNP Q8JNX5
AP	214	ASN	THR	engineered mutation	UNP Q8JNX5
CP	214	ASN	THR	engineered mutation	UNP Q8JNX5
BQ	214	ASN	THR	engineered mutation	UNP Q8JNX5
AQ	214	ASN	THR	engineered mutation	UNP Q8JNX5
CQ	214	ASN	THR	engineered mutation	UNP Q8JNX5
BR	214	ASN	THR	engineered mutation	UNP Q8JNX5
AR	214	ASN	THR	engineered mutation	UNP Q8JNX5
CR	214	ASN	THR	engineered mutation	UNP Q8JNX5
BS	214	ASN	THR	engineered mutation	UNP Q8JNX5
AS	214	ASN	THR	engineered mutation	UNP Q8JNX5
CS	214	ASN	THR	engineered mutation	UNP Q8JNX5
BT	214	ASN	THR	engineered mutation	UNP Q8JNX5
AT	214	ASN	THR	engineered mutation	UNP Q8JNX5

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Chain	Residue	Modelled	Actual	Comment	Reference
CT	214	ASN	THR	engineered mutation	UNP Q8JNX5
BU	214	ASN	THR	engineered mutation	UNP Q8JNX5
AU	214	ASN	THR	engineered mutation	UNP Q8JNX5
CU	214	ASN	THR	engineered mutation	UNP Q8JNX5
BV	214	ASN	THR	engineered mutation	UNP Q8JNX5
AV	214	ASN	THR	engineered mutation	UNP Q8JNX5
CV	214	ASN	THR	engineered mutation	UNP Q8JNX5
BW	214	ASN	THR	engineered mutation	UNP Q8JNX5
AW	214	ASN	THR	engineered mutation	UNP Q8JNX5
CW	214	ASN	THR	engineered mutation	UNP Q8JNX5
BX	214	ASN	THR	engineered mutation	UNP Q8JNX5
AX	214	ASN	THR	engineered mutation	UNP Q8JNX5
CX	214	ASN	THR	engineered mutation	UNP Q8JNX5
BY	214	ASN	THR	engineered mutation	UNP Q8JNX5
AY	214	ASN	THR	engineered mutation	UNP Q8JNX5
CY	214	ASN	THR	engineered mutation	UNP Q8JNX5
BZ	214	ASN	THR	engineered mutation	UNP Q8JNX5
AZ	214	ASN	THR	engineered mutation	UNP Q8JNX5
CZ	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ba	214	ASN	THR	engineered mutation	UNP Q8JNX5
Aa	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ca	214	ASN	THR	engineered mutation	UNP Q8JNX5
Bb	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ab	214	ASN	THR	engineered mutation	UNP Q8JNX5
Cb	214	ASN	THR	engineered mutation	UNP Q8JNX5
Bc	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ac	214	ASN	THR	engineered mutation	UNP Q8JNX5
Cc	214	ASN	THR	engineered mutation	UNP Q8JNX5
Bd	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ad	214	ASN	THR	engineered mutation	UNP Q8JNX5
Cd	214	ASN	THR	engineered mutation	UNP Q8JNX5

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	BA	2	Total Ca 2 2	0	0
2	AA	1	Total Ca 1 1	0	0
2	BB	2	Total Ca 2 2	0	0
2	AB	1	Total Ca 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	BC	2	Total Ca 2 2	0	0
2	AC	1	Total Ca 1 1	0	0
2	BD	2	Total Ca 2 2	0	0
2	AD	1	Total Ca 1 1	0	0
2	BE	2	Total Ca 2 2	0	0
2	AE	1	Total Ca 1 1	0	0
2	BF	2	Total Ca 2 2	0	0
2	AF	1	Total Ca 1 1	0	0
2	BG	2	Total Ca 2 2	0	0
2	AG	1	Total Ca 1 1	0	0
2	BH	2	Total Ca 2 2	0	0
2	AH	1	Total Ca 1 1	0	0
2	BI	2	Total Ca 2 2	0	0
2	AI	1	Total Ca 1 1	0	0
2	BJ	2	Total Ca 2 2	0	0
2	AJ	1	Total Ca 1 1	0	0
2	BK	2	Total Ca 2 2	0	0
2	AK	1	Total Ca 1 1	0	0
2	BL	2	Total Ca 2 2	0	0
2	AL	1	Total Ca 1 1	0	0
2	BM	2	Total Ca 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	AM	1	Total Ca 1 1	0	0
2	BN	2	Total Ca 2 2	0	0
2	AN	1	Total Ca 1 1	0	0
2	BO	2	Total Ca 2 2	0	0
2	AO	1	Total Ca 1 1	0	0
2	BP	2	Total Ca 2 2	0	0
2	AP	1	Total Ca 1 1	0	0
2	BQ	2	Total Ca 2 2	0	0
2	AQ	1	Total Ca 1 1	0	0
2	BR	2	Total Ca 2 2	0	0
2	AR	1	Total Ca 1 1	0	0
2	BS	2	Total Ca 2 2	0	0
2	AS	1	Total Ca 1 1	0	0
2	BT	2	Total Ca 2 2	0	0
2	AT	1	Total Ca 1 1	0	0
2	BU	2	Total Ca 2 2	0	0
2	AU	1	Total Ca 1 1	0	0
2	BV	2	Total Ca 2 2	0	0
2	AV	1	Total Ca 1 1	0	0
2	BW	2	Total Ca 2 2	0	0
2	AW	1	Total Ca 1 1	0	0

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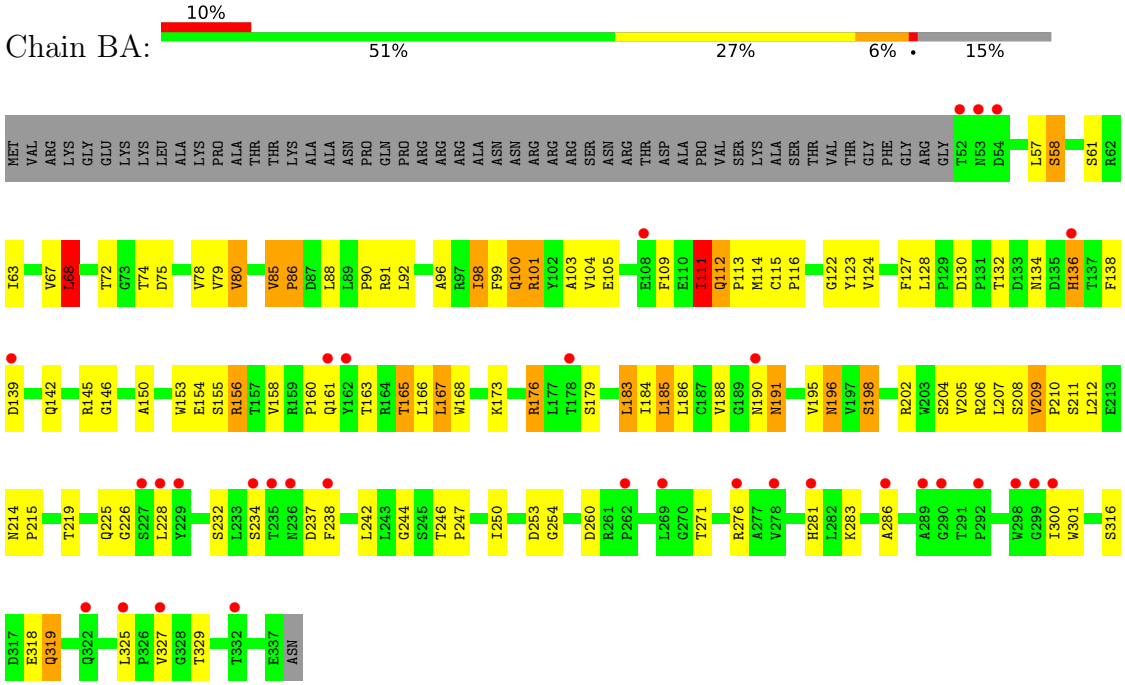
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	BX	2	Total Ca 2 2	0	0
2	AX	1	Total Ca 1 1	0	0
2	BY	2	Total Ca 2 2	0	0
2	AY	1	Total Ca 1 1	0	0
2	BZ	2	Total Ca 2 2	0	0
2	AZ	1	Total Ca 1 1	0	0
2	Ba	2	Total Ca 2 2	0	0
2	Aa	1	Total Ca 1 1	0	0
2	Bb	2	Total Ca 2 2	0	0
2	Ab	1	Total Ca 1 1	0	0
2	Bc	2	Total Ca 2 2	0	0
2	Ac	1	Total Ca 1 1	0	0
2	Bd	2	Total Ca 2 2	0	0
2	Ad	1	Total Ca 1 1	0	0

3 Residue-property plots (i)

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

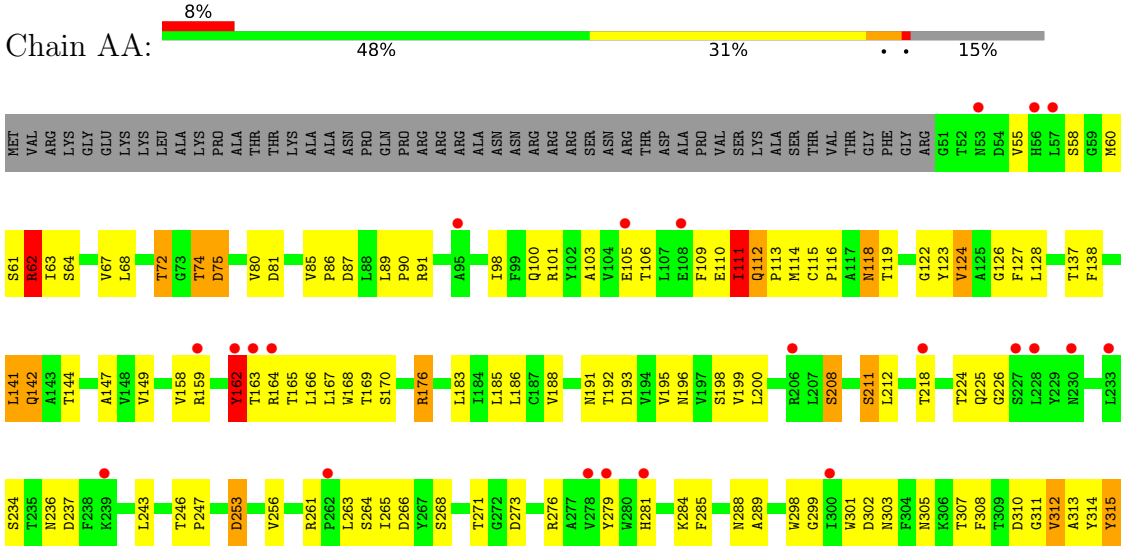
• Molecule 1: Coat protein

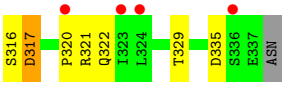
Chain BA:



• Molecule 1: Coat protein

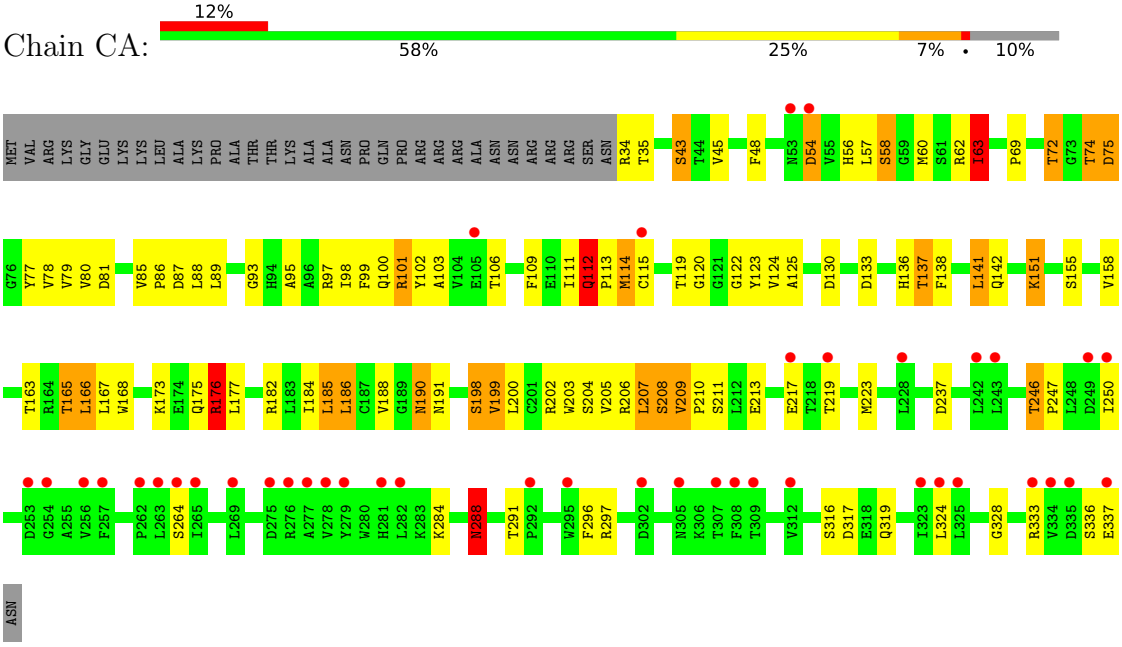
Chain AA:





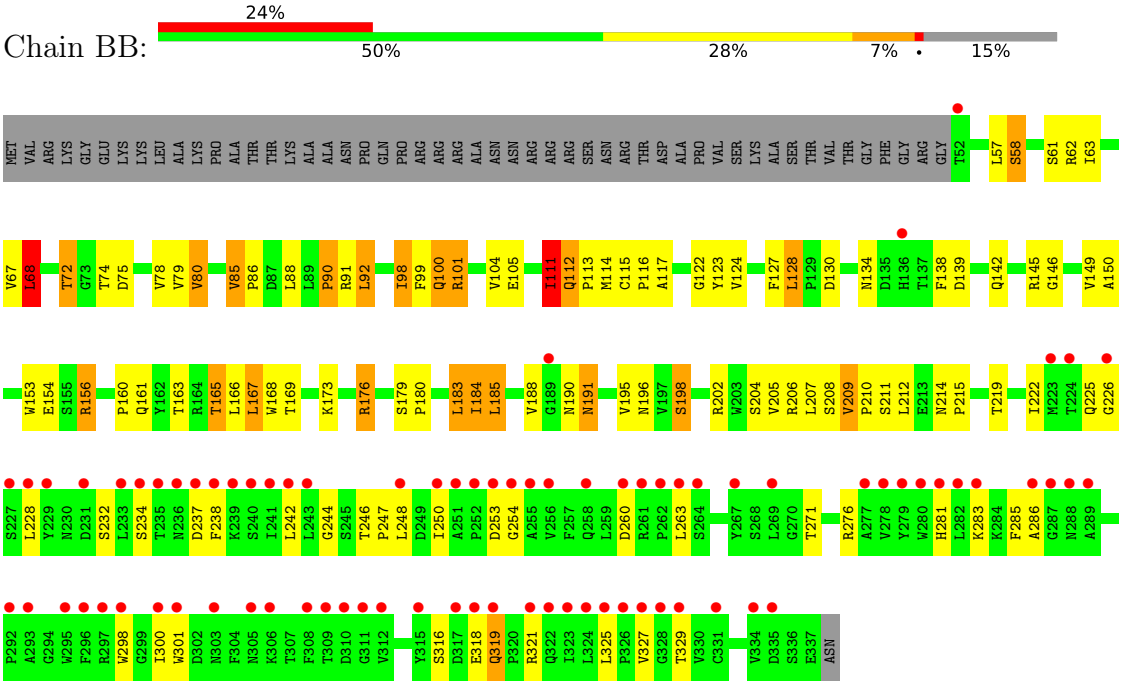
• Molecule 1: Coat protein

Chain CA:



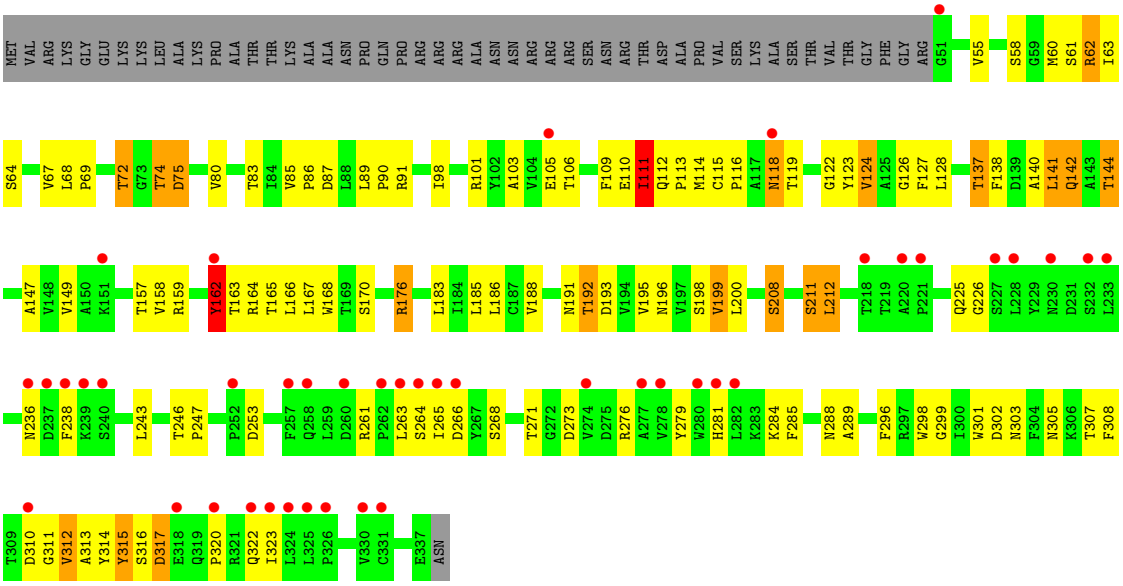
• Molecule 1: Coat protein

Chain BB:



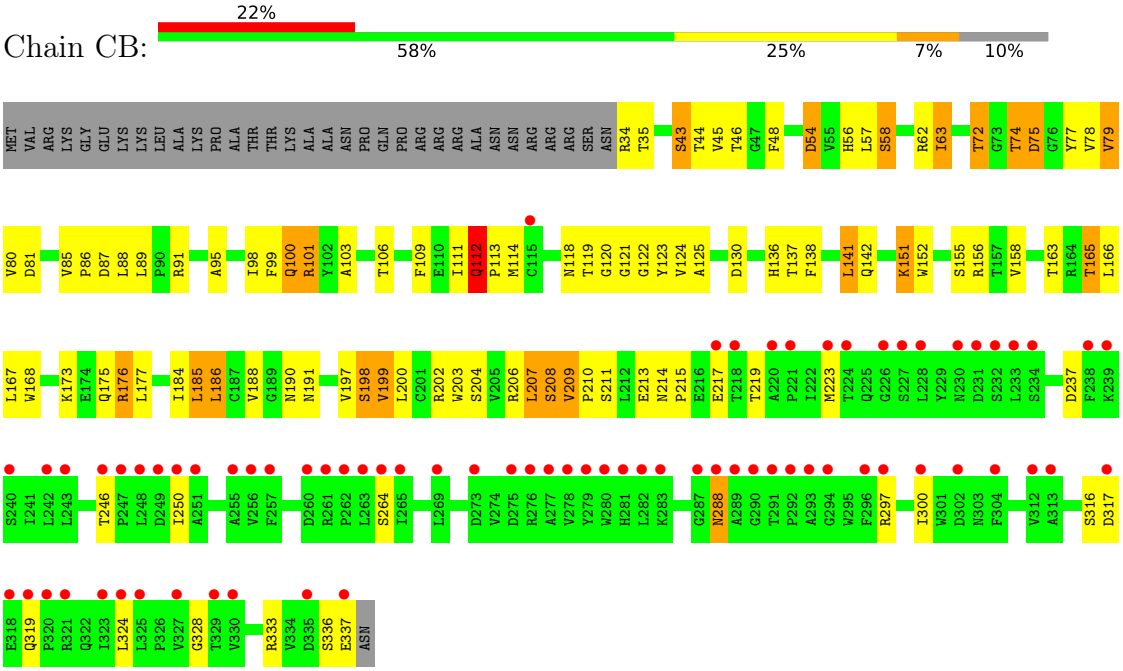
• Molecule 1: Coat protein

Chain AB:



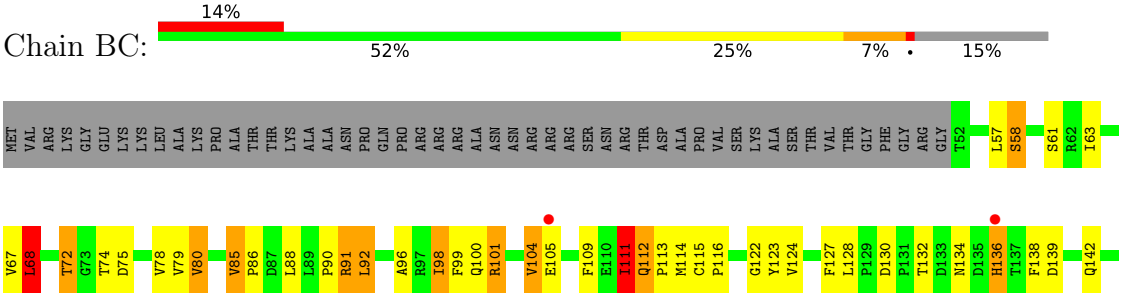
• Molecule 1: Coat protein

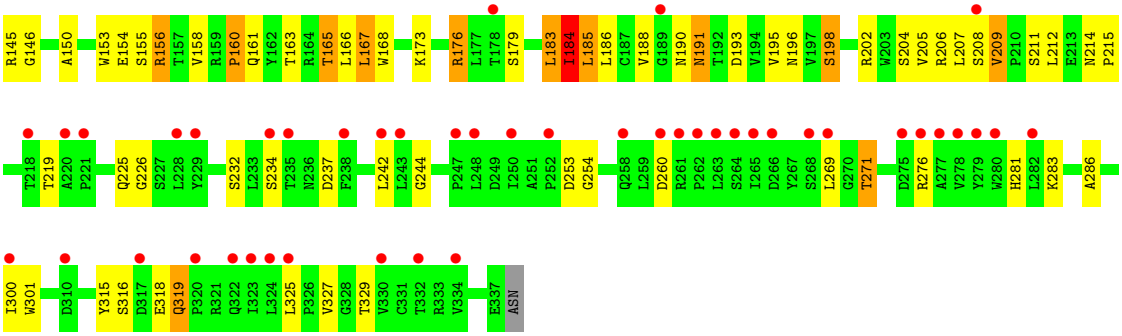
Chain CB:



• Molecule 1: Coat protein

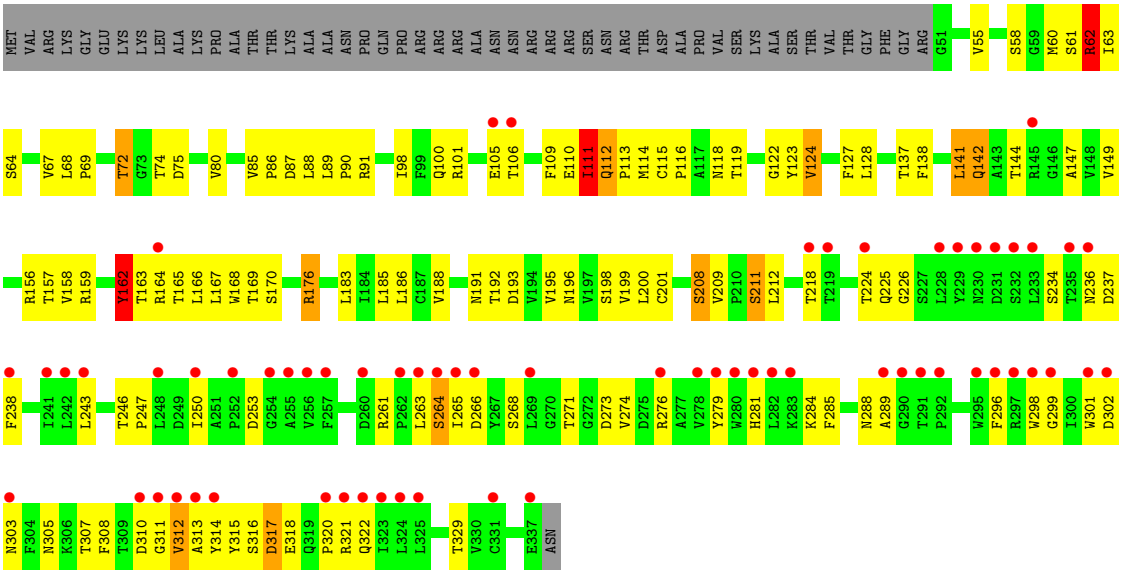
Chain BC:





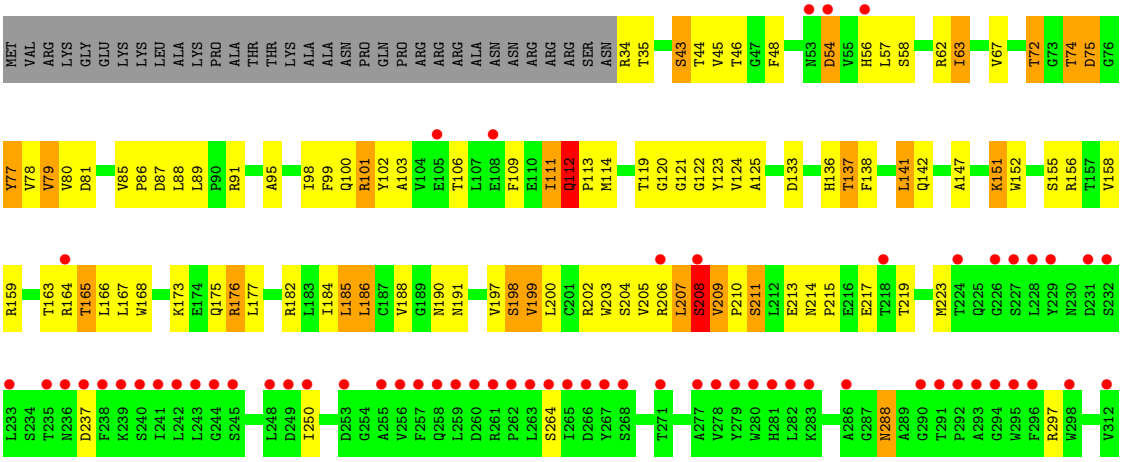
• Molecule 1: Coat protein

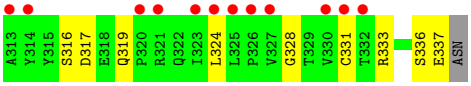
Chain AC:



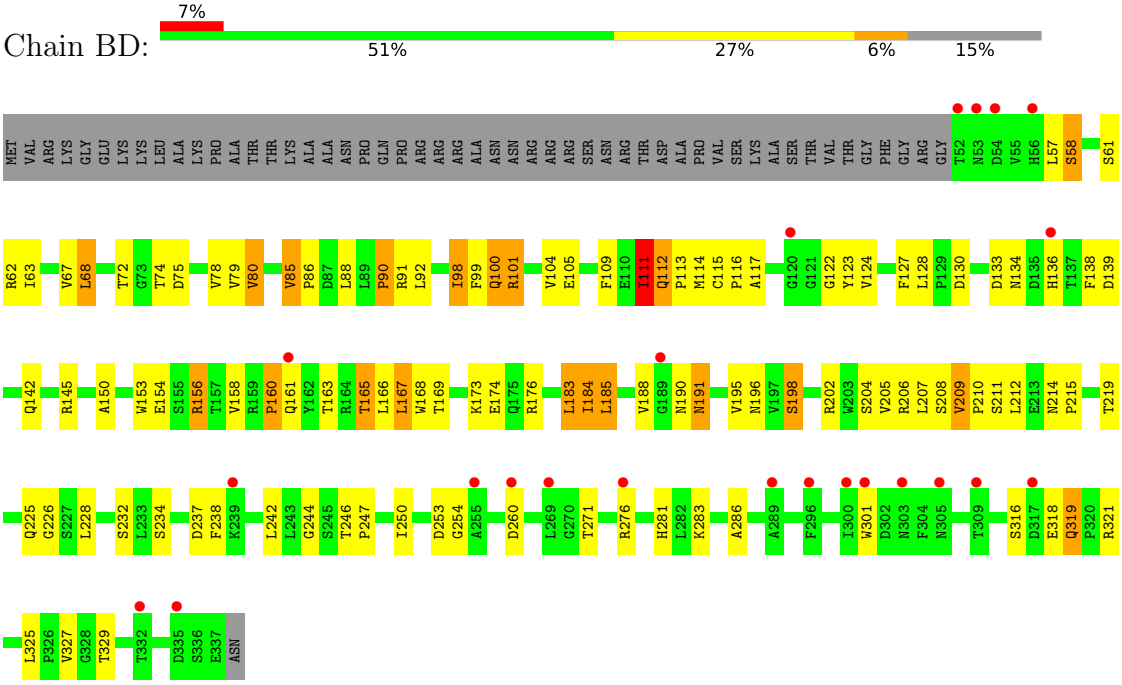
• Molecule 1: Coat protein

Chain CC:

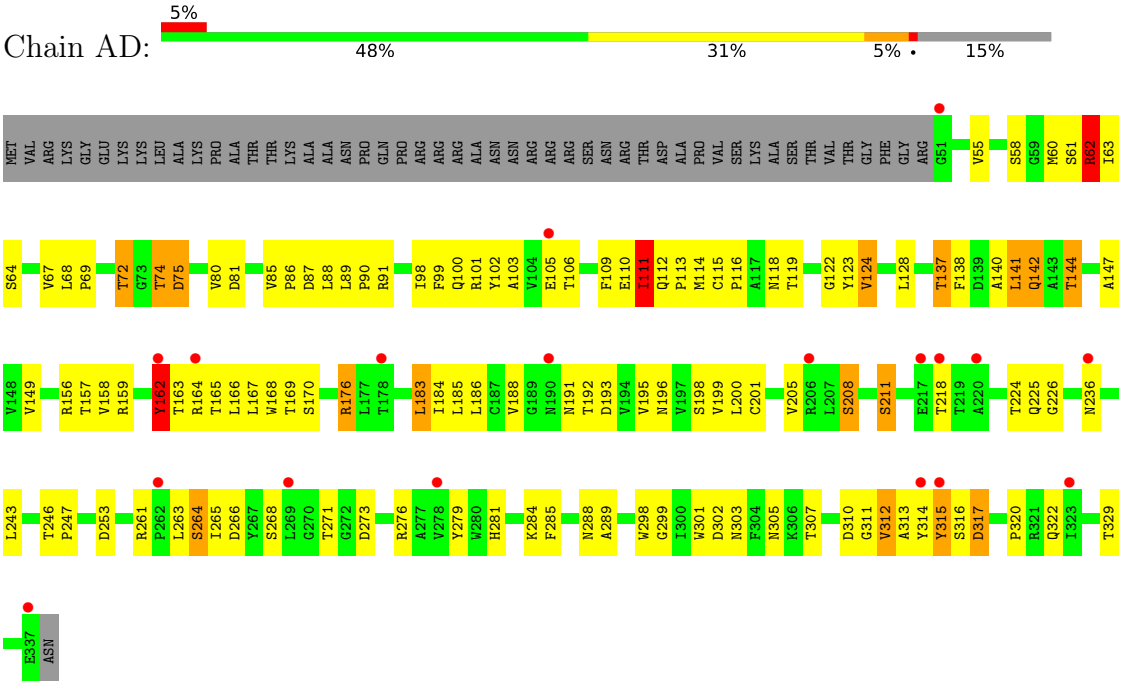




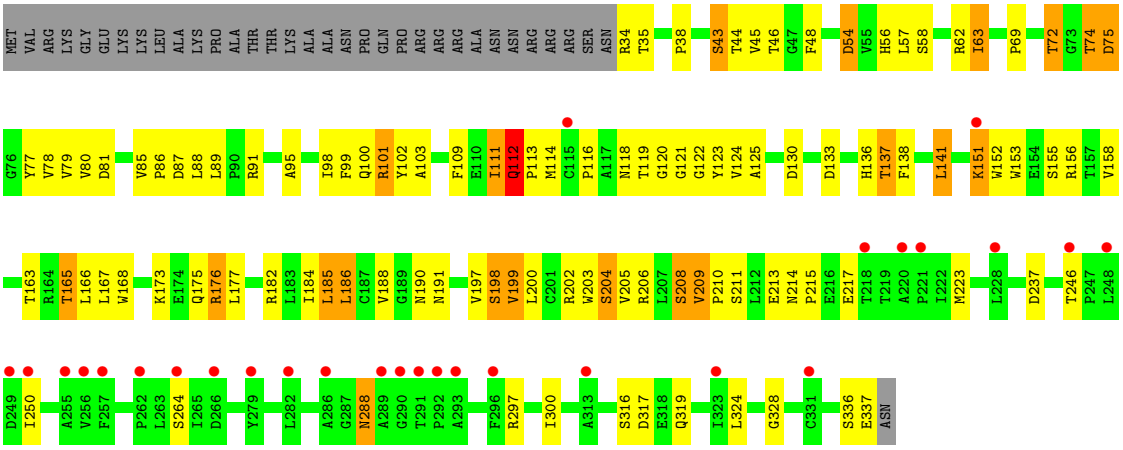
• Molecule 1: Coat protein



• Molecule 1: Coat protein

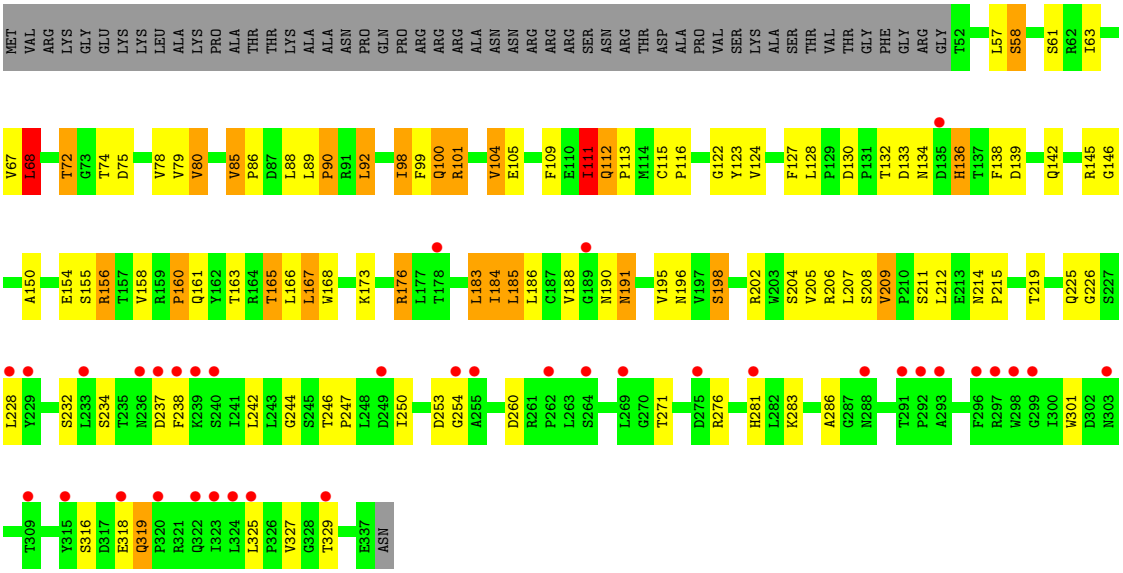


• Molecule 1: Coat protein



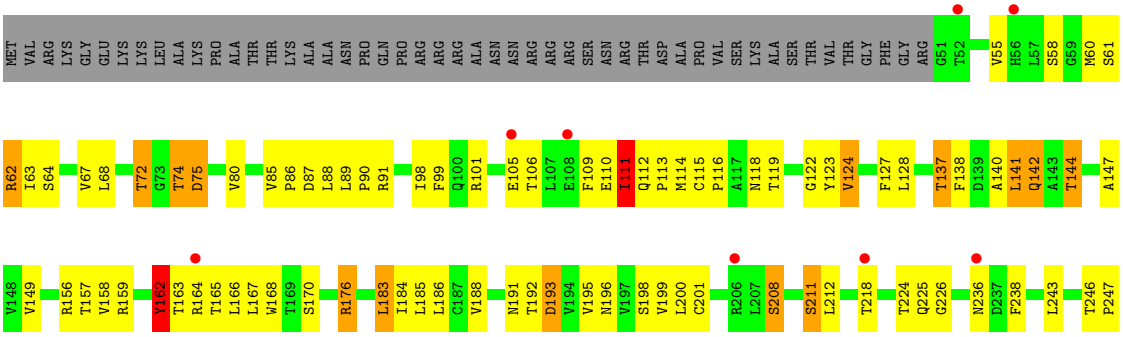
• Molecule 1: Coat protein

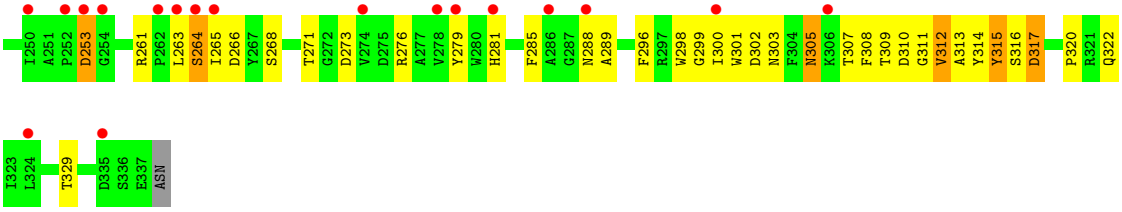
Chain BE:



• Molecule 1: Coat protein

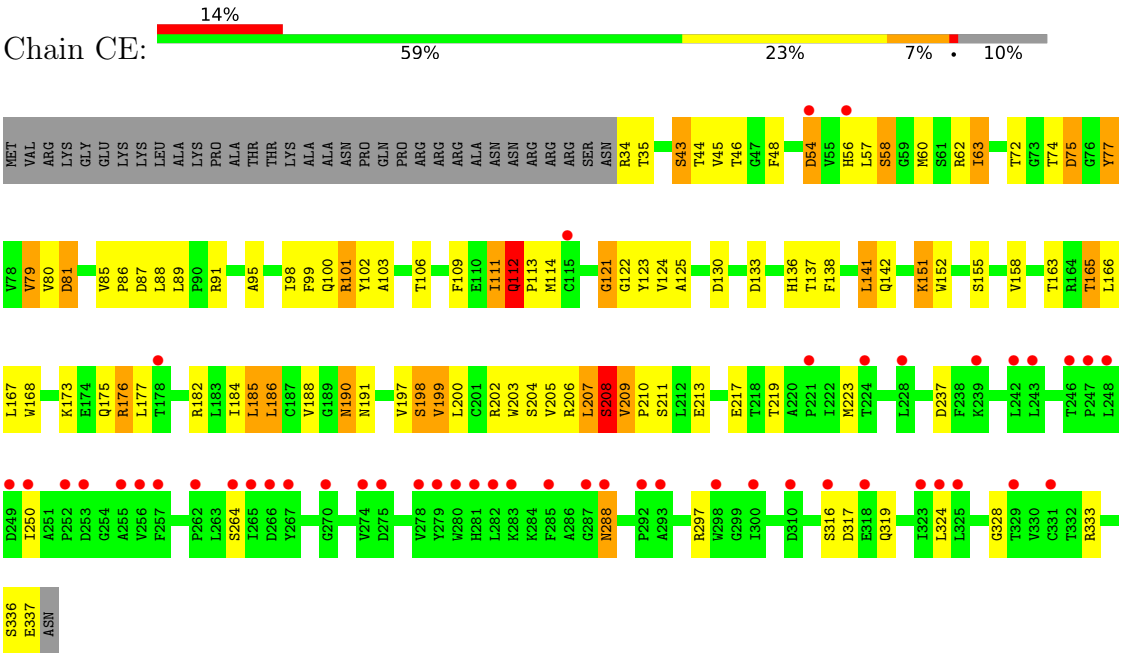
Chain AE:





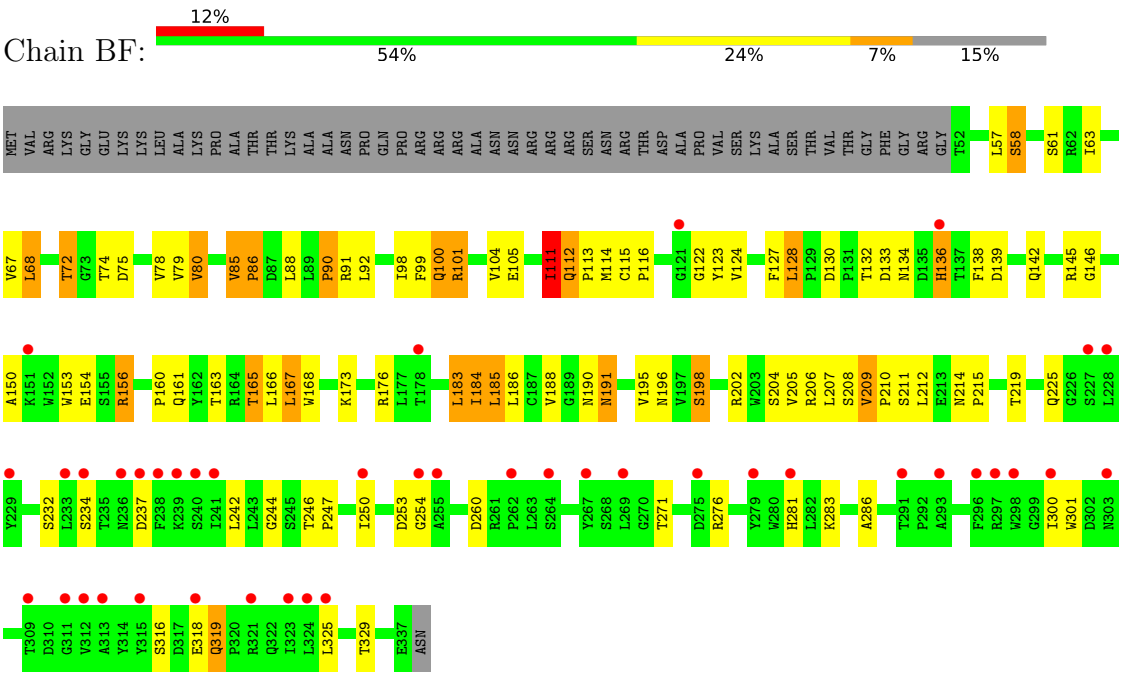
• Molecule 1: Coat protein

Chain CE:



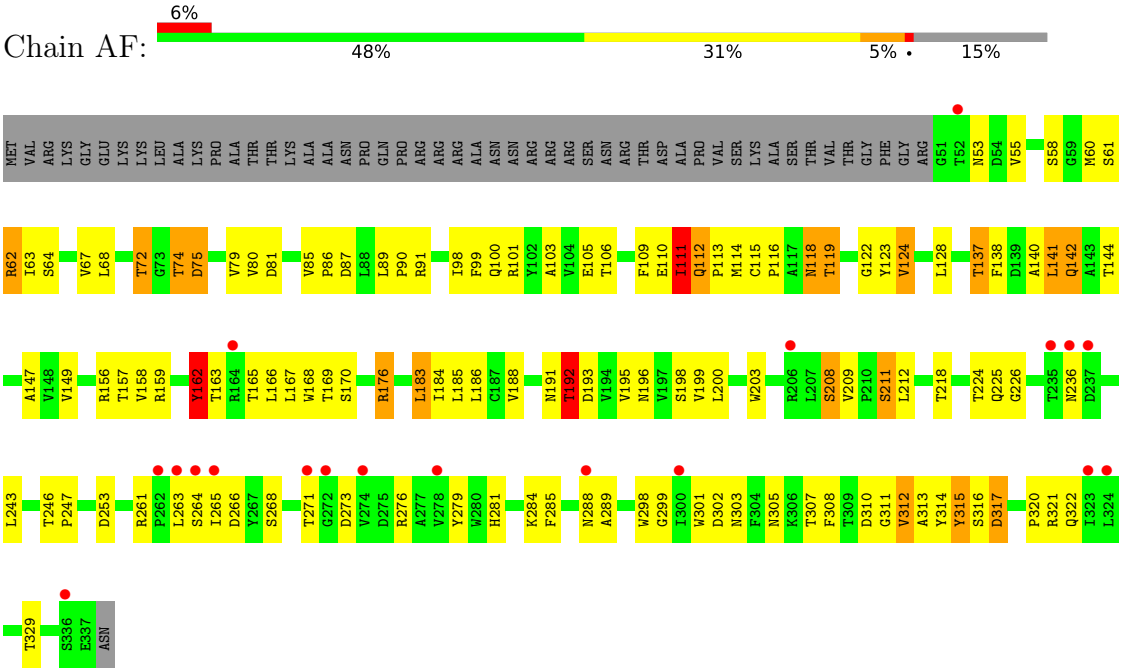
• Molecule 1: Coat protein

Chain BF:



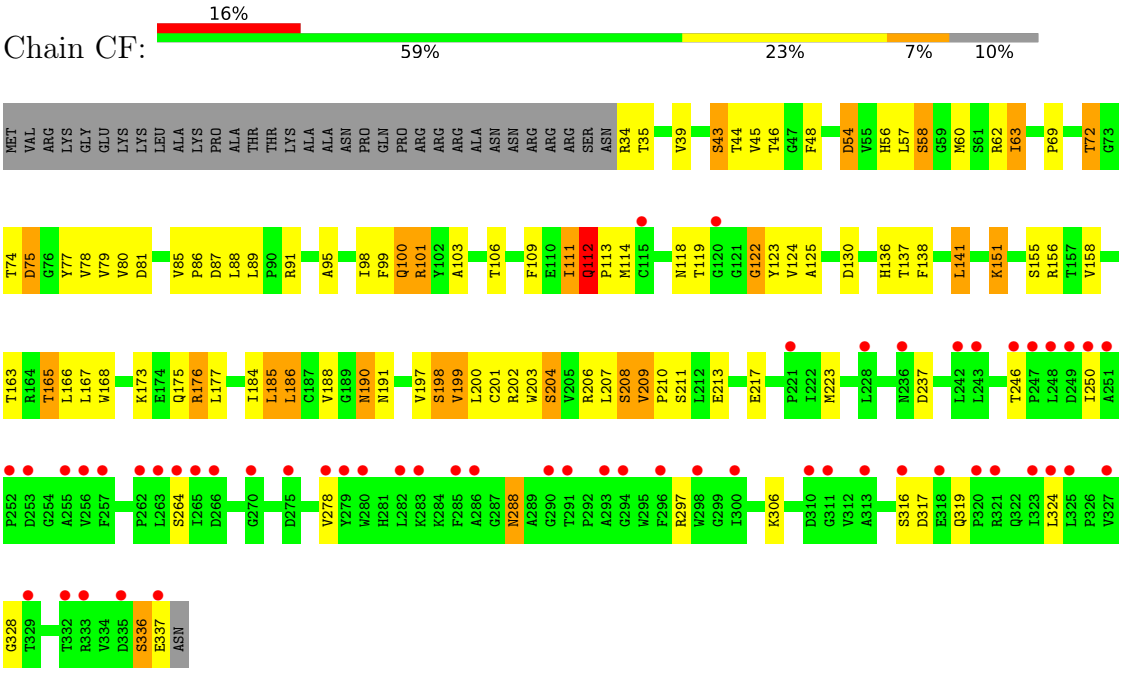
• Molecule 1: Coat protein

Chain AF:



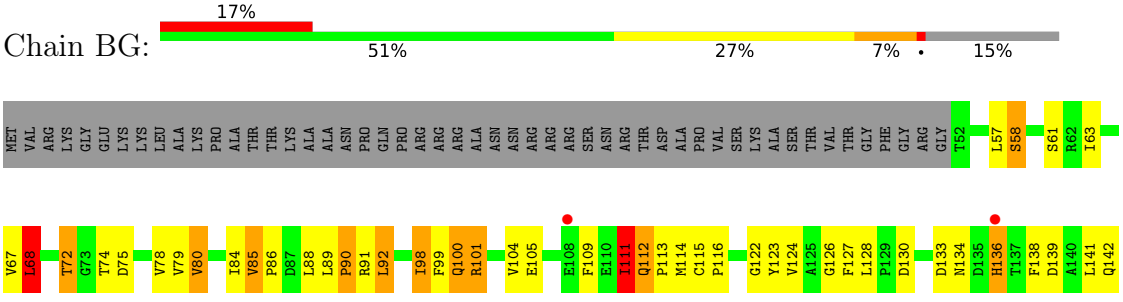
• Molecule 1: Coat protein

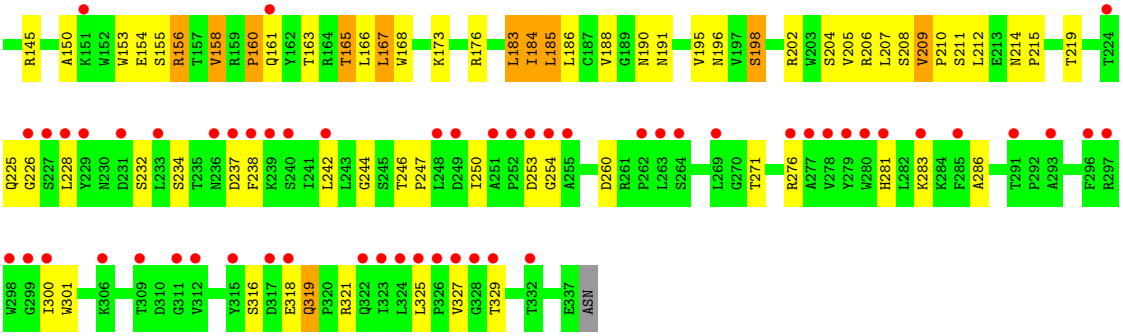
Chain CF:



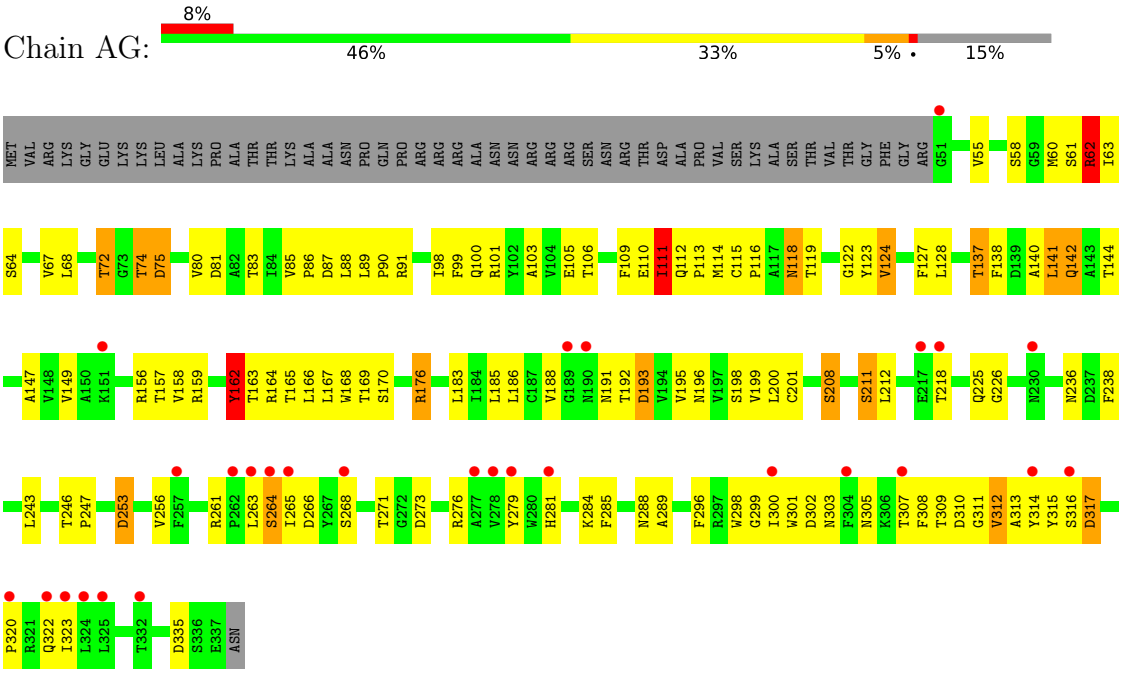
• Molecule 1: Coat protein

Chain BG:

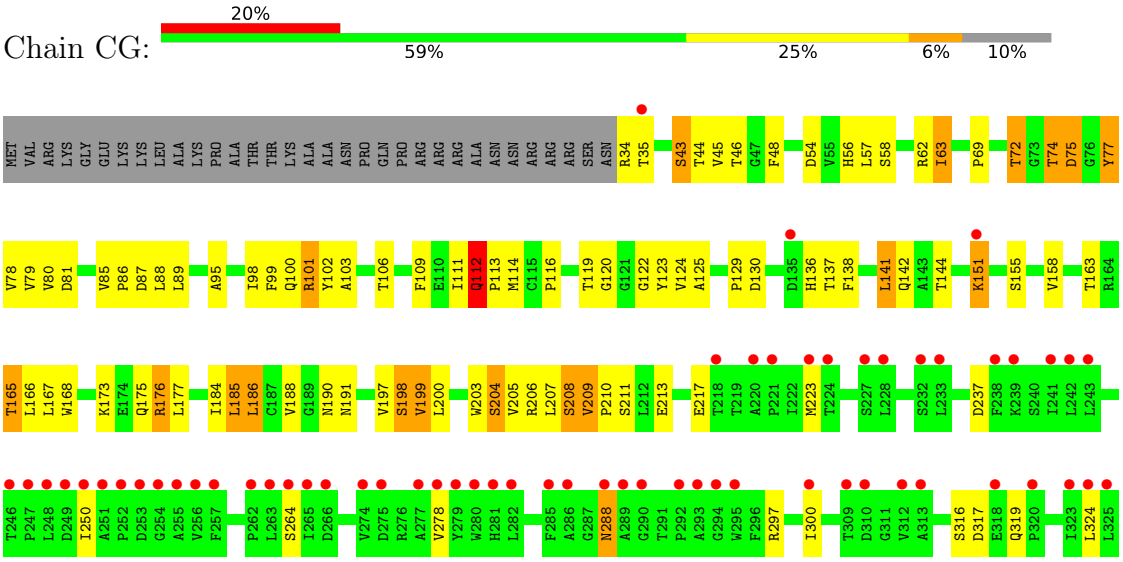


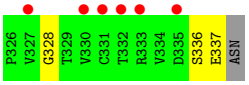


• Molecule 1: Coat protein



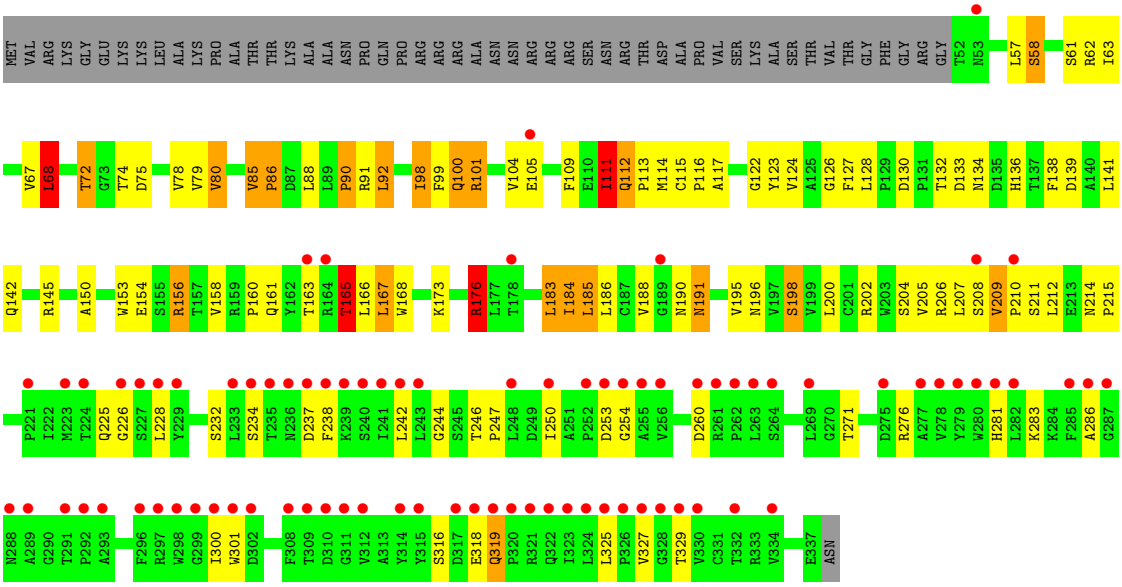
• Molecule 1: Coat protein





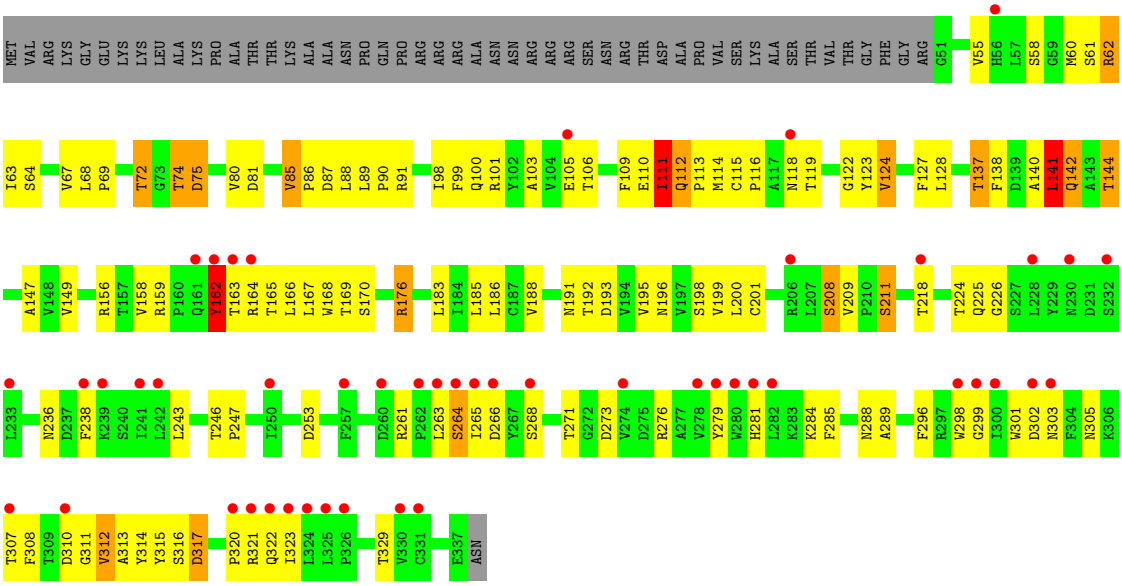
• Molecule 1: Coat protein

Chain BH:



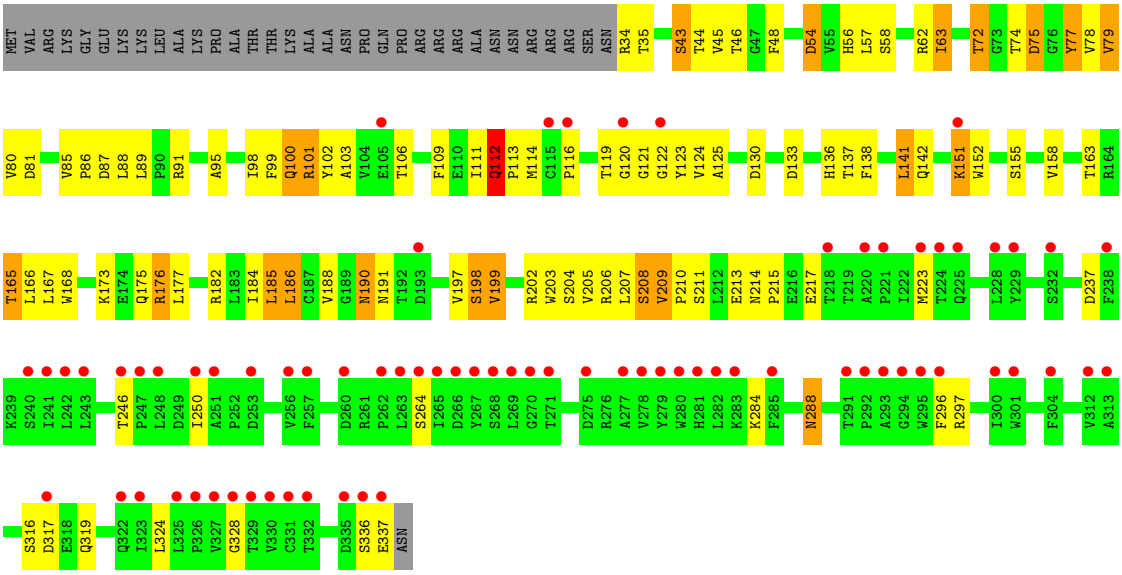
• Molecule 1: Coat protein

Chain AH:



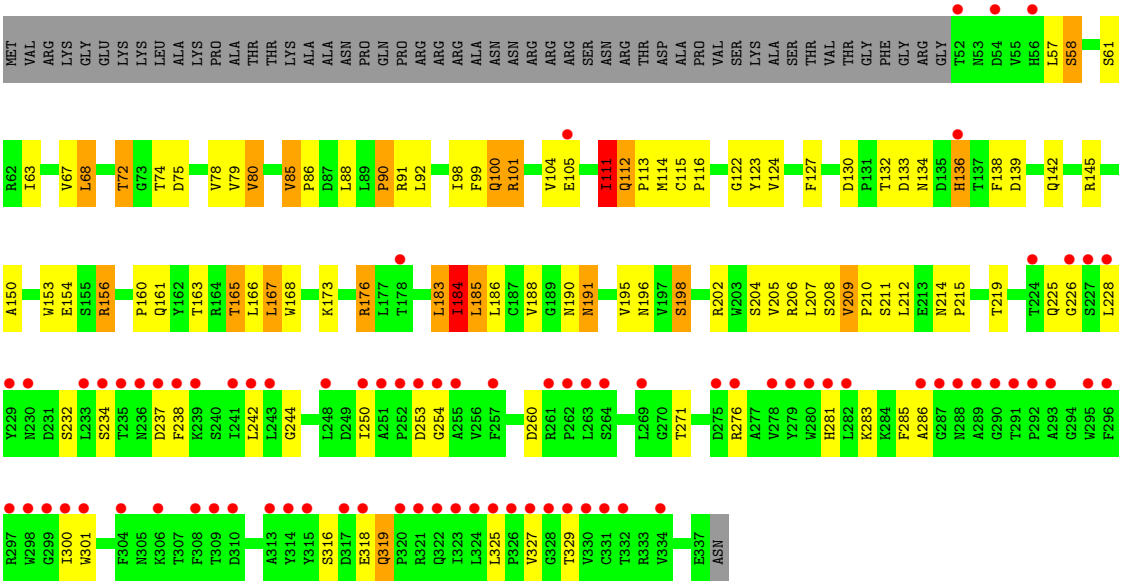
• Molecule 1: Coat protein

Chain CH:



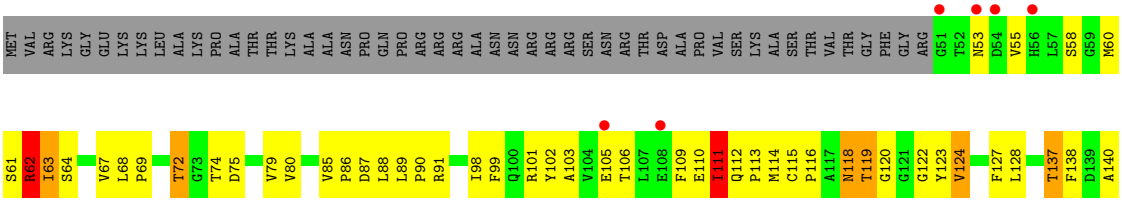
• Molecule 1: Coat protein

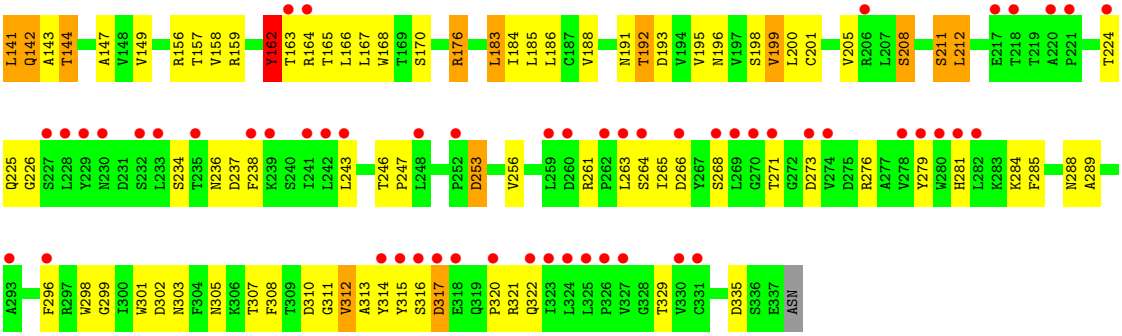
Chain BI:



• Molecule 1: Coat protein

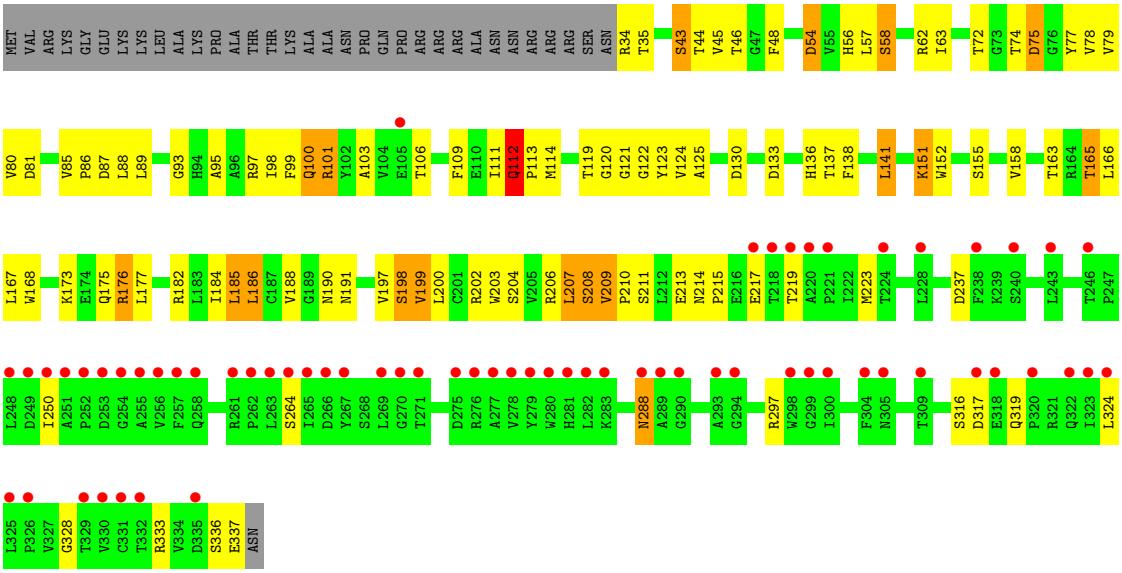
Chain AI:





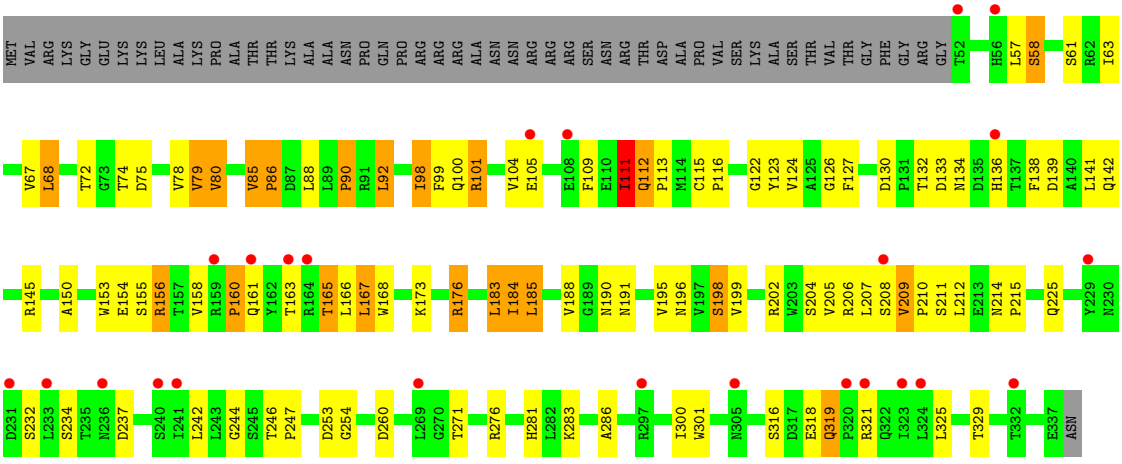
• Molecule 1: Coat protein

Chain CI:



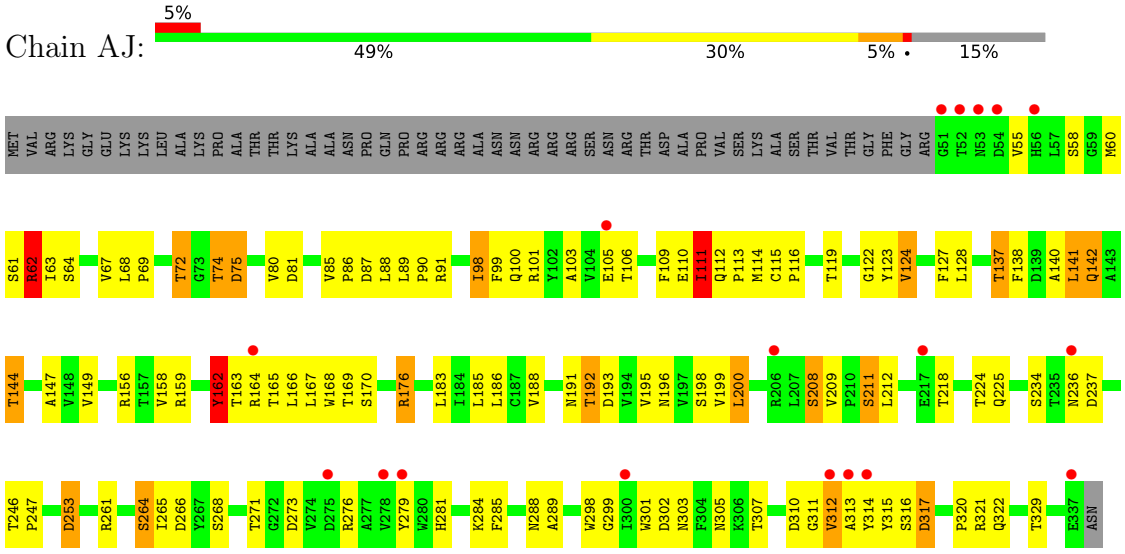
• Molecule 1: Coat protein

Chain BJ:



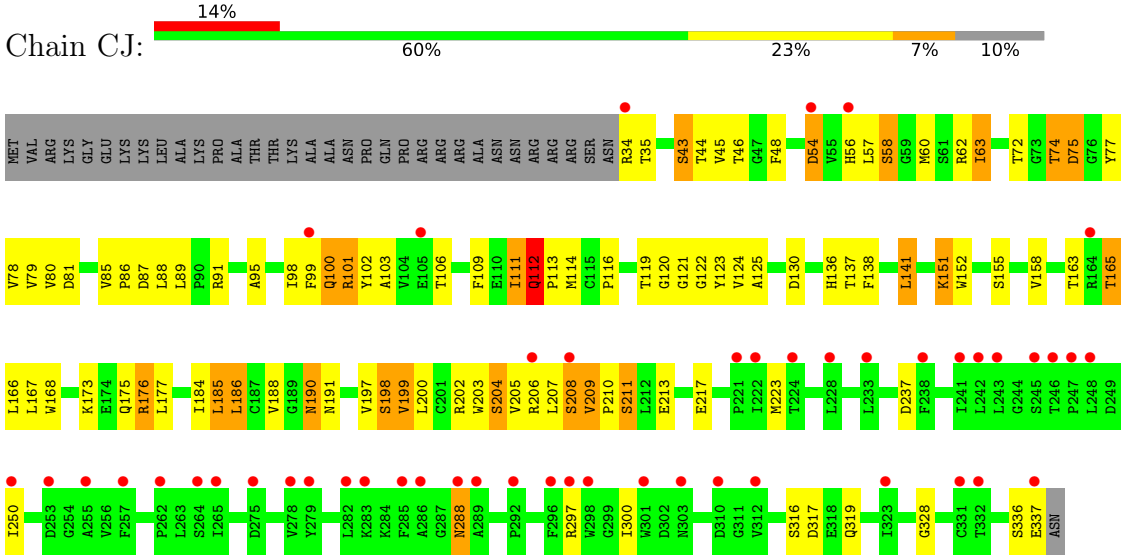
• Molecule 1: Coat protein

Chain AJ:



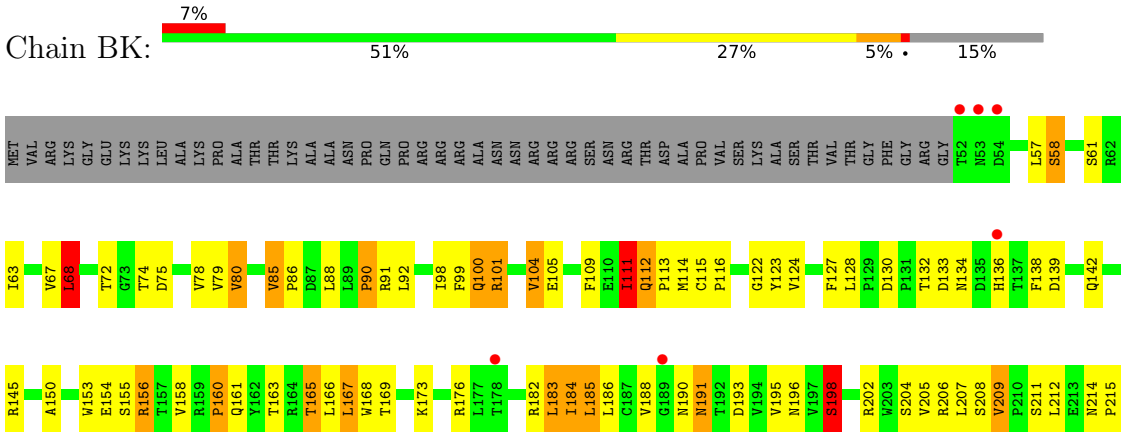
• Molecule 1: Coat protein

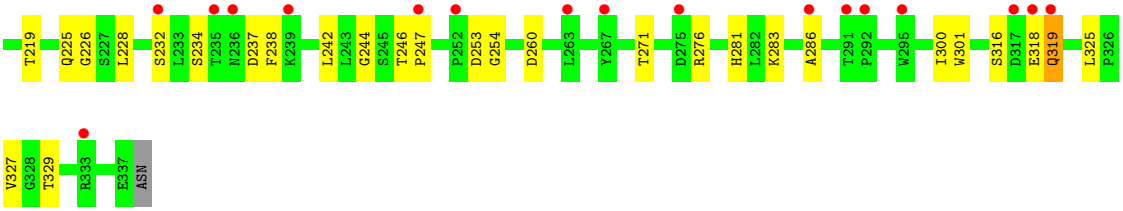
Chain CJ:



• Molecule 1: Coat protein

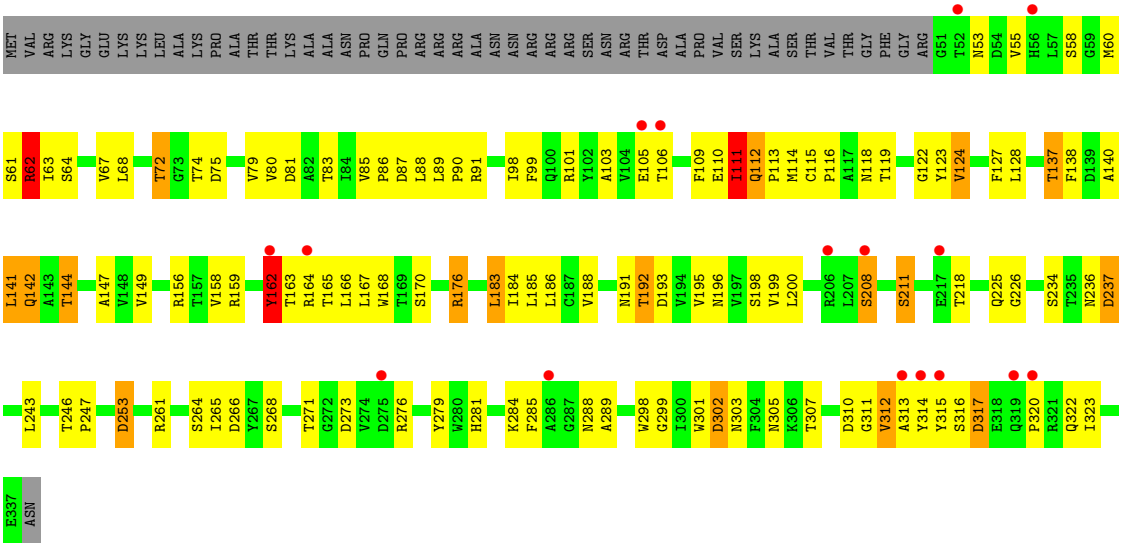
Chain BK:





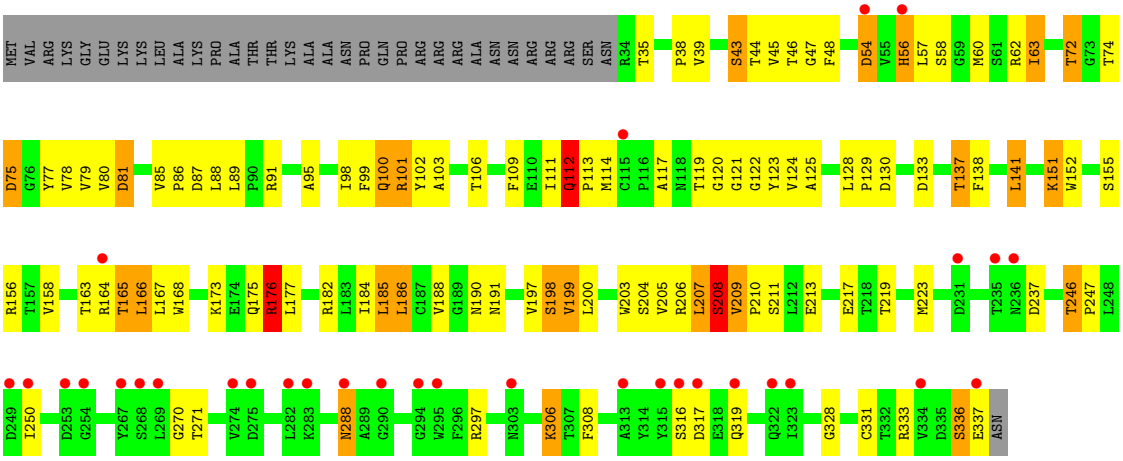
• Molecule 1: Coat protein

Chain AK:



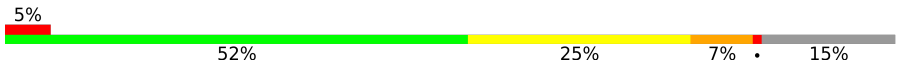
• Molecule 1: Coat protein

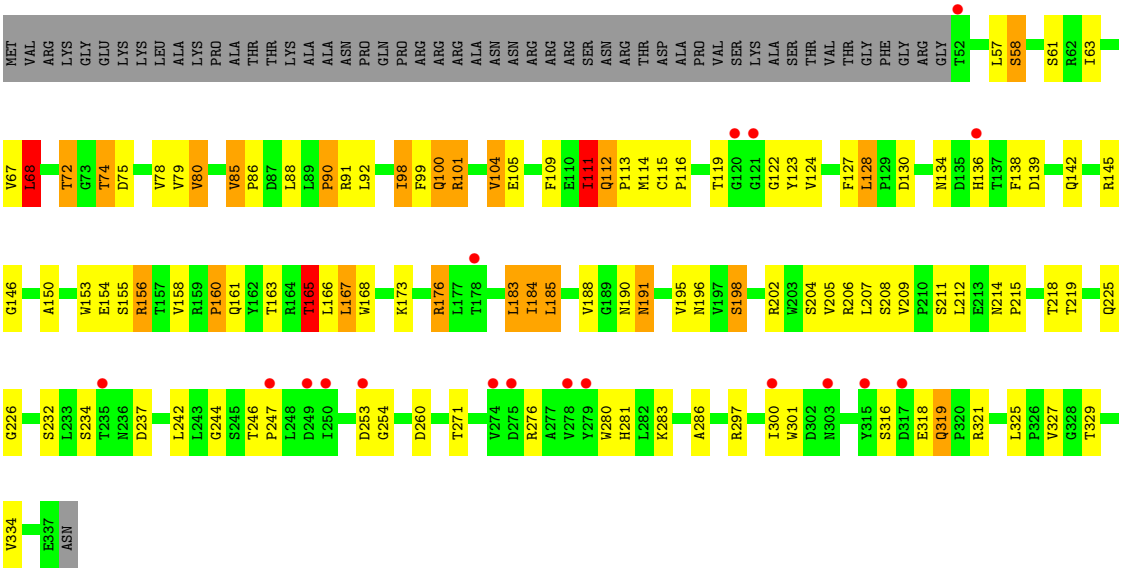
Chain CK:



• Molecule 1: Coat protein

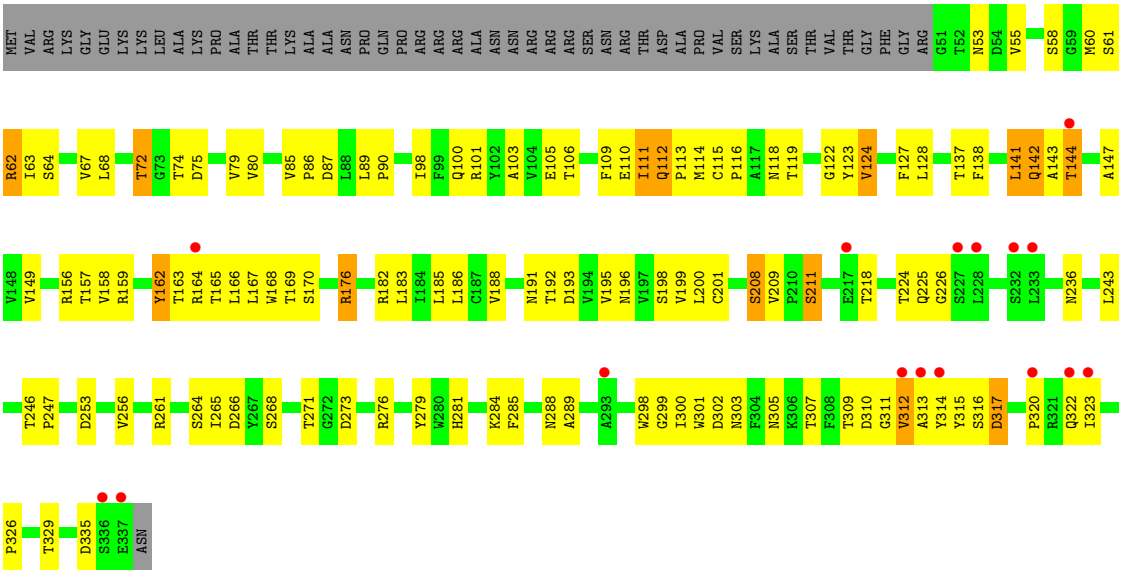
Chain BL:





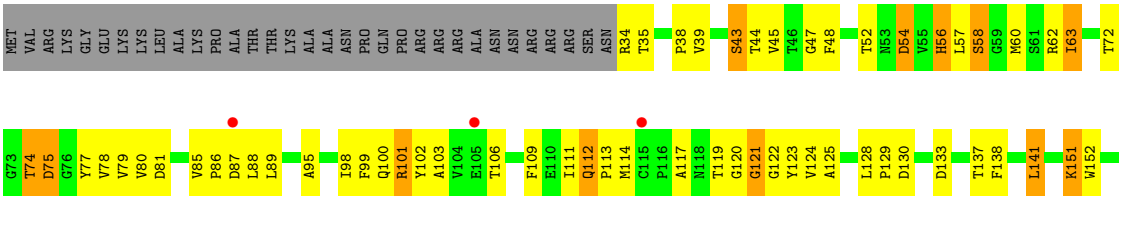
• Molecule 1: Coat protein

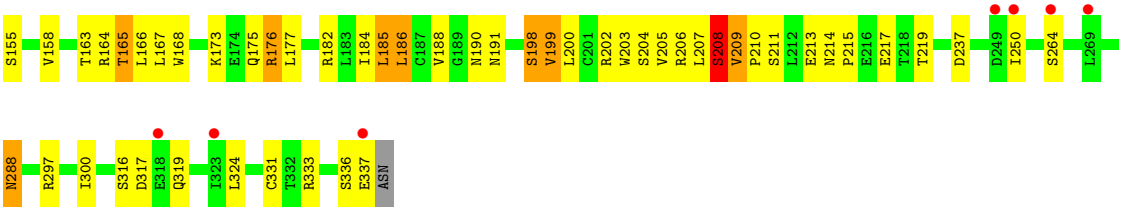
Chain AL:



• Molecule 1: Coat protein

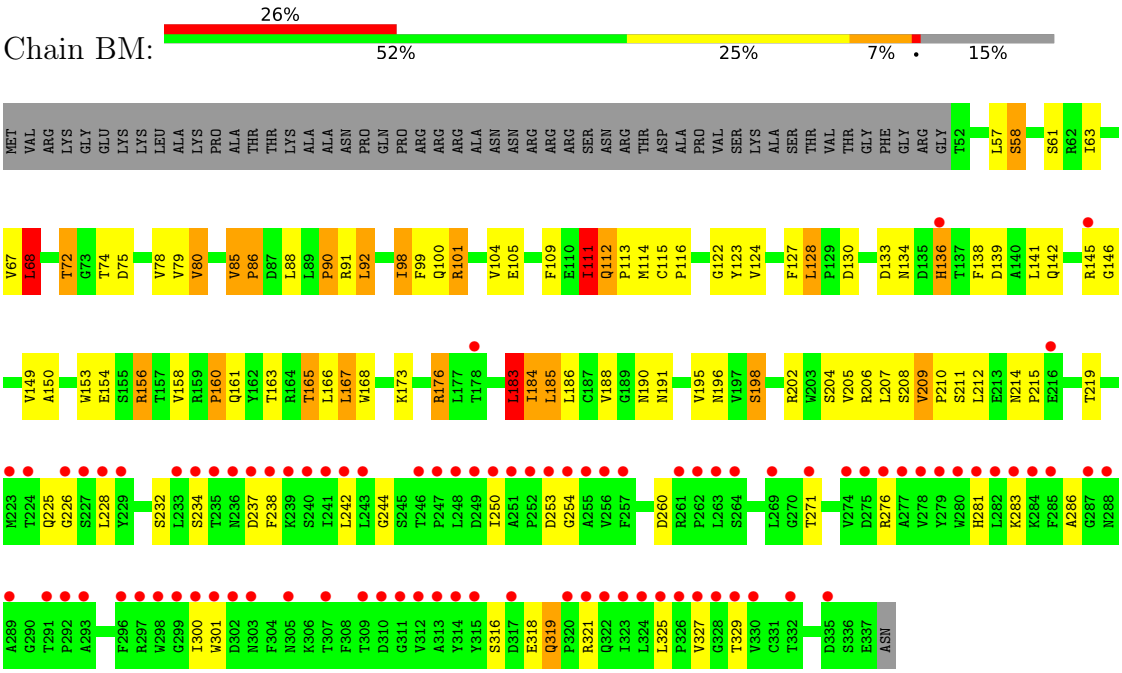
Chain CL:





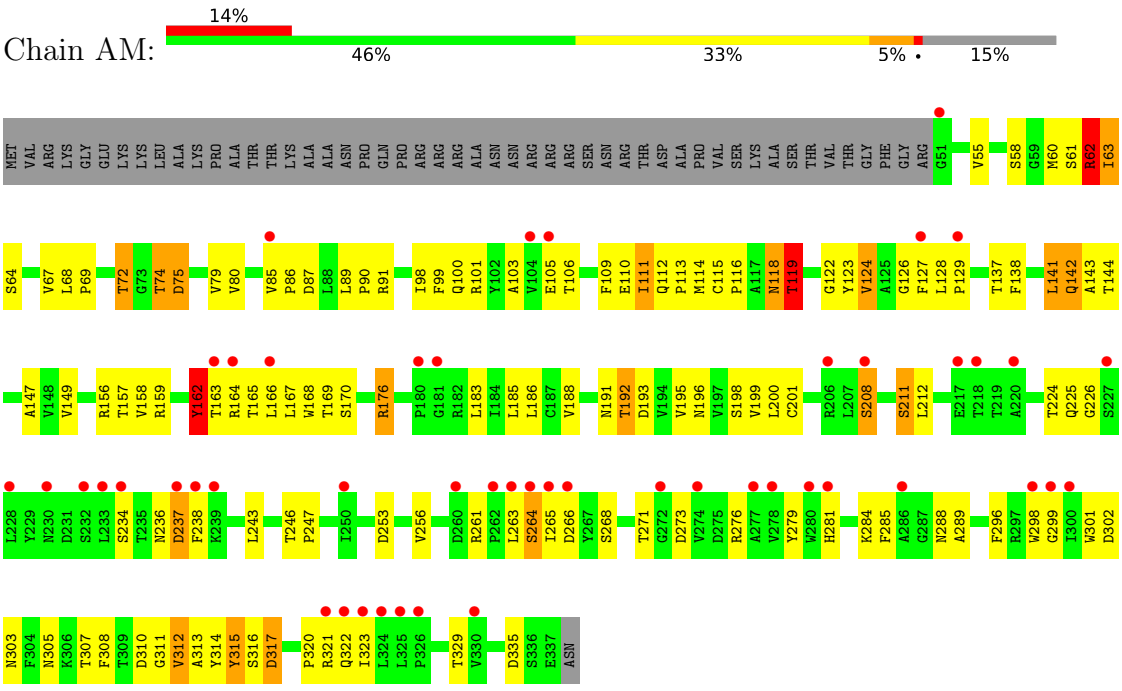
• Molecule 1: Coat protein

Chain BM:



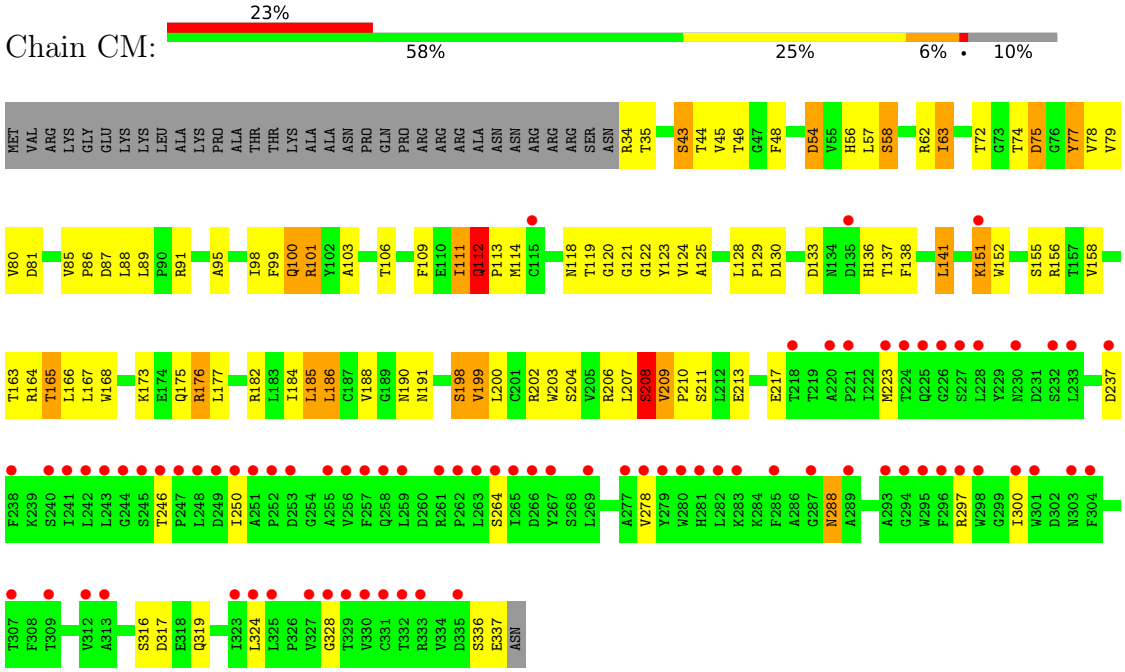
• Molecule 1: Coat protein

Chain AM:



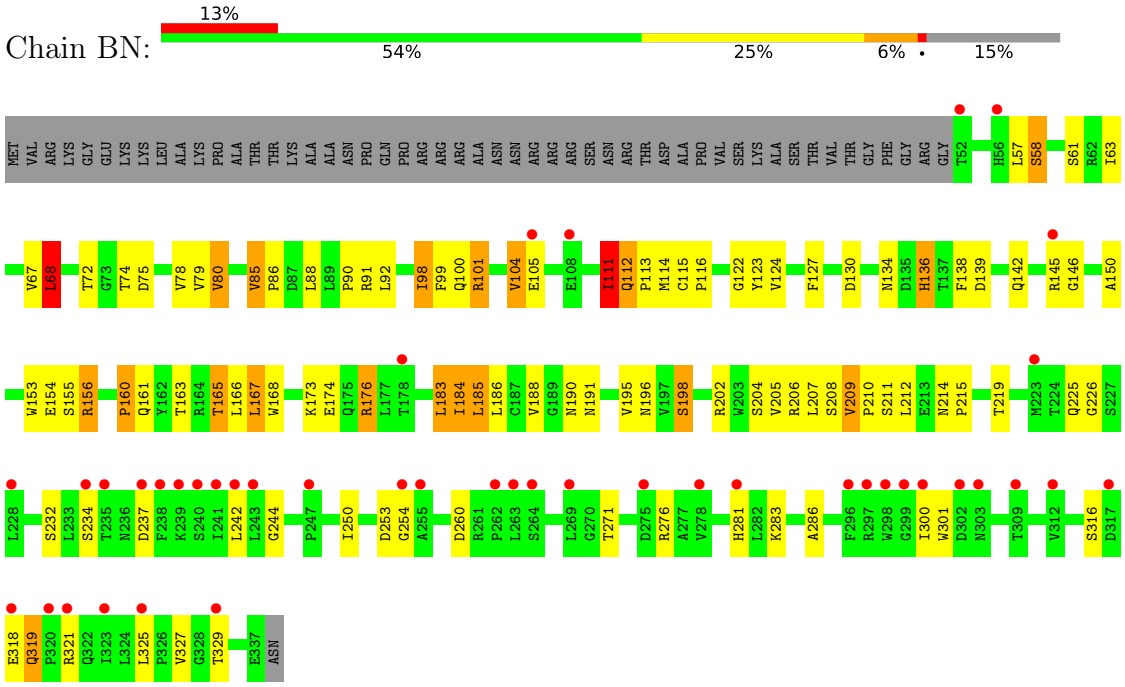
• Molecule 1: Coat protein

Chain CM:



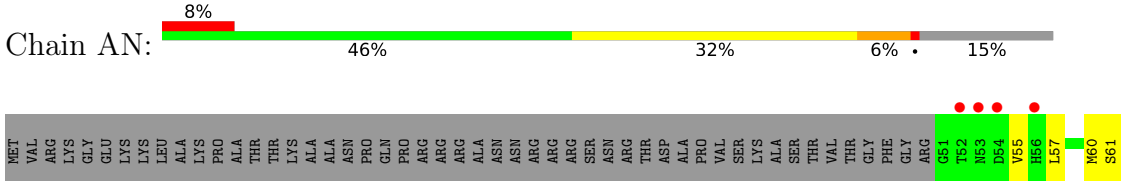
• Molecule 1: Coat protein

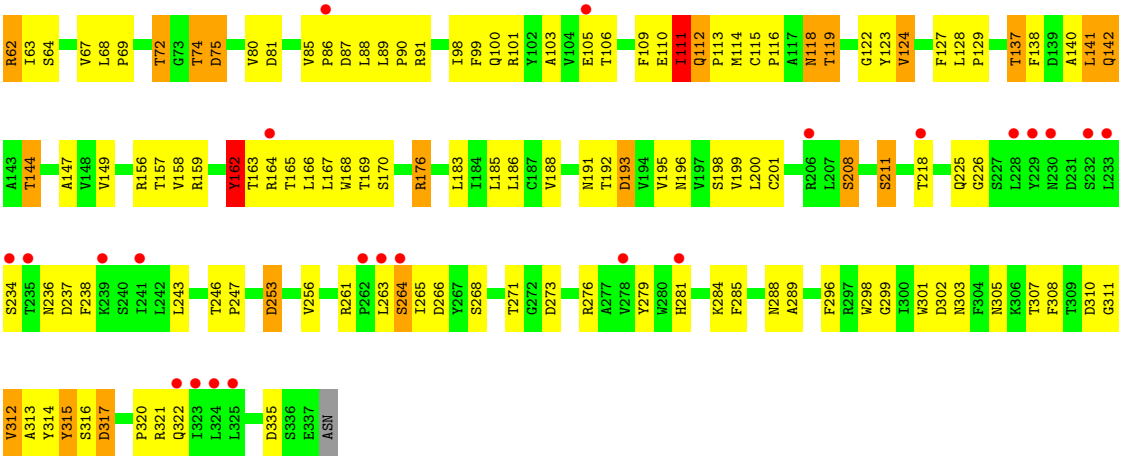
Chain BN:



• Molecule 1: Coat protein

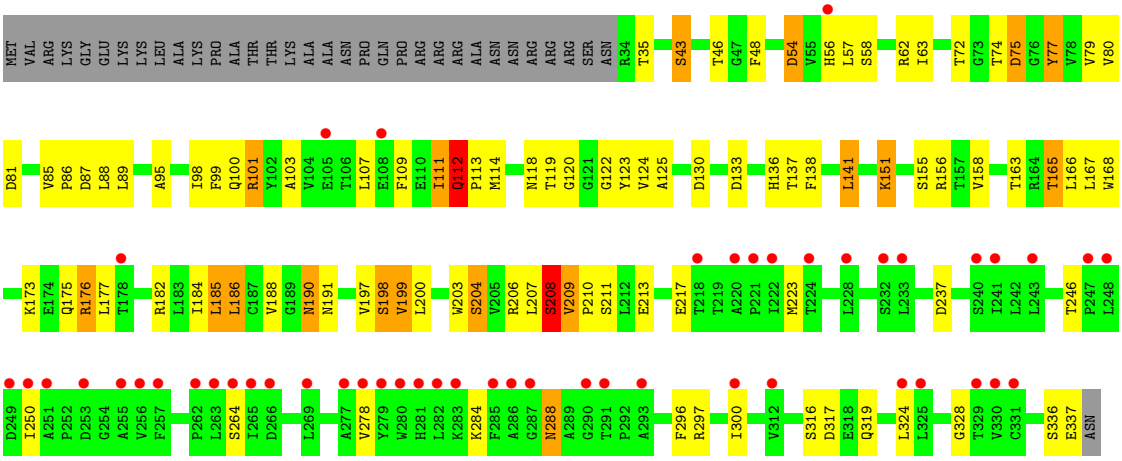
Chain AN:





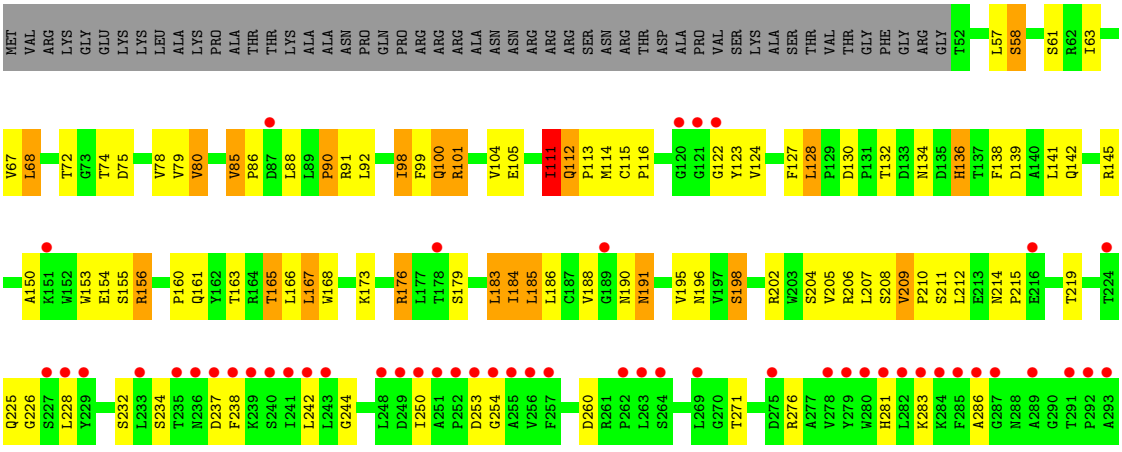
• Molecule 1: Coat protein

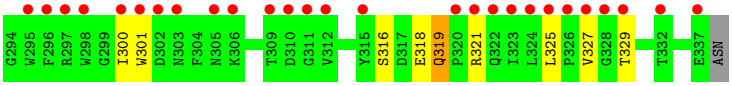
Chain CN:



• Molecule 1: Coat protein

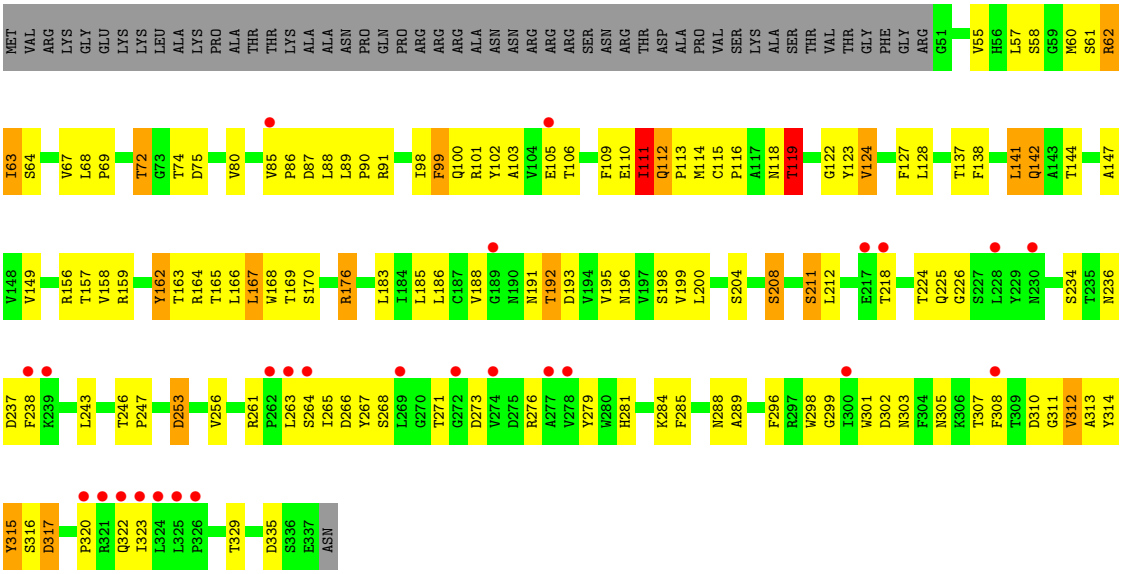
Chain BO:





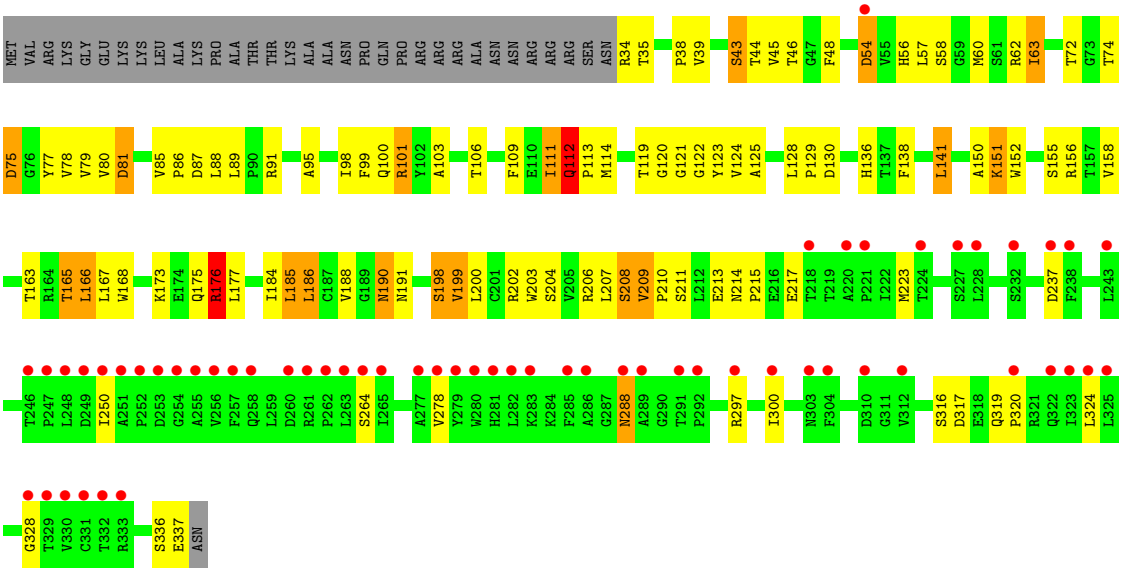
• Molecule 1: Coat protein

Chain AO:



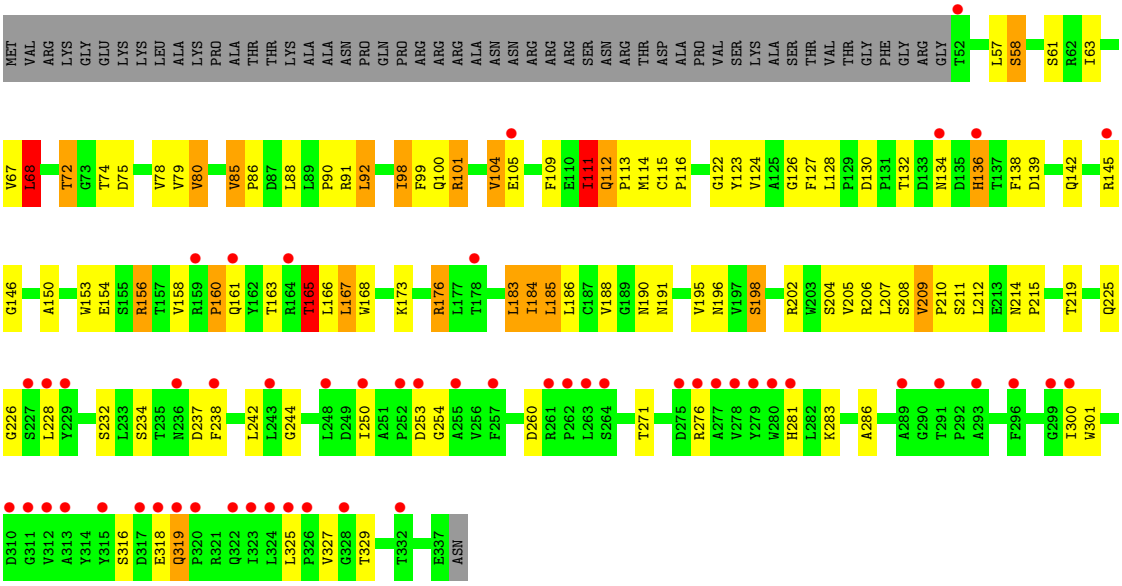
• Molecule 1: Coat protein

Chain CO:

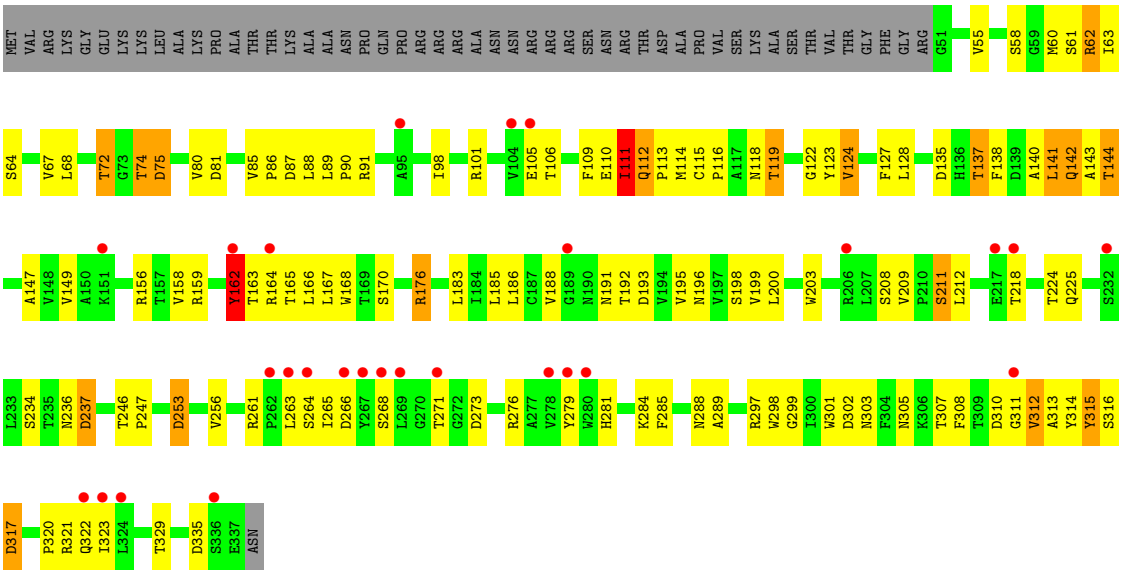


• Molecule 1: Coat protein

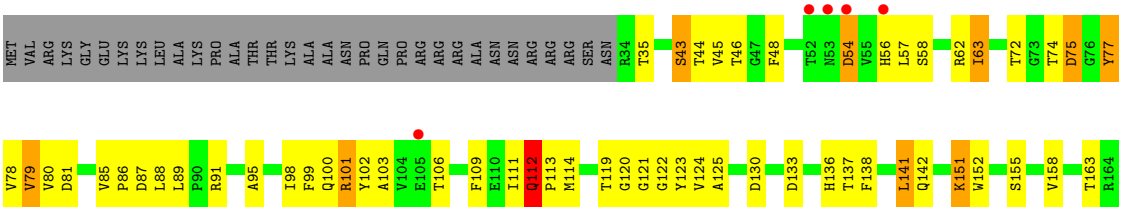
Chain BP:

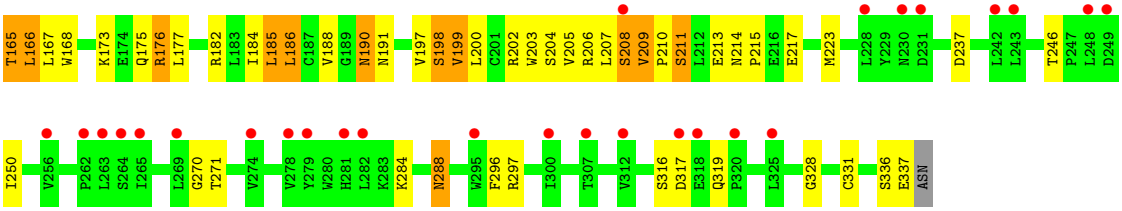


• Molecule 1: Coat protein



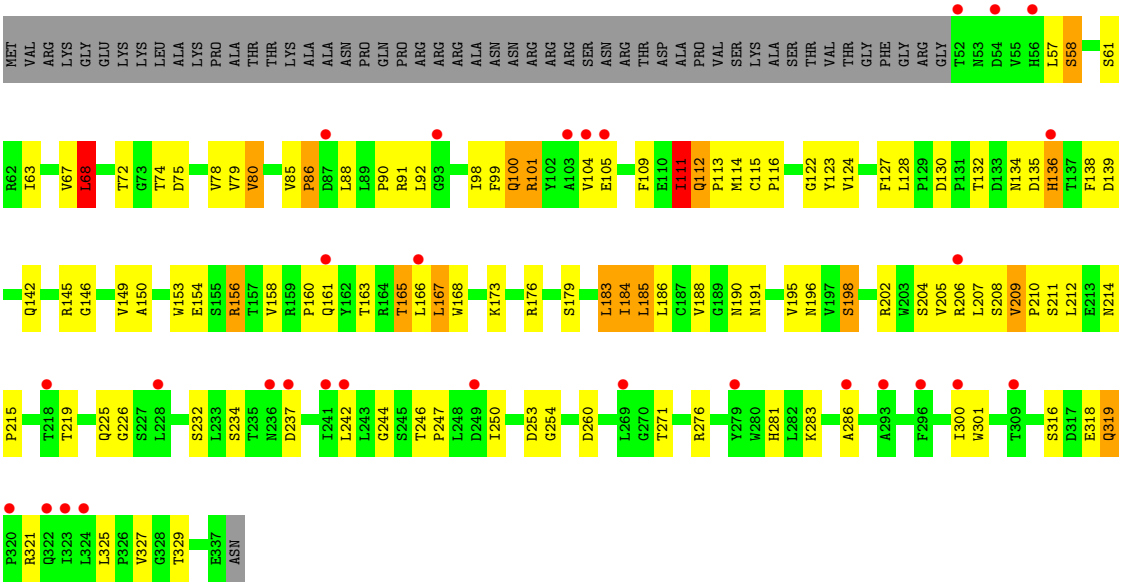
• Molecule 1: Coat protein





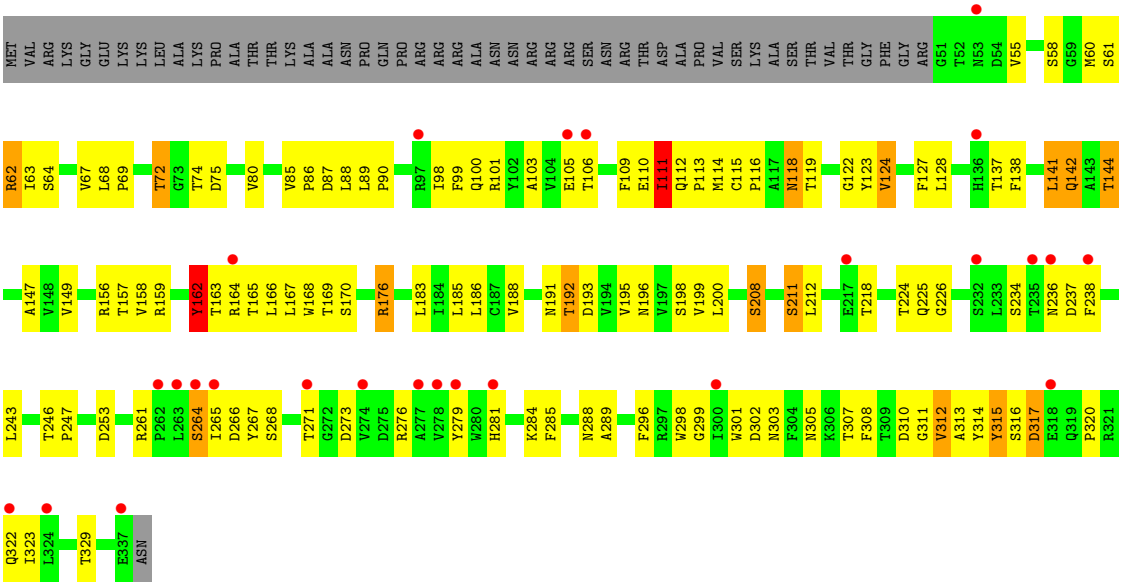
• Molecule 1: Coat protein

Chain BQ:



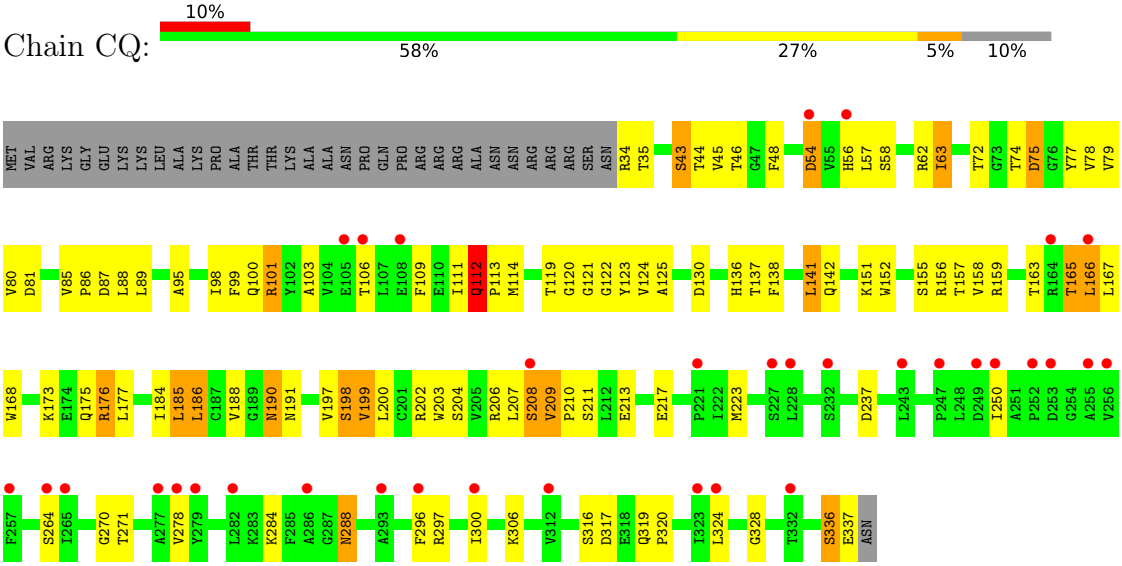
• Molecule 1: Coat protein

Chain AQ:



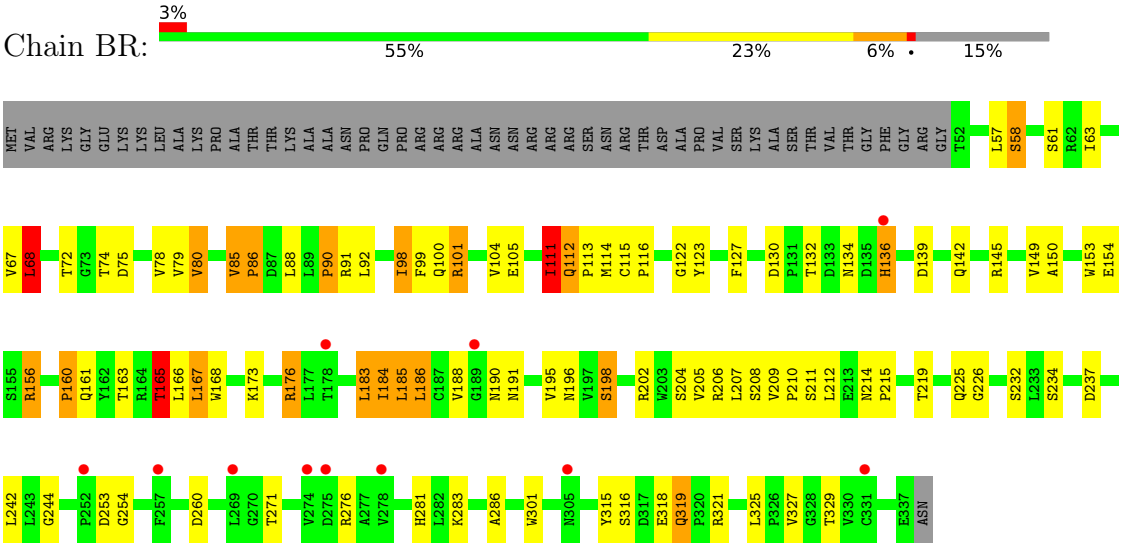
• Molecule 1: Coat protein

Chain CQ:



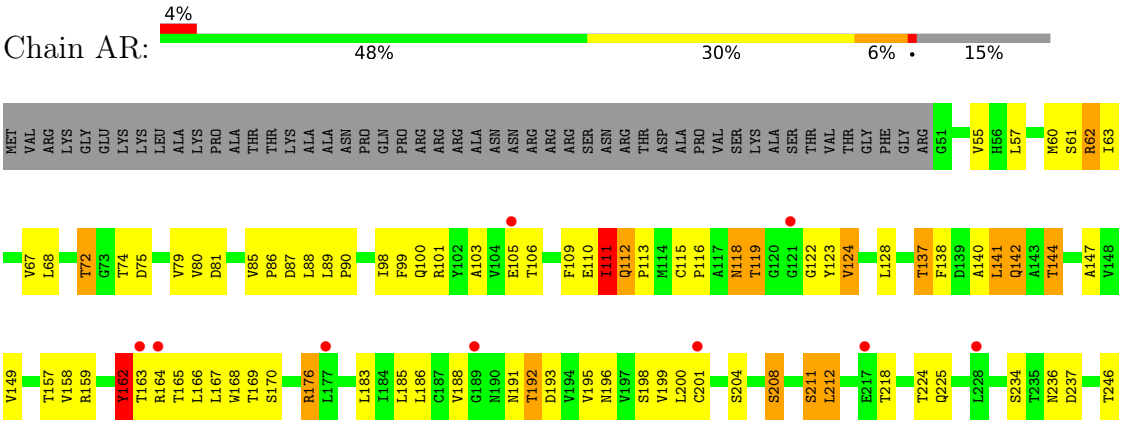
• Molecule 1: Coat protein

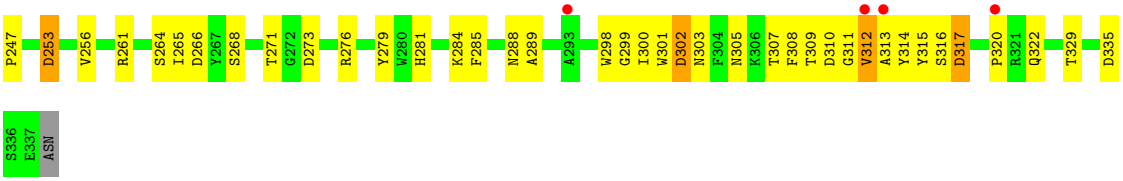
Chain BR:



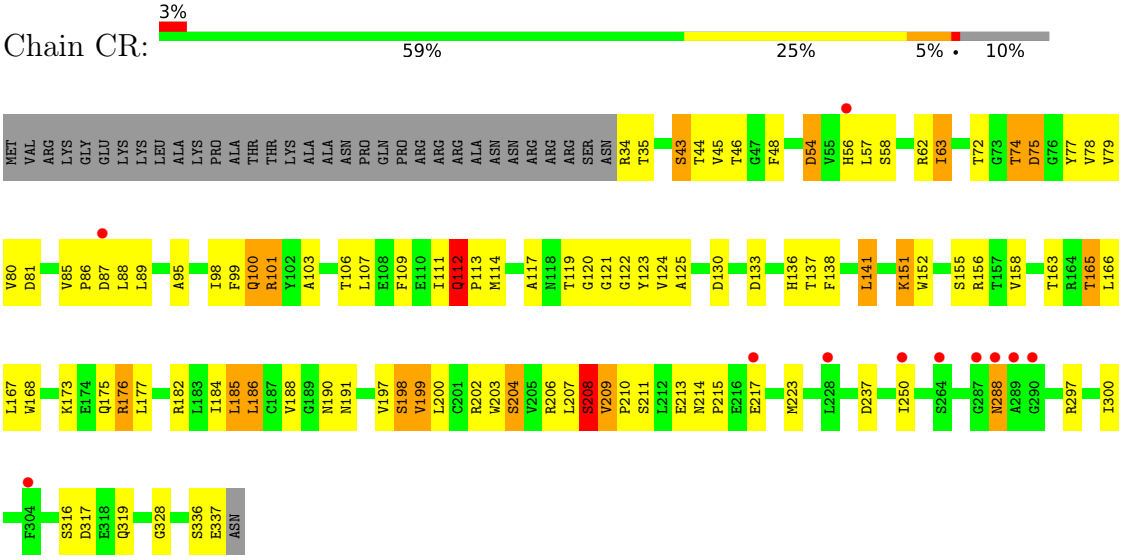
• Molecule 1: Coat protein

Chain AR:

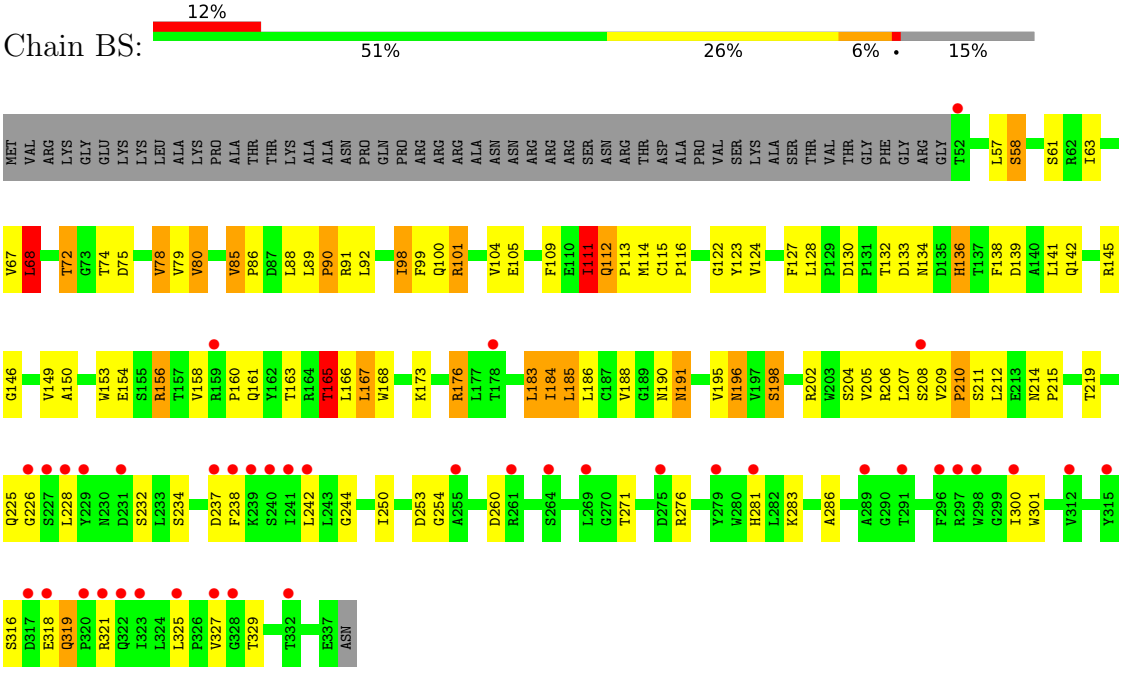




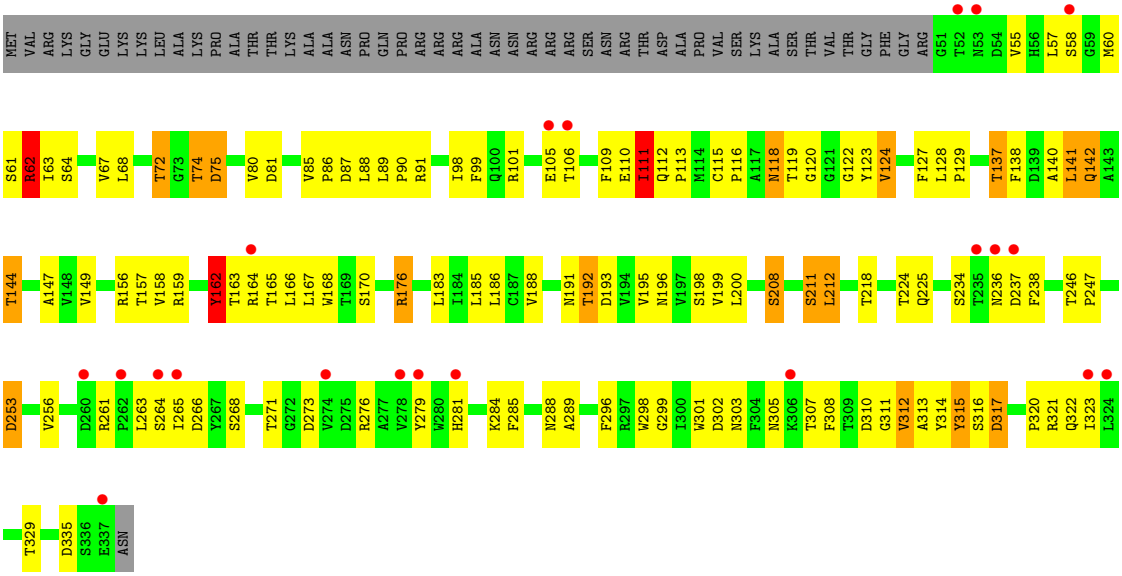
• Molecule 1: Coat protein



• Molecule 1: Coat protein

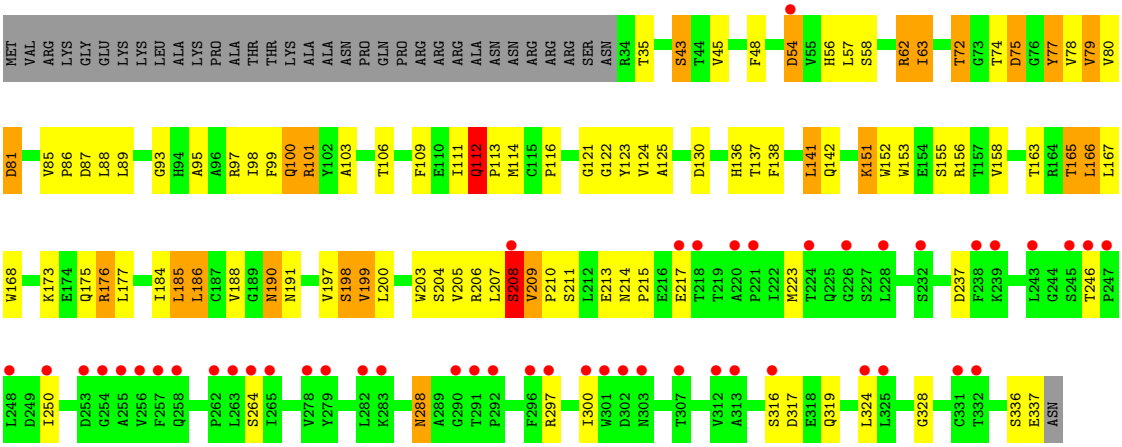


• Molecule 1: Coat protein



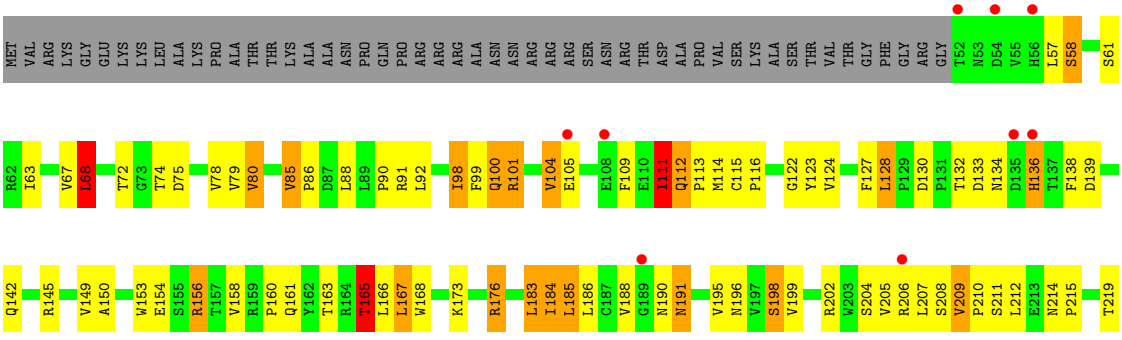
• Molecule 1: Coat protein

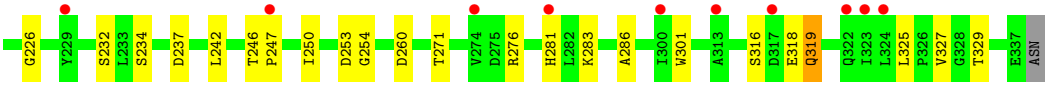
Chain CS:



• Molecule 1: Coat protein

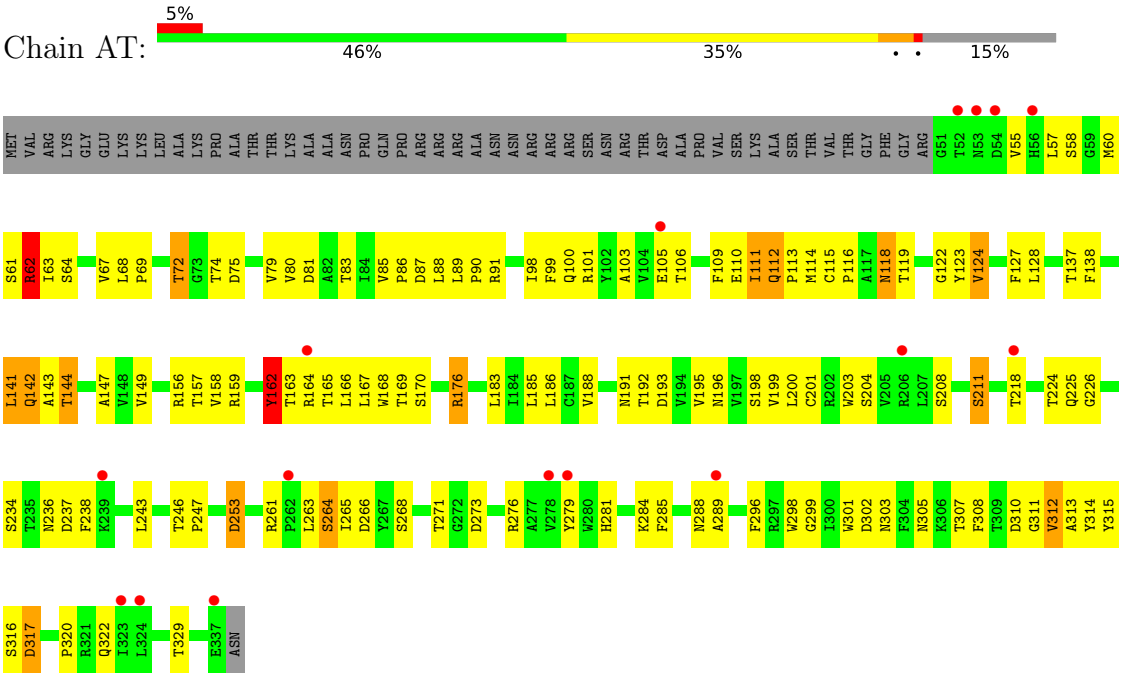
Chain BT:





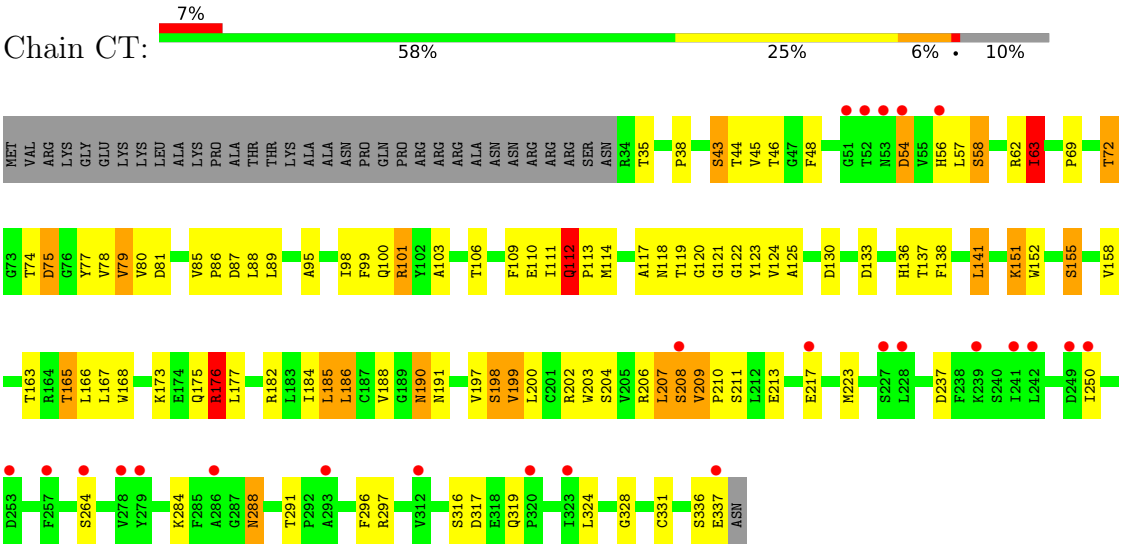
• Molecule 1: Coat protein

Chain AT:



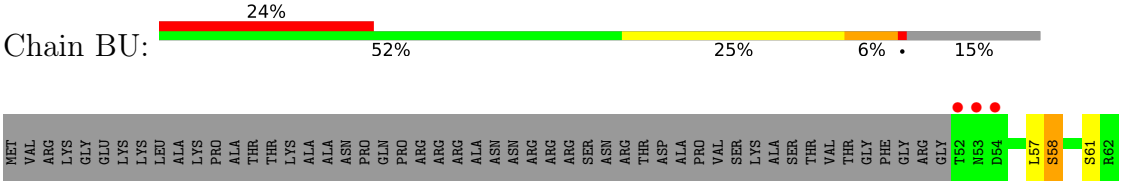
• Molecule 1: Coat protein

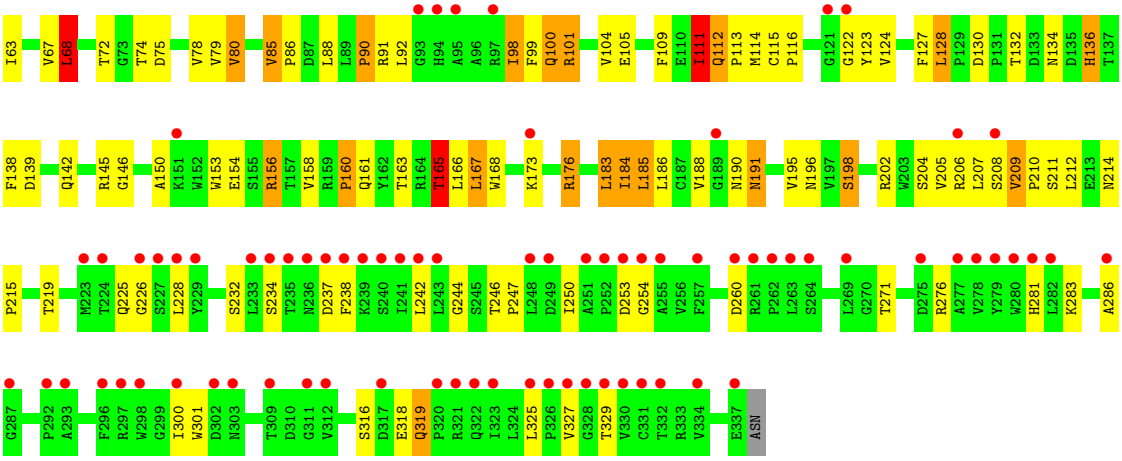
Chain CT:



• Molecule 1: Coat protein

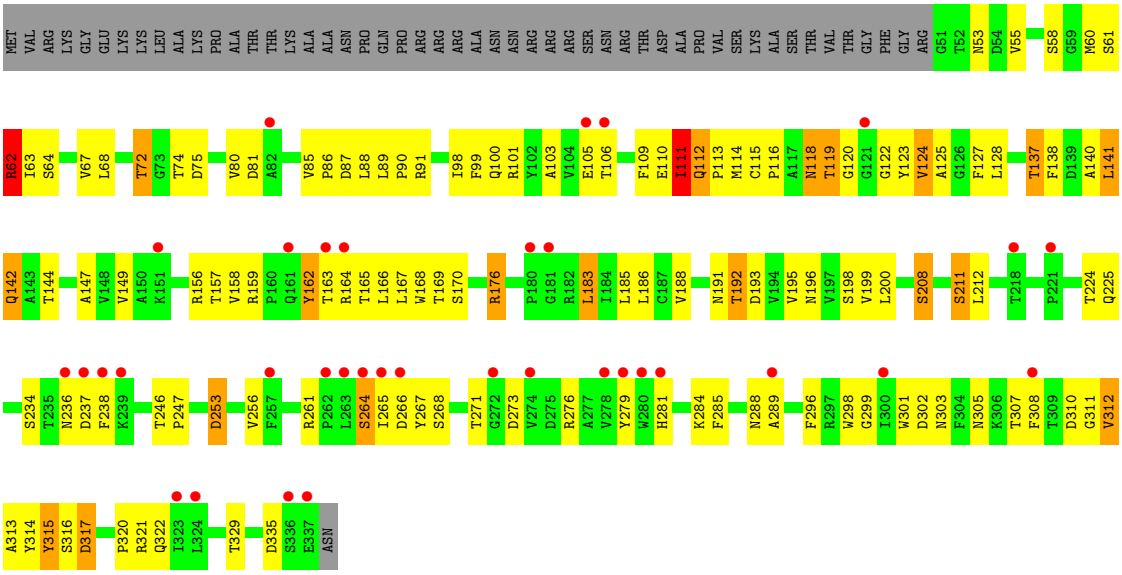
Chain BU:





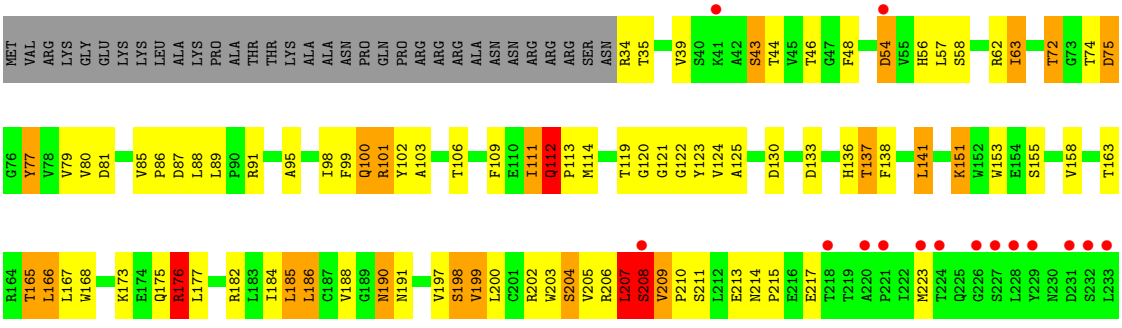
• Molecule 1: Coat protein

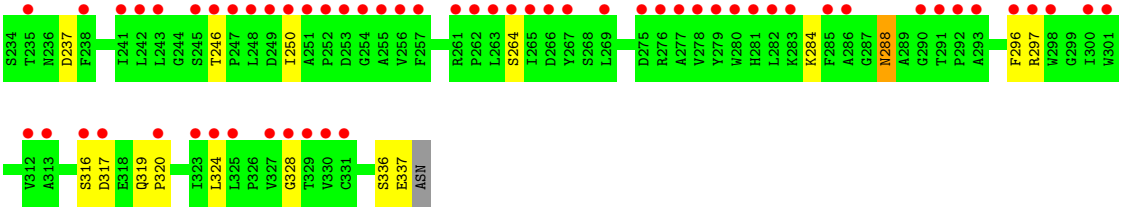
Chain AU:



• Molecule 1: Coat protein

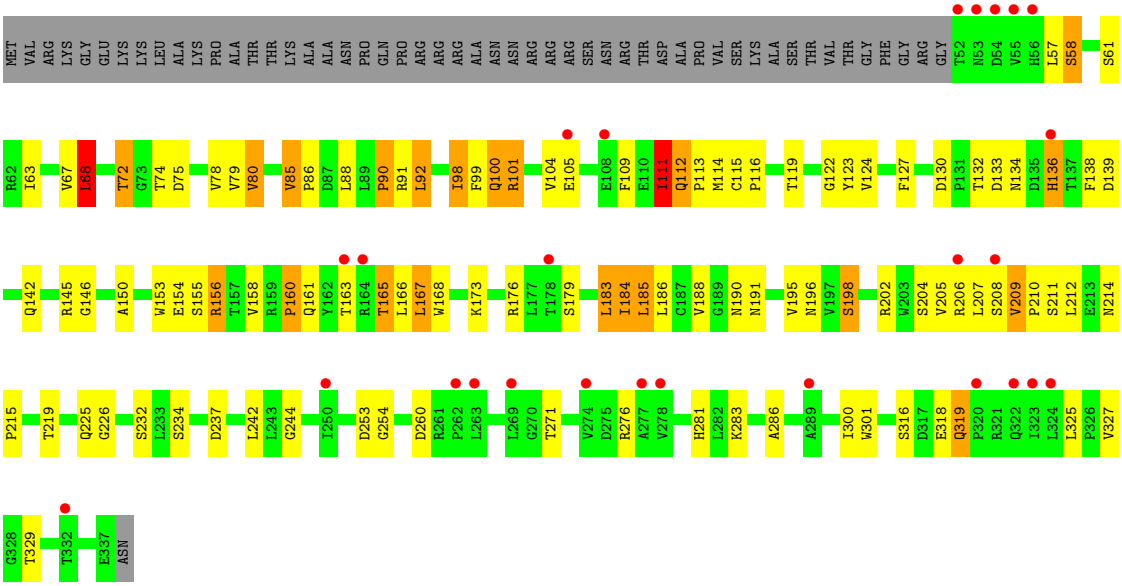
Chain CU:





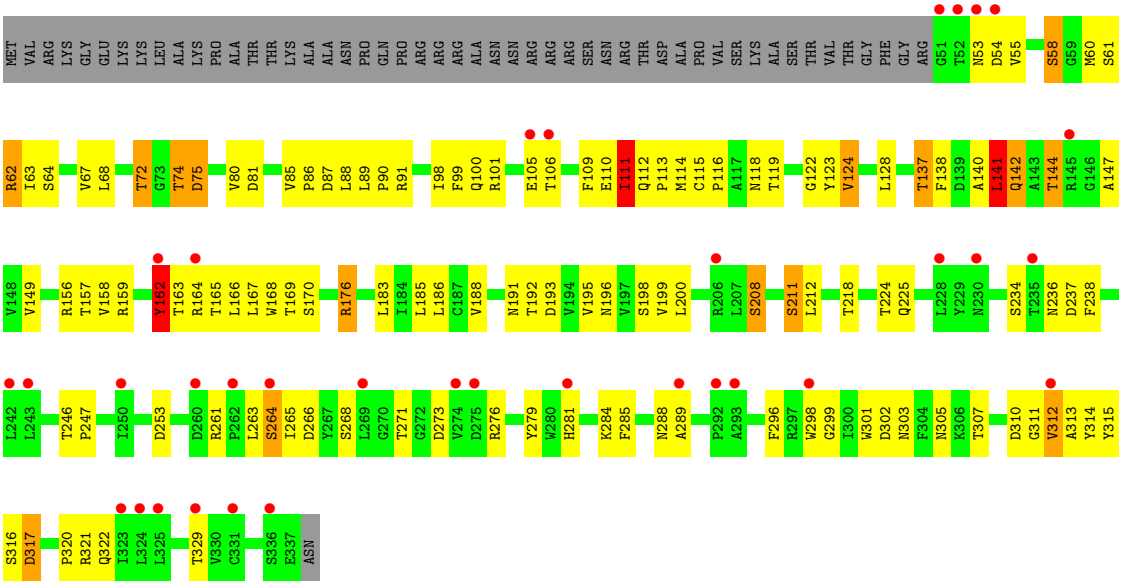
• Molecule 1: Coat protein

Chain BV:



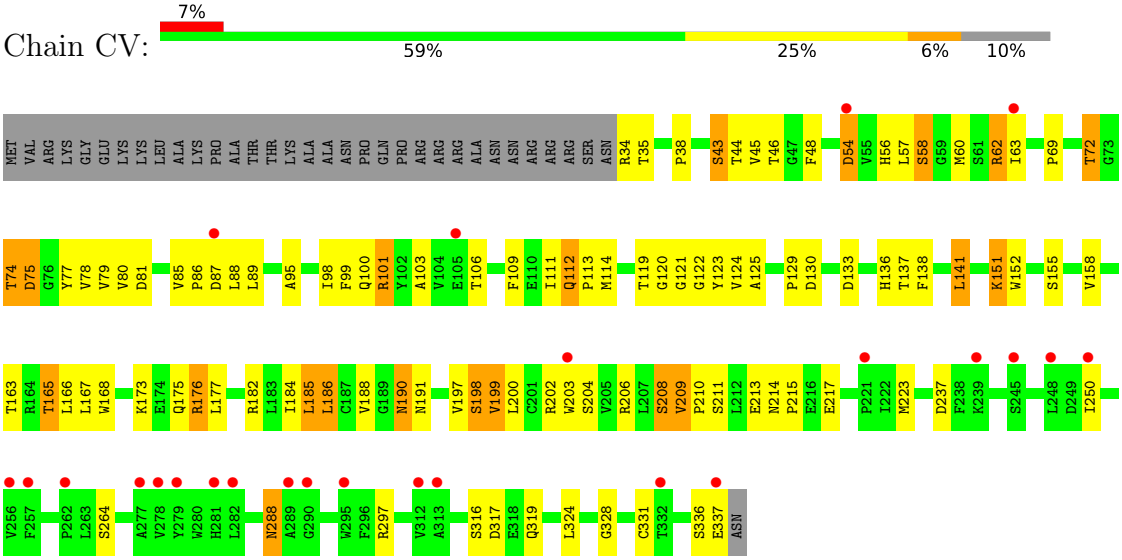
• Molecule 1: Coat protein

Chain AV:



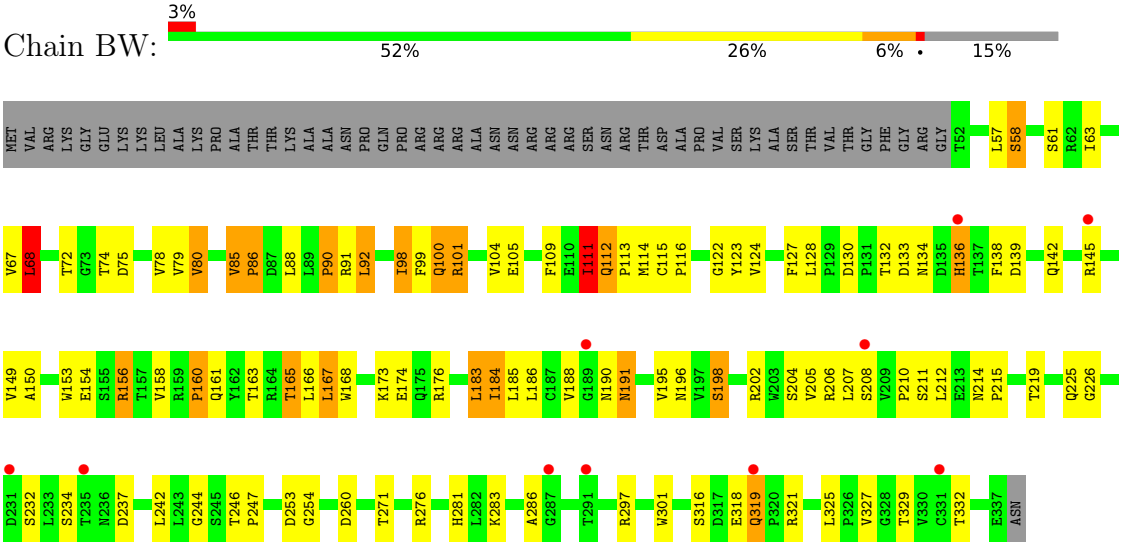
• Molecule 1: Coat protein

Chain CV:



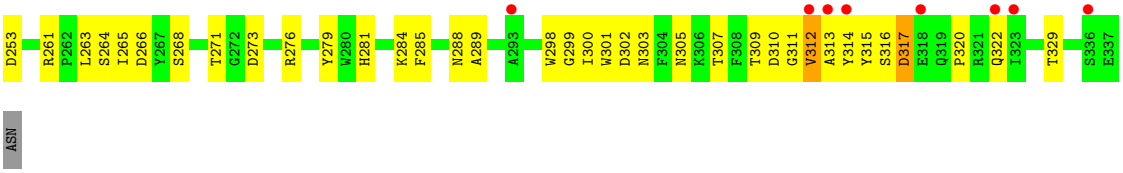
• Molecule 1: Coat protein

Chain BW:

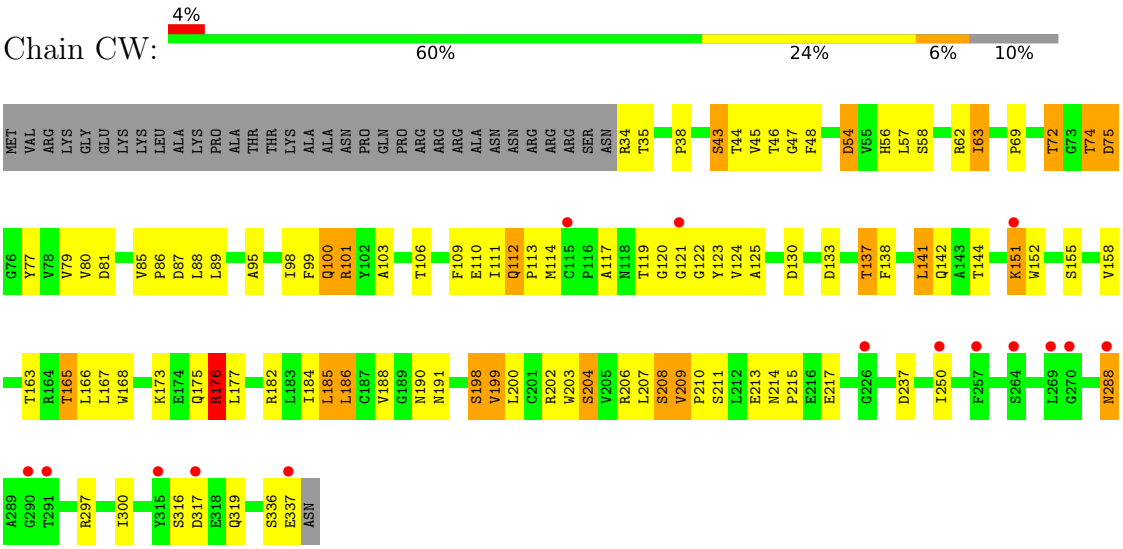


• Molecule 1: Coat protein

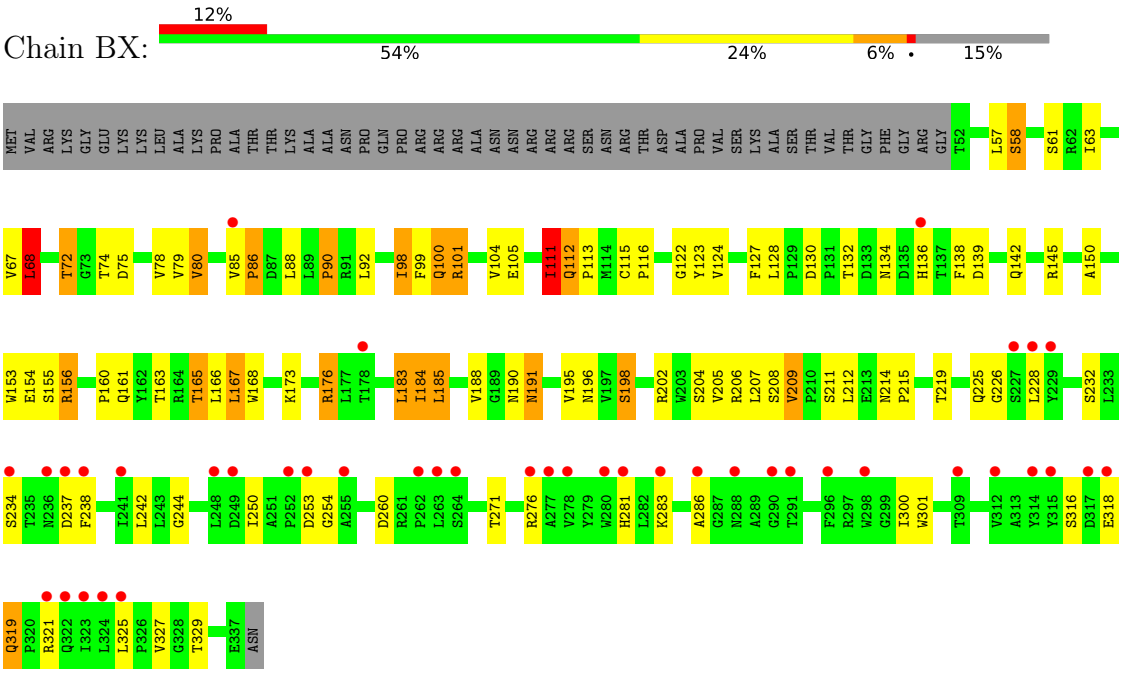
Chain AW:



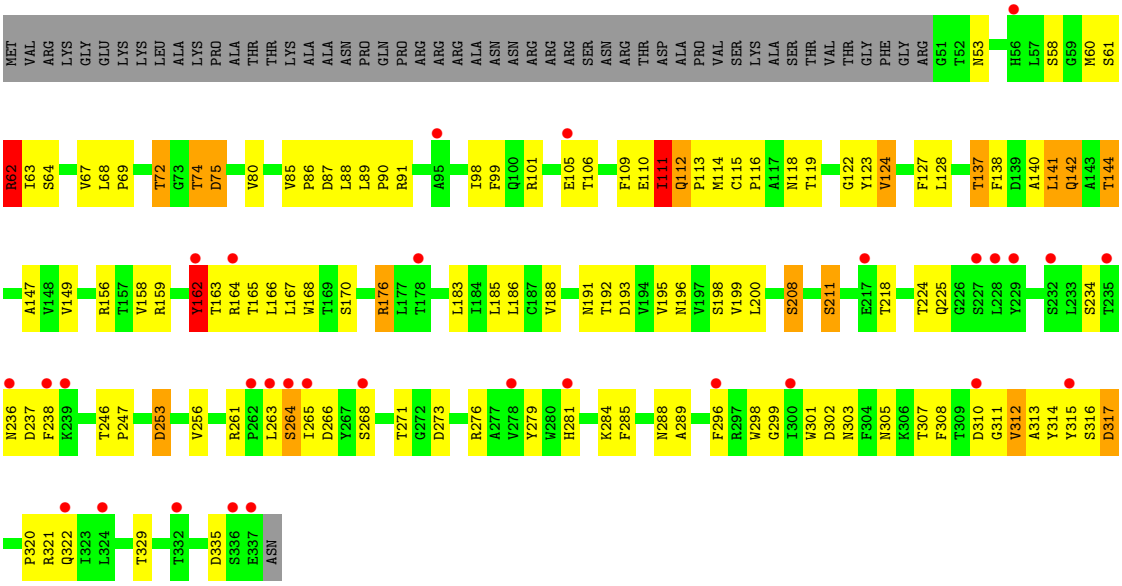
• Molecule 1: Coat protein



• Molecule 1: Coat protein

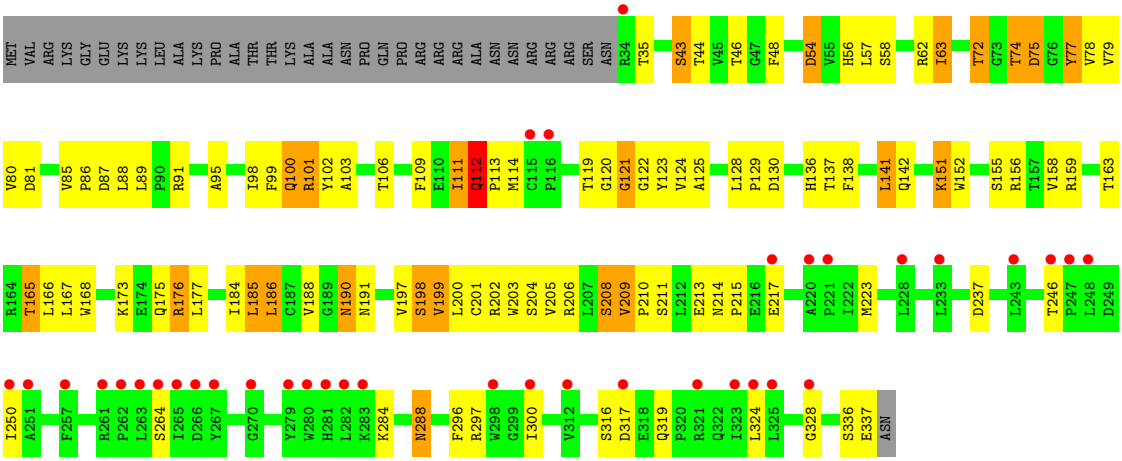


• Molecule 1: Coat protein



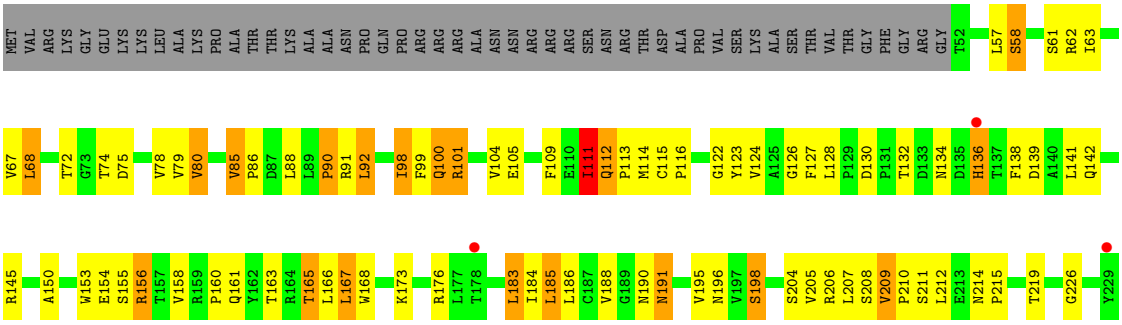
• Molecule 1: Coat protein

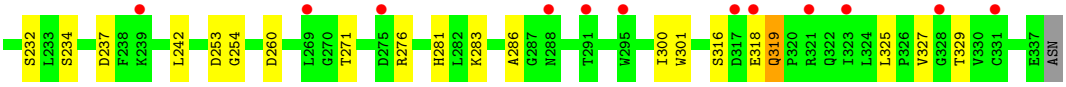
Chain CX:



• Molecule 1: Coat protein

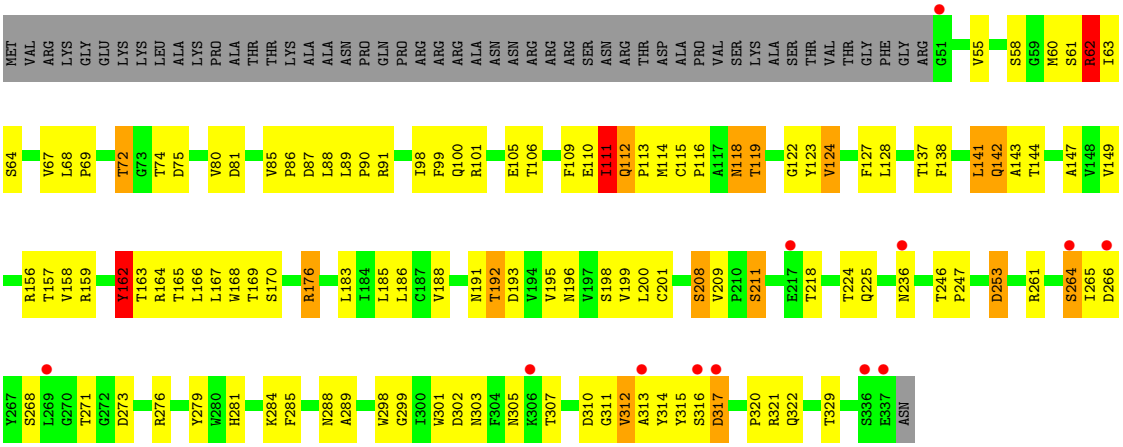
Chain BY:





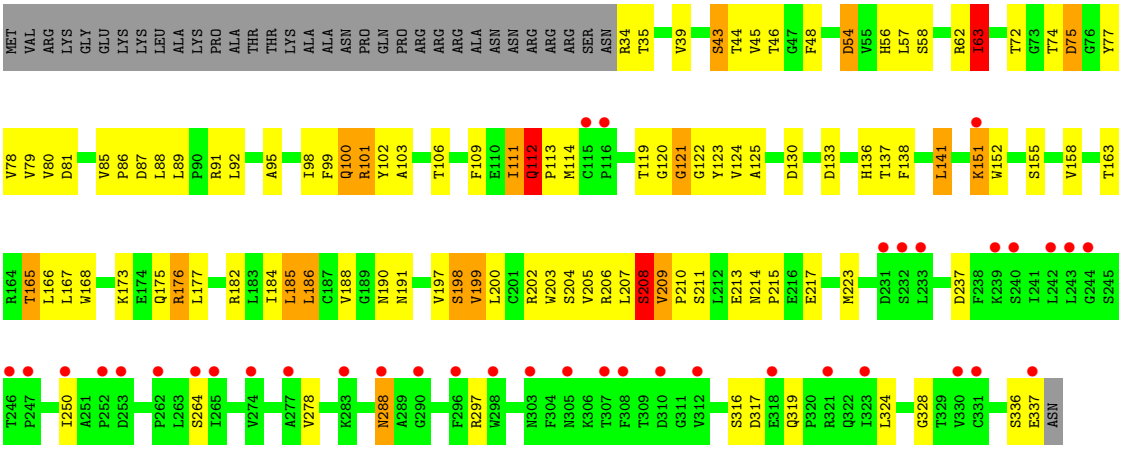
• Molecule 1: Coat protein

Chain AY:



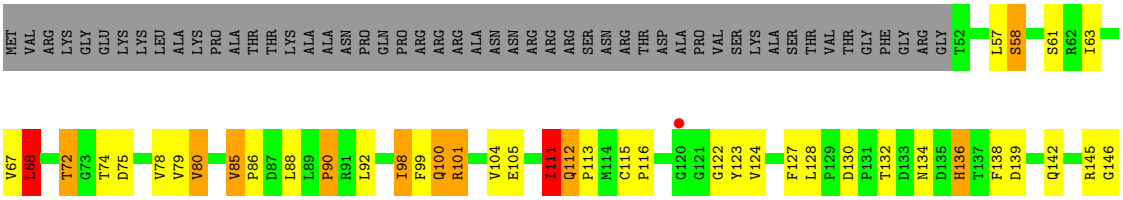
• Molecule 1: Coat protein

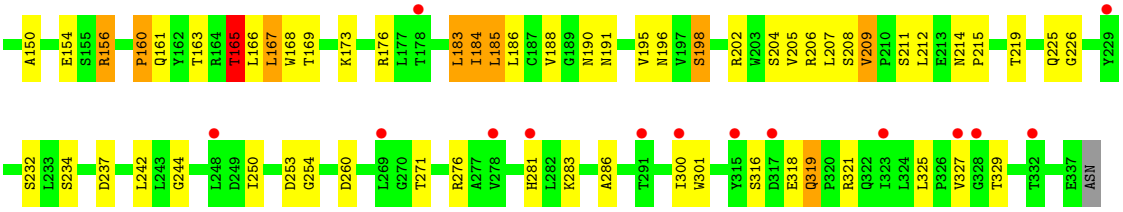
Chain CY:



• Molecule 1: Coat protein

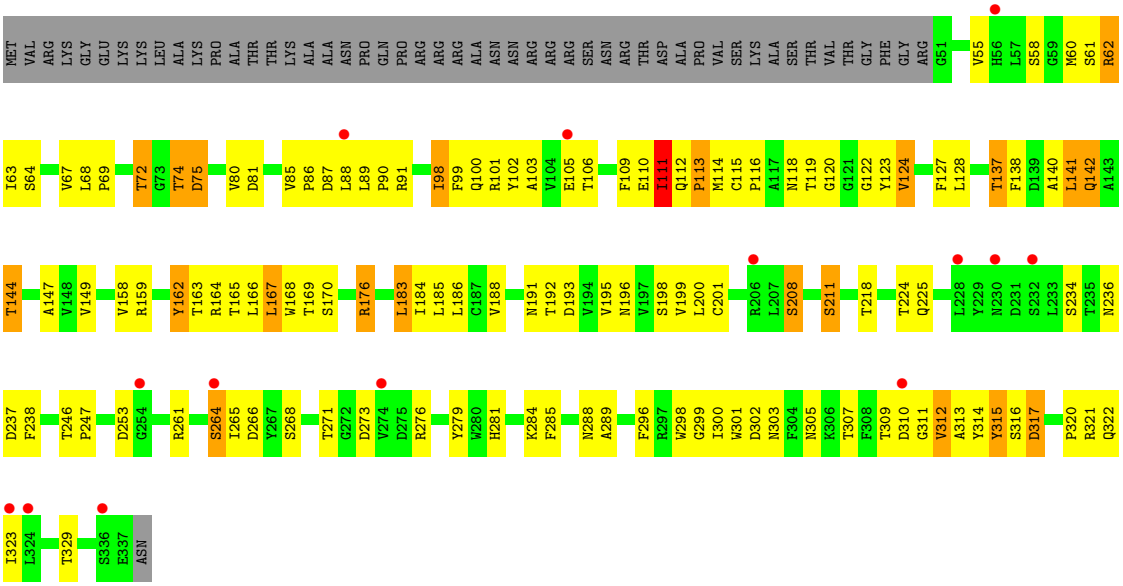
Chain BZ:





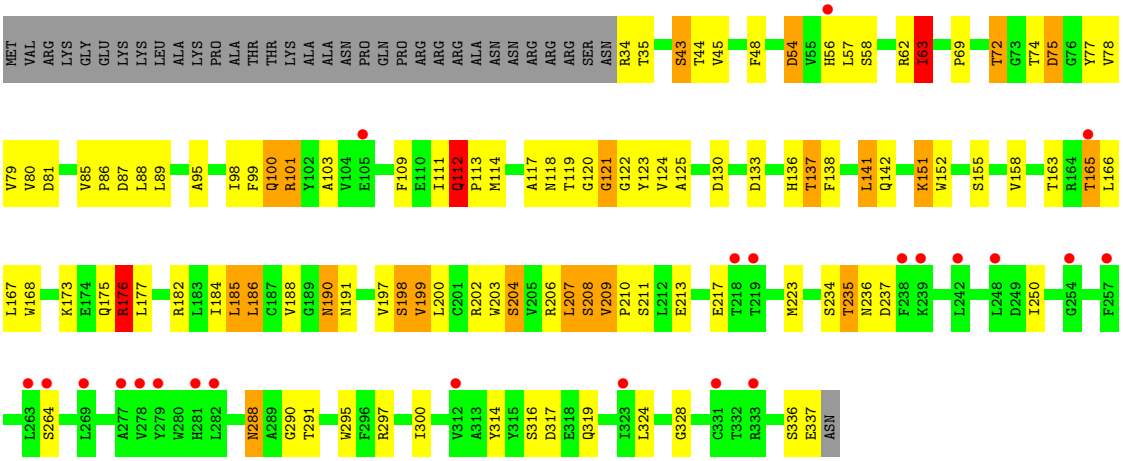
• Molecule 1: Coat protein

Chain AZ:



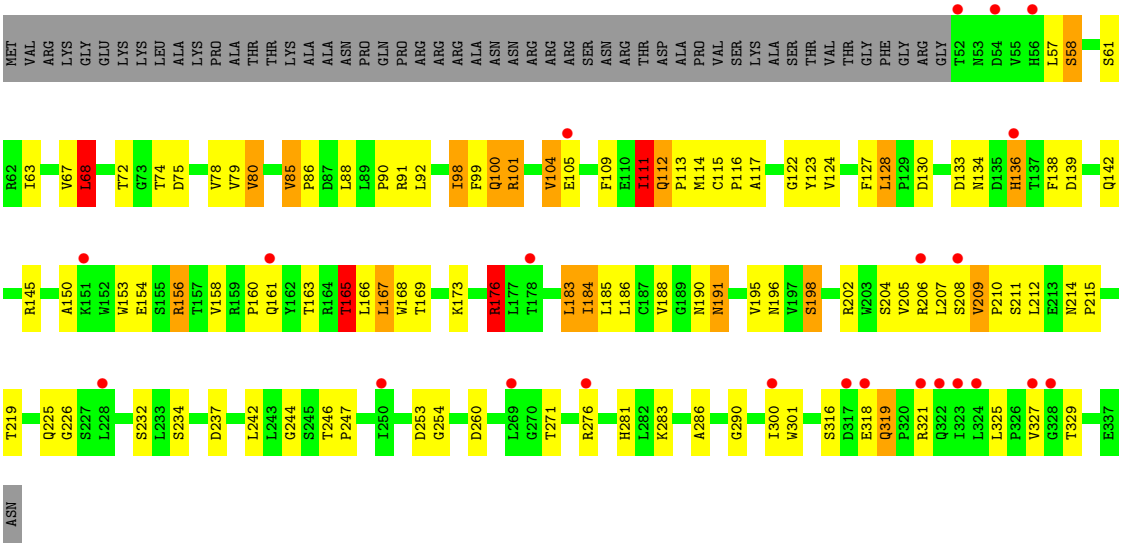
• Molecule 1: Coat protein

Chain CZ:



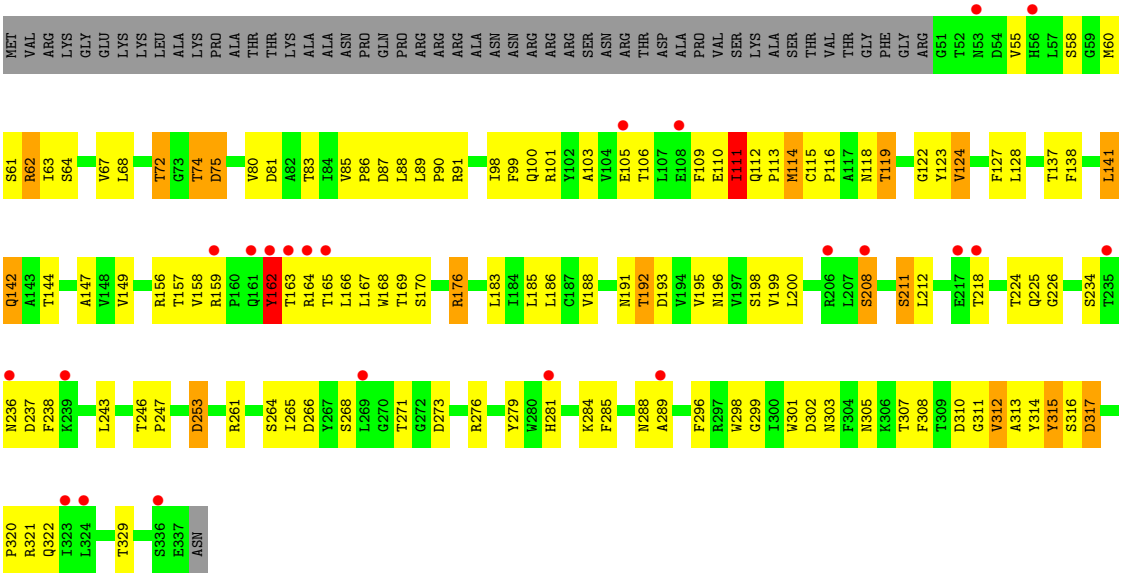
• Molecule 1: Coat protein

Chain Ba:



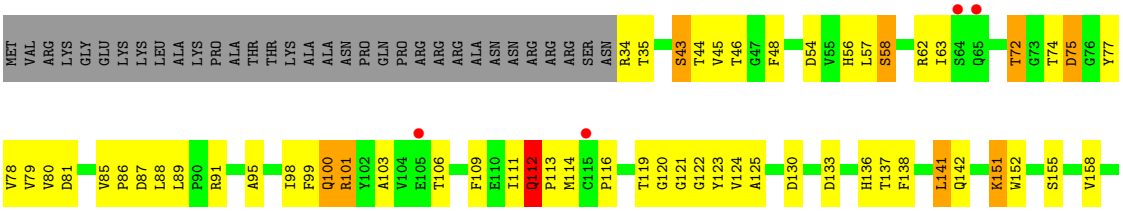
• Molecule 1: Coat protein

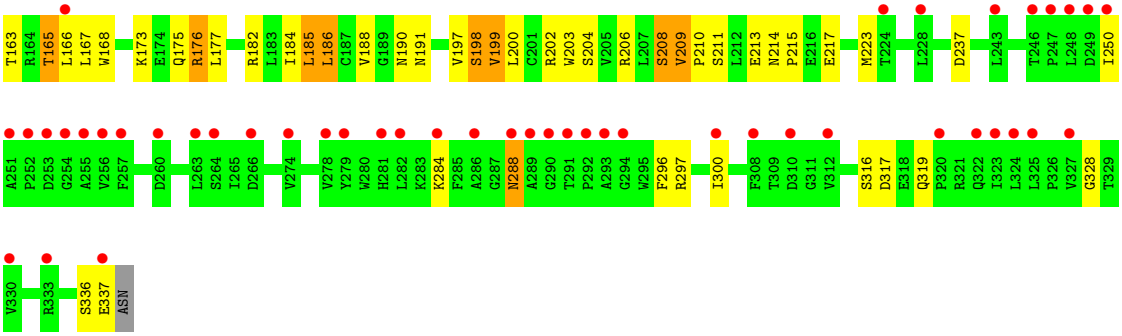
Chain Aa:



• Molecule 1: Coat protein

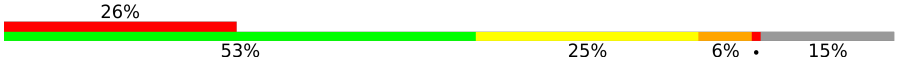
Chain Ca:

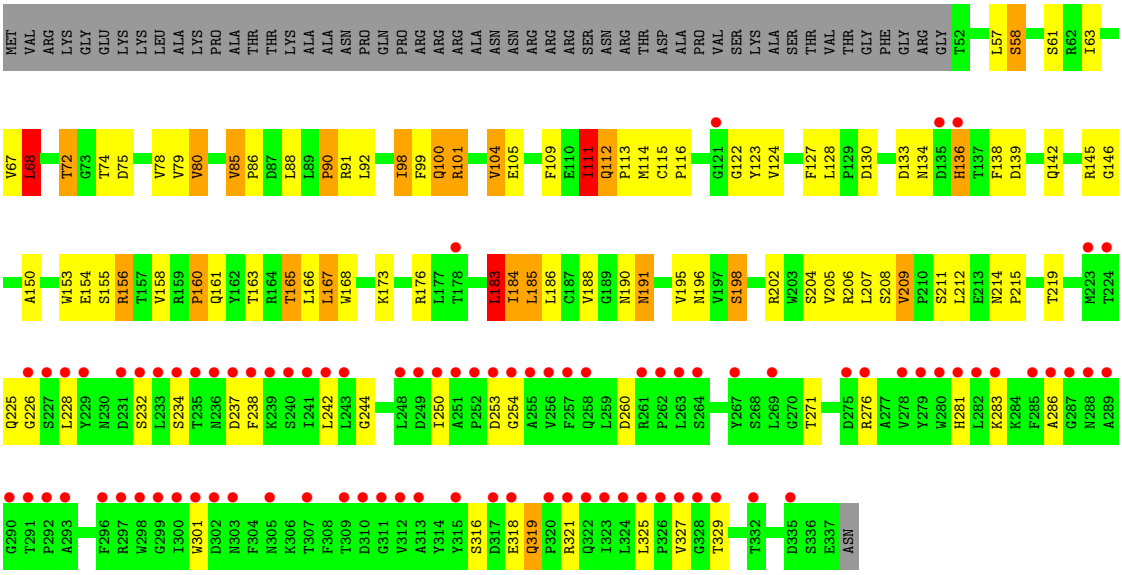




• Molecule 1: Coat protein

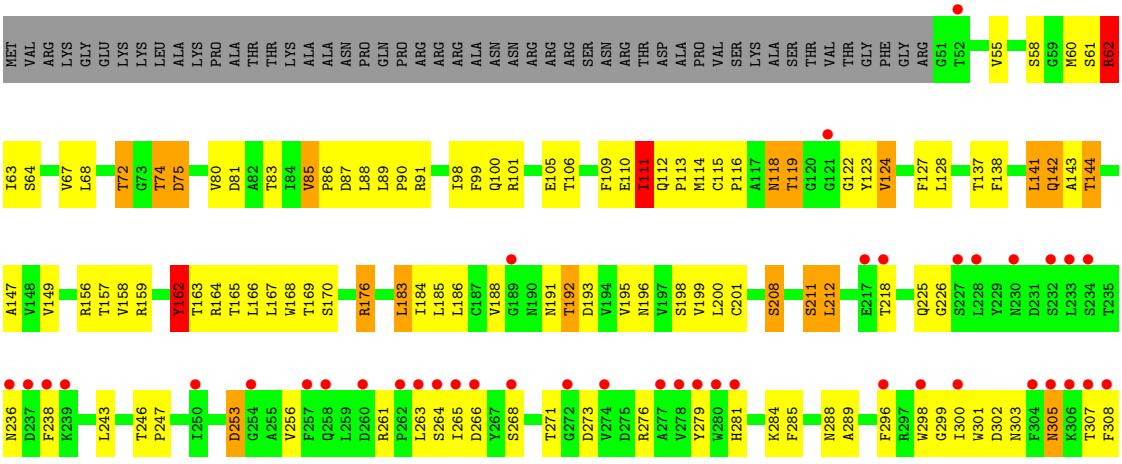
Chain Bb:

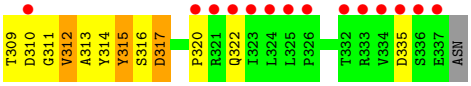




• Molecule 1: Coat protein

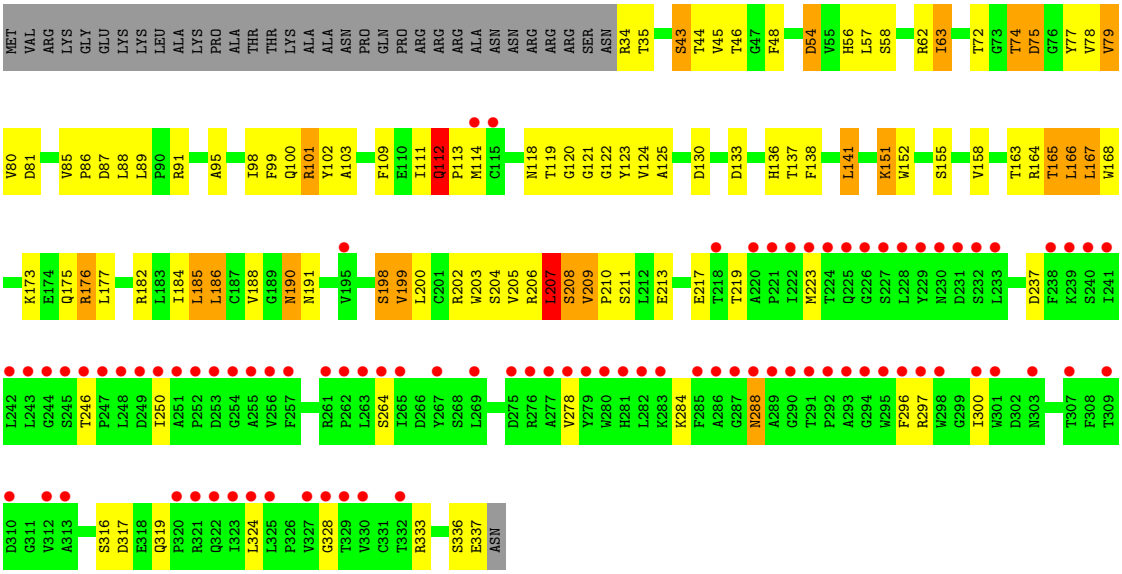
Chain Ab:





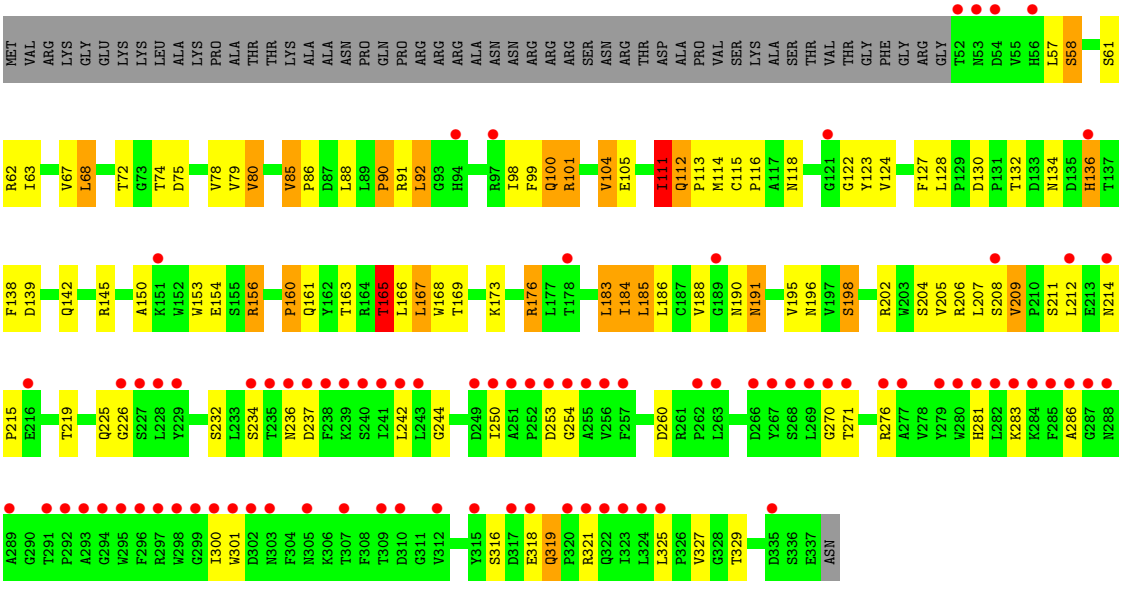
• Molecule 1: Coat protein

Chain Cb:



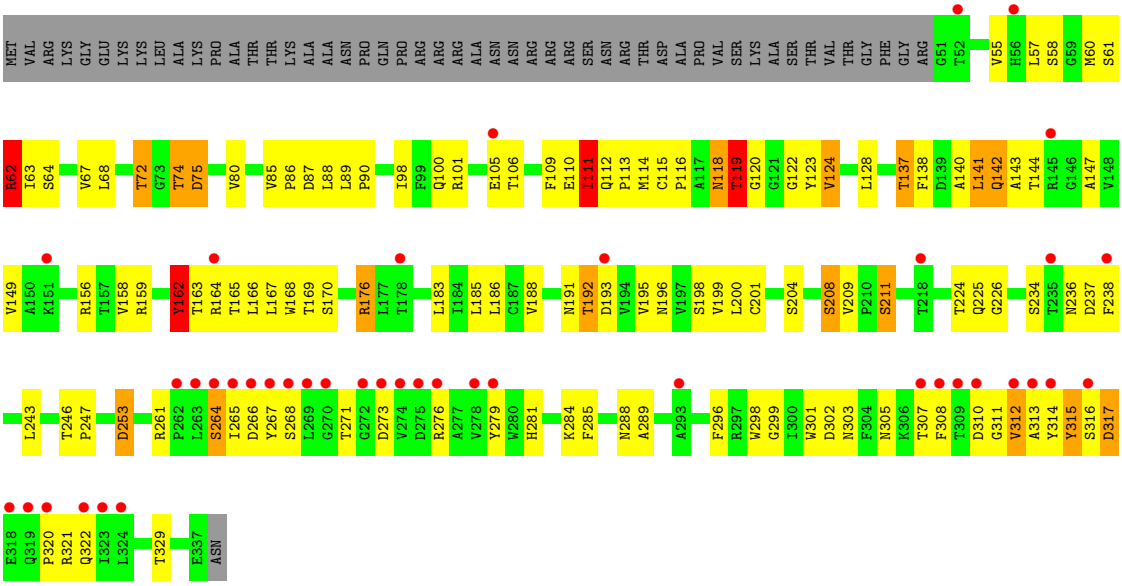
• Molecule 1: Coat protein

Chain Bc:



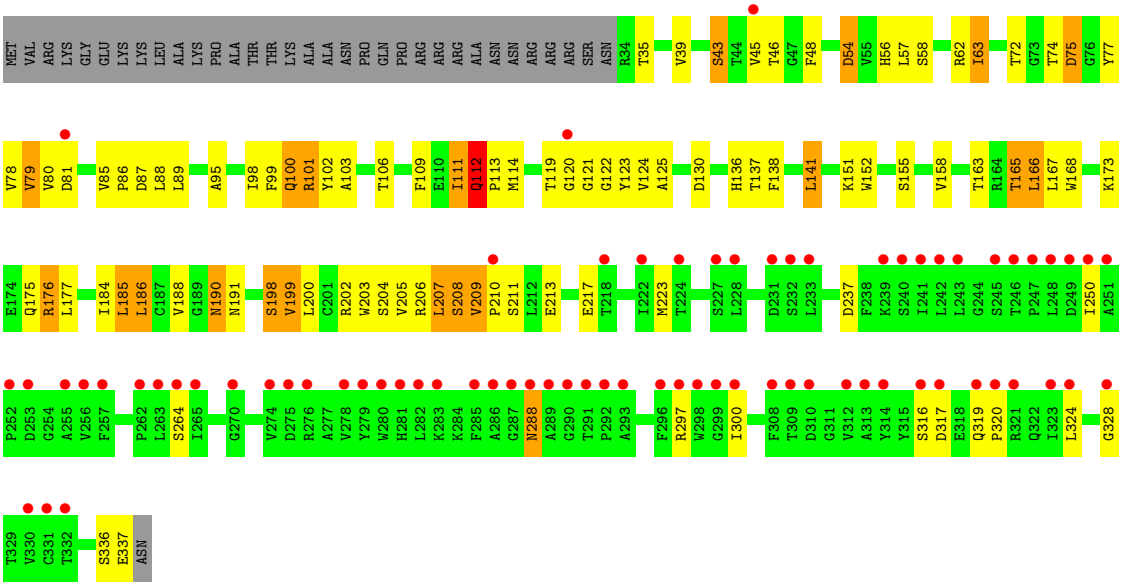
• Molecule 1: Coat protein

Chain Ac:



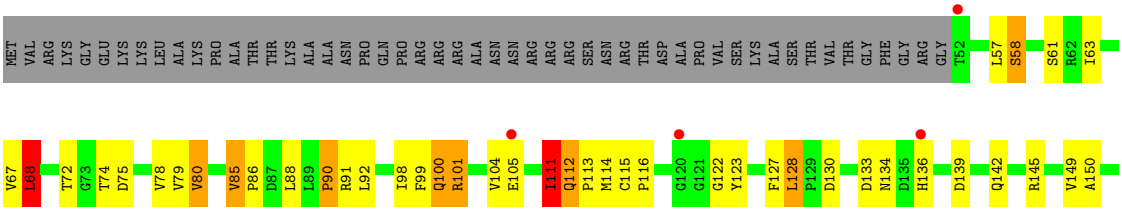
• Molecule 1: Coat protein

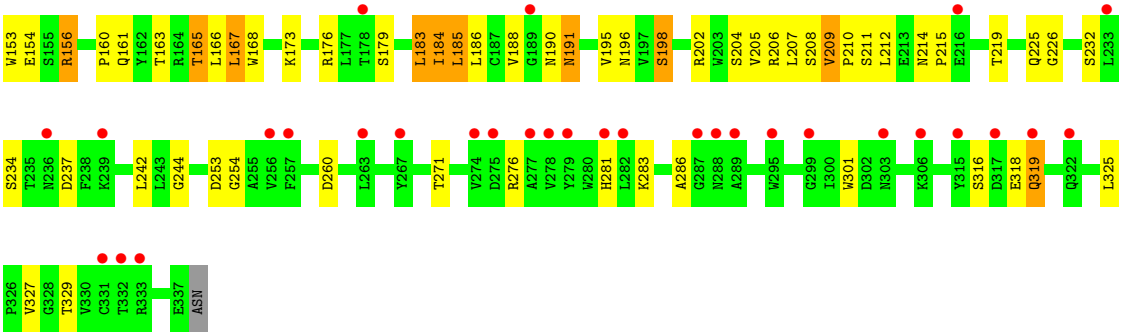
Chain Cc:



• Molecule 1: Coat protein

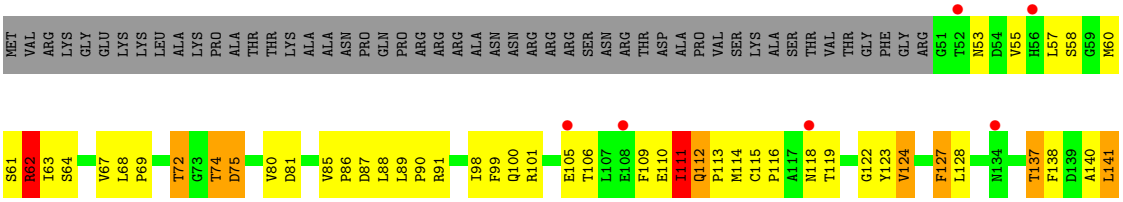
Chain Bd:

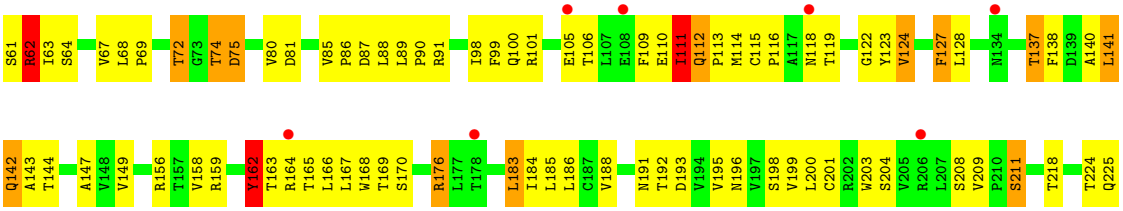


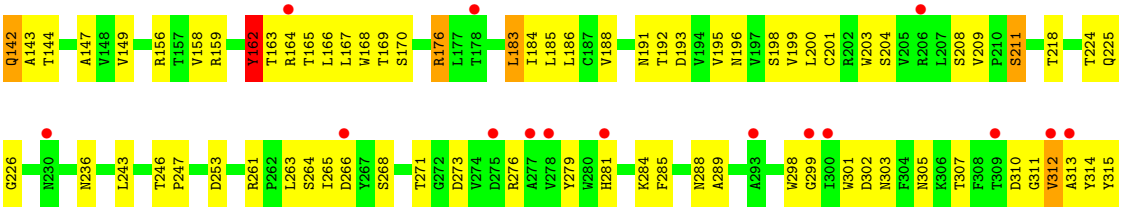


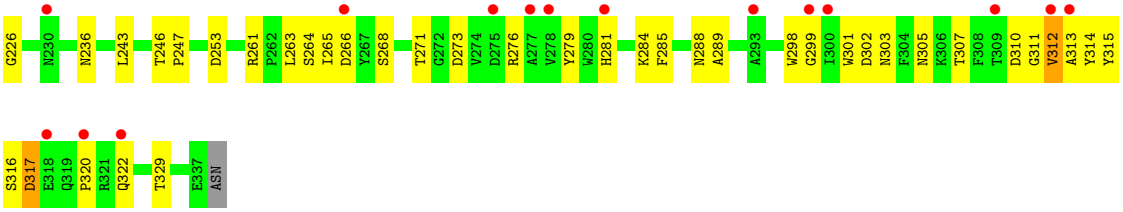
• Molecule 1: Coat protein

Chain Ad:



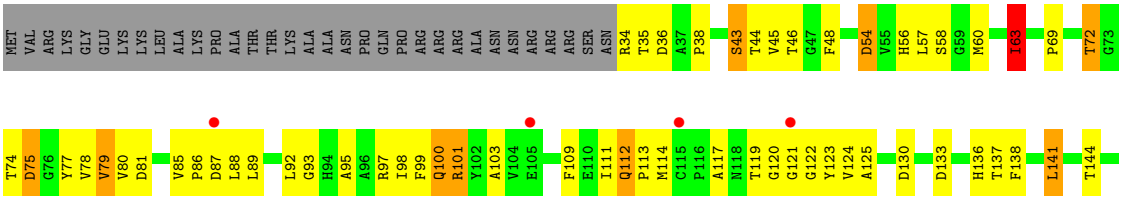


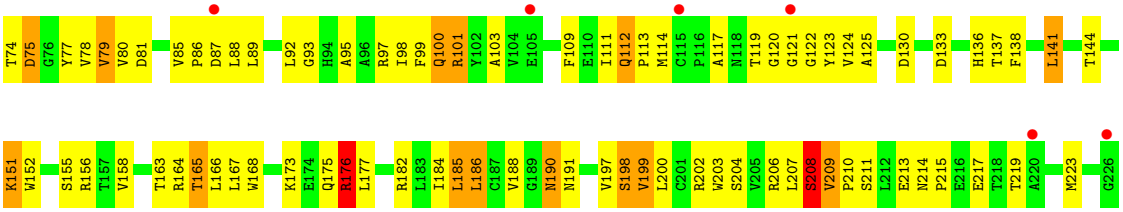


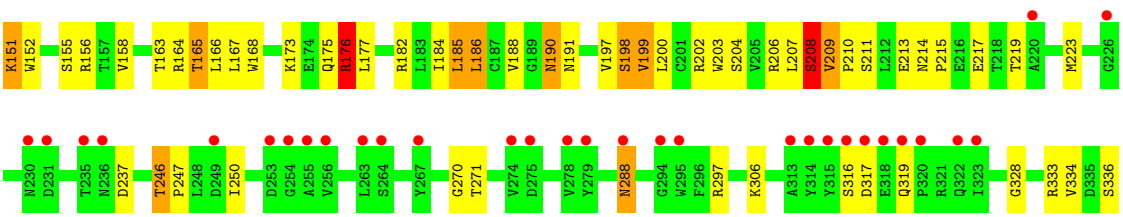


• Molecule 1: Coat protein

Chain Cd:







E337
ASN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	477.36Å 422.74Å 337.89Å 90.00° 134.03° 90.00°	Depositor
Resolution (Å)	263.91 – 3.60 263.91 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.2 (263.91-3.60) 99.3 (263.91-3.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.85 (at 3.58Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.255 , 0.297 0.255 , 0.294	Depositor DCC
R_{free} test set	27556 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	75.1	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 88.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.000 for h+2*l,k,-h-l 0.000 for h,-k,-h-l 0.000 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	203250	wwPDB-VP
Average B, all atoms (Å^2)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.66% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	AA	1.01	1/2274 (0.0%)	1.10	8/3112 (0.3%)
1	AB	1.11	1/2274 (0.0%)	1.13	5/3112 (0.2%)
1	AC	1.10	3/2274 (0.1%)	1.13	6/3112 (0.2%)
1	AD	1.03	0/2274	1.11	6/3112 (0.2%)
1	AE	1.03	1/2274 (0.0%)	1.11	7/3112 (0.2%)
1	AF	1.08	3/2274 (0.1%)	1.13	7/3112 (0.2%)
1	AG	1.02	1/2274 (0.0%)	1.09	6/3112 (0.2%)
1	AH	1.08	4/2274 (0.2%)	1.12	9/3112 (0.3%)
1	AI	1.03	1/2274 (0.0%)	1.10	11/3112 (0.4%)
1	AJ	1.09	2/2274 (0.1%)	1.14	7/3112 (0.2%)
1	AK	1.24	1/2274 (0.0%)	1.23	11/3112 (0.4%)
1	AL	1.17	4/2274 (0.2%)	1.19	8/3112 (0.3%)
1	AM	0.99	1/2274 (0.0%)	1.08	9/3112 (0.3%)
1	AN	1.00	2/2274 (0.1%)	1.11	7/3112 (0.2%)
1	AO	1.05	2/2274 (0.1%)	1.11	8/3112 (0.3%)
1	AP	1.08	3/2274 (0.1%)	1.12	5/3112 (0.2%)
1	AQ	1.01	1/2274 (0.0%)	1.10	5/3112 (0.2%)
1	AR	1.08	1/2274 (0.0%)	1.14	9/3112 (0.3%)
1	AS	1.10	1/2274 (0.0%)	1.14	8/3112 (0.3%)
1	AT	1.01	1/2274 (0.0%)	1.10	6/3112 (0.2%)
1	AU	1.11	4/2274 (0.2%)	1.12	7/3112 (0.2%)
1	AV	1.00	3/2274 (0.1%)	1.09	6/3112 (0.2%)
1	AW	1.11	0/2274	1.13	6/3112 (0.2%)
1	AX	1.07	1/2274 (0.0%)	1.12	8/3112 (0.3%)
1	AY	1.11	2/2274 (0.1%)	1.14	7/3112 (0.2%)
1	AZ	1.03	1/2274 (0.0%)	1.10	7/3112 (0.2%)
1	Aa	1.00	0/2274	1.09	6/3112 (0.2%)
1	Ab	1.07	0/2274	1.11	9/3112 (0.3%)
1	Ac	1.05	1/2274 (0.0%)	1.13	7/3112 (0.2%)
1	Ad	1.12	3/2274 (0.1%)	1.16	6/3112 (0.2%)
1	BA	1.02	0/2270	1.15	14/3107 (0.5%)
1	BB	1.16	2/2270 (0.1%)	1.19	14/3107 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	BC	1.05	3/2270 (0.1%)	1.14	17/3107 (0.5%)
1	BD	1.06	4/2270 (0.2%)	1.15	12/3107 (0.4%)
1	BE	1.08	3/2270 (0.1%)	1.16	16/3107 (0.5%)
1	BF	1.09	3/2270 (0.1%)	1.16	14/3107 (0.5%)
1	BG	1.05	3/2270 (0.1%)	1.16	13/3107 (0.4%)
1	BH	1.09	2/2270 (0.1%)	1.16	12/3107 (0.4%)
1	BI	1.07	2/2270 (0.1%)	1.16	11/3107 (0.4%)
1	BJ	1.14	2/2270 (0.1%)	1.18	14/3107 (0.5%)
1	BK	1.22	5/2270 (0.2%)	1.19	12/3107 (0.4%)
1	BL	1.22	4/2270 (0.2%)	1.21	17/3107 (0.5%)
1	BM	1.10	3/2270 (0.1%)	1.17	14/3107 (0.5%)
1	BN	1.08	2/2270 (0.1%)	1.16	14/3107 (0.5%)
1	BO	1.09	1/2270 (0.0%)	1.16	12/3107 (0.4%)
1	BP	1.08	1/2270 (0.0%)	1.16	17/3107 (0.5%)
1	BQ	1.06	1/2270 (0.0%)	1.13	14/3107 (0.5%)
1	BR	1.12	4/2270 (0.2%)	1.15	13/3107 (0.4%)
1	BS	1.13	4/2270 (0.2%)	1.19	16/3107 (0.5%)
1	BT	1.03	0/2270	1.14	15/3107 (0.5%)
1	BU	1.12	3/2270 (0.1%)	1.18	15/3107 (0.5%)
1	BV	1.05	2/2270 (0.1%)	1.14	16/3107 (0.5%)
1	BW	1.14	4/2270 (0.2%)	1.17	10/3107 (0.3%)
1	BX	1.05	1/2270 (0.0%)	1.15	14/3107 (0.5%)
1	BY	1.07	1/2270 (0.0%)	1.15	12/3107 (0.4%)
1	BZ	1.05	2/2270 (0.1%)	1.14	16/3107 (0.5%)
1	Ba	1.06	0/2270	1.16	14/3107 (0.5%)
1	Bb	1.17	6/2270 (0.3%)	1.20	16/3107 (0.5%)
1	Bc	1.09	2/2270 (0.1%)	1.15	13/3107 (0.4%)
1	Bd	1.10	2/2270 (0.1%)	1.15	11/3107 (0.4%)
1	CA	1.05	4/2398 (0.2%)	1.13	11/3280 (0.3%)
1	CB	1.12	4/2398 (0.2%)	1.11	8/3280 (0.2%)
1	CC	1.19	8/2398 (0.3%)	1.15	8/3280 (0.2%)
1	CD	1.07	4/2398 (0.2%)	1.11	6/3280 (0.2%)
1	CE	1.11	5/2398 (0.2%)	1.12	10/3280 (0.3%)
1	CF	1.14	7/2398 (0.3%)	1.13	7/3280 (0.2%)
1	CG	1.06	4/2398 (0.2%)	1.11	6/3280 (0.2%)
1	CH	1.05	3/2398 (0.1%)	1.11	7/3280 (0.2%)
1	CI	1.04	4/2398 (0.2%)	1.10	7/3280 (0.2%)
1	CJ	1.11	3/2398 (0.1%)	1.13	8/3280 (0.2%)
1	CK	1.31	14/2398 (0.6%)	1.23	10/3280 (0.3%)
1	CL	1.23	4/2398 (0.2%)	1.18	9/3280 (0.3%)
1	CM	1.09	5/2398 (0.2%)	1.12	9/3280 (0.3%)
1	CN	1.07	6/2398 (0.3%)	1.10	6/3280 (0.2%)
1	CO	1.10	5/2398 (0.2%)	1.12	9/3280 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	CP	1.09	7/2398 (0.3%)	1.11	6/3280 (0.2%)
1	CQ	1.09	5/2398 (0.2%)	1.12	5/3280 (0.2%)
1	CR	1.06	6/2398 (0.3%)	1.12	6/3280 (0.2%)
1	CS	1.18	14/2398 (0.6%)	1.16	6/3280 (0.2%)
1	CT	1.08	3/2398 (0.1%)	1.14	9/3280 (0.3%)
1	CU	1.14	7/2398 (0.3%)	1.14	11/3280 (0.3%)
1	CV	1.03	1/2398 (0.0%)	1.10	6/3280 (0.2%)
1	CW	1.14	3/2398 (0.1%)	1.14	6/3280 (0.2%)
1	CX	1.09	8/2398 (0.3%)	1.12	8/3280 (0.2%)
1	CY	1.09	3/2398 (0.1%)	1.13	10/3280 (0.3%)
1	CZ	1.04	3/2398 (0.1%)	1.10	10/3280 (0.3%)
1	Ca	1.03	4/2398 (0.2%)	1.10	6/3280 (0.2%)
1	Cb	1.10	2/2398 (0.1%)	1.13	8/3280 (0.2%)
1	Cc	1.10	5/2398 (0.2%)	1.12	7/3280 (0.2%)
1	Cd	1.19	2/2398 (0.1%)	1.19	10/3280 (0.3%)
All	All	1.09	274/208260 (0.1%)	1.14	870/284970 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	CU	0	1
1	Cb	0	1
All	All	0	2

All (274) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Bb	112	GLN	C-O	-10.78	1.18	1.23
1	CC	112	GLN	CA-CB	8.71	1.58	1.52
1	AY	112	GLN	N-CA	8.55	1.52	1.46
1	CO	112	GLN	N-CA	8.19	1.52	1.46
1	CP	112	GLN	CA-CB	8.13	1.58	1.52
1	AF	112	GLN	N-CA	8.13	1.52	1.46
1	CK	112	GLN	N-CA	8.06	1.52	1.46
1	CO	112	GLN	CA-CB	8.04	1.58	1.52
1	AK	112	GLN	N-CA	7.99	1.52	1.46
1	AH	112	GLN	N-CA	7.96	1.52	1.46
1	CX	112	GLN	N-CA	7.95	1.52	1.46
1	BL	160	PRO	CA-C	-7.90	1.45	1.53

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AP	112	GLN	N-CA	7.83	1.52	1.46
1	CB	112	GLN	CA-CB	7.82	1.58	1.52
1	AT	112	GLN	N-CA	7.50	1.51	1.46
1	CE	112	GLN	CA-CB	7.46	1.57	1.52
1	CD	112	GLN	CA-CB	7.24	1.57	1.52
1	Cc	112	GLN	CA-CB	7.24	1.57	1.52
1	CB	112	GLN	N-CA	7.17	1.51	1.46
1	BU	160	PRO	CA-C	-7.14	1.46	1.53
1	CZ	235	THR	N-CA	7.05	1.55	1.46
1	CP	112	GLN	C-O	-7.04	1.20	1.23
1	CM	112	GLN	CA-CB	7.00	1.57	1.52
1	Bb	90	PRO	C-O	6.99	1.33	1.24
1	CG	112	GLN	CA-CB	6.98	1.57	1.52
1	BK	90	PRO	C-O	6.89	1.32	1.24
1	AX	112	GLN	N-CA	6.86	1.51	1.46
1	CS	77	TYR	C-O	-6.84	1.15	1.24
1	BB	90	PRO	C-O	6.84	1.32	1.24
1	CL	199	VAL	C-O	-6.84	1.16	1.24
1	BE	112	GLN	CA-C	6.82	1.58	1.53
1	CM	112	GLN	N-CA	6.80	1.51	1.46
1	CS	112	GLN	CA-CB	6.76	1.57	1.52
1	CP	112	GLN	N-CA	6.75	1.51	1.46
1	BW	160	PRO	CA-C	-6.74	1.46	1.53
1	CQ	112	GLN	CA-CB	6.74	1.58	1.52
1	Cd	100	GLN	CA-C	-6.68	1.43	1.52
1	BL	90	PRO	C-O	6.65	1.32	1.24
1	CT	112	GLN	CA-CB	6.61	1.57	1.52
1	CE	207	LEU	C-O	-6.60	1.16	1.24
1	CY	100	GLN	CA-C	-6.60	1.43	1.52
1	BR	160	PRO	CA-C	-6.59	1.46	1.53
1	BV	160	PRO	CA-C	-6.58	1.46	1.53
1	CC	112	GLN	N-CA	6.54	1.51	1.46
1	CK	166	LEU	CA-C	-6.50	1.44	1.52
1	CG	112	GLN	N-CA	6.49	1.51	1.46
1	AO	112	GLN	N-CA	6.47	1.51	1.46
1	CL	209	VAL	CA-CB	-6.45	1.49	1.54
1	CN	112	GLN	CA-CB	6.38	1.58	1.52
1	CR	208	SER	CA-C	-6.37	1.46	1.52
1	AR	112	GLN	N-CA	6.37	1.50	1.46
1	CS	112	GLN	C-O	-6.36	1.21	1.23
1	CY	208	SER	C-O	-6.35	1.14	1.23
1	BU	90	PRO	C-O	6.34	1.32	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BW	174	GLU	CA-C	-6.31	1.45	1.52
1	BE	160	PRO	CA-C	-6.30	1.46	1.53
1	CJ	116	PRO	N-CA	-6.24	1.40	1.46
1	BS	210	PRO	C-O	6.24	1.30	1.23
1	AC	112	GLN	N-CA	6.20	1.50	1.46
1	CF	100	GLN	CA-C	-6.20	1.44	1.52
1	CC	147	ALA	C-O	-6.16	1.16	1.23
1	CR	209	VAL	N-CA	6.16	1.51	1.46
1	CU	77	TYR	C-O	-6.16	1.16	1.24
1	Bd	90	PRO	C-O	6.15	1.31	1.24
1	CH	77	TYR	C-O	-6.15	1.16	1.24
1	CS	166	LEU	CA-C	-6.12	1.45	1.52
1	BF	112	GLN	N-CA	6.11	1.51	1.46
1	CQ	159	ARG	C-O	-6.06	1.16	1.24
1	BW	210	PRO	C-O	6.05	1.30	1.23
1	CS	112	GLN	N-CA	6.04	1.50	1.46
1	CD	116	PRO	N-CA	-6.04	1.41	1.46
1	BG	90	PRO	C-O	6.04	1.31	1.24
1	Ca	112	GLN	CA-CB	6.04	1.56	1.52
1	CG	77	TYR	C-O	-6.02	1.16	1.24
1	CK	209	VAL	N-CA	6.01	1.51	1.46
1	BM	90	PRO	C-O	6.01	1.31	1.24
1	BI	90	PRO	C-O	6.00	1.31	1.24
1	CW	100	GLN	CA-C	-6.00	1.44	1.52
1	AH	209	VAL	CA-C	-6.00	1.47	1.52
1	AL	112	GLN	N-CA	5.99	1.50	1.46
1	BM	160	PRO	CA-C	-5.98	1.47	1.53
1	CU	112	GLN	CA-CB	5.98	1.56	1.52
1	BY	90	PRO	C-O	5.98	1.31	1.24
1	CS	116	PRO	N-CA	-5.96	1.40	1.46
1	CK	112	GLN	C-O	-5.95	1.21	1.23
1	CF	201	CYS	CA-C	-5.95	1.45	1.52
1	CK	208	SER	C-O	-5.94	1.15	1.23
1	Cb	207	LEU	C-O	-5.93	1.16	1.24
1	BS	90	PRO	C-O	5.92	1.31	1.24
1	BJ	90	PRO	C-O	5.91	1.31	1.24
1	BF	112	GLN	CA-C	5.90	1.57	1.53
1	Bb	112	GLN	N-CA	5.90	1.51	1.46
1	BD	90	PRO	C-O	5.90	1.31	1.24
1	CF	112	GLN	N-CA	5.88	1.50	1.46
1	AU	112	GLN	N-CA	5.87	1.50	1.46
1	CN	209	VAL	N-CA	5.86	1.51	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Bb	183	LEU	C-O	-5.86	1.17	1.24
1	BZ	90	PRO	C-O	5.84	1.31	1.24
1	CF	112	GLN	CA-CB	5.84	1.56	1.52
1	CF	209	VAL	CA-CB	-5.83	1.50	1.54
1	AP	209	VAL	CA-C	-5.83	1.47	1.52
1	CL	56	HIS	CA-C	-5.83	1.45	1.52
1	Bb	160	PRO	CA-C	-5.83	1.47	1.53
1	CN	208	SER	C-O	-5.82	1.16	1.23
1	BW	90	PRO	C-O	5.82	1.31	1.24
1	CN	77	TYR	C-O	-5.79	1.17	1.24
1	BJ	160	PRO	CA-C	-5.79	1.47	1.53
1	BL	98	ILE	CA-CB	-5.78	1.47	1.54
1	BR	90	PRO	C-O	5.77	1.31	1.24
1	AJ	209	VAL	CA-C	-5.75	1.47	1.52
1	CQ	112	GLN	N-CA	5.75	1.50	1.46
1	CC	208	SER	C-O	-5.74	1.16	1.23
1	BP	160	PRO	CA-C	-5.73	1.47	1.53
1	BK	198	SER	C-O	-5.73	1.17	1.24
1	CY	208	SER	CA-C	-5.73	1.46	1.52
1	CI	100	GLN	CA-C	-5.73	1.44	1.52
1	CR	100	GLN	CA-C	-5.71	1.44	1.52
1	CZ	100	GLN	CA-C	-5.71	1.44	1.52
1	CA	112	GLN	N-CA	5.71	1.50	1.46
1	Cc	166	LEU	CA-C	-5.69	1.45	1.52
1	BC	160	PRO	CA-C	-5.68	1.47	1.53
1	CE	208	SER	CA-C	-5.66	1.47	1.52
1	CT	155	SER	CA-C	-5.66	1.45	1.53
1	CW	199	VAL	C-O	-5.66	1.18	1.24
1	AL	182	ARG	C-O	-5.65	1.17	1.23
1	CM	100	GLN	CA-C	-5.65	1.44	1.52
1	BS	98	ILE	CA-CB	-5.65	1.47	1.54
1	AP	135	ASP	C-O	-5.64	1.17	1.24
1	CU	100	GLN	CA-C	-5.64	1.44	1.52
1	CB	207	LEU	C-O	-5.63	1.17	1.24
1	AJ	200	LEU	CA-C	-5.63	1.46	1.52
1	BB	180	PRO	CA-C	-5.63	1.45	1.52
1	BV	90	PRO	C-O	5.61	1.31	1.24
1	BR	98	ILE	CA-CB	-5.60	1.47	1.54
1	AU	125	ALA	CA-C	-5.59	1.45	1.52
1	CM	208	SER	CA-C	-5.58	1.47	1.52
1	CX	121	GLY	CA-C	-5.58	1.46	1.52
1	CA	207	LEU	C-O	-5.57	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CQ	166	LEU	C-O	-5.56	1.17	1.24
1	CD	209	VAL	N-CA	5.56	1.51	1.46
1	CX	159	ARG	C-O	-5.56	1.17	1.24
1	BZ	160	PRO	CA-C	-5.55	1.47	1.53
1	Ad	112	GLN	N-CA	5.54	1.50	1.46
1	CR	107	LEU	CA-C	-5.53	1.45	1.52
1	CX	100	GLN	CA-C	-5.53	1.44	1.52
1	CT	207	LEU	C-O	-5.52	1.17	1.24
1	BC	193	ASP	CA-C	-5.52	1.46	1.52
1	AH	209	VAL	CA-CB	-5.52	1.49	1.54
1	BK	160	PRO	CA-C	-5.51	1.47	1.53
1	BO	90	PRO	C-O	5.51	1.31	1.24
1	CG	116	PRO	N-CA	-5.50	1.41	1.46
1	CX	201	CYS	CA-C	-5.49	1.46	1.52
1	BX	90	PRO	C-O	5.48	1.31	1.24
1	CS	72	THR	CA-C	-5.46	1.45	1.53
1	Ca	100	GLN	CA-C	-5.46	1.45	1.52
1	Cc	166	LEU	C-O	-5.45	1.17	1.24
1	AF	192	THR	C-O	-5.44	1.17	1.24
1	AC	209	VAL	CA-C	-5.44	1.48	1.52
1	CV	62	ARG	CA-C	-5.44	1.45	1.52
1	AY	209	VAL	CA-CB	-5.43	1.49	1.54
1	Bc	160	PRO	CA-C	-5.43	1.47	1.53
1	CS	62	ARG	CA-C	-5.42	1.45	1.52
1	CK	56	HIS	CA-C	-5.42	1.45	1.52
1	CX	112	GLN	CA-CB	5.42	1.57	1.52
1	BG	160	PRO	CA-C	-5.41	1.47	1.53
1	CU	207	LEU	C-O	-5.41	1.17	1.24
1	CP	77	TYR	C-O	-5.39	1.17	1.24
1	CE	77	TYR	C-O	-5.38	1.17	1.24
1	CE	81	ASP	CA-C	-5.38	1.47	1.53
1	BL	74	THR	C-O	5.38	1.30	1.23
1	AI	199	VAL	CA-C	5.37	1.59	1.52
1	AH	141	LEU	C-O	-5.37	1.17	1.24
1	BE	90	PRO	C-O	5.36	1.30	1.24
1	CS	208	SER	CA-C	-5.36	1.47	1.52
1	CQ	112	GLN	C-O	-5.36	1.21	1.23
1	CK	165	THR	C-O	5.35	1.31	1.23
1	AE	193	ASP	CA-C	-5.34	1.45	1.52
1	CK	207	LEU	C-O	-5.34	1.17	1.24
1	CK	112	GLN	CA-CB	5.33	1.57	1.52
1	CA	112	GLN	CA-CB	5.33	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CS	81	ASP	CA-C	-5.33	1.47	1.53
1	CN	107	LEU	CA-C	-5.32	1.46	1.52
1	CP	165	THR	C-O	5.32	1.30	1.23
1	AV	54	ASP	CA-C	-5.32	1.46	1.52
1	Ac	209	VAL	CA-CB	-5.31	1.49	1.54
1	BC	184	ILE	C-O	-5.31	1.18	1.24
1	AL	209	VAL	CA-C	-5.31	1.48	1.52
1	AV	58	SER	CA-C	-5.29	1.46	1.52
1	BM	183	LEU	C-O	-5.29	1.17	1.24
1	AB	199	VAL	CA-C	5.28	1.58	1.52
1	AU	62	ARG	CD-NE	5.28	1.53	1.46
1	AV	141	LEU	C-O	-5.28	1.17	1.24
1	CW	110	GLU	C-O	-5.28	1.17	1.23
1	AC	201	CYS	CA-C	-5.27	1.46	1.52
1	BF	90	PRO	C-O	5.26	1.30	1.24
1	BQ	135	ASP	C-O	-5.26	1.17	1.23
1	CX	77	TYR	C-O	-5.26	1.17	1.24
1	CP	166	LEU	C-O	-5.25	1.17	1.24
1	BH	176	ARG	C-O	-5.25	1.16	1.24
1	Bc	90	PRO	C-O	5.24	1.30	1.24
1	CN	112	GLN	N-CA	5.24	1.50	1.46
1	Ad	209	VAL	CA-C	-5.24	1.48	1.52
1	CP	166	LEU	CA-C	-5.23	1.46	1.52
1	BD	112	GLN	CA-C	5.23	1.57	1.53
1	BD	174	GLU	CA-C	-5.23	1.46	1.52
1	BH	90	PRO	C-O	5.23	1.30	1.24
1	CK	209	VAL	CA-CB	-5.23	1.50	1.54
1	CU	208	SER	CA-C	-5.22	1.47	1.52
1	CS	207	LEU	C-O	-5.22	1.17	1.24
1	AM	129	PRO	C-O	-5.22	1.17	1.24
1	BN	174	GLU	CA-C	-5.22	1.46	1.52
1	CZ	207	LEU	C-O	-5.21	1.17	1.24
1	Cc	207	LEU	C-O	-5.21	1.17	1.24
1	CK	166	LEU	C-O	-5.20	1.17	1.24
1	BR	186	LEU	CA-C	-5.20	1.46	1.52
1	CS	209	VAL	N-CA	5.20	1.50	1.46
1	BK	193	ASP	CA-C	-5.19	1.46	1.52
1	Ca	112	GLN	N-CA	5.19	1.50	1.46
1	AA	112	GLN	N-CA	5.19	1.50	1.46
1	CC	159	ARG	C-O	-5.19	1.17	1.24
1	CR	112	GLN	CA-CB	5.18	1.57	1.52
1	CR	112	GLN	N-CA	5.18	1.50	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CH	116	PRO	N-CA	-5.17	1.42	1.46
1	CJ	112	GLN	CA-CB	5.17	1.57	1.52
1	BD	160	PRO	CA-C	-5.16	1.48	1.53
1	CI	209	VAL	N-CA	5.16	1.50	1.46
1	CL	208	SER	C-O	-5.15	1.17	1.23
1	CO	166	LEU	CA-C	-5.15	1.46	1.52
1	Cd	208	SER	C-N	-5.15	1.29	1.33
1	CJ	100	GLN	CA-C	-5.14	1.45	1.52
1	CS	208	SER	C-O	-5.14	1.16	1.23
1	BN	160	PRO	CA-C	-5.14	1.48	1.53
1	CC	77	TYR	C-O	-5.14	1.17	1.24
1	CF	165	THR	C-O	5.13	1.30	1.23
1	CM	77	TYR	C-O	-5.13	1.17	1.24
1	AN	193	ASP	CA-C	-5.13	1.46	1.52
1	CA	209	VAL	N-CA	5.13	1.50	1.46
1	CK	100	GLN	CA-C	-5.13	1.45	1.52
1	Cc	100	GLN	CA-C	-5.13	1.45	1.52
1	AL	201	CYS	CA-C	-5.12	1.46	1.52
1	BI	184	ILE	C-O	-5.12	1.18	1.24
1	CO	60	MET	CA-C	-5.12	1.46	1.52
1	CI	112	GLN	N-CA	5.12	1.50	1.46
1	AO	99	PHE	CA-C	-5.11	1.46	1.52
1	CS	100	GLN	CA-C	-5.10	1.45	1.52
1	CC	207	LEU	C-O	-5.09	1.17	1.24
1	CC	67	VAL	C-O	-5.09	1.19	1.24
1	CK	199	VAL	C-O	-5.09	1.18	1.24
1	AN	129	PRO	C-O	-5.09	1.17	1.24
1	CI	207	LEU	C-O	-5.08	1.17	1.24
1	AS	129	PRO	C-O	-5.07	1.18	1.24
1	CU	209	VAL	N-CA	5.07	1.50	1.46
1	BG	158	VAL	C-O	5.07	1.30	1.24
1	CB	100	GLN	CA-C	-5.07	1.45	1.52
1	AZ	113	PRO	C-O	5.07	1.28	1.23
1	AQ	192	THR	C-O	-5.06	1.17	1.24
1	Bd	186	LEU	C-O	-5.06	1.17	1.23
1	Ad	127	PHE	C-O	-5.05	1.18	1.24
1	AU	183	LEU	C-O	-5.05	1.17	1.24
1	BU	98	ILE	CA-CB	-5.04	1.48	1.54
1	Cb	167	LEU	C-O	5.04	1.30	1.23
1	CX	54	ASP	CA-C	-5.04	1.46	1.52
1	CD	199	VAL	C-O	-5.03	1.18	1.24
1	AF	209	VAL	CA-C	-5.03	1.48	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BK	182	ARG	CA-C	-5.03	1.46	1.52
1	BS	78	VAL	C-O	-5.03	1.19	1.24
1	Ca	116	PRO	N-CA	-5.03	1.42	1.46
1	CH	100	GLN	CA-C	-5.02	1.45	1.52
1	CO	81	ASP	CA-C	-5.02	1.48	1.53
1	CU	112	GLN	C-O	-5.02	1.21	1.23
1	Bb	98	ILE	CA-CB	-5.02	1.48	1.54
1	CF	122	GLY	CA-C	-5.01	1.47	1.51
1	CK	308	PHE	CA-C	5.01	1.58	1.52
1	AG	193	ASP	CA-C	-5.00	1.46	1.52

All (870) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BI	111	ILE	N-CA-C	9.01	119.82	110.72
1	BL	111	ILE	N-CA-C	8.99	119.80	110.72
1	BG	111	ILE	N-CA-C	8.85	119.66	110.72
1	BV	111	ILE	N-CA-C	8.77	119.57	110.72
1	BM	111	ILE	N-CA-C	8.65	119.46	110.72
1	AL	111	ILE	N-CA-C	8.63	119.20	110.82
1	Ba	111	ILE	N-CA-C	8.62	119.42	110.72
1	BD	111	ILE	N-CA-C	8.36	119.16	110.72
1	BR	111	ILE	N-CA-C	8.35	119.15	110.72
1	AR	111	ILE	N-CA-C	8.21	118.25	110.53
1	AY	111	ILE	N-CA-C	8.19	118.76	110.82
1	BA	111	ILE	N-CA-C	8.13	119.86	111.00
1	BZ	111	ILE	N-CA-C	8.12	118.92	110.72
1	AK	112	GLN	CB-CA-C	-8.07	105.47	111.20
1	BK	112	GLN	N-CA-C	8.02	127.54	109.81
1	BA	112	GLN	N-CA-C	7.97	127.43	109.81
1	BW	111	ILE	N-CA-C	7.96	118.76	110.72
1	AA	111	ILE	N-CA-C	7.96	118.54	110.82
1	AK	218	THR	N-CA-C	7.96	121.05	111.82
1	BC	112	GLN	N-CA-C	7.95	127.39	109.81
1	BF	112	GLN	CB-CA-C	-7.92	103.26	110.71
1	BP	112	GLN	N-CA-C	7.91	127.28	109.81
1	BH	112	GLN	N-CA-C	7.87	127.20	109.81
1	BJ	111	ILE	N-CA-C	7.87	119.58	111.00
1	CY	336	SER	N-CA-C	7.80	121.59	109.96
1	BV	112	GLN	N-CA-C	7.79	127.03	109.81
1	Bd	112	GLN	N-CA-C	7.77	126.99	109.81
1	BO	112	GLN	N-CA-C	7.77	126.97	109.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BZ	112	GLN	N-CA-C	7.74	126.92	109.81
1	CD	336	SER	N-CA-C	7.74	121.49	109.96
1	CJ	336	SER	N-CA-C	7.73	121.48	109.96
1	BW	112	GLN	N-CA-C	7.72	126.88	109.81
1	Bb	111	ILE	N-CA-C	7.71	119.41	111.00
1	BU	112	GLN	N-CA-C	7.71	126.84	109.81
1	BX	112	GLN	N-CA-C	7.70	126.83	109.81
1	BI	112	GLN	N-CA-C	7.70	126.81	109.81
1	BN	112	GLN	N-CA-C	7.68	126.78	109.81
1	BB	112	GLN	N-CA-C	7.66	126.73	109.81
1	CO	336	SER	N-CA-C	7.64	121.34	109.96
1	CR	209	VAL	N-CA-C	7.63	116.69	107.61
1	BR	112	GLN	N-CA-C	7.62	126.65	109.81
1	BU	111	ILE	N-CA-C	7.61	119.29	111.00
1	CG	336	SER	N-CA-C	7.57	121.24	109.96
1	Cc	336	SER	N-CA-C	7.55	121.21	109.96
1	BO	111	ILE	N-CA-C	7.54	119.22	111.00
1	BL	112	GLN	N-CA-C	7.53	126.45	109.81
1	BG	112	GLN	N-CA-C	7.52	126.44	109.81
1	BS	111	ILE	N-CA-C	7.52	119.20	111.00
1	CS	336	SER	N-CA-C	7.52	121.16	109.96
1	Bd	111	ILE	N-CA-C	7.51	119.18	111.00
1	BQ	112	GLN	N-CA-C	7.50	126.38	109.81
1	BR	208	SER	N-CA-C	7.50	122.40	112.13
1	CE	336	SER	N-CA-C	7.49	121.12	109.96
1	CU	336	SER	N-CA-C	7.48	121.11	109.96
1	CB	336	SER	N-CA-C	7.48	121.11	109.96
1	BB	111	ILE	N-CA-C	7.47	119.14	111.00
1	CI	336	SER	N-CA-C	7.47	121.08	109.96
1	BS	112	GLN	N-CA-C	7.47	126.31	109.81
1	BY	112	GLN	N-CA-C	7.46	126.31	109.81
1	CF	336	SER	N-CA-C	7.46	121.08	109.96
1	AY	218	THR	N-CA-C	7.45	120.46	111.82
1	AF	112	GLN	CB-CA-C	-7.45	105.91	111.20
1	BM	112	GLN	N-CA-C	7.44	126.26	109.81
1	CX	336	SER	N-CA-C	7.43	121.04	109.96
1	CH	336	SER	N-CA-C	7.42	121.01	109.96
1	Cb	336	SER	N-CA-C	7.42	121.01	109.96
1	Ba	112	GLN	N-CA-C	7.41	126.19	109.81
1	CI	112	GLN	CB-CA-C	-7.41	105.94	111.20
1	CN	336	SER	N-CA-C	7.41	121.00	109.96
1	CZ	336	SER	N-CA-C	7.40	120.99	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	CM	336	SER	N-CA-C	7.39	120.97	109.96
1	AV	111	ILE	N-CA-C	7.37	117.97	110.82
1	BL	98	ILE	CB-CA-C	-7.37	104.23	111.30
1	CA	336	SER	N-CA-C	7.36	120.92	109.96
1	CP	336	SER	N-CA-C	7.34	120.90	109.96
1	CW	336	SER	N-CA-C	7.34	120.90	109.96
1	AW	111	ILE	N-CA-C	7.32	117.92	110.82
1	CQ	336	SER	N-CA-C	7.32	120.86	109.96
1	Bc	111	ILE	N-CA-C	7.27	118.92	111.00
1	CC	336	SER	N-CA-C	7.27	120.79	109.96
1	Bc	112	GLN	N-CA-C	7.26	125.85	109.81
1	BP	111	ILE	N-CA-C	7.21	118.86	111.00
1	CT	209	VAL	N-CA-C	7.21	116.19	107.61
1	AL	218	THR	N-CA-C	7.21	121.33	112.54
1	BT	112	GLN	N-CA-C	7.18	125.68	109.81
1	CL	336	SER	N-CA-C	7.18	120.66	109.96
1	BQ	111	ILE	N-CA-C	7.18	118.82	111.00
1	BH	208	SER	N-CA-C	7.18	121.96	112.13
1	CV	336	SER	N-CA-C	7.17	120.65	109.96
1	BC	208	SER	N-CA-C	7.17	121.95	112.13
1	BJ	112	GLN	CB-CA-C	-7.16	103.98	110.71
1	Ca	336	SER	N-CA-C	7.15	120.61	109.96
1	BX	111	ILE	N-CA-C	7.14	118.78	111.00
1	AN	111	ILE	N-CA-C	7.13	117.74	110.82
1	CT	336	SER	N-CA-C	7.13	120.58	109.96
1	Cd	336	SER	N-CA-C	7.12	120.57	109.96
1	BY	208	SER	N-CA-C	7.12	121.89	112.13
1	BT	111	ILE	N-CA-C	7.12	118.76	111.00
1	BK	208	SER	N-CA-C	7.11	121.86	112.13
1	BF	112	GLN	N-CA-C	7.09	127.08	112.40
1	CF	111	ILE	N-CA-C	7.09	117.64	111.90
1	AL	112	GLN	CB-CA-C	-7.07	106.18	111.20
1	CG	209	VAL	N-CA-C	7.06	116.01	107.61
1	BH	111	ILE	N-CA-C	7.05	118.69	111.00
1	BJ	208	SER	N-CA-C	7.05	121.78	112.13
1	CR	336	SER	N-CA-C	7.05	120.46	109.96
1	CK	336	SER	N-CA-C	7.04	120.45	109.96
1	BK	111	ILE	N-CA-C	7.04	118.67	111.00
1	CF	209	VAL	N-CA-C	7.03	115.98	107.61
1	BI	208	SER	N-CA-C	7.03	121.77	112.13
1	AP	111	ILE	N-CA-C	7.03	117.63	110.82
1	CZ	209	VAL	N-CA-C	7.02	115.97	107.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BT	208	SER	N-CA-C	6.98	121.70	112.13
1	BC	111	ILE	N-CA-C	6.96	118.59	111.00
1	BP	208	SER	N-CA-C	6.95	121.65	112.13
1	BF	111	ILE	N-CA-C	6.94	118.56	111.00
1	BL	208	SER	CA-C-N	-6.94	115.80	123.43
1	BL	208	SER	C-N-CA	-6.94	115.80	123.43
1	BM	208	SER	N-CA-C	6.93	121.63	112.13
1	BN	111	ILE	N-CA-C	6.93	118.55	111.00
1	BB	208	SER	CA-C-N	-6.92	115.81	123.43
1	BB	208	SER	C-N-CA	-6.92	115.81	123.43
1	BD	112	GLN	N-CA-C	6.91	126.71	112.40
1	Ac	111	ILE	N-CA-C	6.91	117.52	110.82
1	BA	208	SER	N-CA-C	6.90	121.69	111.96
1	Bb	208	SER	N-CA-C	6.89	121.57	112.13
1	BJ	209	VAL	CA-C-N	-6.89	112.87	119.76
1	BJ	209	VAL	C-N-CA	-6.89	112.87	119.76
1	AT	111	ILE	N-CA-C	6.89	118.51	111.00
1	AC	218	THR	N-CA-C	6.88	119.81	111.82
1	AR	112	GLN	CB-CA-C	-6.88	106.31	111.20
1	AX	162	TYR	N-CA-C	-6.88	98.85	109.24
1	BE	112	GLN	CB-CA-C	-6.88	104.25	110.71
1	BU	208	SER	CA-C-N	-6.87	115.87	123.43
1	BU	208	SER	C-N-CA	-6.87	115.87	123.43
1	BD	208	SER	N-CA-C	6.86	121.53	112.13
1	BS	208	SER	N-CA-C	6.85	121.52	112.13
1	Ba	208	SER	N-CA-C	6.82	121.48	112.13
1	Ad	218	THR	N-CA-C	6.82	119.73	111.82
1	CI	209	VAL	N-CA-C	6.82	115.72	107.61
1	CP	209	VAL	N-CA-C	6.81	115.72	107.61
1	AW	218	THR	N-CA-C	6.79	120.83	112.54
1	BQ	208	SER	N-CA-C	6.79	121.42	112.13
1	AC	111	ILE	N-CA-C	6.78	117.40	110.82
1	BY	111	ILE	N-CA-C	6.78	118.39	111.00
1	CV	209	VAL	N-CA-C	6.77	115.67	107.61
1	CO	209	VAL	N-CA-C	6.75	115.65	107.61
1	BE	112	GLN	N-CA-C	6.75	126.37	112.40
1	CW	209	VAL	N-CA-C	6.73	115.62	107.61
1	Bb	209	VAL	CA-C-N	-6.73	113.03	119.76
1	Bb	209	VAL	C-N-CA	-6.73	113.03	119.76
1	BF	208	SER	N-CA-C	6.72	121.34	112.13
1	AP	162	TYR	N-CA-C	-6.71	99.11	109.24
1	BJ	112	GLN	N-CA-C	6.70	126.28	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	CG	199	VAL	N-CA-C	6.70	117.37	106.72
1	BD	112	GLN	CB-CA-C	-6.70	104.42	110.71
1	Aa	162	TYR	N-CA-C	-6.69	99.14	109.24
1	AO	112	GLN	CB-CA-C	-6.67	106.47	111.20
1	AQ	218	THR	N-CA-C	6.66	119.54	111.82
1	BB	208	SER	N-CA-C	6.65	121.25	112.13
1	CB	199	VAL	N-CA-C	6.65	117.29	106.72
1	CY	199	VAL	N-CA-C	6.64	117.28	106.72
1	Cb	209	VAL	N-CA-C	6.64	115.51	107.61
1	Ca	209	VAL	N-CA-C	6.63	115.50	107.61
1	Bd	208	SER	N-CA-C	6.63	121.21	112.13
1	AK	162	TYR	N-CA-C	-6.62	99.24	109.24
1	CX	199	VAL	N-CA-C	6.62	117.25	106.72
1	CD	209	VAL	N-CA-C	6.59	115.46	107.61
1	Ba	98	ILE	CB-CA-C	-6.59	104.97	111.30
1	BY	209	VAL	CA-C-N	-6.57	113.19	119.76
1	BY	209	VAL	C-N-CA	-6.57	113.19	119.76
1	BD	209	VAL	CA-C-N	-6.57	113.19	119.76
1	BD	209	VAL	C-N-CA	-6.57	113.19	119.76
1	BK	209	VAL	CA-C-N	-6.53	113.23	119.76
1	BK	209	VAL	C-N-CA	-6.53	113.23	119.76
1	Bb	112	GLN	CB-CA-C	-6.52	104.58	110.71
1	BE	111	ILE	N-CA-C	6.51	118.09	111.00
1	BE	209	VAL	CA-C-N	-6.50	113.26	119.76
1	BE	209	VAL	C-N-CA	-6.50	113.26	119.76
1	BZ	208	SER	N-CA-C	6.49	121.02	112.13
1	BG	208	SER	N-CA-C	6.49	121.02	112.13
1	AF	111	ILE	N-CA-C	6.48	117.11	110.82
1	AN	112	GLN	CB-CA-C	-6.47	106.61	111.20
1	AQ	162	TYR	N-CA-C	-6.47	99.48	109.24
1	AS	162	TYR	N-CA-C	-6.47	99.48	109.24
1	BV	68	LEU	CB-CA-C	6.46	117.34	110.17
1	BG	209	VAL	CA-C-N	-6.46	113.31	119.76
1	BG	209	VAL	C-N-CA	-6.46	113.31	119.76
1	Ca	199	VAL	N-CA-C	6.45	116.98	106.72
1	BW	208	SER	CA-C-N	-6.45	116.34	123.43
1	BW	208	SER	C-N-CA	-6.45	116.34	123.43
1	AM	162	TYR	N-CA-C	-6.44	99.51	109.24
1	CA	209	VAL	N-CA-C	6.44	115.27	107.61
1	Ad	112	GLN	CB-CA-C	-6.44	106.63	111.20
1	AB	111	ILE	N-CA-C	6.43	117.06	110.82
1	CH	209	VAL	N-CA-C	6.42	115.25	107.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AX	218	THR	N-CA-C	6.42	119.27	111.82
1	BC	208	SER	CA-C-N	-6.42	116.37	123.43
1	BC	208	SER	C-N-CA	-6.42	116.37	123.43
1	BB	209	VAL	CA-C-N	-6.40	113.36	119.76
1	BB	209	VAL	C-N-CA	-6.40	113.36	119.76
1	BV	208	SER	CA-C-N	-6.39	116.40	123.43
1	BV	208	SER	C-N-CA	-6.39	116.40	123.43
1	BV	208	SER	N-CA-C	6.39	120.89	112.13
1	BR	208	SER	CA-C-N	-6.39	116.40	123.43
1	BR	208	SER	C-N-CA	-6.39	116.40	123.43
1	CX	209	VAL	N-CA-C	6.39	115.21	107.61
1	BN	208	SER	N-CA-C	6.38	120.88	112.13
1	Bb	112	GLN	N-CA-C	6.38	125.60	112.40
1	Bc	208	SER	N-CA-C	6.38	120.95	111.96
1	Cd	209	VAL	N-CA-C	6.37	115.19	107.61
1	AJ	111	ILE	N-CA-C	6.37	117.00	110.82
1	AN	218	THR	N-CA-C	6.36	119.19	111.82
1	AZ	218	THR	N-CA-C	6.36	120.29	112.54
1	AY	112	GLN	CB-CA-C	-6.34	106.70	111.20
1	BX	208	SER	N-CA-C	6.33	120.81	112.13
1	BH	68	LEU	CB-CA-C	6.33	117.19	110.17
1	CE	209	VAL	N-CA-C	6.30	115.11	107.61
1	CL	165	THR	CA-C-N	-6.30	114.23	123.05
1	CL	165	THR	C-N-CA	-6.30	114.23	123.05
1	CK	209	VAL	N-CA-C	6.30	115.11	107.61
1	CK	165	THR	CA-C-N	-6.30	114.23	123.05
1	CK	165	THR	C-N-CA	-6.30	114.23	123.05
1	BR	98	ILE	CB-CA-C	-6.30	105.26	111.30
1	Ac	162	TYR	N-CA-C	-6.29	99.73	109.24
1	Cc	209	VAL	N-CA-C	6.29	115.10	107.61
1	Aa	218	THR	N-CA-C	6.27	119.09	111.82
1	BV	98	ILE	CB-CA-C	-6.27	105.28	111.30
1	AQ	111	ILE	N-CA-C	6.26	116.89	110.82
1	Cc	111	ILE	N-CA-C	6.24	116.93	111.56
1	AJ	218	THR	N-CA-C	6.24	120.15	112.54
1	AD	111	ILE	N-CA-C	6.23	116.87	110.82
1	AK	111	ILE	N-CA-C	6.23	116.87	110.82
1	CT	199	VAL	N-CA-C	6.23	116.63	106.72
1	AG	162	TYR	N-CA-C	-6.21	99.86	109.24
1	AX	112	GLN	CB-CA-C	-6.21	106.79	111.20
1	BU	98	ILE	CB-CA-C	-6.21	105.34	111.30
1	CC	111	ILE	N-CA-C	6.21	116.90	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	Ba	209	VAL	CA-C-N	-6.20	113.56	119.76
1	Ba	209	VAL	C-N-CA	-6.20	113.56	119.76
1	CE	111	ILE	N-CA-C	6.20	116.89	111.56
1	CL	209	VAL	N-CA-C	6.19	114.98	107.61
1	AT	162	TYR	N-CA-C	-6.19	99.89	109.24
1	CC	209	VAL	N-CA-C	6.19	114.97	107.61
1	CJ	112	GLN	CB-CA-C	-6.18	106.81	111.20
1	BS	209	VAL	CA-C-N	-6.18	113.58	119.76
1	BS	209	VAL	C-N-CA	-6.18	113.58	119.76
1	AD	162	TYR	N-CA-C	-6.18	99.91	109.24
1	CY	112	GLN	CB-CA-C	-6.16	106.82	111.20
1	BE	208	SER	N-CA-C	6.16	120.57	112.13
1	Ba	208	SER	CA-C-N	-6.16	116.66	123.43
1	Ba	208	SER	C-N-CA	-6.16	116.66	123.43
1	Ad	111	ILE	N-CA-C	6.15	116.79	110.82
1	BO	219	THR	N-CA-C	6.15	118.72	110.35
1	CU	165	THR	CA-C-N	-6.15	114.44	123.05
1	CU	165	THR	C-N-CA	-6.15	114.44	123.05
1	CQ	209	VAL	N-CA-C	6.15	114.93	107.61
1	Bd	219	THR	N-CA-C	6.13	118.69	110.35
1	CC	199	VAL	N-CA-C	6.12	117.00	107.28
1	CO	176	ARG	NE-CZ-NH2	6.11	124.70	119.20
1	CN	209	VAL	N-CA-C	6.11	114.88	107.61
1	BX	208	SER	CA-C-N	-6.10	116.72	123.43
1	BX	208	SER	C-N-CA	-6.10	116.72	123.43
1	BU	208	SER	N-CA-C	6.10	120.49	112.13
1	CF	165	THR	CA-C-N	-6.10	114.51	123.05
1	CF	165	THR	C-N-CA	-6.10	114.51	123.05
1	AN	208	SER	N-CA-C	6.10	121.29	113.18
1	BG	208	SER	CA-C-N	-6.09	116.73	123.43
1	BG	208	SER	C-N-CA	-6.09	116.73	123.43
1	BS	208	SER	CA-C-N	-6.09	116.73	123.43
1	BS	208	SER	C-N-CA	-6.09	116.73	123.43
1	CN	165	THR	CA-C-N	-6.09	114.53	123.05
1	CN	165	THR	C-N-CA	-6.09	114.53	123.05
1	CO	165	THR	CA-C-N	-6.08	114.53	123.05
1	CO	165	THR	C-N-CA	-6.08	114.53	123.05
1	BI	208	SER	CA-C-N	-6.08	116.75	123.43
1	BI	208	SER	C-N-CA	-6.08	116.75	123.43
1	AC	162	TYR	N-CA-C	-6.07	100.07	109.24
1	AF	162	TYR	N-CA-C	-6.07	100.07	109.24
1	BC	68	LEU	CB-CA-C	6.07	116.91	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AT	112	GLN	CB-CA-C	-6.07	106.89	111.20
1	Bd	208	SER	CA-C-N	-6.07	116.76	123.43
1	Bd	208	SER	C-N-CA	-6.07	116.76	123.43
1	BY	98	ILE	CB-CA-C	-6.06	105.48	111.30
1	BZ	209	VAL	CA-C-N	-6.06	113.70	119.76
1	BZ	209	VAL	C-N-CA	-6.06	113.70	119.76
1	CC	165	THR	CA-C-N	-6.06	114.57	123.05
1	CC	165	THR	C-N-CA	-6.06	114.57	123.05
1	Bb	219	THR	N-CA-C	6.06	118.59	110.35
1	AH	218	THR	N-CA-C	6.05	118.84	111.82
1	AR	218	THR	N-CA-C	6.05	119.92	112.54
1	CY	209	VAL	N-CA-C	6.05	114.81	107.61
1	Ad	162	TYR	N-CA-C	-6.05	100.10	109.24
1	AI	162	TYR	N-CA-C	-6.05	100.10	109.24
1	Cd	165	THR	CA-C-N	-6.05	114.58	123.05
1	Cd	165	THR	C-N-CA	-6.05	114.58	123.05
1	BK	219	THR	N-CA-C	6.04	118.57	110.35
1	Bd	68	LEU	CB-CA-C	6.04	116.88	110.17
1	CA	199	VAL	N-CA-C	6.04	116.88	107.28
1	CS	199	VAL	N-CA-C	6.04	116.88	107.28
1	AU	162	TYR	N-CA-C	-6.03	100.13	109.24
1	BX	209	VAL	N-CA-C	6.03	114.46	107.89
1	CX	112	GLN	CB-CA-C	-6.03	106.92	111.20
1	BK	104	VAL	CB-CA-C	-6.02	103.32	111.15
1	BW	98	ILE	CB-CA-C	-6.02	105.52	111.30
1	AO	111	ILE	N-CA-C	6.01	116.65	110.82
1	AY	162	TYR	N-CA-C	-6.01	100.17	109.24
1	AJ	162	TYR	N-CA-C	-6.00	100.18	109.24
1	AB	162	TYR	N-CA-C	-5.99	100.20	109.24
1	Ab	162	TYR	N-CA-C	-5.99	100.20	109.24
1	BM	209	VAL	CA-C-N	-5.99	113.78	119.76
1	BM	209	VAL	C-N-CA	-5.99	113.78	119.76
1	BX	209	VAL	CA-C-N	-5.97	113.78	119.76
1	BX	209	VAL	C-N-CA	-5.97	113.78	119.76
1	AV	162	TYR	N-CA-C	-5.97	100.22	109.24
1	AR	162	TYR	N-CA-C	-5.97	100.22	109.24
1	BY	209	VAL	N-CA-C	5.96	114.39	107.89
1	CH	165	THR	CA-C-N	-5.96	114.70	123.05
1	CH	165	THR	C-N-CA	-5.96	114.70	123.05
1	AX	111	ILE	N-CA-C	5.96	116.60	110.82
1	BZ	208	SER	CA-C-N	-5.96	116.87	123.43
1	BZ	208	SER	C-N-CA	-5.96	116.87	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BU	219	THR	N-CA-C	5.96	118.45	110.35
1	BG	219	THR	N-CA-C	5.95	118.44	110.35
1	CV	165	THR	CA-C-N	-5.95	114.72	123.05
1	CV	165	THR	C-N-CA	-5.95	114.72	123.05
1	CL	39	VAL	N-CA-C	-5.94	104.72	110.72
1	CM	209	VAL	N-CA-C	5.94	114.68	107.61
1	CP	199	VAL	N-CA-C	5.94	116.72	107.28
1	Ba	68	LEU	CB-CA-C	5.94	116.76	110.17
1	BL	219	THR	N-CA-C	5.94	118.42	110.35
1	CK	209	VAL	CB-CA-C	-5.93	104.38	110.13
1	AP	112	GLN	CB-CA-C	-5.93	106.99	111.20
1	CW	199	VAL	N-CA-C	5.93	116.70	107.28
1	Cb	165	THR	CA-C-N	-5.92	114.77	123.05
1	Cb	165	THR	C-N-CA	-5.92	114.77	123.05
1	BD	98	ILE	CB-CA-C	-5.91	105.62	111.30
1	BE	98	ILE	CB-CA-C	-5.91	105.62	111.30
1	BD	208	SER	CA-C-N	-5.91	116.93	123.43
1	BD	208	SER	C-N-CA	-5.91	116.93	123.43
1	AT	218	THR	N-CA-C	5.91	119.75	112.54
1	CT	176	ARG	NE-CZ-NH2	5.91	124.52	119.20
1	AW	162	TYR	N-CA-C	-5.91	100.32	109.24
1	BL	104	VAL	CB-CA-C	-5.91	103.47	111.15
1	BB	68	LEU	CB-CA-C	5.89	116.71	110.17
1	AY	208	SER	CA-C-N	-5.89	114.97	123.28
1	AY	208	SER	C-N-CA	-5.89	114.97	123.28
1	CF	199	VAL	N-CA-C	5.89	116.65	107.28
1	BM	136	HIS	N-CA-C	5.89	120.16	113.15
1	BN	68	LEU	CB-CA-C	5.89	116.70	110.17
1	BA	98	ILE	CB-CA-C	-5.89	105.65	111.30
1	AA	112	GLN	CB-CA-C	-5.88	107.02	111.20
1	CI	165	THR	CA-C-N	-5.88	114.82	123.05
1	CI	165	THR	C-N-CA	-5.88	114.82	123.05
1	Aa	111	ILE	N-CA-C	5.88	116.52	110.82
1	AA	162	TYR	N-CA-C	-5.87	100.38	109.24
1	BF	219	THR	N-CA-C	5.86	118.32	110.35
1	CM	165	THR	CA-C-N	-5.86	114.98	122.77
1	CM	165	THR	C-N-CA	-5.86	114.98	122.77
1	CS	165	THR	CA-C-N	-5.86	114.85	123.05
1	CS	165	THR	C-N-CA	-5.86	114.85	123.05
1	BF	209	VAL	CA-C-N	-5.85	113.91	119.76
1	BF	209	VAL	C-N-CA	-5.85	113.91	119.76
1	BU	209	VAL	N-CA-C	5.85	114.27	107.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BD	219	THR	N-CA-C	5.84	118.29	110.35
1	CJ	165	THR	CA-C-N	-5.84	114.88	123.05
1	CJ	165	THR	C-N-CA	-5.84	114.88	123.05
1	BL	146	GLY	N-CA-C	-5.84	106.96	113.79
1	Bb	209	VAL	N-CA-C	5.84	114.25	107.89
1	Ac	208	SER	CA-C-N	-5.84	115.05	123.28
1	Ac	208	SER	C-N-CA	-5.84	115.05	123.28
1	CT	79	VAL	CB-CA-C	-5.83	104.26	112.14
1	CA	288	ASN	N-CA-C	5.83	118.73	109.81
1	BO	208	SER	N-CA-C	5.83	120.11	112.13
1	AU	112	GLN	CB-CA-C	-5.83	107.06	111.20
1	CB	209	VAL	N-CA-C	5.82	114.53	107.61
1	CB	112	GLN	CB-CA-C	-5.82	105.94	111.00
1	Bc	219	THR	N-CA-C	5.82	118.26	110.35
1	Ab	218	THR	N-CA-C	5.81	118.56	111.82
1	BS	98	ILE	CB-CA-C	-5.81	105.72	111.30
1	BE	104	VAL	CB-CA-C	-5.81	103.60	111.15
1	BX	219	THR	N-CA-C	5.81	118.25	110.35
1	CS	209	VAL	N-CA-C	5.80	114.52	107.61
1	CU	176	ARG	NE-CZ-NH2	5.80	124.42	119.20
1	Ac	119	THR	N-CA-C	5.80	117.60	111.28
1	AR	79	VAL	CB-CA-C	-5.80	104.64	111.94
1	AZ	111	ILE	N-CA-C	5.80	116.44	110.82
1	Bb	98	ILE	CB-CA-C	-5.79	105.74	111.30
1	BT	98	ILE	CB-CA-C	-5.79	105.74	111.30
1	AN	162	TYR	N-CA-C	-5.78	100.51	109.24
1	CK	112	GLN	CB-CA-C	-5.78	107.10	111.20
1	CZ	199	VAL	N-CA-C	5.78	116.46	107.28
1	CU	199	VAL	N-CA-C	5.77	116.46	107.28
1	CU	209	VAL	N-CA-C	5.77	114.48	107.61
1	BX	98	ILE	CB-CA-C	-5.77	105.76	111.30
1	CY	121	GLY	CA-C-N	-5.77	117.17	121.61
1	CY	121	GLY	C-N-CA	-5.77	117.17	121.61
1	CW	165	THR	CA-C-N	-5.77	114.98	123.05
1	CW	165	THR	C-N-CA	-5.77	114.98	123.05
1	BA	68	LEU	CB-CA-C	5.77	116.57	110.17
1	BT	219	THR	N-CA-C	5.77	118.19	110.35
1	BQ	208	SER	CA-C-N	-5.76	117.09	123.43
1	BQ	208	SER	C-N-CA	-5.76	117.09	123.43
1	AS	111	ILE	N-CA-C	5.76	116.41	110.82
1	BM	68	LEU	CB-CA-C	5.76	116.56	110.17
1	Ab	111	ILE	N-CA-C	5.76	116.40	110.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BM	98	ILE	CB-CA-C	-5.75	105.78	111.30
1	CG	165	THR	CA-C-N	-5.75	115.00	123.05
1	CG	165	THR	C-N-CA	-5.75	115.00	123.05
1	BI	219	THR	N-CA-C	5.75	118.17	110.35
1	CP	165	THR	CA-C-N	-5.75	115.13	122.77
1	CP	165	THR	C-N-CA	-5.75	115.13	122.77
1	BF	208	SER	CA-C-N	-5.75	117.11	123.43
1	BF	208	SER	C-N-CA	-5.75	117.11	123.43
1	BR	219	THR	N-CA-C	5.75	118.16	110.35
1	AU	111	ILE	N-CA-C	5.75	116.39	110.82
1	BU	68	LEU	CB-CA-C	5.74	116.54	110.17
1	CE	165	THR	CA-C-N	-5.74	115.01	123.05
1	CE	165	THR	C-N-CA	-5.74	115.01	123.05
1	BK	208	SER	CA-C-N	-5.74	117.12	123.43
1	BK	208	SER	C-N-CA	-5.74	117.12	123.43
1	BY	219	THR	N-CA-C	5.74	118.16	110.35
1	BV	179	SER	N-CA-C	5.73	117.52	108.23
1	CX	111	ILE	N-CA-C	5.73	116.49	111.56
1	BZ	219	THR	N-CA-C	5.73	118.14	110.35
1	BJ	208	SER	CA-C-N	-5.73	117.13	123.43
1	BJ	208	SER	C-N-CA	-5.73	117.13	123.43
1	AE	111	ILE	N-CA-C	5.73	116.38	110.82
1	Cc	165	THR	CA-C-N	-5.73	115.03	123.05
1	Cc	165	THR	C-N-CA	-5.73	115.03	123.05
1	AH	111	ILE	N-CA-C	5.72	116.37	110.82
1	AM	119	THR	N-CA-C	5.72	117.51	111.28
1	CM	63	ILE	CB-CA-C	5.72	117.11	110.88
1	BT	208	SER	CA-C-N	-5.71	117.15	123.43
1	BT	208	SER	C-N-CA	-5.71	117.15	123.43
1	CW	176	ARG	NE-CZ-NH2	5.71	124.34	119.20
1	BI	136	HIS	N-CA-C	5.71	119.94	113.15
1	CZ	112	GLN	CB-CA-C	-5.71	107.15	111.20
1	Cd	63	ILE	CB-CA-C	5.71	117.10	110.88
1	BS	219	THR	N-CA-C	5.70	118.11	110.35
1	BM	208	SER	CA-C-N	-5.70	117.16	123.43
1	BM	208	SER	C-N-CA	-5.70	117.16	123.43
1	CN	111	ILE	N-CA-C	5.70	116.52	111.90
1	AO	218	THR	N-CA-C	5.70	118.43	111.82
1	BH	98	ILE	CB-CA-C	-5.70	105.83	111.30
1	BS	68	LEU	CB-CA-C	5.70	116.50	110.17
1	Cc	199	VAL	N-CA-C	5.69	116.33	107.28
1	AO	119	THR	N-CA-C	5.69	117.48	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BA	208	SER	CA-C-N	-5.69	117.17	123.43
1	BA	208	SER	C-N-CA	-5.69	117.17	123.43
1	AL	162	TYR	N-CA-C	-5.69	100.65	109.24
1	BX	136	HIS	N-CA-C	5.68	119.91	113.15
1	BT	136	HIS	N-CA-C	5.68	119.90	113.15
1	BH	209	VAL	CA-C-N	-5.67	114.09	119.76
1	BH	209	VAL	C-N-CA	-5.67	114.09	119.76
1	BK	68	LEU	CB-CA-C	5.67	116.46	110.17
1	CA	165	THR	CA-C-N	-5.67	115.12	123.05
1	CA	165	THR	C-N-CA	-5.67	115.12	123.05
1	BC	98	ILE	CB-CA-C	-5.67	105.86	111.30
1	BN	208	SER	CA-C-N	-5.66	117.20	123.43
1	BN	208	SER	C-N-CA	-5.66	117.20	123.43
1	BU	209	VAL	CA-C-N	-5.66	114.10	119.76
1	BU	209	VAL	C-N-CA	-5.66	114.10	119.76
1	Bb	136	HIS	N-CA-C	5.66	119.89	113.15
1	BP	68	LEU	CB-CA-C	5.66	116.45	110.17
1	CR	112	GLN	CB-CA-C	-5.66	107.18	111.20
1	BC	104	VAL	CB-CA-C	-5.66	103.80	111.15
1	CJ	209	VAL	N-CA-C	5.66	114.34	107.61
1	CX	165	THR	CA-C-N	-5.66	115.13	123.05
1	CX	165	THR	C-N-CA	-5.66	115.13	123.05
1	Bc	208	SER	CA-C-N	-5.65	117.21	123.43
1	Bc	208	SER	C-N-CA	-5.65	117.21	123.43
1	AD	218	THR	N-CA-C	5.65	119.44	112.54
1	BE	219	THR	N-CA-C	5.65	118.03	110.35
1	CM	199	VAL	N-CA-C	5.64	116.25	107.28
1	CQ	199	VAL	N-CA-C	5.64	116.25	107.28
1	BW	219	THR	N-CA-C	5.64	118.02	110.35
1	BW	208	SER	N-CA-C	5.64	119.86	112.13
1	AJ	98	ILE	N-CA-C	5.63	116.41	110.72
1	Ba	219	THR	N-CA-C	5.63	118.01	110.35
1	BV	132	THR	CA-C-O	-5.63	113.49	119.97
1	CO	199	VAL	N-CA-C	5.63	116.23	107.28
1	BA	219	THR	N-CA-C	5.63	118.00	110.35
1	CJ	111	ILE	N-CA-C	5.63	116.40	111.56
1	BJ	98	ILE	CB-CA-C	-5.62	105.90	111.30
1	BP	146	GLY	N-CA-C	-5.62	106.94	114.25
1	AS	208	SER	N-CA-C	5.62	120.66	113.18
1	CV	199	VAL	N-CA-C	5.62	116.22	107.28
1	BL	208	SER	N-CA-C	5.62	119.83	112.13
1	BO	136	HIS	N-CA-C	5.62	119.83	113.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	CD	165	THR	CA-C-N	-5.61	115.20	123.05
1	CD	165	THR	C-N-CA	-5.61	115.20	123.05
1	CT	165	THR	CA-C-N	-5.61	115.20	123.05
1	CT	165	THR	C-N-CA	-5.61	115.20	123.05
1	BG	98	ILE	CB-CA-C	-5.60	105.92	111.30
1	BR	209	VAL	CA-C-N	-5.60	114.16	119.76
1	BR	209	VAL	C-N-CA	-5.60	114.16	119.76
1	Bb	208	SER	CA-C-N	-5.60	117.27	123.43
1	Bb	208	SER	C-N-CA	-5.60	117.27	123.43
1	CM	111	ILE	N-CA-C	5.60	116.37	111.56
1	BE	136	HIS	N-CA-C	5.60	119.81	113.15
1	AE	162	TYR	N-CA-C	-5.60	100.79	109.24
1	CK	306	LYS	N-CA-C	5.60	120.06	113.23
1	AJ	208	SER	CA-C-N	-5.59	115.39	123.28
1	AJ	208	SER	C-N-CA	-5.59	115.39	123.28
1	BA	209	VAL	CA-C-N	-5.59	114.17	119.76
1	BA	209	VAL	C-N-CA	-5.59	114.17	119.76
1	BL	209	VAL	CA-C-N	-5.59	114.17	119.76
1	BL	209	VAL	C-N-CA	-5.59	114.17	119.76
1	BQ	68	LEU	CB-CA-C	5.58	116.37	110.17
1	CH	199	VAL	N-CA-C	5.58	116.15	107.28
1	BB	98	ILE	CB-CA-C	-5.58	105.95	111.30
1	AK	79	VAL	CB-CA-C	-5.58	104.92	111.94
1	Ba	104	VAL	CB-CA-C	-5.57	103.91	111.15
1	CH	79	VAL	CB-CA-C	-5.56	104.75	112.04
1	Aa	208	SER	N-CA-C	5.56	120.58	113.18
1	BG	209	VAL	N-CA-C	5.56	113.95	107.89
1	BA	132	THR	CA-C-O	-5.56	113.58	119.97
1	BE	132	THR	CA-C-O	-5.56	113.58	119.97
1	BU	136	HIS	N-CA-C	5.56	119.76	113.15
1	CL	199	VAL	N-CA-C	5.56	116.11	107.28
1	BG	136	HIS	N-CA-C	5.55	119.76	113.15
1	BD	209	VAL	N-CA-C	5.55	113.94	107.89
1	BN	136	HIS	N-CA-C	5.55	119.75	113.15
1	BV	136	HIS	N-CA-C	5.55	119.75	113.15
1	BC	179	SER	N-CA-C	5.55	117.22	108.23
1	Cb	112	GLN	CB-CA-C	-5.55	107.26	111.20
1	AA	218	THR	N-CA-C	5.55	119.31	112.54
1	BM	72	THR	CB-CA-C	-5.55	99.38	110.42
1	Ba	136	HIS	N-CA-C	5.55	119.75	113.15
1	BC	132	THR	CA-C-O	-5.54	113.59	119.97
1	BY	136	HIS	N-CA-C	5.54	119.74	113.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BP	209	VAL	CA-C-N	-5.53	114.23	119.76
1	BP	209	VAL	C-N-CA	-5.53	114.23	119.76
1	AR	208	SER	N-CA-C	5.53	120.53	113.18
1	BX	72	THR	CB-CA-C	-5.53	99.86	109.64
1	CD	111	ILE	N-CA-C	5.52	116.31	111.56
1	AS	218	THR	N-CA-C	5.52	119.28	112.54
1	CM	112	GLN	CB-CA-C	-5.52	106.20	111.00
1	CK	166	LEU	N-CA-CB	5.52	119.21	110.55
1	BB	209	VAL	N-CA-C	5.51	113.90	107.89
1	CR	165	THR	CA-C-N	-5.51	115.33	123.05
1	CR	165	THR	C-N-CA	-5.51	115.33	123.05
1	AK	208	SER	CA-C-N	-5.51	115.51	123.28
1	AK	208	SER	C-N-CA	-5.51	115.51	123.28
1	AH	112	GLN	CB-CA-C	-5.51	107.29	111.20
1	CS	79	VAL	CB-CA-C	-5.51	104.82	112.04
1	AH	162	TYR	N-CA-C	-5.51	100.92	109.24
1	BT	165	THR	N-CA-C	-5.50	101.10	108.86
1	AL	79	VAL	CB-CA-C	-5.50	105.01	111.94
1	CU	121	GLY	CA-C-N	-5.50	117.37	121.61
1	CU	121	GLY	C-N-CA	-5.50	117.37	121.61
1	Bb	72	THR	CB-CA-C	-5.50	99.90	109.64
1	AG	218	THR	N-CA-C	5.50	118.20	111.82
1	BH	132	THR	CA-C-O	-5.50	113.65	119.97
1	BG	72	THR	CB-CA-C	-5.49	99.92	109.64
1	BP	98	ILE	CB-CA-C	-5.49	106.03	111.30
1	BM	219	THR	N-CA-C	5.49	117.82	110.35
1	AG	62	ARG	CG-CD-NE	5.49	124.07	112.00
1	AM	63	ILE	N-CA-C	-5.49	106.35	111.45
1	BN	104	VAL	CB-CA-C	-5.48	104.02	111.15
1	BB	219	THR	N-CA-C	5.48	117.80	110.35
1	BW	136	HIS	N-CA-C	5.48	119.67	113.15
1	AF	218	THR	N-CA-C	5.47	119.22	112.54
1	CC	112	GLN	CB-CA-C	-5.47	106.24	111.00
1	BL	68	LEU	CB-CA-C	5.47	116.24	110.17
1	BS	132	THR	CA-C-O	-5.47	113.68	119.97
1	BE	208	SER	CA-C-N	-5.46	117.42	123.43
1	BE	208	SER	C-N-CA	-5.46	117.42	123.43
1	AZ	162	TYR	N-CA-C	-5.46	100.99	109.24
1	BS	210	PRO	O-C-N	5.46	129.65	123.10
1	AE	208	SER	CA-C-N	-5.46	115.58	123.28
1	AE	208	SER	C-N-CA	-5.46	115.58	123.28
1	BJ	132	THR	CA-C-O	-5.46	113.69	119.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AF	53	ASN	N-CA-C	5.46	120.30	113.43
1	Bc	132	THR	CA-C-O	-5.46	113.69	119.97
1	BW	68	LEU	CB-CA-C	5.45	116.22	110.17
1	CC	79	VAL	CB-CA-C	-5.45	104.90	112.04
1	AP	218	THR	N-CA-C	5.45	119.19	112.54
1	BI	132	THR	CA-C-O	-5.45	113.70	119.97
1	Cc	79	VAL	CB-CA-C	-5.45	104.91	112.04
1	AW	79	VAL	CB-CA-C	-5.44	105.08	111.94
1	AV	218	THR	N-CA-C	5.44	119.18	112.54
1	BP	132	THR	CA-C-O	-5.43	113.73	119.97
1	BZ	132	THR	CA-C-O	-5.43	113.73	119.97
1	BP	219	THR	N-CA-C	5.43	117.73	110.35
1	CL	58	SER	N-CA-C	5.43	116.52	108.60
1	BZ	165	THR	N-CA-C	-5.42	101.21	108.86
1	Bd	209	VAL	CA-C-N	-5.42	114.34	119.76
1	Bd	209	VAL	C-N-CA	-5.42	114.34	119.76
1	AO	162	TYR	N-CA-C	-5.42	101.05	109.24
1	AU	62	ARG	CG-CD-NE	5.42	123.93	112.00
1	BE	72	THR	CB-CA-C	-5.42	100.05	109.64
1	BH	208	SER	CA-C-N	-5.42	117.47	123.43
1	BH	208	SER	C-N-CA	-5.42	117.47	123.43
1	BP	208	SER	CA-C-N	-5.41	117.48	123.43
1	BP	208	SER	C-N-CA	-5.41	117.48	123.43
1	BM	209	VAL	N-CA-C	5.41	113.78	107.89
1	BP	72	THR	CB-CA-C	-5.41	100.07	109.64
1	BF	132	THR	CA-C-O	-5.41	113.75	119.97
1	BV	219	THR	N-CA-C	5.40	117.70	110.35
1	BC	136	HIS	N-CA-C	5.40	119.58	113.15
1	CD	199	VAL	N-CA-C	5.40	115.87	107.28
1	Bc	136	HIS	N-CA-C	5.40	119.58	113.15
1	CK	199	VAL	N-CA-C	5.40	115.86	107.28
1	AI	53	ASN	N-CA-C	5.39	120.22	113.43
1	BO	98	ILE	CB-CA-C	-5.39	106.12	111.30
1	Cd	176	ARG	NE-CZ-NH2	5.39	124.05	119.20
1	BZ	68	LEU	CB-CA-C	5.39	116.15	110.17
1	BP	104	VAL	CB-CA-C	-5.39	104.14	111.15
1	BK	132	THR	CA-C-O	-5.39	113.78	119.97
1	BA	146	GLY	N-CA-C	-5.38	107.25	114.25
1	BB	146	GLY	N-CA-C	-5.38	107.25	114.25
1	BU	165	THR	N-CA-C	-5.38	101.27	108.86
1	BS	72	THR	CB-CA-C	-5.38	100.12	109.64
1	BK	209	VAL	N-CA-C	5.37	113.74	107.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AI	111	ILE	N-CA-C	5.37	116.03	110.82
1	BN	209	VAL	CA-C-N	-5.37	114.39	119.76
1	BN	209	VAL	C-N-CA	-5.37	114.39	119.76
1	BO	176	ARG	NE-CZ-NH2	5.37	124.03	119.20
1	BL	136	HIS	N-CA-C	5.37	119.54	113.15
1	Ab	62	ARG	CG-CD-NE	5.36	123.79	112.00
1	AS	62	ARG	CG-CD-NE	5.36	123.79	112.00
1	CZ	165	THR	CA-C-N	-5.36	115.55	123.05
1	CZ	165	THR	C-N-CA	-5.36	115.55	123.05
1	BZ	72	THR	CB-CA-C	-5.36	100.16	109.64
1	BN	98	ILE	CB-CA-C	-5.35	106.16	111.30
1	AI	79	VAL	CB-CA-C	-5.35	105.20	111.94
1	AC	208	SER	N-CA-C	5.35	120.29	113.18
1	CY	63	ILE	CB-CA-C	5.35	116.71	110.88
1	CZ	63	ILE	CB-CA-C	5.34	116.70	110.88
1	CY	165	THR	CA-C-N	-5.34	115.57	123.05
1	CY	165	THR	C-N-CA	-5.34	115.57	123.05
1	AL	208	SER	CA-C-N	-5.34	115.75	123.28
1	AL	208	SER	C-N-CA	-5.34	115.75	123.28
1	BZ	209	VAL	N-CA-C	5.34	113.71	107.89
1	BT	209	VAL	CA-C-N	-5.33	114.43	119.76
1	BT	209	VAL	C-N-CA	-5.33	114.43	119.76
1	Ba	176	ARG	NE-CZ-NH2	5.33	123.99	119.20
1	BC	209	VAL	CA-C-N	-5.33	114.43	119.76
1	BC	209	VAL	C-N-CA	-5.33	114.43	119.76
1	BJ	176	ARG	NE-CZ-NH2	5.33	123.99	119.20
1	BW	132	THR	CA-C-O	-5.33	113.85	119.97
1	Bb	104	VAL	CB-CA-C	-5.33	104.23	111.15
1	AE	218	THR	N-CA-C	5.32	119.03	112.54
1	BT	104	VAL	CB-CA-C	-5.32	104.23	111.15
1	BA	136	HIS	N-CA-C	5.31	119.47	113.15
1	AB	208	SER	N-CA-C	5.31	120.25	113.18
1	AC	112	GLN	CB-CA-C	-5.31	107.43	111.20
1	CY	111	ILE	N-CA-C	5.31	116.20	111.90
1	CT	58	SER	N-CA-C	5.31	116.35	108.60
1	BI	72	THR	CB-CA-C	-5.31	100.25	109.64
1	BL	165	THR	N-CA-C	-5.31	101.38	108.86
1	CR	199	VAL	N-CA-C	5.31	115.72	107.28
1	AZ	120	GLY	N-CA-C	5.30	122.42	115.47
1	AI	119	THR	N-CA-C	5.30	117.06	111.28
1	BL	334	VAL	CB-CA-C	-5.30	106.40	111.06
1	BY	208	SER	CA-C-N	-5.30	117.60	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	BY	208	SER	C-N-CA	-5.30	117.60	123.43
1	BB	179	SER	N-CA-C	5.29	116.81	108.23
1	AI	62	ARG	CG-CD-NE	5.29	123.65	112.00
1	BT	132	THR	CA-C-O	-5.29	113.88	119.97
1	BN	219	THR	N-CA-C	5.29	117.55	110.35
1	BQ	209	VAL	CA-C-N	-5.28	114.48	119.76
1	BQ	209	VAL	C-N-CA	-5.28	114.48	119.76
1	BU	146	GLY	N-CA-C	-5.28	107.38	114.25
1	AM	208	SER	N-CA-C	5.28	120.20	113.18
1	BQ	219	THR	N-CA-C	5.28	117.52	110.35
1	Bc	209	VAL	N-CA-C	5.27	113.64	107.89
1	BT	209	VAL	N-CA-C	5.27	113.63	107.89
1	AB	208	SER	CA-C-N	-5.26	115.86	123.28
1	AB	208	SER	C-N-CA	-5.26	115.86	123.28
1	AW	53	ASN	N-CA-C	5.26	120.06	113.43
1	BZ	98	ILE	CB-CA-C	-5.26	106.25	111.30
1	Ad	53	ASN	N-CA-C	5.26	120.06	113.43
1	Cd	79	VAL	CB-CA-C	-5.26	105.04	112.14
1	BP	165	THR	N-CA-C	-5.26	101.44	108.86
1	AV	53	ASN	N-CA-C	5.26	120.05	113.43
1	BQ	146	GLY	N-CA-C	-5.25	107.42	114.25
1	CX	63	ILE	CB-CA-C	5.25	116.61	110.88
1	CB	79	VAL	CB-CA-C	-5.25	105.16	112.04
1	BQ	209	VAL	N-CA-C	5.25	113.61	107.89
1	AU	120	GLY	N-CA-C	5.25	122.52	115.59
1	BV	209	VAL	CA-C-N	-5.25	114.51	119.76
1	BV	209	VAL	C-N-CA	-5.25	114.51	119.76
1	BJ	136	HIS	N-CA-C	5.25	119.40	113.15
1	AS	120	GLY	N-CA-C	5.25	122.52	115.59
1	BA	179	SER	N-CA-C	5.25	116.73	108.23
1	BS	146	GLY	N-CA-C	-5.25	107.43	114.25
1	CZ	121	GLY	CA-C-N	-5.24	117.57	121.61
1	CZ	121	GLY	C-N-CA	-5.24	117.57	121.61
1	BF	136	HIS	N-CA-C	5.24	119.38	113.15
1	BM	146	GLY	N-CA-C	-5.24	107.44	114.25
1	AM	208	SER	CA-C-N	-5.23	115.90	123.28
1	AM	208	SER	C-N-CA	-5.23	115.90	123.28
1	CG	112	GLN	CB-CA-C	-5.23	106.45	111.00
1	AH	85	VAL	CA-C-N	-5.23	113.53	119.28
1	AH	85	VAL	C-N-CA	-5.23	113.53	119.28
1	BL	218	THR	N-CA-C	5.23	117.72	111.71
1	Cb	199	VAL	N-CA-C	5.23	115.59	107.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	Bc	165	THR	N-CA-C	-5.23	101.49	108.86
1	BF	209	VAL	N-CA-C	5.23	113.59	107.89
1	Ac	62	ARG	CG-CD-NE	5.23	123.50	112.00
1	Ab	85	VAL	CA-C-N	-5.22	113.53	119.28
1	Ab	85	VAL	C-N-CA	-5.22	113.53	119.28
1	AG	111	ILE	N-CA-C	5.22	115.88	110.82
1	CE	199	VAL	N-CA-C	5.21	115.57	107.28
1	BJ	210	PRO	O-C-N	5.21	129.36	123.10
1	Ca	58	SER	N-CA-C	5.21	116.21	108.60
1	Ca	165	THR	CA-C-N	-5.21	115.84	122.77
1	Ca	165	THR	C-N-CA	-5.21	115.84	122.77
1	AM	79	VAL	CB-CA-C	-5.21	105.26	112.24
1	AU	208	SER	N-CA-C	5.21	120.11	113.18
1	BI	209	VAL	CA-C-N	-5.21	114.55	119.76
1	BI	209	VAL	C-N-CA	-5.21	114.55	119.76
1	BF	146	GLY	N-CA-C	-5.21	107.48	114.25
1	Bd	136	HIS	N-CA-C	5.21	119.34	113.15
1	CN	199	VAL	N-CA-C	5.20	115.55	107.28
1	CU	111	ILE	N-CA-C	5.20	116.03	111.56
1	AA	208	SER	CA-C-N	-5.20	115.95	123.28
1	AA	208	SER	C-N-CA	-5.20	115.95	123.28
1	CE	79	VAL	CB-CA-C	-5.20	105.23	112.04
1	AY	62	ARG	CG-CD-NE	5.19	123.42	112.00
1	CB	58	SER	N-CA-C	5.19	116.18	108.60
1	BG	68	LEU	CB-CA-C	5.19	115.93	110.17
1	Bd	179	SER	N-CA-C	5.19	116.64	108.23
1	AV	208	SER	CA-C-N	-5.19	115.96	123.28
1	AV	208	SER	C-N-CA	-5.19	115.96	123.28
1	BC	104	VAL	N-CA-C	5.19	115.74	108.89
1	CA	166	LEU	N-CA-CB	5.18	118.69	110.55
1	AQ	208	SER	CA-C-N	-5.18	115.97	123.28
1	AQ	208	SER	C-N-CA	-5.18	115.97	123.28
1	BT	68	LEU	CB-CA-C	5.18	115.92	110.17
1	BV	72	THR	CB-CA-C	-5.18	100.47	109.64
1	AG	208	SER	CA-C-N	-5.18	115.98	123.28
1	AG	208	SER	C-N-CA	-5.18	115.98	123.28
1	BV	132	THR	N-CA-CB	5.18	118.31	110.28
1	AN	208	SER	CA-C-N	-5.18	115.98	123.28
1	AN	208	SER	C-N-CA	-5.18	115.98	123.28
1	BQ	132	THR	CA-C-O	-5.18	114.02	119.97
1	BB	72	THR	CB-CA-C	-5.17	100.48	109.64
1	AK	302	ASP	CB-CA-C	5.17	117.97	109.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	CK	176	ARG	NE-CZ-NH2	5.17	123.86	119.20
1	AX	53	ASN	N-CA-C	5.17	119.95	113.43
1	BO	176	ARG	NE-CZ-NH1	-5.17	116.33	121.50
1	Cd	199	VAL	N-CA-C	5.17	115.50	107.28
1	CA	112	GLN	CB-CA-C	-5.17	107.53	111.20
1	BC	219	THR	N-CA-C	5.17	117.38	110.35
1	Ba	165	THR	N-CA-C	-5.16	101.58	108.86
1	BV	146	GLY	N-CA-C	-5.16	107.54	114.25
1	BP	132	THR	N-CA-CB	5.16	118.28	110.28
1	AD	208	SER	CA-C-N	-5.16	116.01	123.28
1	AD	208	SER	C-N-CA	-5.16	116.01	123.28
1	CI	199	VAL	N-CA-C	5.16	115.48	107.28
1	Aa	208	SER	CA-C-N	-5.15	116.02	123.28
1	Aa	208	SER	C-N-CA	-5.15	116.02	123.28
1	CT	63	ILE	CB-CA-C	5.15	116.49	110.88
1	Ab	208	SER	CA-C-N	-5.15	116.02	123.28
1	Ab	208	SER	C-N-CA	-5.15	116.02	123.28
1	AK	53	ASN	N-CA-C	5.15	119.91	113.43
1	BJ	209	VAL	N-CA-C	5.14	113.50	107.89
1	BN	146	GLY	N-CA-C	-5.14	107.56	114.25
1	BN	176	ARG	NE-CZ-NH2	5.14	123.83	119.20
1	BC	72	THR	CB-CA-C	-5.14	100.54	109.64
1	BH	72	THR	CB-CA-C	-5.14	100.54	109.64
1	Ac	208	SER	N-CA-C	5.14	120.02	113.18
1	CO	150	ALA	N-CA-C	5.14	116.33	108.52
1	BR	68	LEU	CB-CA-C	5.14	115.87	110.17
1	AO	63	ILE	N-CA-C	-5.13	106.67	111.45
1	BD	136	HIS	N-CA-C	5.13	119.25	113.15
1	CH	112	GLN	CB-CA-C	-5.13	106.54	111.00
1	CI	58	SER	N-CA-C	5.13	116.09	108.60
1	CJ	199	VAL	N-CA-C	5.13	115.44	107.28
1	BP	136	HIS	N-CA-C	5.13	119.25	113.15
1	Bb	146	GLY	N-CA-C	-5.13	107.58	114.25
1	AE	208	SER	N-CA-C	5.13	120.00	113.18
1	BR	136	HIS	N-CA-C	5.12	119.25	113.15
1	CA	63	ILE	CB-CA-C	5.12	116.46	110.88
1	AH	208	SER	N-CA-C	5.12	119.99	113.18
1	AT	79	VAL	CB-CA-C	-5.12	105.38	112.24
1	CV	58	SER	N-CA-C	5.12	116.08	108.60
1	Bc	209	VAL	CA-C-N	-5.12	114.64	119.76
1	Bc	209	VAL	C-N-CA	-5.12	114.64	119.76
1	BZ	136	HIS	N-CA-C	5.12	119.24	113.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AD	62	ARG	CG-CD-NE	5.12	123.26	112.00
1	CO	166	LEU	N-CA-CB	5.12	118.59	110.55
1	Cd	306	LYS	N-CA-C	5.12	119.47	113.23
1	CM	58	SER	N-CA-C	5.11	116.06	108.60
1	BQ	179	SER	N-CA-C	5.11	116.51	108.23
1	AH	208	SER	CA-C-N	-5.11	116.08	123.28
1	AH	208	SER	C-N-CA	-5.11	116.08	123.28
1	AM	62	ARG	CG-CD-NE	5.10	123.23	112.00
1	BX	68	LEU	CB-CA-C	5.10	115.83	110.17
1	AL	53	ASN	N-CA-C	5.10	120.36	114.04
1	BC	146	GLY	N-CA-C	-5.10	107.62	114.25
1	AC	62	ARG	CG-CD-NE	5.09	123.21	112.00
1	BL	72	THR	CB-CA-C	-5.09	100.62	109.64
1	BO	179	SER	N-CA-C	5.09	116.48	108.23
1	BH	165	THR	N-CA-C	-5.09	101.68	108.86
1	BO	132	THR	CA-C-O	-5.09	114.11	119.97
1	AJ	62	ARG	CG-CD-NE	5.09	123.20	112.00
1	CU	166	LEU	N-CA-CB	5.09	118.54	110.55
1	CQ	165	THR	CA-C-N	-5.08	115.94	123.05
1	CQ	165	THR	C-N-CA	-5.08	115.94	123.05
1	AU	53	ASN	N-CA-C	5.08	119.83	113.43
1	CF	58	SER	N-CA-C	5.08	116.02	108.60
1	CA	176	ARG	NE-CZ-NH2	5.08	123.77	119.20
1	BF	72	THR	CB-CA-C	-5.08	100.65	109.64
1	AX	62	ARG	CG-CD-NE	5.08	123.17	112.00
1	Bc	104	VAL	CB-CA-C	-5.08	104.55	111.15
1	BY	132	THR	CA-C-O	-5.08	114.13	119.97
1	CU	112	GLN	CB-CA-C	-5.07	106.59	111.00
1	Cd	334	VAL	CB-CA-C	-5.07	105.35	110.88
1	CE	58	SER	N-CA-C	5.07	116.00	108.60
1	CE	121	GLY	CA-C-N	-5.07	117.71	121.61
1	CE	121	GLY	C-N-CA	-5.07	117.71	121.61
1	CP	79	VAL	CB-CA-C	-5.07	105.40	112.04
1	AA	208	SER	N-CA-C	5.07	119.92	113.18
1	AI	208	SER	CA-C-N	-5.07	116.14	123.28
1	AI	208	SER	C-N-CA	-5.07	116.14	123.28
1	AZ	208	SER	CA-C-N	-5.06	116.14	123.28
1	AZ	208	SER	C-N-CA	-5.06	116.14	123.28
1	AF	79	VAL	CB-CA-C	-5.06	105.56	111.94
1	AW	120	GLY	N-CA-C	5.06	122.10	115.47
1	BE	146	GLY	N-CA-C	-5.06	107.67	114.25
1	CB	165	THR	CA-C-N	-5.06	115.97	123.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	CB	165	THR	C-N-CA	-5.06	115.97	123.05
1	AI	120	GLY	N-CA-C	5.06	122.10	115.47
1	Cb	166	LEU	N-CA-CB	5.06	118.49	110.55
1	AI	208	SER	N-CA-C	5.06	119.91	113.18
1	AS	208	SER	CA-C-N	-5.05	116.16	123.28
1	AS	208	SER	C-N-CA	-5.05	116.16	123.28
1	BR	165	THR	N-CA-C	-5.05	101.74	108.86
1	BS	165	THR	N-CA-C	-5.05	101.74	108.86
1	BZ	146	GLY	N-CA-C	-5.05	107.69	114.25
1	BO	209	VAL	CA-C-N	-5.05	114.71	119.76
1	BO	209	VAL	C-N-CA	-5.05	114.71	119.76
1	AI	63	ILE	N-CA-C	-5.04	106.76	111.45
1	CO	111	ILE	N-CA-C	5.04	115.99	111.90
1	BX	132	THR	CA-C-O	-5.04	114.17	119.97
1	CJ	58	SER	N-CA-C	5.04	115.96	108.60
1	AT	62	ARG	CG-CD-NE	5.04	123.09	112.00
1	Bb	68	LEU	CB-CA-C	5.04	115.76	110.17
1	BE	68	LEU	CB-CA-C	5.04	115.76	110.17
1	BQ	136	HIS	N-CA-C	5.04	119.14	113.15
1	Ab	305	ASN	N-CA-C	5.04	117.15	111.11
1	Ad	62	ARG	CG-CD-NE	5.04	123.08	112.00
1	AR	302	ASP	CB-CA-C	5.03	117.75	109.90
1	BS	136	HIS	N-CA-C	5.03	119.14	113.15
1	AE	305	ASN	N-CA-C	5.03	117.15	111.11
1	BR	132	THR	CA-C-O	-5.03	114.19	119.97
1	AK	237	ASP	N-CA-C	5.03	115.94	108.60
1	AO	208	SER	CA-C-N	-5.03	116.19	123.28
1	AO	208	SER	C-N-CA	-5.03	116.19	123.28
1	CZ	176	ARG	NE-CZ-NH2	5.03	123.72	119.20
1	Cb	79	VAL	CB-CA-C	-5.02	105.46	112.04
1	CL	121	GLY	CA-C-N	-5.02	117.74	121.61
1	CL	121	GLY	C-N-CA	-5.02	117.74	121.61
1	AM	237	ASP	N-CA-C	5.02	115.93	108.60
1	AZ	98	ILE	N-CA-C	5.02	115.79	110.72
1	AA	62	ARG	CG-CD-NE	5.02	123.04	112.00
1	AX	208	SER	CA-C-N	-5.02	116.21	123.28
1	AX	208	SER	C-N-CA	-5.02	116.21	123.28
1	AK	62	ARG	CG-CD-NE	5.01	123.03	112.00
1	AR	208	SER	CA-C-N	-5.01	116.21	123.28
1	AR	208	SER	C-N-CA	-5.01	116.21	123.28
1	CA	58	SER	N-CA-C	5.01	115.91	108.60
1	BU	132	THR	CA-C-O	-5.00	114.22	119.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AF	208	SER	N-CA-C	5.00	119.83	113.18
1	AP	237	ASP	N-CA-C	5.00	115.90	108.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	CU	207	LEU	Peptide
1	Cb	207	LEU	Peptide

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	2218	0	2155	139	0
1	AB	2218	0	2155	143	0
1	AC	2218	0	2155	139	19
1	AD	2218	0	2155	143	0
1	AE	2218	0	2155	135	0
1	AF	2218	0	2155	137	0
1	AG	2218	0	2155	148	0
1	AH	2218	0	2155	140	0
1	AI	2218	0	2155	148	0
1	AJ	2218	0	2155	142	1
1	AK	2218	0	2155	133	0
1	AL	2218	0	2155	122	0
1	AM	2218	0	2155	148	0
1	AN	2218	0	2155	142	0
1	AO	2218	0	2155	142	0
1	AP	2218	0	2155	137	1
1	AQ	2218	0	2155	132	0
1	AR	2218	0	2155	128	0
1	AS	2218	0	2155	142	0
1	AT	2218	0	2155	146	0
1	AU	2218	0	2155	143	0
1	AV	2218	0	2155	142	0
1	AW	2218	0	2155	138	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AX	2218	0	2155	132	0
1	AY	2218	0	2155	136	0
1	AZ	2218	0	2155	144	0
1	Aa	2218	0	2155	147	0
1	Ab	2218	0	2155	135	0
1	Ac	2218	0	2155	131	0
1	Ad	2218	0	2155	141	0
1	BA	2214	0	2153	100	0
1	BB	2214	0	2153	104	0
1	BC	2214	0	2153	96	13
1	BD	2214	0	2153	104	0
1	BE	2214	0	2153	88	0
1	BF	2214	0	2153	94	0
1	BG	2214	0	2153	97	0
1	BH	2214	0	2153	109	0
1	BI	2214	0	2153	98	8
1	BJ	2214	0	2153	87	1
1	BK	2214	0	2153	98	0
1	BL	2214	0	2153	93	7
1	BM	2214	0	2153	104	0
1	BN	2214	0	2153	88	0
1	BO	2214	0	2153	101	0
1	BP	2214	0	2153	97	0
1	BQ	2214	0	2153	98	0
1	BR	2214	0	2153	88	1
1	BS	2214	0	2153	100	0
1	BT	2214	0	2153	96	0
1	BU	2214	0	2153	91	0
1	BV	2214	0	2153	97	0
1	BW	2214	0	2153	93	6
1	BX	2214	0	2153	81	1
1	BY	2214	0	2153	101	0
1	BZ	2214	0	2153	84	0
1	Ba	2214	0	2153	98	11
1	Bb	2214	0	2153	102	0
1	Bc	2214	0	2153	105	1
1	Bd	2214	0	2153	92	0
1	CA	2340	0	2280	119	1
1	CB	2340	0	2280	132	0
1	CC	2340	0	2280	124	0
1	CD	2340	0	2280	125	0
1	CE	2340	0	2280	113	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CF	2340	0	2280	124	0
1	CG	2340	0	2280	116	0
1	CH	2340	0	2280	120	0
1	CI	2340	0	2280	123	0
1	CJ	2340	0	2280	117	0
1	CK	2340	0	2280	130	6
1	CL	2340	0	2280	125	1
1	CM	2340	0	2280	125	0
1	CN	2340	0	2280	103	0
1	CO	2340	0	2280	123	0
1	CP	2340	0	2280	117	2
1	CQ	2340	0	2280	121	11
1	CR	2340	0	2280	122	1
1	CS	2340	0	2280	108	0
1	CT	2340	0	2280	122	2
1	CU	2340	0	2280	116	0
1	CV	2340	0	2280	119	0
1	CW	2340	0	2280	127	0
1	CX	2340	0	2280	113	0
1	CY	2340	0	2280	122	0
1	CZ	2340	0	2280	118	32
1	Ca	2340	0	2280	114	0
1	Cb	2340	0	2280	118	0
1	Cc	2340	0	2280	113	0
1	Cd	2340	0	2280	144	7
2	AA	1	0	0	0	0
2	AB	1	0	0	0	0
2	AC	1	0	0	0	0
2	AD	1	0	0	0	0
2	AE	1	0	0	0	0
2	AF	1	0	0	0	0
2	AG	1	0	0	0	0
2	AH	1	0	0	0	0
2	AI	1	0	0	0	0
2	AJ	1	0	0	0	0
2	AK	1	0	0	0	0
2	AL	1	0	0	0	0
2	AM	1	0	0	0	0
2	AN	1	0	0	0	0
2	AO	1	0	0	0	0
2	AP	1	0	0	0	0
2	AQ	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AR	1	0	0	0	0
2	AS	1	0	0	0	0
2	AT	1	0	0	0	0
2	AU	1	0	0	0	0
2	AV	1	0	0	0	0
2	AW	1	0	0	0	0
2	AX	1	0	0	0	0
2	AY	1	0	0	0	0
2	AZ	1	0	0	0	0
2	Aa	1	0	0	0	0
2	Ab	1	0	0	0	0
2	Ac	1	0	0	0	0
2	Ad	1	0	0	0	0
2	BA	2	0	0	0	0
2	BB	2	0	0	0	0
2	BC	2	0	0	0	0
2	BD	2	0	0	0	0
2	BE	2	0	0	0	0
2	BF	2	0	0	0	0
2	BG	2	0	0	0	0
2	BH	2	0	0	0	0
2	BI	2	0	0	0	0
2	BJ	2	0	0	0	0
2	BK	2	0	0	0	0
2	BL	2	0	0	0	0
2	BM	2	0	0	0	0
2	BN	2	0	0	0	0
2	BO	2	0	0	0	0
2	BP	2	0	0	0	0
2	BQ	2	0	0	0	0
2	BR	2	0	0	0	0
2	BS	2	0	0	0	0
2	BT	2	0	0	0	0
2	BU	2	0	0	0	0
2	BV	2	0	0	0	0
2	BW	2	0	0	0	0
2	BX	2	0	0	0	0
2	BY	2	0	0	0	0
2	BZ	2	0	0	0	0
2	Ba	2	0	0	0	0
2	Bb	2	0	0	0	0
2	Bc	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Bd	2	0	0	0	0
All	All	203250	0	197640	9639	71

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 24.

All (9639) 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:Ad:298:TRP:NE1	1:Ad:312:VAL:HG12	1.22	1.53
1:AA:298:TRP:NE1	1:AA:312:VAL:HG12	1.24	1.53
1:AI:298:TRP:NE1	1:AI:312:VAL:HG12	1.24	1.50
1:AK:298:TRP:NE1	1:AK:312:VAL:HG12	1.21	1.50
1:AB:298:TRP:NE1	1:AB:312:VAL:HG12	1.23	1.49
1:Ac:298:TRP:NE1	1:Ac:312:VAL:HG12	1.23	1.48
1:AU:298:TRP:NE1	1:AU:312:VAL:HG12	1.23	1.48
1:AO:298:TRP:NE1	1:AO:312:VAL:HG12	1.22	1.47
1:AC:298:TRP:NE1	1:AC:312:VAL:HG12	1.24	1.47
1:AJ:298:TRP:NE1	1:AJ:312:VAL:HG12	1.22	1.46
1:AL:298:TRP:NE1	1:AL:312:VAL:HG12	1.21	1.46
1:AS:298:TRP:NE1	1:AS:312:VAL:HG12	1.22	1.46
1:AF:298:TRP:NE1	1:AF:312:VAL:HG12	1.22	1.45
1:AN:298:TRP:NE1	1:AN:312:VAL:HG12	1.23	1.45
1:AM:298:TRP:NE1	1:AM:312:VAL:HG12	1.22	1.44
1:AV:298:TRP:NE1	1:AV:312:VAL:HG12	1.24	1.44
1:Aa:298:TRP:NE1	1:Aa:312:VAL:HG12	1.23	1.44
1:AH:298:TRP:NE1	1:AH:312:VAL:HG12	1.23	1.43
1:AY:298:TRP:NE1	1:AY:312:VAL:HG12	1.23	1.43
1:AW:298:TRP:NE1	1:AW:312:VAL:HG12	1.21	1.43
1:Ab:298:TRP:NE1	1:Ab:312:VAL:HG12	1.24	1.43
1:AZ:298:TRP:NE1	1:AZ:312:VAL:HG12	1.24	1.43
1:Ad:298:TRP:CE2	1:Ad:312:VAL:HG12	1.54	1.43
1:AX:298:TRP:NE1	1:AX:312:VAL:HG12	1.23	1.42
1:AD:298:TRP:CE2	1:AD:312:VAL:HG12	1.55	1.42
1:AQ:298:TRP:NE1	1:AQ:312:VAL:HG12	1.23	1.41
1:AG:298:TRP:NE1	1:AG:312:VAL:HG12	1.22	1.41
1:AP:298:TRP:NE1	1:AP:312:VAL:HG12	1.22	1.41
1:AZ:298:TRP:CE2	1:AZ:312:VAL:HG12	1.54	1.41
1:AC:298:TRP:CE2	1:AC:312:VAL:HG12	1.54	1.41
1:AR:298:TRP:NE1	1:AR:312:VAL:HG12	1.24	1.41
1:Aa:298:TRP:CE2	1:Aa:312:VAL:HG12	1.55	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:298:TRP:CE2	1:AI:312:VAL:HG12	1.56	1.40
1:AL:298:TRP:CE2	1:AL:312:VAL:HG12	1.53	1.40
1:AN:298:TRP:CE2	1:AN:312:VAL:HG12	1.56	1.40
1:AT:298:TRP:CE2	1:AT:312:VAL:HG12	1.54	1.40
1:AE:298:TRP:NE1	1:AE:312:VAL:HG12	1.24	1.40
1:AP:298:TRP:CE2	1:AP:312:VAL:HG12	1.54	1.40
1:AD:298:TRP:NE1	1:AD:312:VAL:HG12	1.23	1.40
1:AQ:298:TRP:CE2	1:AQ:312:VAL:HG12	1.56	1.40
1:AE:298:TRP:CE2	1:AE:312:VAL:HG12	1.56	1.39
1:AT:298:TRP:NE1	1:AT:312:VAL:HG12	1.23	1.39
1:AV:298:TRP:CE2	1:AV:312:VAL:HG12	1.54	1.39
1:AW:298:TRP:CE2	1:AW:312:VAL:HG12	1.54	1.39
1:AA:298:TRP:CE2	1:AA:312:VAL:HG12	1.55	1.39
1:AO:298:TRP:CE2	1:AO:312:VAL:HG12	1.56	1.39
1:AR:298:TRP:CE2	1:AR:312:VAL:HG12	1.56	1.39
1:AJ:298:TRP:CE2	1:AJ:312:VAL:HG12	1.56	1.39
1:AK:298:TRP:CE2	1:AK:312:VAL:HG12	1.54	1.39
1:AM:298:TRP:CE2	1:AM:312:VAL:HG12	1.57	1.39
1:AX:298:TRP:CE2	1:AX:312:VAL:HG12	1.56	1.39
1:AY:298:TRP:CE2	1:AY:312:VAL:HG12	1.55	1.38
1:AF:298:TRP:CE2	1:AF:312:VAL:HG12	1.56	1.38
1:AH:298:TRP:CE2	1:AH:312:VAL:HG12	1.56	1.38
1:Ab:298:TRP:CE2	1:Ab:312:VAL:HG12	1.57	1.38
1:AU:298:TRP:CE2	1:AU:312:VAL:HG12	1.56	1.38
1:Ac:298:TRP:CE2	1:Ac:312:VAL:HG12	1.57	1.38
1:AG:298:TRP:CE2	1:AG:312:VAL:HG12	1.56	1.37
1:AB:298:TRP:CE2	1:AB:312:VAL:HG12	1.57	1.37
1:Ad:298:TRP:CD1	1:Ad:312:VAL:HG12	1.60	1.37
1:AR:298:TRP:CD1	1:AR:312:VAL:HG12	1.60	1.36
1:AS:298:TRP:CE2	1:AS:312:VAL:HG12	1.57	1.36
1:AB:298:TRP:CD1	1:AB:312:VAL:HG12	1.62	1.35
1:AK:298:TRP:CD1	1:AK:312:VAL:HG12	1.61	1.35
1:AL:298:TRP:CD1	1:AL:312:VAL:HG12	1.60	1.35
1:Aa:298:TRP:CD1	1:Aa:312:VAL:HG12	1.60	1.35
1:AG:298:TRP:CD1	1:AG:312:VAL:HG12	1.62	1.35
1:AW:298:TRP:CD1	1:AW:312:VAL:HG12	1.60	1.34
1:AT:298:TRP:CD1	1:AT:312:VAL:HG12	1.61	1.34
1:AD:298:TRP:CD1	1:AD:312:VAL:HG12	1.62	1.34
1:AJ:298:TRP:CD1	1:AJ:312:VAL:HG12	1.62	1.34
1:AC:298:TRP:CD1	1:AC:312:VAL:HG12	1.61	1.33
1:AO:298:TRP:CD1	1:AO:312:VAL:HG12	1.62	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:298:TRP:CD1	1:AH:312:VAL:HG12	1.62	1.33
1:AP:298:TRP:CD1	1:AP:312:VAL:HG12	1.61	1.33
1:AV:298:TRP:CD1	1:AV:312:VAL:HG12	1.62	1.33
1:AX:298:TRP:CD1	1:AX:312:VAL:HG12	1.62	1.33
1:AZ:298:TRP:CD1	1:AZ:312:VAL:HG12	1.62	1.33
1:Ac:298:TRP:CD1	1:Ac:312:VAL:HG12	1.62	1.33
1:AA:298:TRP:CD1	1:AA:312:VAL:HG12	1.63	1.33
1:AE:298:TRP:CD1	1:AE:312:VAL:HG12	1.63	1.32
1:AN:298:TRP:CD1	1:AN:312:VAL:HG12	1.62	1.32
1:AQ:298:TRP:CD1	1:AQ:312:VAL:HG12	1.62	1.32
1:AM:298:TRP:CD1	1:AM:312:VAL:HG12	1.62	1.31
1:AU:298:TRP:CD1	1:AU:312:VAL:HG12	1.64	1.31
1:AF:298:TRP:CD1	1:AF:312:VAL:HG12	1.62	1.31
1:AI:298:TRP:CD1	1:AI:312:VAL:HG12	1.63	1.31
1:Ab:298:TRP:CD1	1:Ab:312:VAL:HG12	1.64	1.30
1:AY:298:TRP:CD1	1:AY:312:VAL:HG12	1.63	1.30
1:AS:298:TRP:CD1	1:AS:312:VAL:HG12	1.64	1.29
1:AH:253:ASP:OD1	1:AH:284:LYS:O	1.52	1.27
1:AM:253:ASP:OD1	1:AM:284:LYS:O	1.53	1.27
1:AN:253:ASP:OD1	1:AN:284:LYS:O	1.53	1.27
1:AT:253:ASP:OD1	1:AT:284:LYS:O	1.53	1.27
1:AO:253:ASP:OD1	1:AO:284:LYS:O	1.53	1.26
1:Ab:253:ASP:OD1	1:Ab:284:LYS:O	1.52	1.26
1:AP:253:ASP:OD1	1:AP:284:LYS:O	1.53	1.26
1:AI:253:ASP:OD1	1:AI:284:LYS:O	1.53	1.25
1:AU:253:ASP:OD1	1:AU:284:LYS:O	1.52	1.25
1:AV:253:ASP:OD1	1:AV:284:LYS:O	1.53	1.25
1:AW:253:ASP:OD1	1:AW:284:LYS:O	1.54	1.25
1:AJ:253:ASP:OD1	1:AJ:284:LYS:O	1.54	1.24
1:AZ:253:ASP:OD1	1:AZ:284:LYS:O	1.54	1.24
1:Aa:253:ASP:OD1	1:Aa:284:LYS:O	1.53	1.24
1:Ad:253:ASP:OD1	1:Ad:284:LYS:O	1.53	1.24
1:Ac:253:ASP:OD1	1:Ac:284:LYS:O	1.53	1.24
1:AD:253:ASP:OD1	1:AD:284:LYS:O	1.54	1.24
1:AQ:253:ASP:OD1	1:AQ:284:LYS:O	1.52	1.23
1:AC:253:ASP:OD1	1:AC:284:LYS:O	1.53	1.23
1:AG:253:ASP:OD1	1:AG:284:LYS:O	1.53	1.23
1:AS:253:ASP:OD1	1:AS:284:LYS:O	1.53	1.23
1:AA:253:ASP:OD1	1:AA:284:LYS:O	1.53	1.23
1:AR:253:ASP:OD1	1:AR:284:LYS:O	1.54	1.22
1:AL:253:ASP:OD1	1:AL:284:LYS:O	1.53	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:253:ASP:OD1	1:AF:284:LYS:O	1.53	1.22
1:AK:253:ASP:OD1	1:AK:284:LYS:O	1.54	1.22
1:Ad:302:ASP:C	1:Ad:305:ASN:OD1	1.83	1.22
1:AB:253:ASP:OD1	1:AB:284:LYS:O	1.52	1.21
1:AC:302:ASP:C	1:AC:305:ASN:OD1	1.84	1.21
1:AK:302:ASP:C	1:AK:305:ASN:OD1	1.83	1.21
1:AX:253:ASP:OD1	1:AX:284:LYS:O	1.53	1.21
1:AP:302:ASP:C	1:AP:305:ASN:OD1	1.84	1.21
1:AT:302:ASP:C	1:AT:305:ASN:OD1	1.84	1.21
1:AJ:302:ASP:C	1:AJ:305:ASN:OD1	1.84	1.21
1:AX:302:ASP:C	1:AX:305:ASN:OD1	1.84	1.21
1:Aa:302:ASP:C	1:Aa:305:ASN:OD1	1.84	1.21
1:Ab:302:ASP:C	1:Ab:305:ASN:OD1	1.84	1.21
1:AG:302:ASP:C	1:AG:305:ASN:OD1	1.84	1.21
1:AU:302:ASP:C	1:AU:305:ASN:OD1	1.84	1.21
1:AY:253:ASP:OD1	1:AY:284:LYS:O	1.53	1.21
1:AA:302:ASP:C	1:AA:305:ASN:OD1	1.83	1.20
1:AM:302:ASP:C	1:AM:305:ASN:OD1	1.84	1.20
1:AL:302:ASP:C	1:AL:305:ASN:OD1	1.84	1.20
1:AD:302:ASP:C	1:AD:305:ASN:OD1	1.84	1.20
1:AF:302:ASP:C	1:AF:305:ASN:OD1	1.84	1.20
1:AQ:302:ASP:C	1:AQ:305:ASN:OD1	1.84	1.20
1:AE:302:ASP:C	1:AE:305:ASN:OD1	1.84	1.20
1:AI:302:ASP:C	1:AI:305:ASN:OD1	1.84	1.20
1:AO:302:ASP:C	1:AO:305:ASN:OD1	1.85	1.20
1:AH:302:ASP:C	1:AH:305:ASN:OD1	1.84	1.20
1:AZ:302:ASP:C	1:AZ:305:ASN:OD1	1.84	1.19
1:AR:302:ASP:C	1:AR:305:ASN:OD1	1.83	1.19
1:AB:302:ASP:C	1:AB:305:ASN:OD1	1.84	1.19
1:AS:302:ASP:C	1:AS:305:ASN:OD1	1.84	1.19
1:AV:302:ASP:C	1:AV:305:ASN:OD1	1.84	1.19
1:AY:302:ASP:C	1:AY:305:ASN:OD1	1.84	1.19
1:AM:298:TRP:CD1	1:AM:312:VAL:CG1	2.26	1.19
1:AN:302:ASP:C	1:AN:305:ASN:OD1	1.84	1.19
1:AT:298:TRP:CD1	1:AT:312:VAL:CG1	2.26	1.19
1:Ac:302:ASP:C	1:Ac:305:ASN:OD1	1.84	1.19
1:AW:302:ASP:C	1:AW:305:ASN:OD1	1.85	1.18
1:AC:298:TRP:CD1	1:AC:312:VAL:CG1	2.27	1.18
1:AN:298:TRP:CD1	1:AN:312:VAL:CG1	2.27	1.18
1:AP:298:TRP:CD1	1:AP:312:VAL:CG1	2.26	1.18
1:AL:298:TRP:CD1	1:AL:312:VAL:CG1	2.26	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:298:TRP:CD1	1:AW:312:VAL:CG1	2.26	1.18
1:AH:298:TRP:CD1	1:AH:312:VAL:CG1	2.27	1.17
1:AQ:298:TRP:CD1	1:AQ:312:VAL:CG1	2.28	1.17
1:AI:298:TRP:CD1	1:AI:312:VAL:CG1	2.28	1.17
1:AR:298:TRP:CD1	1:AR:312:VAL:CG1	2.26	1.17
1:Aa:298:TRP:CD1	1:Aa:312:VAL:CG1	2.25	1.17
1:Ad:298:TRP:CD1	1:Ad:312:VAL:CG1	2.27	1.17
1:AA:298:TRP:CD1	1:AA:312:VAL:CG1	2.28	1.17
1:AF:298:TRP:CD1	1:AF:312:VAL:CG1	2.28	1.17
1:Ab:298:TRP:CD1	1:Ab:312:VAL:CG1	2.28	1.17
1:Cd:141:LEU:HD21	1:Cd:184:ILE:HD11	1.24	1.17
1:AO:298:TRP:CD1	1:AO:312:VAL:CG1	2.27	1.16
1:AE:298:TRP:CD1	1:AE:312:VAL:CG1	2.29	1.16
1:Ac:298:TRP:CD1	1:Ac:312:VAL:CG1	2.27	1.16
1:AB:298:TRP:CD1	1:AB:312:VAL:CG1	2.26	1.16
1:AG:298:TRP:CD1	1:AG:312:VAL:CG1	2.27	1.16
1:AK:298:TRP:CD1	1:AK:312:VAL:CG1	2.28	1.16
1:AU:298:TRP:CD1	1:AU:312:VAL:CG1	2.29	1.16
1:AV:298:TRP:CD1	1:AV:312:VAL:CG1	2.28	1.16
1:AX:298:TRP:CD1	1:AX:312:VAL:CG1	2.28	1.16
1:AZ:298:TRP:CD1	1:AZ:312:VAL:CG1	2.28	1.16
1:AD:298:TRP:CD1	1:AD:312:VAL:CG1	2.27	1.15
1:AJ:298:TRP:CD1	1:AJ:312:VAL:CG1	2.28	1.15
1:AS:298:TRP:CD1	1:AS:312:VAL:CG1	2.29	1.15
1:CR:141:LEU:HD21	1:CR:184:ILE:HD11	1.30	1.14
1:CX:141:LEU:HD21	1:CX:184:ILE:HD11	1.27	1.14
1:AY:298:TRP:CD1	1:AY:312:VAL:CG1	2.30	1.14
1:AP:298:TRP:NE1	1:AP:312:VAL:CG1	2.12	1.13
1:CT:141:LEU:HD21	1:CT:184:ILE:HD11	1.29	1.13
1:CI:141:LEU:HD21	1:CI:184:ILE:HD11	1.30	1.13
1:CW:141:LEU:HD21	1:CW:184:ILE:HD11	1.31	1.13
1:AG:298:TRP:NE1	1:AG:312:VAL:CG1	2.12	1.12
1:CM:141:LEU:HD21	1:CM:184:ILE:HD11	1.30	1.12
1:AF:298:TRP:NE1	1:AF:312:VAL:CG1	2.13	1.12
1:CZ:141:LEU:HD21	1:CZ:184:ILE:HD11	1.26	1.12
1:AM:298:TRP:NE1	1:AM:312:VAL:CG1	2.13	1.12
1:AW:298:TRP:NE1	1:AW:312:VAL:CG1	2.12	1.12
1:AU:298:TRP:NE1	1:AU:312:VAL:CG1	2.13	1.11
1:CP:141:LEU:HD21	1:CP:184:ILE:HD11	1.31	1.11
1:AY:298:TRP:NE1	1:AY:312:VAL:CG1	2.13	1.11
1:CB:141:LEU:HD21	1:CB:184:ILE:HD11	1.29	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:298:TRP:NE1	1:AK:312:VAL:CG1	2.13	1.11
1:AC:298:TRP:NE1	1:AC:312:VAL:CG1	2.13	1.11
1:AH:298:TRP:NE1	1:AH:312:VAL:CG1	2.13	1.11
1:AE:298:TRP:NE1	1:AE:312:VAL:CG1	2.14	1.11
1:AS:298:TRP:NE1	1:AS:312:VAL:CG1	2.13	1.11
1:AB:298:TRP:NE1	1:AB:312:VAL:CG1	2.13	1.10
1:AO:298:TRP:NE1	1:AO:312:VAL:CG1	2.13	1.10
1:CO:141:LEU:HD21	1:CO:184:ILE:HD11	1.31	1.10
1:AI:141:LEU:O	1:AI:144:THR:HG22	1.50	1.10
1:AJ:298:TRP:NE1	1:AJ:312:VAL:CG1	2.13	1.10
1:CN:141:LEU:HD21	1:CN:184:ILE:HD11	1.32	1.10
1:AX:298:TRP:NE1	1:AX:312:VAL:CG1	2.14	1.10
1:Ab:298:TRP:NE1	1:Ab:312:VAL:CG1	2.14	1.10
1:AQ:298:TRP:NE1	1:AQ:312:VAL:CG1	2.13	1.10
1:Ad:141:LEU:O	1:Ad:144:THR:HG22	1.51	1.10
1:AA:298:TRP:NE1	1:AA:312:VAL:CG1	2.14	1.10
1:CD:141:LEU:HD21	1:CD:184:ILE:HD11	1.31	1.10
1:AL:298:TRP:NE1	1:AL:312:VAL:CG1	2.12	1.10
1:AN:298:TRP:NE1	1:AN:312:VAL:CG1	2.13	1.10
1:AD:298:TRP:NE1	1:AD:312:VAL:CG1	2.13	1.10
1:CL:141:LEU:HD21	1:CL:184:ILE:HD11	1.31	1.09
1:AV:298:TRP:NE1	1:AV:312:VAL:CG1	2.14	1.09
1:AA:141:LEU:O	1:AA:144:THR:HG22	1.52	1.09
1:AI:298:TRP:NE1	1:AI:312:VAL:CG1	2.14	1.09
1:Ac:298:TRP:NE1	1:Ac:312:VAL:CG1	2.14	1.09
1:AT:298:TRP:NE1	1:AT:312:VAL:CG1	2.13	1.09
1:CH:141:LEU:HD21	1:CH:184:ILE:HD11	1.31	1.09
1:CK:141:LEU:HD21	1:CK:184:ILE:HD11	1.31	1.09
1:Ad:298:TRP:NE1	1:Ad:312:VAL:CG1	2.13	1.09
1:CA:141:LEU:HD21	1:CA:184:ILE:HD11	1.35	1.09
1:Aa:298:TRP:NE1	1:Aa:312:VAL:CG1	2.13	1.09
1:BH:114:MET:SD	1:Cd:122:GLY:HA3	1.93	1.08
1:Ca:141:LEU:HD21	1:Ca:184:ILE:HD11	1.34	1.08
1:CY:141:LEU:HD21	1:CY:184:ILE:HD11	1.36	1.08
1:AZ:298:TRP:NE1	1:AZ:312:VAL:CG1	2.13	1.08
1:CS:141:LEU:HD21	1:CS:184:ILE:HD11	1.34	1.08
1:AR:298:TRP:NE1	1:AR:312:VAL:CG1	2.14	1.07
1:CC:141:LEU:HD21	1:CC:184:ILE:HD11	1.33	1.07
1:CV:141:LEU:HD21	1:CV:184:ILE:HD11	1.34	1.07
1:AX:141:LEU:O	1:AX:144:THR:HG22	1.53	1.07
1:CJ:141:LEU:HD21	1:CJ:184:ILE:HD11	1.37	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:141:LEU:HD21	1:CG:184:ILE:HD11	1.32	1.06
1:BN:61:SER:HB3	1:BN:90:PRO:HD2	1.37	1.06
1:AC:141:LEU:O	1:AC:144:THR:HG22	1.55	1.06
1:AL:298:TRP:CE2	1:AL:312:VAL:CG1	2.39	1.06
1:CE:141:LEU:HD21	1:CE:184:ILE:HD11	1.36	1.06
1:BO:61:SER:HB3	1:BO:90:PRO:HD2	1.36	1.06
1:Bc:61:SER:HB3	1:Bc:90:PRO:HD2	1.38	1.06
1:CQ:141:LEU:HD21	1:CQ:184:ILE:HD11	1.30	1.06
1:AQ:141:LEU:O	1:AQ:144:THR:HG22	1.55	1.05
1:AN:141:LEU:O	1:AN:144:THR:HG22	1.56	1.05
1:AT:141:LEU:O	1:AT:144:THR:HG22	1.55	1.05
1:AU:141:LEU:O	1:AU:144:THR:HG22	1.55	1.05
1:AK:141:LEU:O	1:AK:144:THR:HG22	1.57	1.05
1:AK:298:TRP:CE2	1:AK:312:VAL:CG1	2.39	1.05
1:BG:61:SER:HB3	1:BG:90:PRO:HD2	1.39	1.05
1:Ad:298:TRP:CE2	1:Ad:312:VAL:CG1	2.39	1.05
1:BE:61:SER:HB3	1:BE:90:PRO:HD2	1.38	1.04
1:CF:141:LEU:HD21	1:CF:184:ILE:HD11	1.35	1.04
1:AT:298:TRP:CE2	1:AT:312:VAL:CG1	2.40	1.04
1:AV:298:TRP:CE2	1:AV:312:VAL:CG1	2.40	1.04
1:Ac:141:LEU:O	1:Ac:144:THR:HG22	1.57	1.04
1:BI:61:SER:HB3	1:BI:90:PRO:HD2	1.37	1.04
1:BA:61:SER:HB3	1:BA:90:PRO:HD2	1.40	1.04
1:AM:141:LEU:O	1:AM:144:THR:HG22	1.55	1.04
1:BY:254:GLY:HA2	1:BY:283:LYS:HE3	1.39	1.04
1:AD:298:TRP:CE2	1:AD:312:VAL:CG1	2.41	1.04
1:BH:61:SER:HB3	1:BH:90:PRO:HD2	1.39	1.04
1:AH:141:LEU:O	1:AH:144:THR:HG22	1.58	1.04
1:BV:61:SER:HB3	1:BV:90:PRO:HD2	1.38	1.04
1:AV:141:LEU:O	1:AV:144:THR:HG22	1.56	1.04
1:AY:141:LEU:O	1:AY:144:THR:HG22	1.56	1.04
1:AY:298:TRP:CE2	1:AY:312:VAL:CG1	2.41	1.04
1:AZ:298:TRP:CE2	1:AZ:312:VAL:CG1	2.40	1.04
1:BD:254:GLY:HA2	1:BD:283:LYS:HE3	1.39	1.04
1:AO:141:LEU:O	1:AO:144:THR:HG22	1.58	1.04
1:BI:254:GLY:HA2	1:BI:283:LYS:HE3	1.37	1.03
1:BS:61:SER:HB3	1:BS:90:PRO:HD2	1.36	1.03
1:AW:141:LEU:O	1:AW:144:THR:HG22	1.58	1.03
1:Cc:141:LEU:HD21	1:Cc:184:ILE:HD11	1.37	1.03
1:BA:254:GLY:HA2	1:BA:283:LYS:HE3	1.38	1.03
1:AC:298:TRP:CE2	1:AC:312:VAL:CG1	2.41	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:141:LEU:O	1:AE:144:THR:HG22	1.56	1.03
1:BG:254:GLY:HA2	1:BG:283:LYS:HE3	1.40	1.03
1:AW:298:TRP:CE2	1:AW:312:VAL:CG1	2.40	1.03
1:BZ:61:SER:HB3	1:BZ:90:PRO:HD2	1.39	1.03
1:Ab:141:LEU:O	1:Ab:144:THR:HG22	1.58	1.03
1:AD:141:LEU:O	1:AD:144:THR:HG22	1.58	1.03
1:BE:254:GLY:HA2	1:BE:283:LYS:HE3	1.41	1.03
1:AJ:141:LEU:O	1:AJ:144:THR:HG22	1.58	1.03
1:AN:298:TRP:CE2	1:AN:312:VAL:CG1	2.42	1.03
1:AP:298:TRP:CE2	1:AP:312:VAL:CG1	2.40	1.03
1:Bd:254:GLY:HA2	1:Bd:283:LYS:HE3	1.39	1.03
1:AF:141:LEU:O	1:AF:144:THR:HG22	1.59	1.03
1:Aa:298:TRP:CE2	1:Aa:312:VAL:CG1	2.42	1.03
1:Bb:61:SER:HB3	1:Bb:90:PRO:HD2	1.40	1.03
1:AR:298:TRP:CE2	1:AR:312:VAL:CG1	2.42	1.02
1:Bb:254:GLY:HA2	1:Bb:283:LYS:HE3	1.41	1.02
1:AA:298:TRP:CE2	1:AA:312:VAL:CG1	2.42	1.02
1:AG:141:LEU:O	1:AG:144:THR:HG22	1.57	1.02
1:BK:254:GLY:HA2	1:BK:283:LYS:HE3	1.41	1.02
1:BX:61:SER:HB3	1:BX:90:PRO:HD2	1.40	1.02
1:BC:254:GLY:HA2	1:BC:283:LYS:HE3	1.42	1.02
1:AI:298:TRP:CE2	1:AI:312:VAL:CG1	2.43	1.02
1:BL:254:GLY:HA2	1:BL:283:LYS:HE3	1.39	1.02
1:BM:61:SER:HB3	1:BM:90:PRO:HD2	1.41	1.02
1:AU:298:TRP:CE2	1:AU:312:VAL:CG1	2.43	1.02
1:Ba:254:GLY:HA2	1:Ba:283:LYS:HE3	1.40	1.02
1:BC:61:SER:HB3	1:BC:90:PRO:HD2	1.42	1.02
1:CC:101:ARG:HB2	1:CC:208:SER:OG	1.59	1.02
1:AH:298:TRP:CE2	1:AH:312:VAL:CG1	2.43	1.02
1:BL:61:SER:HB3	1:BL:90:PRO:HD2	1.40	1.02
1:AL:279:TYR:CZ	1:AL:311:GLY:O	2.13	1.02
1:AM:253:ASP:OD1	1:AM:284:LYS:C	2.03	1.02
1:AO:298:TRP:CE2	1:AO:312:VAL:CG1	2.42	1.02
1:AE:298:TRP:CE2	1:AE:312:VAL:CG1	2.42	1.01
1:AJ:298:TRP:CE2	1:AJ:312:VAL:CG1	2.43	1.01
1:AQ:298:TRP:CE2	1:AQ:312:VAL:CG1	2.42	1.01
1:BT:254:GLY:HA2	1:BT:283:LYS:HE3	1.41	1.01
1:CU:141:LEU:HD21	1:CU:184:ILE:HD11	1.35	1.01
1:AC:253:ASP:OD1	1:AC:284:LYS:C	2.04	1.01
1:AF:279:TYR:CZ	1:AF:311:GLY:O	2.14	1.01
1:BJ:61:SER:HB3	1:BJ:90:PRO:HD2	1.40	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:253:ASP:OD1	1:AN:284:LYS:C	2.03	1.01
1:AX:298:TRP:CE2	1:AX:312:VAL:CG1	2.42	1.01
1:AF:298:TRP:CE2	1:AF:312:VAL:CG1	2.42	1.01
1:AG:298:TRP:CE2	1:AG:312:VAL:CG1	2.42	1.01
1:BM:254:GLY:HA2	1:BM:283:LYS:HE3	1.41	1.01
1:CM:75:ASP:OD1	1:CM:188:VAL:O	1.79	1.01
1:BN:254:GLY:HA2	1:BN:283:LYS:HE3	1.42	1.01
1:BU:61:SER:HB3	1:BU:90:PRO:HD2	1.39	1.01
1:Aa:141:LEU:O	1:Aa:144:THR:HG22	1.58	1.01
1:Ac:298:TRP:CE2	1:Ac:312:VAL:CG1	2.44	1.01
1:AC:279:TYR:CZ	1:AC:311:GLY:O	2.14	1.01
1:AH:279:TYR:CZ	1:AH:311:GLY:O	2.14	1.01
1:BK:98:ILE:O	1:BK:211:SER:O	1.79	1.01
1:AR:253:ASP:OD1	1:AR:284:LYS:C	2.04	1.01
1:AV:253:ASP:OD1	1:AV:284:LYS:C	2.04	1.01
1:BB:61:SER:HB3	1:BB:90:PRO:HD2	1.41	1.01
1:AH:253:ASP:OD1	1:AH:284:LYS:C	2.03	1.01
1:AK:253:ASP:OD1	1:AK:284:LYS:C	2.04	1.01
1:AM:279:TYR:CZ	1:AM:311:GLY:O	2.14	1.01
1:AR:141:LEU:O	1:AR:144:THR:HG22	1.60	1.01
1:BS:254:GLY:HA2	1:BS:283:LYS:HE3	1.39	1.01
1:BX:254:GLY:HA2	1:BX:283:LYS:HE3	1.41	1.01
1:Aa:253:ASP:OD1	1:Aa:284:LYS:C	2.03	1.01
1:Ab:253:ASP:OD1	1:Ab:284:LYS:C	2.04	1.01
1:Cb:141:LEU:HD21	1:Cb:184:ILE:HD11	1.42	1.01
1:Ad:253:ASP:OD1	1:Ad:284:LYS:C	2.02	1.01
1:AB:253:ASP:OD1	1:AB:284:LYS:C	2.03	1.00
1:AE:279:TYR:CZ	1:AE:311:GLY:O	2.14	1.00
1:AF:253:ASP:OD1	1:AF:284:LYS:C	2.04	1.00
1:AI:253:ASP:OD1	1:AI:284:LYS:C	2.03	1.00
1:AM:298:TRP:CE2	1:AM:312:VAL:CG1	2.43	1.00
1:AM:314:TYR:CE1	1:AM:315:TYR:C	2.40	1.00
1:AO:314:TYR:CE1	1:AO:315:TYR:C	2.39	1.00
1:BR:254:GLY:HA2	1:BR:283:LYS:HE3	1.41	1.00
1:Ab:298:TRP:CE2	1:Ab:312:VAL:CG1	2.43	1.00
1:AB:141:LEU:O	1:AB:144:THR:HG22	1.59	1.00
1:AB:298:TRP:CE2	1:AB:312:VAL:CG1	2.44	1.00
1:AP:279:TYR:CZ	1:AP:311:GLY:O	2.15	1.00
1:AX:253:ASP:OD1	1:AX:284:LYS:C	2.04	1.00
1:AX:314:TYR:CE1	1:AX:315:TYR:C	2.39	1.00
1:AZ:253:ASP:OD1	1:AZ:284:LYS:C	2.04	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:253:ASP:OD1	1:AA:284:LYS:C	2.04	1.00
1:AA:279:TYR:CZ	1:AA:311:GLY:O	2.14	1.00
1:AJ:279:TYR:CZ	1:AJ:311:GLY:O	2.14	1.00
1:BK:61:SER:HB3	1:BK:90:PRO:HD2	1.42	1.00
1:AS:141:LEU:O	1:AS:144:THR:HG22	1.60	1.00
1:AU:253:ASP:OD1	1:AU:284:LYS:C	2.04	1.00
1:BY:61:SER:HB3	1:BY:90:PRO:HD2	1.41	1.00
1:Ba:61:SER:HB3	1:Ba:90:PRO:HD2	1.40	1.00
1:Aa:279:TYR:CZ	1:Aa:311:GLY:O	2.15	1.00
1:Ac:279:TYR:CZ	1:Ac:311:GLY:O	2.15	1.00
1:AL:253:ASP:OD1	1:AL:284:LYS:C	2.04	1.00
1:AP:141:LEU:O	1:AP:144:THR:HG22	1.62	1.00
1:AD:253:ASP:OD1	1:AD:284:LYS:C	2.04	1.00
1:BH:254:GLY:HA2	1:BH:283:LYS:HE3	1.40	1.00
1:AI:279:TYR:CZ	1:AI:311:GLY:O	2.14	1.00
1:BP:61:SER:HB3	1:BP:90:PRO:HD2	1.40	1.00
1:AT:253:ASP:OD1	1:AT:284:LYS:C	2.04	1.00
1:Ad:279:TYR:CZ	1:Ad:311:GLY:O	2.14	1.00
1:AB:279:TYR:CZ	1:AB:311:GLY:O	2.15	1.00
1:AD:279:TYR:CZ	1:AD:311:GLY:O	2.14	1.00
1:BO:254:GLY:HA2	1:BO:283:LYS:HE3	1.40	1.00
1:AU:314:TYR:CE1	1:AU:315:TYR:C	2.40	1.00
1:AG:253:ASP:OD1	1:AG:284:LYS:C	2.04	0.99
1:BQ:61:SER:HB3	1:BQ:90:PRO:HD2	1.40	0.99
1:Aa:299:GLY:HA3	1:Aa:310:ASP:O	1.62	0.99
1:Bd:98:ILE:O	1:Bd:211:SER:O	1.80	0.99
1:BP:254:GLY:HA2	1:BP:283:LYS:HE3	1.41	0.99
1:AP:253:ASP:OD1	1:AP:284:LYS:C	2.04	0.99
1:AR:279:TYR:CZ	1:AR:311:GLY:O	2.15	0.99
1:BV:254:GLY:HA2	1:BV:283:LYS:HE3	1.41	0.99
1:BZ:254:GLY:HA2	1:BZ:283:LYS:HE3	1.41	0.99
1:CZ:101:ARG:HB2	1:CZ:208:SER:OG	1.63	0.99
1:Ab:279:TYR:CZ	1:Ab:311:GLY:O	2.15	0.99
1:AK:279:TYR:CZ	1:AK:311:GLY:O	2.16	0.99
1:AO:253:ASP:OD1	1:AO:284:LYS:C	2.04	0.99
1:AQ:279:TYR:CZ	1:AQ:311:GLY:O	2.15	0.99
1:AQ:314:TYR:CE1	1:AQ:315:TYR:C	2.41	0.99
1:AT:279:TYR:CZ	1:AT:311:GLY:O	2.14	0.99
1:Ab:299:GLY:HA3	1:Ab:310:ASP:O	1.63	0.99
1:BM:98:ILE:O	1:BM:211:SER:O	1.80	0.99
1:AZ:141:LEU:O	1:AZ:144:THR:HG22	1.60	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:314:TYR:CE1	1:AA:315:TYR:C	2.40	0.99
1:BF:61:SER:HB3	1:BF:90:PRO:HD2	1.44	0.99
1:CI:75:ASP:OD1	1:CI:188:VAL:O	1.81	0.99
1:AN:279:TYR:CZ	1:AN:311:GLY:O	2.15	0.99
1:BP:98:ILE:O	1:BP:211:SER:O	1.81	0.99
1:AS:298:TRP:CE2	1:AS:312:VAL:CG1	2.43	0.99
1:AW:253:ASP:OD1	1:AW:284:LYS:C	2.04	0.99
1:AZ:299:GLY:HA3	1:AZ:310:ASP:O	1.62	0.99
1:AL:298:TRP:CD2	1:AL:312:VAL:HG12	1.98	0.99
1:CL:75:ASP:OD1	1:CL:188:VAL:O	1.79	0.99
1:BQ:254:GLY:HA2	1:BQ:283:LYS:HE3	1.41	0.99
1:BT:61:SER:HB3	1:BT:90:PRO:HD2	1.41	0.99
1:BD:61:SER:HB3	1:BD:90:PRO:HD2	1.41	0.99
1:BV:98:ILE:O	1:BV:211:SER:O	1.81	0.99
1:BW:254:GLY:HA2	1:BW:283:LYS:HE3	1.43	0.99
1:AW:279:TYR:CZ	1:AW:311:GLY:O	2.14	0.99
1:AW:298:TRP:CD2	1:AW:312:VAL:HG12	1.98	0.99
1:AZ:279:TYR:CZ	1:AZ:311:GLY:O	2.16	0.99
1:AJ:253:ASP:OD1	1:AJ:284:LYS:C	2.05	0.99
1:AB:314:TYR:CE1	1:AB:315:TYR:C	2.40	0.99
1:AG:314:TYR:CE1	1:AG:315:TYR:C	2.41	0.99
1:AN:314:TYR:CE1	1:AN:315:TYR:C	2.41	0.99
1:AO:279:TYR:CZ	1:AO:311:GLY:O	2.15	0.99
1:BU:254:GLY:HA2	1:BU:283:LYS:HE3	1.41	0.99
1:AV:279:TYR:CZ	1:AV:311:GLY:O	2.16	0.99
1:BF:98:ILE:O	1:BF:211:SER:O	1.81	0.98
1:AG:279:TYR:CZ	1:AG:311:GLY:O	2.15	0.98
1:AQ:253:ASP:OD1	1:AQ:284:LYS:C	2.04	0.98
1:AS:279:TYR:CZ	1:AS:311:GLY:O	2.16	0.98
1:BW:61:SER:HB3	1:BW:90:PRO:HD2	1.41	0.98
1:Ab:314:TYR:CE1	1:Ab:315:TYR:C	2.41	0.98
1:AH:314:TYR:CE1	1:AH:315:TYR:C	2.41	0.98
1:BI:98:ILE:O	1:BI:211:SER:O	1.81	0.98
1:AV:314:TYR:CE1	1:AV:315:TYR:C	2.41	0.98
1:AF:314:TYR:CE1	1:AF:315:TYR:C	2.41	0.98
1:AL:141:LEU:O	1:AL:144:THR:HG22	1.61	0.98
1:AN:299:GLY:HA3	1:AN:310:ASP:O	1.63	0.98
1:AG:299:GLY:HA3	1:AG:310:ASP:O	1.63	0.98
1:AU:299:GLY:HA3	1:AU:310:ASP:O	1.63	0.98
1:Bc:254:GLY:HA2	1:Bc:283:LYS:HE3	1.42	0.98
1:Bd:61:SER:HB3	1:Bd:90:PRO:HD2	1.41	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:299:GLY:HA3	1:AC:310:ASP:O	1.63	0.98
1:AK:298:TRP:CD2	1:AK:312:VAL:HG12	1.99	0.98
1:AM:299:GLY:HA3	1:AM:310:ASP:O	1.62	0.98
1:BP:98:ILE:O	1:BP:211:SER:N	1.95	0.98
1:AS:253:ASP:OD1	1:AS:284:LYS:C	2.04	0.98
1:AV:299:GLY:HA3	1:AV:310:ASP:O	1.63	0.98
1:CW:75:ASP:OD1	1:CW:188:VAL:O	1.81	0.98
1:AY:253:ASP:OD1	1:AY:284:LYS:C	2.06	0.98
1:AB:299:GLY:HA3	1:AB:310:ASP:O	1.63	0.98
1:AS:314:TYR:CE1	1:AS:315:TYR:C	2.41	0.98
1:AU:279:TYR:CZ	1:AU:311:GLY:O	2.15	0.98
1:BB:98:ILE:O	1:BB:211:SER:O	1.81	0.98
1:AI:314:TYR:CE1	1:AI:315:TYR:C	2.41	0.98
1:CL:101:ARG:HB2	1:CL:208:SER:OG	1.64	0.98
1:BR:61:SER:HB3	1:BR:90:PRO:HD2	1.42	0.98
1:AT:299:GLY:HA3	1:AT:310:ASP:O	1.64	0.98
1:BX:98:ILE:O	1:BX:211:SER:O	1.80	0.98
1:Aa:314:TYR:CE1	1:Aa:315:TYR:C	2.42	0.98
1:AH:299:GLY:HA3	1:AH:310:ASP:O	1.62	0.98
1:CH:101:ARG:HB2	1:CH:208:SER:OG	1.64	0.98
1:AI:299:GLY:HA3	1:AI:310:ASP:O	1.62	0.98
1:Cc:101:ARG:HB2	1:Cc:208:SER:OG	1.63	0.98
1:Ad:298:TRP:CD2	1:Ad:312:VAL:HG12	1.99	0.98
1:AE:299:GLY:HA3	1:AE:310:ASP:O	1.63	0.98
1:AE:314:TYR:CE1	1:AE:315:TYR:C	2.41	0.98
1:BJ:254:GLY:HA2	1:BJ:283:LYS:HE3	1.42	0.98
1:AP:299:GLY:HA3	1:AP:310:ASP:O	1.64	0.98
1:CU:101:ARG:HB2	1:CU:208:SER:OG	1.64	0.98
1:AA:299:GLY:HA3	1:AA:310:ASP:O	1.63	0.98
1:AD:314:TYR:CE1	1:AD:315:TYR:C	2.42	0.98
1:BS:98:ILE:O	1:BS:211:SER:O	1.82	0.98
1:Ac:253:ASP:OD1	1:Ac:284:LYS:C	2.05	0.98
1:AR:298:TRP:CD2	1:AR:312:VAL:HG12	1.98	0.97
1:CR:101:ARG:HB2	1:CR:208:SER:OG	1.64	0.97
1:AX:299:GLY:HA3	1:AX:310:ASP:O	1.64	0.97
1:Bb:98:ILE:O	1:Bb:211:SER:O	1.81	0.97
1:AY:279:TYR:CZ	1:AY:311:GLY:O	2.16	0.97
1:Ac:314:TYR:CE1	1:Ac:315:TYR:C	2.41	0.97
1:CB:101:ARG:HB2	1:CB:208:SER:OG	1.63	0.97
1:AJ:314:TYR:CE1	1:AJ:315:TYR:C	2.42	0.97
1:AL:314:TYR:CE1	1:AL:315:TYR:C	2.42	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:298:TRP:CD2	1:AV:312:VAL:HG12	1.99	0.97
1:BB:254:GLY:HA2	1:BB:283:LYS:HE3	1.41	0.97
1:BC:98:ILE:O	1:BC:211:SER:O	1.82	0.97
1:BL:98:ILE:O	1:BL:211:SER:O	1.82	0.97
1:BO:98:ILE:O	1:BO:211:SER:O	1.82	0.97
1:AX:279:TYR:CZ	1:AX:311:GLY:O	2.17	0.97
1:CX:101:ARG:HB2	1:CX:208:SER:OG	1.65	0.97
1:AZ:314:TYR:CE1	1:AZ:315:TYR:C	2.42	0.97
1:AF:299:GLY:HA3	1:AF:310:ASP:O	1.64	0.97
1:BJ:98:ILE:O	1:BJ:211:SER:O	1.81	0.97
1:CO:75:ASP:OD1	1:CO:188:VAL:O	1.83	0.97
1:Bc:98:ILE:O	1:Bc:211:SER:O	1.80	0.97
1:CA:122:GLY:HA3	1:BV:114:MET:SD	2.04	0.97
1:AT:298:TRP:CD2	1:AT:312:VAL:HG12	2.00	0.97
1:AT:314:TYR:CE1	1:AT:315:TYR:C	2.42	0.97
1:Cb:75:ASP:OD1	1:Cb:188:VAL:O	1.82	0.97
1:CB:75:ASP:OD1	1:CB:188:VAL:O	1.82	0.97
1:AL:299:GLY:HA3	1:AL:310:ASP:O	1.65	0.97
1:BU:98:ILE:O	1:BU:211:SER:O	1.81	0.97
1:AW:314:TYR:CE1	1:AW:315:TYR:C	2.42	0.97
1:AY:314:TYR:CE1	1:AY:315:TYR:C	2.43	0.97
1:CD:101:ARG:HB2	1:CD:208:SER:OG	1.65	0.97
1:CI:101:ARG:HB2	1:CI:208:SER:OG	1.64	0.97
1:AJ:299:GLY:HA3	1:AJ:310:ASP:O	1.65	0.97
1:AC:314:TYR:CE1	1:AC:315:TYR:C	2.42	0.97
1:CC:75:ASP:OD1	1:CC:188:VAL:O	1.82	0.97
1:CY:75:ASP:OD1	1:CY:188:VAL:O	1.83	0.97
1:BD:98:ILE:O	1:BD:211:SER:O	1.81	0.97
1:BN:98:ILE:O	1:BN:211:SER:N	1.98	0.97
1:CQ:75:ASP:OD1	1:CQ:188:VAL:O	1.83	0.97
1:BA:98:ILE:O	1:BA:211:SER:O	1.82	0.96
1:BE:98:ILE:O	1:BE:211:SER:O	1.83	0.96
1:CF:75:ASP:OD1	1:CF:188:VAL:O	1.83	0.96
1:AP:314:TYR:CE1	1:AP:315:TYR:C	2.43	0.96
1:CP:101:ARG:HB2	1:CP:208:SER:OG	1.65	0.96
1:AR:299:GLY:HA3	1:AR:310:ASP:O	1.64	0.96
1:CE:101:ARG:HB2	1:CE:208:SER:OG	1.64	0.96
1:BN:98:ILE:O	1:BN:211:SER:O	1.82	0.96
1:AJ:302:ASP:O	1:AJ:305:ASN:OD1	1.83	0.96
1:AK:314:TYR:CE1	1:AK:315:TYR:C	2.43	0.96
1:AZ:298:TRP:CD2	1:AZ:312:VAL:HG12	1.98	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:298:TRP:CD2	1:AC:312:VAL:HG12	2.00	0.96
1:CI:80:VAL:HG12	1:CI:185:LEU:HB3	1.47	0.96
1:CJ:101:ARG:HB2	1:CJ:208:SER:OG	1.64	0.96
1:AQ:298:TRP:CD2	1:AQ:312:VAL:HG12	2.00	0.96
1:AQ:299:GLY:HA3	1:AQ:310:ASP:O	1.65	0.96
1:AR:314:TYR:CE1	1:AR:315:TYR:C	2.43	0.96
1:Ca:75:ASP:OD1	1:Ca:188:VAL:O	1.82	0.96
1:CW:101:ARG:HB2	1:CW:208:SER:OG	1.66	0.96
1:Ad:314:TYR:CE1	1:Ad:315:TYR:C	2.43	0.96
1:BD:98:ILE:O	1:BD:211:SER:N	1.98	0.96
1:CT:101:ARG:HB2	1:CT:208:SER:OG	1.65	0.96
1:Ba:98:ILE:O	1:Ba:211:SER:N	1.98	0.96
1:Aa:298:TRP:CD2	1:Aa:312:VAL:HG12	2.00	0.96
1:AD:299:GLY:HA3	1:AD:310:ASP:O	1.65	0.96
1:CQ:101:ARG:HB2	1:CQ:208:SER:OG	1.64	0.96
1:BT:98:ILE:O	1:BT:211:SER:O	1.82	0.96
1:AV:302:ASP:O	1:AV:305:ASN:OD1	1.84	0.96
1:CA:75:ASP:OD1	1:CA:188:VAL:O	1.84	0.96
1:BW:98:ILE:O	1:BW:211:SER:O	1.81	0.96
1:BZ:98:ILE:O	1:BZ:211:SER:N	1.98	0.96
1:BF:254:GLY:HA2	1:BF:283:LYS:HE3	1.44	0.96
1:BH:98:ILE:O	1:BH:211:SER:N	1.97	0.96
1:AO:299:GLY:HA3	1:AO:310:ASP:O	1.64	0.96
1:AO:302:ASP:O	1:AO:305:ASN:OD1	1.84	0.96
1:CQ:80:VAL:HG12	1:CQ:185:LEU:HB3	1.47	0.96
1:AA:298:TRP:CD2	1:AA:312:VAL:HG12	2.00	0.96
1:AP:302:ASP:O	1:AP:305:ASN:OD1	1.84	0.96
1:AT:302:ASP:O	1:AT:305:ASN:OD1	1.84	0.96
1:BV:98:ILE:O	1:BV:211:SER:N	1.99	0.96
1:BZ:98:ILE:O	1:BZ:211:SER:O	1.84	0.96
1:CZ:75:ASP:OD1	1:CZ:188:VAL:O	1.83	0.96
1:Ba:98:ILE:O	1:Ba:211:SER:O	1.84	0.96
1:CG:75:ASP:OD1	1:CG:188:VAL:O	1.84	0.95
1:CR:98:ILE:O	1:CR:211:SER:O	1.84	0.95
1:AV:61:SER:HB3	1:AV:90:PRO:HD2	1.48	0.95
1:CV:101:ARG:HB2	1:CV:208:SER:OG	1.64	0.95
1:BR:98:ILE:O	1:BR:211:SER:O	1.84	0.95
1:Ab:302:ASP:O	1:Ab:305:ASN:OD1	1.84	0.95
1:Ac:302:ASP:O	1:Ac:305:ASN:OD1	1.84	0.95
1:Cd:75:ASP:OD1	1:Cd:188:VAL:O	1.84	0.95
1:BE:98:ILE:O	1:BE:211:SER:N	1.98	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:98:ILE:O	1:BH:211:SER:O	1.82	0.95
1:BO:98:ILE:O	1:BO:211:SER:N	1.99	0.95
1:AS:299:GLY:HA3	1:AS:310:ASP:O	1.65	0.95
1:AW:299:GLY:HA3	1:AW:310:ASP:O	1.66	0.95
1:BY:98:ILE:O	1:BY:211:SER:N	1.99	0.95
1:Aa:302:ASP:O	1:Aa:305:ASN:OD1	1.84	0.95
1:Bd:98:ILE:O	1:Bd:211:SER:N	1.97	0.95
1:BA:98:ILE:O	1:BA:211:SER:N	1.99	0.95
1:AX:298:TRP:CD2	1:AX:312:VAL:HG12	2.01	0.95
1:CK:56:HIS:CE1	1:CK:206:ARG:HD2	2.01	0.95
1:CO:101:ARG:HB2	1:CO:208:SER:OG	1.66	0.95
1:BQ:98:ILE:O	1:BQ:211:SER:O	1.83	0.95
1:AX:302:ASP:O	1:AX:305:ASN:OD1	1.83	0.95
1:Cc:98:ILE:O	1:Cc:211:SER:O	1.85	0.95
1:CH:80:VAL:HG12	1:CH:185:LEU:HB3	1.48	0.95
1:Bc:98:ILE:O	1:Bc:211:SER:N	1.99	0.95
1:Cd:101:ARG:HB2	1:Cd:208:SER:OG	1.66	0.95
1:AN:302:ASP:O	1:AN:305:ASN:OD1	1.84	0.95
1:Ad:302:ASP:O	1:Ad:305:ASN:OD1	1.84	0.95
1:AD:302:ASP:O	1:AD:305:ASN:OD1	1.84	0.95
1:AE:302:ASP:O	1:AE:305:ASN:OD1	1.84	0.95
1:AP:298:TRP:CD2	1:AP:312:VAL:HG12	2.01	0.95
1:AF:302:ASP:O	1:AF:305:ASN:OD1	1.84	0.95
1:BI:98:ILE:O	1:BI:211:SER:N	1.98	0.95
1:CI:98:ILE:O	1:CI:211:SER:O	1.85	0.95
1:BK:98:ILE:O	1:BK:211:SER:N	1.99	0.95
1:AL:298:TRP:CG	1:AL:312:VAL:HG12	2.02	0.95
1:CL:56:HIS:CE1	1:CL:206:ARG:HD2	2.01	0.95
1:AY:298:TRP:CD2	1:AY:312:VAL:HG12	2.01	0.95
1:BC:98:ILE:O	1:BC:211:SER:N	1.99	0.94
1:BG:98:ILE:O	1:BG:211:SER:O	1.83	0.94
1:AG:61:SER:HB3	1:AG:90:PRO:HD2	1.47	0.94
1:AH:298:TRP:CD2	1:AH:312:VAL:HG12	2.02	0.94
1:AI:298:TRP:CD2	1:AI:312:VAL:HG12	2.02	0.94
1:AI:302:ASP:O	1:AI:305:ASN:OD1	1.84	0.94
1:Ad:299:GLY:HA3	1:Ad:310:ASP:O	1.67	0.94
1:CD:75:ASP:OD1	1:CD:188:VAL:O	1.85	0.94
1:CD:98:ILE:O	1:CD:211:SER:O	1.85	0.94
1:BQ:98:ILE:O	1:BQ:211:SER:N	1.99	0.94
1:AS:302:ASP:O	1:AS:305:ASN:OD1	1.84	0.94
1:AN:298:TRP:CD2	1:AN:312:VAL:HG12	2.02	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:98:ILE:O	1:BT:211:SER:N	2.01	0.94
1:Ad:298:TRP:CG	1:Ad:312:VAL:HG12	2.02	0.94
1:BG:98:ILE:O	1:BG:211:SER:N	2.01	0.94
1:CK:80:VAL:HG12	1:CK:185:LEU:HB3	1.49	0.94
1:CM:101:ARG:HB2	1:CM:208:SER:OG	1.67	0.94
1:CS:101:ARG:HB2	1:CS:208:SER:OG	1.67	0.94
1:CW:80:VAL:HG12	1:CW:185:LEU:HB3	1.46	0.94
1:CX:56:HIS:CE1	1:CX:206:ARG:HD2	2.01	0.94
1:CH:75:ASP:OD1	1:CH:188:VAL:O	1.84	0.94
1:AO:298:TRP:CD2	1:AO:312:VAL:HG12	2.02	0.94
1:CX:75:ASP:OD1	1:CX:188:VAL:O	1.86	0.94
1:BY:98:ILE:O	1:BY:211:SER:O	1.85	0.94
1:CB:98:ILE:O	1:CB:211:SER:O	1.86	0.94
1:AC:302:ASP:O	1:AC:305:ASN:OD1	1.84	0.94
1:AD:298:TRP:CD2	1:AD:312:VAL:HG12	2.00	0.94
1:CF:101:ARG:HB2	1:CF:208:SER:OG	1.65	0.94
1:CO:98:ILE:O	1:CO:211:SER:O	1.86	0.94
1:BB:98:ILE:O	1:BB:211:SER:N	1.99	0.94
1:CE:75:ASP:OD1	1:CE:188:VAL:O	1.84	0.94
1:CG:101:ARG:HB2	1:CG:208:SER:OG	1.65	0.94
1:CI:56:HIS:CE1	1:CI:206:ARG:HD2	2.03	0.94
1:BR:98:ILE:O	1:BR:211:SER:N	1.99	0.94
1:AR:298:TRP:CG	1:AR:312:VAL:HG12	2.01	0.94
1:CR:75:ASP:OD1	1:CR:188:VAL:O	1.84	0.94
1:CT:317:ASP:HB3	1:CT:319:GLN:HG3	1.50	0.94
1:CU:56:HIS:CE1	1:CU:206:ARG:HD2	2.03	0.94
1:AY:302:ASP:O	1:AY:305:ASN:OD1	1.85	0.94
1:Cb:317:ASP:HB3	1:Cb:319:GLN:HG3	1.50	0.94
1:Cc:75:ASP:OD1	1:Cc:188:VAL:O	1.84	0.94
1:AB:302:ASP:O	1:AB:305:ASN:OD1	1.84	0.94
1:CP:75:ASP:OD1	1:CP:188:VAL:O	1.85	0.94
1:CU:98:ILE:O	1:CU:211:SER:O	1.86	0.94
1:AW:298:TRP:CG	1:AW:312:VAL:HG12	2.02	0.94
1:AK:302:ASP:O	1:AK:305:ASN:OD1	1.86	0.94
1:CS:75:ASP:OD1	1:CS:188:VAL:O	1.86	0.93
1:BU:98:ILE:O	1:BU:211:SER:N	2.01	0.93
1:CV:75:ASP:OD1	1:CV:188:VAL:O	1.86	0.93
1:CY:101:ARG:HB2	1:CY:208:SER:OG	1.67	0.93
1:CC:56:HIS:CE1	1:CC:206:ARG:HD2	2.03	0.93
1:CH:317:ASP:HB3	1:CH:319:GLN:HG3	1.50	0.93
1:AL:302:ASP:O	1:AL:305:ASN:OD1	1.85	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:317:ASP:HB3	1:CU:319:GLN:HG3	1.51	0.93
1:AY:299:GLY:HA3	1:AY:310:ASP:O	1.68	0.93
1:AE:298:TRP:CD2	1:AE:312:VAL:HG12	2.02	0.93
1:CP:80:VAL:HG12	1:CP:185:LEU:HB3	1.50	0.93
1:CB:56:HIS:CE1	1:CB:206:ARG:HD2	2.04	0.93
1:AG:302:ASP:O	1:AG:305:ASN:OD1	1.85	0.93
1:CG:80:VAL:HG12	1:CG:185:LEU:HB3	1.49	0.93
1:AJ:298:TRP:CD2	1:AJ:312:VAL:HG12	2.02	0.93
1:CK:101:ARG:HB2	1:CK:208:SER:OG	1.67	0.93
1:CL:317:ASP:HB3	1:CL:319:GLN:HG3	1.50	0.93
1:BM:98:ILE:O	1:BM:211:SER:N	2.00	0.93
1:CM:317:ASP:HB3	1:CM:319:GLN:HG3	1.50	0.93
1:CR:56:HIS:CE1	1:CR:206:ARG:HD2	2.04	0.93
1:Cb:56:HIS:CE1	1:Cb:206:ARG:HD2	2.03	0.93
1:BD:114:MET:SD	1:CW:122:GLY:HA3	2.09	0.93
1:CE:56:HIS:CE1	1:CE:206:ARG:HD2	2.03	0.93
1:AA:302:ASP:O	1:AA:305:ASN:OD1	1.84	0.93
1:AB:298:TRP:CD2	1:AB:312:VAL:HG12	2.03	0.93
1:AF:298:TRP:CD2	1:AF:312:VAL:HG12	2.02	0.93
1:AH:302:ASP:O	1:AH:305:ASN:OD1	1.84	0.93
1:CL:80:VAL:HG12	1:CL:185:LEU:HB3	1.49	0.93
1:CQ:98:ILE:O	1:CQ:211:SER:O	1.85	0.93
1:BW:98:ILE:O	1:BW:211:SER:N	2.02	0.93
1:Aa:298:TRP:CG	1:Aa:312:VAL:HG12	2.04	0.93
1:Cd:56:HIS:CE1	1:Cd:206:ARG:HD2	2.03	0.93
1:CA:101:ARG:HB2	1:CA:208:SER:OG	1.67	0.93
1:BF:98:ILE:O	1:BF:211:SER:N	2.02	0.93
1:AS:298:TRP:CD2	1:AS:312:VAL:HG12	2.04	0.93
1:AU:302:ASP:O	1:AU:305:ASN:OD1	1.84	0.93
1:AX:314:TYR:CE1	1:AX:315:TYR:O	2.22	0.93
1:CA:317:ASP:HB3	1:CA:319:GLN:HG3	1.50	0.93
1:AK:298:TRP:CG	1:AK:312:VAL:HG12	2.02	0.93
1:BL:98:ILE:O	1:BL:211:SER:N	2.02	0.93
1:CS:56:HIS:CE1	1:CS:206:ARG:HD2	2.02	0.93
1:CD:56:HIS:CE1	1:CD:206:ARG:HD2	2.04	0.93
1:CK:75:ASP:OD1	1:CK:188:VAL:O	1.85	0.93
1:AU:298:TRP:CD2	1:AU:312:VAL:HG12	2.04	0.93
1:CU:75:ASP:OD1	1:CU:188:VAL:O	1.85	0.93
1:Ca:56:HIS:CE1	1:Ca:206:ARG:HD2	2.04	0.93
1:Ca:101:ARG:HB2	1:Ca:208:SER:OG	1.67	0.93
1:BJ:98:ILE:O	1:BJ:211:SER:N	2.00	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:302:ASP:O	1:AQ:305:ASN:OD1	1.84	0.93
1:AR:302:ASP:O	1:AR:305:ASN:OD1	1.84	0.93
1:CA:56:HIS:CE1	1:CA:206:ARG:HD2	2.04	0.92
1:AG:298:TRP:CD2	1:AG:312:VAL:HG12	2.03	0.92
1:CN:75:ASP:OD1	1:CN:188:VAL:O	1.86	0.92
1:CK:317:ASP:HB3	1:CK:319:GLN:HG3	1.52	0.92
1:AM:298:TRP:CD2	1:AM:312:VAL:HG12	2.03	0.92
1:CT:56:HIS:CE1	1:CT:206:ARG:HD2	2.04	0.92
1:AZ:302:ASP:O	1:AZ:305:ASN:OD1	1.85	0.92
1:Ab:298:TRP:CD2	1:Ab:312:VAL:HG12	2.04	0.92
1:Cb:101:ARG:HB2	1:Cb:208:SER:OG	1.68	0.92
1:CC:317:ASP:HB3	1:CC:319:GLN:HG3	1.50	0.92
1:CR:317:ASP:HB3	1:CR:319:GLN:HG3	1.52	0.92
1:CY:56:HIS:CE1	1:CY:206:ARG:HD2	2.05	0.92
1:Cd:80:VAL:HG12	1:Cd:185:LEU:HB3	1.49	0.92
1:CB:80:VAL:HG12	1:CB:185:LEU:HB3	1.49	0.92
1:AC:298:TRP:CG	1:AC:312:VAL:HG12	2.04	0.92
1:AK:299:GLY:HA3	1:AK:310:ASP:O	1.70	0.92
1:AM:302:ASP:O	1:AM:305:ASN:OD1	1.84	0.92
1:AQ:298:TRP:CG	1:AQ:312:VAL:HG12	2.04	0.92
1:CW:317:ASP:HB3	1:CW:319:GLN:HG3	1.52	0.92
1:BB:114:MET:SD	1:CK:122:GLY:HA3	2.09	0.92
1:CV:56:HIS:CE1	1:CV:206:ARG:HD2	2.05	0.92
1:BA:101:ARG:CZ	1:BA:166:LEU:HD12	2.00	0.92
1:CD:317:ASP:HB3	1:CD:319:GLN:HG3	1.51	0.92
1:CO:80:VAL:HG12	1:CO:185:LEU:HB3	1.50	0.92
1:BX:98:ILE:O	1:BX:211:SER:N	2.01	0.92
1:AZ:298:TRP:CG	1:AZ:312:VAL:HG12	2.04	0.92
1:CW:56:HIS:CE1	1:CW:206:ARG:HD2	2.05	0.92
1:CZ:80:VAL:HG12	1:CZ:185:LEU:HB3	1.51	0.92
1:Cc:317:ASP:HB3	1:Cc:319:GLN:HG3	1.50	0.92
1:CF:317:ASP:HB3	1:CF:319:GLN:HG3	1.51	0.92
1:CG:56:HIS:CE1	1:CG:206:ARG:HD2	2.03	0.92
1:CG:317:ASP:HB3	1:CG:319:GLN:HG3	1.51	0.92
1:CS:317:ASP:HB3	1:CS:319:GLN:HG3	1.51	0.92
1:CT:80:VAL:HG12	1:CT:185:LEU:HB3	1.50	0.92
1:CX:317:ASP:HB3	1:CX:319:GLN:HG3	1.50	0.92
1:CJ:56:HIS:CE1	1:CJ:206:ARG:HD2	2.05	0.92
1:AO:314:TYR:CE1	1:AO:315:TYR:O	2.23	0.92
1:AT:298:TRP:CG	1:AT:312:VAL:HG12	2.04	0.92
1:Cd:98:ILE:O	1:Cd:211:SER:O	1.88	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:298:TRP:CG	1:AD:312:VAL:HG12	2.04	0.92
1:AV:314:TYR:CE1	1:AV:315:TYR:O	2.23	0.92
1:Ac:298:TRP:CD2	1:Ac:312:VAL:HG12	2.03	0.92
1:AO:298:TRP:CG	1:AO:312:VAL:HG12	2.05	0.91
1:CO:317:ASP:HB3	1:CO:319:GLN:HG3	1.52	0.91
1:CT:98:ILE:O	1:CT:211:SER:O	1.88	0.91
1:Ca:98:ILE:O	1:Ca:211:SER:O	1.88	0.91
1:Bb:98:ILE:O	1:Bb:211:SER:N	2.03	0.91
1:Ac:299:GLY:HA3	1:Ac:310:ASP:O	1.68	0.91
1:Cc:56:HIS:CE1	1:Cc:206:ARG:HD2	2.05	0.91
1:CJ:75:ASP:OD1	1:CJ:188:VAL:O	1.88	0.91
1:CM:98:ILE:O	1:CM:211:SER:O	1.88	0.91
1:AH:61:SER:HB3	1:AH:90:PRO:HD2	1.52	0.91
1:AM:298:TRP:CG	1:AM:312:VAL:HG12	2.06	0.91
1:CN:101:ARG:HB2	1:CN:208:SER:OG	1.69	0.91
1:AO:61:SER:HB3	1:AO:90:PRO:HD2	1.51	0.91
1:AU:61:SER:HB3	1:AU:90:PRO:HD2	1.52	0.91
1:CN:56:HIS:CE1	1:CN:206:ARG:HD2	2.05	0.91
1:AW:302:ASP:O	1:AW:305:ASN:OD1	1.86	0.91
1:CF:56:HIS:CE1	1:CF:206:ARG:HD2	2.04	0.91
1:CJ:98:ILE:O	1:CJ:211:SER:O	1.89	0.91
1:CR:80:VAL:HG12	1:CR:185:LEU:HB3	1.49	0.91
1:AU:314:TYR:CE1	1:AU:315:TYR:O	2.24	0.91
1:AY:302:ASP:HB3	1:AY:305:ASN:ND2	1.86	0.91
1:CH:98:ILE:O	1:CH:211:SER:O	1.89	0.91
1:AJ:302:ASP:HB3	1:AJ:305:ASN:ND2	1.86	0.91
1:CJ:80:VAL:HG12	1:CJ:185:LEU:HB3	1.53	0.91
1:AQ:61:SER:HB3	1:AQ:90:PRO:HD2	1.52	0.91
1:CZ:98:ILE:O	1:CZ:211:SER:O	1.88	0.91
1:Aa:61:SER:HB3	1:Aa:90:PRO:HD2	1.52	0.91
1:Cb:80:VAL:HG12	1:Cb:185:LEU:HB3	1.52	0.91
1:CE:98:ILE:O	1:CE:211:SER:O	1.89	0.91
1:AF:302:ASP:HB3	1:AF:305:ASN:ND2	1.86	0.91
1:Ac:298:TRP:CG	1:Ac:312:VAL:HG12	2.06	0.91
1:CL:98:ILE:O	1:CL:211:SER:O	1.88	0.91
1:AV:298:TRP:CG	1:AV:312:VAL:HG12	2.04	0.91
1:CE:317:ASP:HB3	1:CE:319:GLN:HG3	1.51	0.91
1:AJ:298:TRP:CG	1:AJ:312:VAL:HG12	2.06	0.91
1:CM:80:VAL:HG12	1:CM:185:LEU:HB3	1.53	0.91
1:CN:317:ASP:HB3	1:CN:319:GLN:HG3	1.51	0.91
1:AO:302:ASP:HB3	1:AO:305:ASN:ND2	1.86	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:56:HIS:CE1	1:CP:206:ARG:HD2	2.05	0.91
1:CS:98:ILE:O	1:CS:211:SER:O	1.89	0.91
1:CH:56:HIS:CE1	1:CH:206:ARG:HD2	2.06	0.91
1:AM:302:ASP:HB3	1:AM:305:ASN:ND2	1.86	0.91
1:AY:298:TRP:CG	1:AY:312:VAL:HG12	2.06	0.91
1:CZ:56:HIS:CE1	1:CZ:206:ARG:HD2	2.05	0.91
1:AI:314:TYR:CE1	1:AI:315:TYR:O	2.24	0.90
1:AX:298:TRP:CG	1:AX:312:VAL:HG12	2.05	0.90
1:AE:298:TRP:CG	1:AE:312:VAL:HG12	2.06	0.90
1:AH:302:ASP:HB3	1:AH:305:ASN:ND2	1.86	0.90
1:CN:98:ILE:O	1:CN:211:SER:O	1.87	0.90
1:CP:98:ILE:O	1:CP:211:SER:O	1.89	0.90
1:CQ:56:HIS:CE1	1:CQ:206:ARG:HD2	2.06	0.90
1:CV:317:ASP:HB3	1:CV:319:GLN:HG3	1.50	0.90
1:Cd:317:ASP:HB3	1:Cd:319:GLN:HG3	1.51	0.90
1:AB:314:TYR:CE1	1:AB:315:TYR:O	2.23	0.90
1:CG:98:ILE:O	1:CG:211:SER:O	1.89	0.90
1:CX:98:ILE:O	1:CX:211:SER:O	1.88	0.90
1:AA:61:SER:HB3	1:AA:90:PRO:HD2	1.52	0.90
1:AN:302:ASP:HB3	1:AN:305:ASN:ND2	1.87	0.90
1:AN:314:TYR:CE1	1:AN:315:TYR:O	2.25	0.90
1:CQ:317:ASP:HB3	1:CQ:319:GLN:HG3	1.51	0.90
1:AS:314:TYR:CE1	1:AS:315:TYR:O	2.24	0.90
1:Ab:314:TYR:CE1	1:Ab:315:TYR:O	2.25	0.90
1:Ac:61:SER:HB3	1:Ac:90:PRO:HD2	1.53	0.90
1:AA:298:TRP:CG	1:AA:312:VAL:HG12	2.05	0.90
1:AB:298:TRP:CG	1:AB:312:VAL:HG12	2.06	0.90
1:AF:298:TRP:CG	1:AF:312:VAL:HG12	2.07	0.90
1:CF:98:ILE:O	1:CF:211:SER:O	1.88	0.90
1:AZ:314:TYR:CE1	1:AZ:315:TYR:O	2.25	0.90
1:Aa:302:ASP:HB3	1:Aa:305:ASN:ND2	1.87	0.90
1:AH:298:TRP:CG	1:AH:312:VAL:HG12	2.06	0.90
1:AI:302:ASP:HB3	1:AI:305:ASN:ND2	1.87	0.90
1:CY:80:VAL:HG12	1:CY:185:LEU:HB3	1.52	0.90
1:CY:317:ASP:HB3	1:CY:319:GLN:HG3	1.51	0.90
1:Cd:141:LEU:HD21	1:Cd:184:ILE:CD1	2.01	0.90
1:AE:302:ASP:HB3	1:AE:305:ASN:ND2	1.86	0.90
1:AG:314:TYR:CE1	1:AG:315:TYR:O	2.25	0.90
1:AH:314:TYR:CE1	1:AH:315:TYR:O	2.25	0.90
1:CM:56:HIS:CE1	1:CM:206:ARG:HD2	2.06	0.90
1:AP:298:TRP:CG	1:AP:312:VAL:HG12	2.05	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:298:TRP:CG	1:AG:312:VAL:HG12	2.07	0.90
1:AI:298:TRP:CG	1:AI:312:VAL:HG12	2.06	0.90
1:CO:56:HIS:CE1	1:CO:206:ARG:HD2	2.06	0.90
1:AS:302:ASP:HB3	1:AS:305:ASN:ND2	1.86	0.90
1:AT:61:SER:HB3	1:AT:90:PRO:HD2	1.52	0.90
1:AC:314:TYR:CE1	1:AC:315:TYR:O	2.25	0.90
1:AE:61:SER:HB3	1:AE:90:PRO:HD2	1.53	0.90
1:AM:314:TYR:CE1	1:AM:315:TYR:O	2.24	0.90
1:CU:80:VAL:HG12	1:CU:185:LEU:HB3	1.51	0.90
1:Ab:302:ASP:HB3	1:Ab:305:ASN:ND2	1.87	0.90
1:AA:314:TYR:CE1	1:AA:315:TYR:O	2.25	0.90
1:CB:317:ASP:HB3	1:CB:319:GLN:HG3	1.50	0.90
1:CJ:317:ASP:HB3	1:CJ:319:GLN:HG3	1.52	0.90
1:AQ:302:ASP:HB3	1:AQ:305:ASN:ND2	1.87	0.90
1:AE:314:TYR:CE1	1:AE:315:TYR:O	2.26	0.89
1:AL:279:TYR:OH	1:AL:311:GLY:O	1.89	0.89
1:AT:302:ASP:HB3	1:AT:305:ASN:ND2	1.87	0.89
1:AP:302:ASP:HB3	1:AP:305:ASN:ND2	1.87	0.89
1:CP:317:ASP:HB3	1:CP:319:GLN:HG3	1.50	0.89
1:BS:98:ILE:O	1:BS:211:SER:N	2.05	0.89
1:AY:61:SER:HB3	1:AY:90:PRO:HD2	1.53	0.89
1:Ac:302:ASP:HB3	1:Ac:305:ASN:ND2	1.86	0.89
1:Ad:314:TYR:CE1	1:Ad:315:TYR:O	2.25	0.89
1:CT:75:ASP:OD1	1:CT:188:VAL:O	1.89	0.89
1:CY:98:ILE:O	1:CY:211:SER:O	1.87	0.89
1:Cc:80:VAL:HG12	1:Cc:185:LEU:HB3	1.55	0.89
1:CC:80:VAL:HG12	1:CC:185:LEU:HB3	1.53	0.89
1:AD:302:ASP:HB3	1:AD:305:ASN:ND2	1.87	0.89
1:AP:314:TYR:CE1	1:AP:315:TYR:O	2.26	0.89
1:AR:314:TYR:CE1	1:AR:315:TYR:O	2.25	0.89
1:CA:98:ILE:O	1:CA:211:SER:O	1.88	0.89
1:AG:302:ASP:HB3	1:AG:305:ASN:ND2	1.87	0.89
1:CI:317:ASP:HB3	1:CI:319:GLN:HG3	1.52	0.89
1:AN:298:TRP:CG	1:AN:312:VAL:HG12	2.06	0.89
1:AS:298:TRP:CG	1:AS:312:VAL:HG12	2.08	0.89
1:Ca:80:VAL:HG12	1:Ca:185:LEU:HB3	1.51	0.89
1:BC:101:ARG:CZ	1:BC:166:LEU:HD12	2.03	0.89
1:AL:314:TYR:CE1	1:AL:315:TYR:O	2.25	0.89
1:CS:80:VAL:HG12	1:CS:185:LEU:HB3	1.55	0.89
1:CD:80:VAL:HG12	1:CD:185:LEU:HB3	1.53	0.89
1:AK:279:TYR:OH	1:AK:311:GLY:O	1.91	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:302:ASP:HB3	1:AW:305:ASN:ND2	1.86	0.89
1:AZ:302:ASP:HB3	1:AZ:305:ASN:ND2	1.88	0.89
1:Aa:314:TYR:CE1	1:Aa:315:TYR:O	2.25	0.89
1:Ad:61:SER:HB3	1:Ad:90:PRO:HD2	1.54	0.89
1:CA:80:VAL:HG12	1:CA:185:LEU:HB3	1.51	0.89
1:BK:101:ARG:CZ	1:BK:166:LEU:HD12	2.03	0.89
1:AK:314:TYR:CE1	1:AK:315:TYR:O	2.25	0.89
1:AQ:314:TYR:CE1	1:AQ:315:TYR:O	2.24	0.89
1:AD:314:TYR:CE1	1:AD:315:TYR:O	2.25	0.89
1:AT:314:TYR:CE1	1:AT:315:TYR:O	2.25	0.89
1:AV:302:ASP:HB3	1:AV:305:ASN:ND2	1.88	0.89
1:Cb:98:ILE:O	1:Cb:211:SER:O	1.90	0.89
1:AB:302:ASP:HB3	1:AB:305:ASN:ND2	1.87	0.89
1:CE:80:VAL:HG12	1:CE:185:LEU:HB3	1.54	0.89
1:BI:101:ARG:CZ	1:BI:166:LEU:HD12	2.02	0.89
1:AU:298:TRP:CG	1:AU:312:VAL:HG12	2.08	0.88
1:Ca:317:ASP:HB3	1:Ca:319:GLN:HG3	1.51	0.88
1:Ab:61:SER:HB3	1:Ab:90:PRO:HD2	1.55	0.88
1:Ac:314:TYR:CE1	1:Ac:315:TYR:O	2.25	0.88
1:BH:101:ARG:CZ	1:BH:166:LEU:HD12	2.03	0.88
1:AK:302:ASP:HB3	1:AK:305:ASN:ND2	1.88	0.88
1:CN:80:VAL:HG12	1:CN:185:LEU:HB3	1.53	0.88
1:Ad:298:TRP:CG	1:Ad:312:VAL:CG1	2.56	0.88
1:AA:302:ASP:HB3	1:AA:305:ASN:ND2	1.87	0.88
1:AR:61:SER:HB3	1:AR:90:PRO:HD2	1.53	0.88
1:AU:302:ASP:HB3	1:AU:305:ASN:ND2	1.86	0.88
1:Ad:302:ASP:HB3	1:Ad:305:ASN:ND2	1.88	0.88
1:AX:61:SER:HB3	1:AX:90:PRO:HD2	1.55	0.88
1:CX:80:VAL:HG12	1:CX:185:LEU:HB3	1.55	0.88
1:BD:153:TRP:O	1:CW:151:LYS:NZ	2.07	0.88
1:BN:101:ARG:CZ	1:BN:166:LEU:HD12	2.03	0.88
1:BT:101:ARG:CZ	1:BT:166:LEU:HD12	2.03	0.88
1:AC:302:ASP:HB3	1:AC:305:ASN:ND2	1.88	0.88
1:CC:98:ILE:O	1:CC:211:SER:O	1.91	0.88
1:AK:298:TRP:CG	1:AK:312:VAL:CG1	2.57	0.88
1:CV:79:VAL:HG12	1:CV:185:LEU:O	1.74	0.88
1:CZ:317:ASP:HB3	1:CZ:319:GLN:HG3	1.52	0.88
1:CK:98:ILE:O	1:CK:211:SER:O	1.90	0.88
1:AW:298:TRP:CG	1:AW:312:VAL:CG1	2.57	0.88
1:CW:98:ILE:O	1:CW:211:SER:O	1.90	0.88
1:AJ:314:TYR:CE1	1:AJ:315:TYR:O	2.27	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:302:ASP:HB3	1:AR:305:ASN:ND2	1.88	0.88
1:BU:101:ARG:CZ	1:BU:166:LEU:HD12	2.03	0.88
1:AX:302:ASP:HB3	1:AX:305:ASN:ND2	1.87	0.88
1:CT:122:GLY:HA3	1:Ba:114:MET:SD	2.13	0.88
1:CV:80:VAL:HG12	1:CV:185:LEU:HB3	1.55	0.88
1:Ab:298:TRP:CG	1:Ab:312:VAL:HG12	2.08	0.88
1:CF:80:VAL:HG12	1:CF:185:LEU:HB3	1.53	0.87
1:BG:114:MET:SD	1:CP:122:GLY:HA3	2.13	0.87
1:AK:61:SER:HB3	1:AK:90:PRO:HD2	1.54	0.87
1:AA:279:TYR:OH	1:AA:311:GLY:O	1.92	0.87
1:AE:279:TYR:OH	1:AE:311:GLY:O	1.91	0.87
1:AW:279:TYR:OH	1:AW:311:GLY:O	1.92	0.87
1:AD:61:SER:HB3	1:AD:90:PRO:HD2	1.54	0.87
1:CS:79:VAL:HG12	1:CS:185:LEU:O	1.73	0.87
1:AN:61:SER:HB3	1:AN:90:PRO:HD2	1.54	0.87
1:AJ:61:SER:HB3	1:AJ:90:PRO:HD2	1.56	0.87
1:AR:298:TRP:CG	1:AR:312:VAL:CG1	2.57	0.87
1:Bd:101:ARG:CZ	1:Bd:166:LEU:HD12	2.04	0.87
1:AF:314:TYR:CE1	1:AF:315:TYR:O	2.26	0.87
1:BJ:101:ARG:CZ	1:BJ:166:LEU:HD12	2.04	0.87
1:Aa:298:TRP:CG	1:Aa:312:VAL:CG1	2.58	0.87
1:AC:61:SER:HB3	1:AC:90:PRO:HD2	1.56	0.87
1:BH:153:TRP:O	1:Cd:151:LYS:NZ	2.08	0.87
1:BT:114:MET:SD	1:CV:122:GLY:HA3	2.15	0.87
1:AD:298:TRP:CG	1:AD:312:VAL:CG1	2.58	0.86
1:AF:279:TYR:OH	1:AF:311:GLY:O	1.92	0.86
1:AW:314:TYR:CE1	1:AW:315:TYR:O	2.27	0.86
1:BY:101:ARG:CZ	1:BY:166:LEU:HD12	2.04	0.86
1:AY:314:TYR:CE1	1:AY:315:TYR:O	2.27	0.86
1:CG:79:VAL:HG12	1:CG:185:LEU:O	1.75	0.86
1:BM:122:GLY:C	1:BM:188:VAL:HG22	2.00	0.86
1:AL:298:TRP:CG	1:AL:312:VAL:CG1	2.56	0.86
1:BP:101:ARG:CZ	1:BP:166:LEU:HD12	2.05	0.86
1:AR:279:TYR:OH	1:AR:311:GLY:O	1.93	0.86
1:AT:279:TYR:OH	1:AT:311:GLY:O	1.94	0.86
1:AT:298:TRP:CG	1:AT:312:VAL:CG1	2.59	0.86
1:BX:101:ARG:CZ	1:BX:166:LEU:HD12	2.05	0.86
1:CD:79:VAL:HG12	1:CD:185:LEU:O	1.74	0.86
1:CH:79:VAL:HG12	1:CH:185:LEU:O	1.75	0.86
1:AI:61:SER:HB3	1:AI:90:PRO:HD2	1.57	0.86
1:AL:98:ILE:O	1:AL:211:SER:O	1.93	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:61:SER:HB3	1:AM:90:PRO:HD2	1.56	0.86
1:BV:101:ARG:CZ	1:BV:166:LEU:HD12	2.05	0.86
1:AL:302:ASP:HB3	1:AL:305:ASN:ND2	1.89	0.86
1:BF:101:ARG:CZ	1:BF:166:LEU:HD12	2.06	0.86
1:CX:141:LEU:HD21	1:CX:184:ILE:CD1	2.04	0.86
1:AZ:98:ILE:O	1:AZ:211:SER:O	1.94	0.86
1:AB:305:ASN:ND2	1:AB:307:THR:O	2.09	0.86
1:BL:101:ARG:CZ	1:BL:166:LEU:HD12	2.05	0.86
1:CR:79:VAL:HG12	1:CR:185:LEU:O	1.76	0.86
1:Ba:101:ARG:CZ	1:Ba:166:LEU:HD12	2.05	0.86
1:BG:122:GLY:C	1:BG:188:VAL:HG22	2.01	0.86
1:AI:98:ILE:O	1:AI:211:SER:O	1.92	0.86
1:AW:61:SER:HB3	1:AW:90:PRO:HD2	1.56	0.86
1:Ac:305:ASN:ND2	1:Ac:307:THR:O	2.09	0.86
1:AJ:305:ASN:ND2	1:AJ:307:THR:O	2.08	0.86
1:CY:79:VAL:HG12	1:CY:185:LEU:O	1.74	0.86
1:BG:101:ARG:CZ	1:BG:166:LEU:HD12	2.07	0.85
1:BQ:101:ARG:CZ	1:BQ:166:LEU:HD12	2.06	0.85
1:AQ:279:TYR:OH	1:AQ:311:GLY:O	1.93	0.85
1:Aa:305:ASN:ND2	1:Aa:307:THR:O	2.09	0.85
1:CG:141:LEU:HD21	1:CG:184:ILE:CD1	2.06	0.85
1:CV:98:ILE:O	1:CV:211:SER:O	1.93	0.85
1:CW:141:LEU:HD21	1:CW:184:ILE:CD1	2.06	0.85
1:Ad:279:TYR:OH	1:Ad:311:GLY:O	1.91	0.85
1:AJ:279:TYR:OH	1:AJ:311:GLY:O	1.93	0.85
1:AP:298:TRP:CG	1:AP:312:VAL:CG1	2.59	0.85
1:BW:101:ARG:CZ	1:BW:166:LEU:HD12	2.05	0.85
1:BB:101:ARG:CZ	1:BB:166:LEU:HD12	2.06	0.85
1:AM:305:ASN:ND2	1:AM:307:THR:O	2.09	0.85
1:BO:101:ARG:CZ	1:BO:166:LEU:HD12	2.05	0.85
1:AQ:298:TRP:CG	1:AQ:312:VAL:CG1	2.59	0.85
1:BD:101:ARG:CZ	1:BD:166:LEU:HD12	2.06	0.85
1:AI:305:ASN:ND2	1:AI:307:THR:O	2.09	0.85
1:AO:98:ILE:O	1:AO:211:SER:O	1.95	0.85
1:AS:305:ASN:ND2	1:AS:307:THR:O	2.09	0.85
1:CW:38:PRO:O	1:Cd:117:ALA:HB2	1.77	0.85
1:CZ:79:VAL:HG12	1:CZ:185:LEU:O	1.76	0.85
1:BA:114:MET:SD	1:CI:122:GLY:HA3	2.16	0.85
1:BR:101:ARG:CZ	1:BR:166:LEU:HD12	2.07	0.85
1:BV:122:GLY:C	1:BV:188:VAL:HG22	2.02	0.85
1:Bc:101:ARG:CZ	1:Bc:166:LEU:HD12	2.06	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:98:ILE:O	1:AE:211:SER:O	1.95	0.85
1:CJ:79:VAL:HG12	1:CJ:185:LEU:O	1.77	0.85
1:CO:100:GLN:CG	1:CO:211:SER:OG	2.24	0.85
1:BS:101:ARG:CZ	1:BS:166:LEU:HD12	2.06	0.85
1:BT:122:GLY:C	1:BT:188:VAL:HG22	2.02	0.85
1:Bd:122:GLY:C	1:Bd:188:VAL:HG22	2.02	0.85
1:AB:298:TRP:CG	1:AB:312:VAL:CG1	2.60	0.85
1:AE:298:TRP:CG	1:AE:312:VAL:CG1	2.60	0.85
1:AJ:302:ASP:O	1:AJ:305:ASN:CG	2.20	0.85
1:AN:298:TRP:CG	1:AN:312:VAL:CG1	2.60	0.85
1:BO:122:GLY:C	1:BO:188:VAL:HG22	2.02	0.85
1:AS:61:SER:HB3	1:AS:90:PRO:HD2	1.56	0.85
1:AV:298:TRP:CG	1:AV:312:VAL:CG1	2.59	0.85
1:AW:98:ILE:O	1:AW:211:SER:O	1.93	0.85
1:AZ:61:SER:HB3	1:AZ:90:PRO:HD2	1.58	0.85
1:AK:98:ILE:O	1:AK:211:SER:O	1.93	0.85
1:AL:61:SER:HB3	1:AL:90:PRO:HD2	1.59	0.85
1:CL:141:LEU:HD21	1:CL:184:ILE:CD1	2.07	0.85
1:AO:305:ASN:ND2	1:AO:307:THR:O	2.09	0.85
1:CT:79:VAL:HG12	1:CT:185:LEU:O	1.76	0.85
1:CT:141:LEU:HD21	1:CT:184:ILE:CD1	2.05	0.85
1:AA:105:GLU:O	1:AA:162:TYR:OH	1.95	0.84
1:CB:79:VAL:HG12	1:CB:185:LEU:O	1.76	0.84
1:AH:298:TRP:CG	1:AH:312:VAL:CG1	2.60	0.84
1:AO:298:TRP:CG	1:AO:312:VAL:CG1	2.60	0.84
1:BX:122:GLY:C	1:BX:188:VAL:HG22	2.02	0.84
1:BD:122:GLY:C	1:BD:188:VAL:HG22	2.02	0.84
1:AM:298:TRP:CG	1:AM:312:VAL:CG1	2.60	0.84
1:AO:279:TYR:OH	1:AO:311:GLY:O	1.95	0.84
1:AX:279:TYR:OH	1:AX:311:GLY:O	1.95	0.84
1:AY:279:TYR:OH	1:AY:311:GLY:O	1.94	0.84
1:Ab:305:ASN:ND2	1:Ab:307:THR:O	2.10	0.84
1:AD:98:ILE:O	1:AD:211:SER:O	1.94	0.84
1:CD:141:LEU:HD21	1:CD:184:ILE:CD1	2.05	0.84
1:AG:298:TRP:CG	1:AG:312:VAL:CG1	2.61	0.84
1:AG:305:ASN:ND2	1:AG:307:THR:O	2.10	0.84
1:AH:305:ASN:ND2	1:AH:307:THR:O	2.09	0.84
1:AI:298:TRP:CG	1:AI:312:VAL:CG1	2.60	0.84
1:AJ:298:TRP:CG	1:AJ:312:VAL:CG1	2.60	0.84
1:AP:61:SER:HB3	1:AP:90:PRO:HD2	1.58	0.84
1:AV:98:ILE:O	1:AV:211:SER:O	1.94	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:122:GLY:C	1:BA:188:VAL:HG22	2.03	0.84
1:AC:298:TRP:CG	1:AC:312:VAL:CG1	2.59	0.84
1:CR:141:LEU:HD21	1:CR:184:ILE:CD1	2.06	0.84
1:AX:305:ASN:ND2	1:AX:307:THR:O	2.10	0.84
1:Ad:98:ILE:O	1:Ad:211:SER:O	1.93	0.84
1:AB:61:SER:HB3	1:AB:90:PRO:HD2	1.58	0.84
1:AC:279:TYR:OH	1:AC:311:GLY:O	1.96	0.84
1:CH:141:LEU:HD21	1:CH:184:ILE:CD1	2.08	0.84
1:AI:105:GLU:O	1:AI:162:TYR:OH	1.94	0.84
1:CZ:141:LEU:HD21	1:CZ:184:ILE:CD1	2.04	0.84
1:CA:79:VAL:HG12	1:CA:185:LEU:O	1.77	0.84
1:AM:279:TYR:OH	1:AM:311:GLY:O	1.94	0.84
1:CN:100:GLN:CG	1:CN:211:SER:OG	2.26	0.84
1:AU:302:ASP:O	1:AU:305:ASN:CG	2.21	0.84
1:BZ:101:ARG:CZ	1:BZ:166:LEU:HD12	2.07	0.84
1:Ac:298:TRP:CG	1:Ac:312:VAL:CG1	2.60	0.84
1:CB:141:LEU:HD21	1:CB:184:ILE:CD1	2.06	0.84
1:AD:279:TYR:OH	1:AD:311:GLY:O	1.93	0.84
1:AF:61:SER:HB3	1:AF:90:PRO:HD2	1.58	0.84
1:AS:279:TYR:OH	1:AS:311:GLY:O	1.95	0.84
1:AU:305:ASN:ND2	1:AU:307:THR:O	2.09	0.84
1:AA:298:TRP:CG	1:AA:312:VAL:CG1	2.59	0.84
1:AJ:302:ASP:O	1:AJ:305:ASN:ND2	2.10	0.84
1:AP:98:ILE:O	1:AP:211:SER:O	1.96	0.84
1:BB:153:TRP:O	1:CK:151:LYS:NZ	2.11	0.84
1:BE:101:ARG:CZ	1:BE:166:LEU:HD12	2.07	0.84
1:AH:105:GLU:O	1:AH:162:TYR:OH	1.96	0.84
1:AZ:298:TRP:CG	1:AZ:312:VAL:CG1	2.59	0.84
1:AA:302:ASP:O	1:AA:305:ASN:ND2	2.11	0.84
1:AF:305:ASN:ND2	1:AF:307:THR:O	2.10	0.84
1:AP:279:TYR:OH	1:AP:311:GLY:O	1.95	0.84
1:AZ:302:ASP:O	1:AZ:305:ASN:ND2	2.11	0.84
1:Ac:302:ASP:O	1:Ac:305:ASN:CG	2.21	0.84
1:AH:279:TYR:OH	1:AH:311:GLY:O	1.95	0.83
1:AP:305:ASN:ND2	1:AP:307:THR:O	2.11	0.83
1:Aa:98:ILE:O	1:Aa:211:SER:O	1.96	0.83
1:AD:302:ASP:O	1:AD:305:ASN:CG	2.21	0.83
1:AJ:98:ILE:O	1:AJ:211:SER:O	1.95	0.83
1:CM:79:VAL:HG12	1:CM:185:LEU:O	1.78	0.83
1:AQ:302:ASP:O	1:AQ:305:ASN:CG	2.22	0.83
1:AV:302:ASP:O	1:AV:305:ASN:ND2	2.11	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:302:ASP:O	1:AX:305:ASN:CG	2.21	0.83
1:AF:302:ASP:O	1:AF:305:ASN:ND2	2.11	0.83
1:AI:302:ASP:O	1:AI:305:ASN:ND2	2.11	0.83
1:AM:302:ASP:O	1:AM:305:ASN:CG	2.22	0.83
1:CM:141:LEU:HD21	1:CM:184:ILE:CD1	2.06	0.83
1:AN:279:TYR:OH	1:AN:311:GLY:O	1.95	0.83
1:AV:302:ASP:O	1:AV:305:ASN:CG	2.20	0.83
1:AX:298:TRP:CG	1:AX:312:VAL:CG1	2.59	0.83
1:AX:302:ASP:O	1:AX:305:ASN:ND2	2.11	0.83
1:BY:122:GLY:C	1:BY:188:VAL:HG22	2.02	0.83
1:Ab:98:ILE:O	1:Ab:211:SER:O	1.97	0.83
1:AE:302:ASP:O	1:AE:305:ASN:ND2	2.11	0.83
1:CE:79:VAL:HG12	1:CE:185:LEU:O	1.79	0.83
1:AI:279:TYR:OH	1:AI:311:GLY:O	1.96	0.83
1:AU:302:ASP:O	1:AU:305:ASN:ND2	2.11	0.83
1:Aa:302:ASP:O	1:Aa:305:ASN:CG	2.22	0.83
1:Ac:302:ASP:O	1:Ac:305:ASN:ND2	2.11	0.83
1:AB:302:ASP:O	1:AB:305:ASN:CG	2.21	0.83
1:AS:298:TRP:CG	1:AS:312:VAL:CG1	2.61	0.83
1:AC:302:ASP:O	1:AC:305:ASN:CG	2.21	0.83
1:AC:302:ASP:O	1:AC:305:ASN:ND2	2.11	0.83
1:AG:279:TYR:OH	1:AG:311:GLY:O	1.95	0.83
1:AM:302:ASP:O	1:AM:305:ASN:ND2	2.11	0.83
1:AN:305:ASN:ND2	1:AN:307:THR:O	2.10	0.83
1:AO:302:ASP:O	1:AO:305:ASN:CG	2.22	0.83
1:AT:302:ASP:O	1:AT:305:ASN:CG	2.21	0.83
1:BZ:122:GLY:C	1:BZ:188:VAL:HG22	2.03	0.83
1:Aa:279:TYR:OH	1:Aa:311:GLY:O	1.95	0.83
1:Bb:101:ARG:CZ	1:Bb:166:LEU:HD12	2.09	0.83
1:CC:79:VAL:HG12	1:CC:185:LEU:O	1.78	0.83
1:CF:79:VAL:HG12	1:CF:185:LEU:O	1.79	0.83
1:BL:122:GLY:C	1:BL:188:VAL:HG22	2.04	0.83
1:CP:141:LEU:HD21	1:CP:184:ILE:CD1	2.07	0.83
1:AS:98:ILE:O	1:AS:211:SER:O	1.95	0.83
1:AU:98:ILE:O	1:AU:211:SER:O	1.97	0.83
1:AU:279:TYR:OH	1:AU:311:GLY:O	1.95	0.83
1:CU:79:VAL:HG12	1:CU:185:LEU:O	1.79	0.83
1:AV:305:ASN:ND2	1:AV:307:THR:O	2.11	0.83
1:Cb:100:GLN:CG	1:Cb:211:SER:OG	2.27	0.83
1:AB:98:ILE:O	1:AB:211:SER:O	1.95	0.83
1:AE:305:ASN:ND2	1:AE:307:THR:O	2.09	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:302:ASP:O	1:AF:305:ASN:CG	2.21	0.83
1:AH:302:ASP:O	1:AH:305:ASN:ND2	2.11	0.83
1:BN:122:GLY:C	1:BN:188:VAL:HG22	2.04	0.83
1:CO:79:VAL:HG12	1:CO:185:LEU:O	1.79	0.83
1:AS:302:ASP:O	1:AS:305:ASN:ND2	2.11	0.83
1:AT:105:GLU:O	1:AT:162:TYR:OH	1.97	0.83
1:Aa:302:ASP:O	1:Aa:305:ASN:ND2	2.12	0.83
1:Ab:298:TRP:CG	1:Ab:312:VAL:CG1	2.61	0.83
1:AB:279:TYR:OH	1:AB:311:GLY:O	1.95	0.83
1:AB:302:ASP:O	1:AB:305:ASN:ND2	2.11	0.83
1:AD:305:ASN:ND2	1:AD:307:THR:O	2.11	0.83
1:CF:141:LEU:HD21	1:CF:184:ILE:CD1	2.09	0.83
1:AN:302:ASP:O	1:AN:305:ASN:CG	2.21	0.83
1:AN:302:ASP:O	1:AN:305:ASN:ND2	2.11	0.83
1:AP:302:ASP:O	1:AP:305:ASN:CG	2.21	0.83
1:AQ:302:ASP:O	1:AQ:305:ASN:ND2	2.12	0.83
1:AT:302:ASP:OD2	1:AT:305:ASN:HB3	1.79	0.83
1:AY:305:ASN:ND2	1:AY:307:THR:O	2.11	0.83
1:Ab:279:TYR:OH	1:Ab:311:GLY:O	1.97	0.83
1:AG:302:ASP:O	1:AG:305:ASN:ND2	2.11	0.83
1:AH:302:ASP:O	1:AH:305:ASN:CG	2.21	0.83
1:CO:141:LEU:HD21	1:CO:184:ILE:CD1	2.08	0.83
1:AZ:305:ASN:ND2	1:AZ:307:THR:O	2.12	0.83
1:Ca:79:VAL:HG12	1:Ca:185:LEU:O	1.78	0.83
1:Ac:98:ILE:O	1:Ac:211:SER:O	1.95	0.83
1:AA:302:ASP:O	1:AA:305:ASN:CG	2.21	0.82
1:AJ:91:ARG:HE	1:BR:98:ILE:HG22	1.44	0.82
1:BP:122:GLY:C	1:BP:188:VAL:HG22	2.03	0.82
1:AR:98:ILE:O	1:AR:211:SER:O	1.96	0.82
1:CT:317:ASP:HB3	1:CT:319:GLN:CG	2.10	0.82
1:CK:79:VAL:HG12	1:CK:185:LEU:O	1.79	0.82
1:AN:98:ILE:O	1:AN:211:SER:O	1.97	0.82
1:AQ:305:ASN:ND2	1:AQ:307:THR:O	2.12	0.82
1:CQ:141:LEU:HD21	1:CQ:184:ILE:CD1	2.07	0.82
1:AT:98:ILE:O	1:AT:211:SER:O	1.97	0.82
1:AT:302:ASP:O	1:AT:305:ASN:ND2	2.11	0.82
1:AV:279:TYR:OH	1:AV:311:GLY:O	1.94	0.82
1:AZ:302:ASP:O	1:AZ:305:ASN:CG	2.22	0.82
1:AA:98:ILE:O	1:AA:211:SER:O	1.96	0.82
1:AA:305:ASN:ND2	1:AA:307:THR:O	2.11	0.82
1:AH:98:ILE:O	1:AH:211:SER:O	1.95	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:302:ASP:O	1:AP:305:ASN:ND2	2.12	0.82
1:AU:298:TRP:CG	1:AU:312:VAL:CG1	2.62	0.82
1:AC:305:ASN:ND2	1:AC:307:THR:O	2.10	0.82
1:AD:302:ASP:O	1:AD:305:ASN:ND2	2.11	0.82
1:AE:302:ASP:O	1:AE:305:ASN:CG	2.22	0.82
1:BF:122:GLY:C	1:BF:188:VAL:HG22	2.04	0.82
1:CK:141:LEU:HD21	1:CK:184:ILE:CD1	2.09	0.82
1:BS:122:GLY:C	1:BS:188:VAL:HG22	2.04	0.82
1:AS:302:ASP:O	1:AS:305:ASN:CG	2.21	0.82
1:AW:305:ASN:ND2	1:AW:307:THR:O	2.12	0.82
1:CX:79:VAL:HG12	1:CX:185:LEU:O	1.78	0.82
1:Cd:100:GLN:CG	1:Cd:211:SER:OG	2.28	0.82
1:AC:98:ILE:O	1:AC:211:SER:O	1.97	0.82
1:AF:298:TRP:CG	1:AF:312:VAL:CG1	2.61	0.82
1:AI:302:ASP:O	1:AI:305:ASN:CG	2.21	0.82
1:CI:141:LEU:HD21	1:CI:184:ILE:CD1	2.07	0.82
1:BK:122:GLY:C	1:BK:188:VAL:HG22	2.03	0.82
1:AL:302:ASP:O	1:AL:305:ASN:ND2	2.12	0.82
1:AL:305:ASN:ND2	1:AL:307:THR:O	2.13	0.82
1:AM:105:GLU:O	1:AM:162:TYR:OH	1.96	0.82
1:AO:302:ASP:O	1:AO:305:ASN:ND2	2.11	0.82
1:BQ:122:GLY:C	1:BQ:188:VAL:HG22	2.03	0.82
1:AR:302:ASP:O	1:AR:305:ASN:CG	2.22	0.82
1:AW:105:GLU:O	1:AW:162:TYR:OH	1.97	0.82
1:AY:98:ILE:O	1:AY:211:SER:O	1.97	0.82
1:BC:122:GLY:C	1:BC:188:VAL:HG22	2.04	0.82
1:BJ:122:GLY:C	1:BJ:188:VAL:HG22	2.03	0.82
1:CN:141:LEU:HD21	1:CN:184:ILE:CD1	2.07	0.82
1:AQ:98:ILE:O	1:AQ:211:SER:O	1.98	0.82
1:AR:302:ASP:O	1:AR:305:ASN:ND2	2.12	0.82
1:AR:305:ASN:ND2	1:AR:307:THR:O	2.12	0.82
1:Ab:302:ASP:O	1:Ab:305:ASN:ND2	2.11	0.82
1:Ac:279:TYR:OH	1:Ac:311:GLY:O	1.96	0.82
1:CE:100:GLN:CG	1:CE:211:SER:OG	2.28	0.82
1:AI:302:ASP:OD2	1:AI:305:ASN:HB3	1.80	0.82
1:CI:79:VAL:HG12	1:CI:185:LEU:O	1.79	0.82
1:CV:317:ASP:HB3	1:CV:319:GLN:CG	2.10	0.82
1:Cc:79:VAL:HG12	1:Cc:185:LEU:O	1.80	0.82
1:CA:317:ASP:HB3	1:CA:319:GLN:CG	2.10	0.82
1:CB:100:GLN:CG	1:CB:211:SER:OG	2.27	0.82
1:AG:302:ASP:O	1:AG:305:ASN:CG	2.22	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:100:GLN:CG	1:CK:211:SER:OG	2.27	0.82
1:BM:101:ARG:CZ	1:BM:166:LEU:HD12	2.08	0.82
1:AR:302:ASP:OD2	1:AR:305:ASN:HB3	1.80	0.82
1:BW:122:GLY:C	1:BW:188:VAL:HG22	2.04	0.82
1:AY:298:TRP:CG	1:AY:312:VAL:CG1	2.62	0.82
1:AY:302:ASP:O	1:AY:305:ASN:ND2	2.11	0.82
1:AG:98:ILE:O	1:AG:211:SER:O	1.98	0.82
1:AL:302:ASP:O	1:AL:305:ASN:CG	2.22	0.82
1:CN:79:VAL:HG12	1:CN:185:LEU:O	1.80	0.82
1:AW:302:ASP:O	1:AW:305:ASN:ND2	2.12	0.82
1:Ca:141:LEU:HD21	1:Ca:184:ILE:CD1	2.10	0.82
1:Bb:122:GLY:C	1:Bb:188:VAL:HG22	2.05	0.82
1:Cc:141:LEU:HD21	1:Cc:184:ILE:CD1	2.09	0.82
1:Cd:101:ARG:NH1	1:Cd:166:LEU:HD12	1.95	0.82
1:CC:317:ASP:HB3	1:CC:319:GLN:CG	2.10	0.82
1:BH:122:GLY:C	1:BH:188:VAL:HG22	2.05	0.82
1:CL:79:VAL:HG12	1:CL:185:LEU:O	1.80	0.82
1:AO:253:ASP:OD1	1:AO:285:PHE:HA	1.80	0.82
1:AP:105:GLU:O	1:AP:162:TYR:OH	1.98	0.82
1:CU:141:LEU:HD21	1:CU:184:ILE:CD1	2.10	0.82
1:Ad:302:ASP:O	1:Ad:305:ASN:CG	2.22	0.82
1:BE:122:GLY:C	1:BE:188:VAL:HG22	2.05	0.81
1:CM:317:ASP:HB3	1:CM:319:GLN:CG	2.10	0.81
1:CY:141:LEU:HD21	1:CY:184:ILE:CD1	2.10	0.81
1:Cb:79:VAL:HG12	1:Cb:185:LEU:O	1.79	0.81
1:AM:98:ILE:O	1:AM:211:SER:O	1.98	0.81
1:AP:302:ASP:OD2	1:AP:305:ASN:HB3	1.79	0.81
1:AT:305:ASN:ND2	1:AT:307:THR:O	2.13	0.81
1:AZ:279:TYR:OH	1:AZ:311:GLY:O	1.97	0.81
1:Ab:302:ASP:O	1:Ab:305:ASN:CG	2.21	0.81
1:Cd:79:VAL:HG12	1:Cd:185:LEU:O	1.79	0.81
1:AA:302:ASP:C	1:AA:305:ASN:CG	2.48	0.81
1:BB:122:GLY:C	1:BB:188:VAL:HG22	2.05	0.81
1:AB:253:ASP:OD1	1:AB:285:PHE:HA	1.81	0.81
1:CH:317:ASP:HB3	1:CH:319:GLN:CG	2.10	0.81
1:BI:122:GLY:C	1:BI:188:VAL:HG22	2.04	0.81
1:AK:302:ASP:O	1:AK:305:ASN:CG	2.23	0.81
1:AL:298:TRP:CD2	1:AL:312:VAL:CG1	2.63	0.81
1:AO:105:GLU:O	1:AO:162:TYR:OH	1.97	0.81
1:BR:122:GLY:C	1:BR:188:VAL:HG22	2.05	0.81
1:AR:302:ASP:C	1:AR:305:ASN:CG	2.48	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:302:ASP:C	1:AT:305:ASN:CG	2.48	0.81
1:AW:302:ASP:O	1:AW:305:ASN:CG	2.23	0.81
1:AX:105:GLU:O	1:AX:162:TYR:OH	1.97	0.81
1:AY:302:ASP:O	1:AY:305:ASN:CG	2.22	0.81
1:Cb:317:ASP:HB3	1:Cb:319:GLN:CG	2.10	0.81
1:CG:317:ASP:HB3	1:CG:319:GLN:CG	2.10	0.81
1:AK:302:ASP:O	1:AK:305:ASN:ND2	2.13	0.81
1:AR:105:GLU:O	1:AR:162:TYR:OH	1.98	0.81
1:AW:253:ASP:OD1	1:AW:285:PHE:HA	1.81	0.81
1:CW:100:GLN:CG	1:CW:211:SER:OG	2.28	0.81
1:Cc:317:ASP:HB3	1:Cc:319:GLN:CG	2.10	0.81
1:Ad:302:ASP:O	1:Ad:305:ASN:ND2	2.14	0.81
1:AA:253:ASP:OD1	1:AA:285:PHE:HA	1.80	0.81
1:AC:105:GLU:O	1:AC:162:TYR:OH	1.98	0.81
1:AN:105:GLU:O	1:AN:162:TYR:OH	1.99	0.81
1:AN:253:ASP:OD1	1:AN:285:PHE:HA	1.81	0.81
1:AN:302:ASP:C	1:AN:305:ASN:CG	2.49	0.81
1:AU:302:ASP:C	1:AU:305:ASN:CG	2.49	0.81
1:AY:302:ASP:C	1:AY:305:ASN:CG	2.49	0.81
1:CA:141:LEU:HD21	1:CA:184:ILE:CD1	2.10	0.81
1:CP:101:ARG:NH1	1:CP:166:LEU:HD12	1.95	0.81
1:CU:317:ASP:HB3	1:CU:319:GLN:CG	2.10	0.81
1:Ac:302:ASP:C	1:Ac:305:ASN:CG	2.49	0.81
1:Ad:298:TRP:CD2	1:Ad:312:VAL:CG1	2.63	0.81
1:AE:253:ASP:OD1	1:AE:285:PHE:HA	1.80	0.81
1:AG:105:GLU:O	1:AG:162:TYR:OH	1.98	0.81
1:AK:302:ASP:C	1:AK:305:ASN:CG	2.48	0.81
1:AL:302:ASP:C	1:AL:305:ASN:CG	2.48	0.81
1:AP:302:ASP:C	1:AP:305:ASN:CG	2.48	0.81
1:CP:79:VAL:HG12	1:CP:185:LEU:O	1.79	0.81
1:AZ:302:ASP:C	1:AZ:305:ASN:CG	2.49	0.81
1:Aa:302:ASP:C	1:Aa:305:ASN:CG	2.49	0.81
1:CB:317:ASP:HB3	1:CB:319:GLN:CG	2.10	0.81
1:AC:253:ASP:OD1	1:AC:285:PHE:HA	1.81	0.81
1:BH:98:ILE:HG22	1:Ad:91:ARG:HE	1.45	0.81
1:AQ:302:ASP:C	1:AQ:305:ASN:CG	2.49	0.81
1:AS:253:ASP:OD1	1:AS:285:PHE:HA	1.81	0.81
1:CT:100:GLN:CG	1:CT:211:SER:OG	2.29	0.81
1:Cc:100:GLN:CG	1:Cc:211:SER:OG	2.29	0.81
1:AG:302:ASP:C	1:AG:305:ASN:CG	2.49	0.81
1:AH:302:ASP:C	1:AH:305:ASN:CG	2.49	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:302:ASP:C	1:AJ:305:ASN:CG	2.49	0.81
1:CJ:141:LEU:HD21	1:CJ:184:ILE:CD1	2.10	0.81
1:CK:317:ASP:HB3	1:CK:319:GLN:CG	2.11	0.81
1:AM:302:ASP:C	1:AM:305:ASN:CG	2.49	0.81
1:AM:302:ASP:OD2	1:AM:305:ASN:HB3	1.81	0.81
1:CN:317:ASP:HB3	1:CN:319:GLN:CG	2.10	0.81
1:AU:253:ASP:OD1	1:AU:285:PHE:HA	1.80	0.81
1:CW:38:PRO:O	1:Cd:117:ALA:CB	2.28	0.81
1:CE:317:ASP:HB3	1:CE:319:GLN:CG	2.10	0.81
1:AK:253:ASP:OD1	1:AK:285:PHE:HA	1.81	0.81
1:AQ:253:ASP:OD1	1:AQ:285:PHE:HA	1.81	0.81
1:AS:302:ASP:C	1:AS:305:ASN:CG	2.49	0.81
1:AU:302:ASP:OD2	1:AU:305:ASN:HB3	1.81	0.81
1:AX:253:ASP:OD1	1:AX:285:PHE:HA	1.81	0.81
1:Ac:105:GLU:O	1:Ac:162:TYR:OH	1.98	0.81
1:Ad:302:ASP:C	1:Ad:305:ASN:CG	2.48	0.81
1:AB:302:ASP:C	1:AB:305:ASN:CG	2.49	0.80
1:AD:253:ASP:OD1	1:AD:285:PHE:HA	1.81	0.80
1:CE:141:LEU:HD21	1:CE:184:ILE:CD1	2.09	0.80
1:AH:253:ASP:OD1	1:AH:285:PHE:HA	1.81	0.80
1:AM:298:TRP:CD1	1:AM:312:VAL:HG13	2.16	0.80
1:AS:105:GLU:O	1:AS:162:TYR:OH	1.99	0.80
1:Aa:105:GLU:O	1:Aa:162:TYR:OH	1.97	0.80
1:Bc:122:GLY:C	1:Bc:188:VAL:HG22	2.06	0.80
1:BD:98:ILE:HG22	1:AW:91:ARG:HE	1.47	0.80
1:AI:302:ASP:C	1:AI:305:ASN:CG	2.49	0.80
1:CO:317:ASP:HB3	1:CO:319:GLN:CG	2.11	0.80
1:CP:317:ASP:HB3	1:CP:319:GLN:CG	2.10	0.80
1:AQ:302:ASP:OD2	1:AQ:305:ASN:HB3	1.81	0.80
1:CQ:100:GLN:CG	1:CQ:211:SER:OG	2.29	0.80
1:AA:302:ASP:OD2	1:AA:305:ASN:HB3	1.81	0.80
1:CL:101:ARG:NH1	1:CL:166:LEU:HD12	1.96	0.80
1:AV:105:GLU:O	1:AV:162:TYR:OH	1.99	0.80
1:AV:253:ASP:OD1	1:AV:285:PHE:HA	1.81	0.80
1:AV:302:ASP:C	1:AV:305:ASN:CG	2.49	0.80
1:AW:298:TRP:CD2	1:AW:312:VAL:CG1	2.64	0.80
1:CX:317:ASP:HB3	1:CX:319:GLN:CG	2.10	0.80
1:Ba:122:GLY:C	1:Ba:188:VAL:HG22	2.07	0.80
1:AD:302:ASP:C	1:AD:305:ASN:CG	2.49	0.80
1:AN:302:ASP:OD2	1:AN:305:ASN:HB3	1.82	0.80
1:CQ:317:ASP:HB3	1:CQ:319:GLN:CG	2.11	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:317:ASP:HB3	1:CR:319:GLN:CG	2.11	0.80
1:CW:317:ASP:HB3	1:CW:319:GLN:CG	2.12	0.80
1:AX:302:ASP:OD2	1:AX:305:ASN:HB3	1.81	0.80
1:Aa:302:ASP:OD2	1:Aa:305:ASN:HB3	1.81	0.80
1:AM:253:ASP:OD1	1:AM:285:PHE:HA	1.81	0.80
1:AW:302:ASP:C	1:AW:305:ASN:CG	2.49	0.80
1:CX:100:GLN:CG	1:CX:211:SER:OG	2.30	0.80
1:CY:317:ASP:HB3	1:CY:319:GLN:CG	2.10	0.80
1:AZ:302:ASP:OD2	1:AZ:305:ASN:HB3	1.82	0.80
1:Ad:253:ASP:OD1	1:Ad:285:PHE:HA	1.82	0.80
1:AC:298:TRP:CD1	1:AC:312:VAL:HG13	2.16	0.80
1:AC:302:ASP:C	1:AC:305:ASN:CG	2.48	0.80
1:CJ:100:GLN:CG	1:CJ:211:SER:OG	2.30	0.80
1:CV:141:LEU:HD21	1:CV:184:ILE:CD1	2.09	0.80
1:AW:298:TRP:CD1	1:AW:312:VAL:HG13	2.16	0.80
1:Aa:253:ASP:OD1	1:Aa:285:PHE:HA	1.81	0.80
1:Ad:105:GLU:O	1:Ad:162:TYR:OH	1.99	0.80
1:BD:154:GLU:OE1	1:CD:43:SER:OG	1.99	0.80
1:AE:302:ASP:OD2	1:AE:305:ASN:HB3	1.82	0.80
1:AH:298:TRP:CD1	1:AH:312:VAL:HG13	2.16	0.80
1:CS:317:ASP:HB3	1:CS:319:GLN:CG	2.10	0.80
1:Ad:302:ASP:OD2	1:Ad:305:ASN:HB3	1.81	0.80
1:Cd:141:LEU:CD2	1:Cd:184:ILE:HD11	2.08	0.80
1:CD:100:GLN:CG	1:CD:211:SER:OG	2.30	0.80
1:AG:298:TRP:CD1	1:AG:312:VAL:HG13	2.17	0.80
1:CM:100:GLN:CG	1:CM:211:SER:OG	2.29	0.80
1:AL:298:TRP:CD1	1:AL:312:VAL:HG13	2.17	0.80
1:CF:100:GLN:CG	1:CF:211:SER:OG	2.30	0.80
1:AN:298:TRP:CD1	1:AN:312:VAL:HG13	2.17	0.80
1:AX:98:ILE:O	1:AX:211:SER:O	2.00	0.80
1:AY:105:GLU:O	1:AY:162:TYR:OH	1.99	0.80
1:AY:253:ASP:OD1	1:AY:285:PHE:HA	1.82	0.80
1:Aa:298:TRP:CD1	1:Aa:312:VAL:HG13	2.16	0.80
1:CD:317:ASP:HB3	1:CD:319:GLN:CG	2.12	0.79
1:CN:122:GLY:HA3	1:BP:114:MET:SD	2.23	0.79
1:AV:302:ASP:OD2	1:AV:305:ASN:HB3	1.82	0.79
1:AX:302:ASP:C	1:AX:305:ASN:CG	2.49	0.79
1:CZ:100:GLN:CG	1:CZ:211:SER:OG	2.30	0.79
1:AD:302:ASP:OD2	1:AD:305:ASN:HB3	1.82	0.79
1:AF:302:ASP:C	1:AF:305:ASN:CG	2.49	0.79
1:AJ:302:ASP:OD2	1:AJ:305:ASN:HB3	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:253:ASP:OD1	1:AL:285:PHE:HA	1.82	0.79
1:CP:100:GLN:CG	1:CP:211:SER:OG	2.30	0.79
1:CR:100:GLN:CG	1:CR:211:SER:OG	2.30	0.79
1:AU:105:GLU:O	1:AU:162:TYR:OH	1.99	0.79
1:Ca:100:GLN:CG	1:Ca:211:SER:OG	2.30	0.79
1:CH:100:GLN:CG	1:CH:211:SER:OG	2.30	0.79
1:AK:302:ASP:OD2	1:AK:305:ASN:HB3	1.81	0.79
1:CL:317:ASP:HB3	1:CL:319:GLN:CG	2.11	0.79
1:AO:302:ASP:C	1:AO:305:ASN:CG	2.49	0.79
1:CO:100:GLN:HG3	1:CO:211:SER:OG	1.83	0.79
1:CF:317:ASP:HB3	1:CF:319:GLN:CG	2.10	0.79
1:CI:100:GLN:CG	1:CI:211:SER:OG	2.30	0.79
1:CR:101:ARG:NH1	1:CR:166:LEU:HD12	1.98	0.79
1:AZ:105:GLU:O	1:AZ:162:TYR:OH	2.00	0.79
1:Ab:105:GLU:O	1:Ab:162:TYR:OH	1.98	0.79
1:Ad:305:ASN:ND2	1:Ad:307:THR:O	2.16	0.79
1:AP:298:TRP:CD1	1:AP:312:VAL:HG13	2.16	0.79
1:AS:298:TRP:CD1	1:AS:312:VAL:HG13	2.18	0.79
1:CW:79:VAL:HG12	1:CW:185:LEU:O	1.82	0.79
1:Ab:302:ASP:C	1:Ab:305:ASN:CG	2.49	0.79
1:Ab:302:ASP:OD2	1:Ab:305:ASN:HB3	1.81	0.79
1:Cd:317:ASP:HB3	1:Cd:319:GLN:CG	2.11	0.79
1:AD:298:TRP:CD1	1:AD:312:VAL:HG13	2.18	0.79
1:CI:101:ARG:NH1	1:CI:166:LEU:HD12	1.98	0.79
1:AO:298:TRP:CD1	1:AO:312:VAL:HG13	2.18	0.79
1:AU:314:TYR:HE1	1:AU:316:SER:CA	1.96	0.79
1:AZ:253:ASP:OD1	1:AZ:285:PHE:HA	1.82	0.79
1:CZ:317:ASP:HB3	1:CZ:319:GLN:CG	2.12	0.79
1:Ba:154:GLU:OE1	1:Ca:43:SER:OG	2.00	0.79
1:AB:314:TYR:HE1	1:AB:316:SER:CA	1.96	0.79
1:AF:302:ASP:OD2	1:AF:305:ASN:HB3	1.81	0.79
1:BG:154:GLU:OE1	1:CG:43:SER:OG	2.01	0.79
1:Bd:154:GLU:OE1	1:Cd:43:SER:OG	2.00	0.79
1:CG:100:GLN:CG	1:CG:211:SER:OG	2.31	0.79
1:CK:101:ARG:NH1	1:CK:166:LEU:HD12	1.98	0.79
1:AF:298:TRP:CD1	1:AF:312:VAL:HG13	2.18	0.79
1:AI:253:ASP:OD1	1:AI:285:PHE:HA	1.81	0.79
1:AJ:98:ILE:HG23	1:BR:91:ARG:NH1	1.98	0.79
1:BU:154:GLU:OE1	1:CU:43:SER:OG	2.01	0.79
1:Ca:317:ASP:HB3	1:Ca:319:GLN:CG	2.11	0.79
1:Ac:253:ASP:OD1	1:Ac:285:PHE:HA	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:154:GLU:OE1	1:CA:43:SER:OG	1.99	0.79
1:AE:302:ASP:C	1:AE:305:ASN:CG	2.49	0.79
1:AG:253:ASP:OD1	1:AG:285:PHE:HA	1.82	0.79
1:AH:302:ASP:OD2	1:AH:305:ASN:HB3	1.81	0.79
1:CI:317:ASP:HB3	1:CI:319:GLN:CG	2.12	0.79
1:AJ:253:ASP:OD1	1:AJ:285:PHE:HA	1.83	0.79
1:AK:305:ASN:ND2	1:AK:307:THR:O	2.16	0.79
1:AT:253:ASP:OD1	1:AT:285:PHE:HA	1.81	0.79
1:Cc:101:ARG:NH1	1:Cc:166:LEU:HD12	1.98	0.79
1:CJ:317:ASP:HB3	1:CJ:319:GLN:CG	2.12	0.78
1:AL:302:ASP:OD2	1:AL:305:ASN:HB3	1.81	0.78
1:AR:253:ASP:OD1	1:AR:285:PHE:HA	1.82	0.78
1:AX:298:TRP:CD1	1:AX:312:VAL:HG13	2.18	0.78
1:AX:314:TYR:HE1	1:AX:316:SER:CA	1.96	0.78
1:CC:141:LEU:HD21	1:CC:184:ILE:CD1	2.12	0.78
1:AJ:298:TRP:CD1	1:AJ:312:VAL:HG13	2.18	0.78
1:CT:100:GLN:HG2	1:CT:213:GLU:OE2	1.83	0.78
1:CV:101:ARG:NH1	1:CV:166:LEU:HD12	1.99	0.78
1:AL:105:GLU:O	1:AL:162:TYR:OH	1.99	0.78
1:CN:100:GLN:HG2	1:CN:211:SER:OG	1.84	0.78
1:AQ:105:GLU:O	1:AQ:162:TYR:OH	1.98	0.78
1:AS:302:ASP:OD2	1:AS:305:ASN:HB3	1.83	0.78
1:AZ:298:TRP:CD2	1:AZ:312:VAL:CG1	2.65	0.78
1:AE:105:GLU:O	1:AE:162:TYR:OH	2.00	0.78
1:AF:253:ASP:OD1	1:AF:285:PHE:HA	1.81	0.78
1:AJ:91:ARG:NE	1:BR:98:ILE:HG22	1.99	0.78
1:AJ:105:GLU:O	1:AJ:162:TYR:OH	2.01	0.78
1:BY:154:GLU:OE1	1:CY:43:SER:OG	2.00	0.78
1:AF:105:GLU:O	1:AF:162:TYR:OH	2.01	0.78
1:AG:302:ASP:OD2	1:AG:305:ASN:HB3	1.83	0.78
1:CW:45:VAL:HG23	1:Cd:200:LEU:HD13	1.65	0.78
1:CS:101:ARG:NH1	1:CS:166:LEU:HD12	1.98	0.78
1:AV:298:TRP:CD1	1:AV:312:VAL:HG13	2.19	0.78
1:BH:154:GLU:OE1	1:CH:43:SER:OG	2.02	0.78
1:CS:141:LEU:HD21	1:CS:184:ILE:CD1	2.11	0.78
1:AY:302:ASP:OD2	1:AY:305:ASN:HB3	1.82	0.78
1:Ab:253:ASP:OD1	1:Ab:285:PHE:HA	1.82	0.78
1:AB:302:ASP:OD2	1:AB:305:ASN:HB3	1.83	0.78
1:AK:298:TRP:CD1	1:AK:312:VAL:HG13	2.19	0.78
1:CW:80:VAL:CG1	1:CW:185:LEU:HB3	2.14	0.78
1:AB:105:GLU:O	1:AB:162:TYR:OH	2.00	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:101:ARG:NH1	1:CJ:166:LEU:HD12	1.99	0.78
1:AT:298:TRP:CD1	1:AT:312:VAL:HG13	2.17	0.78
1:CK:100:GLN:HG2	1:CK:211:SER:OG	1.85	0.77
1:AP:253:ASP:OD1	1:AP:285:PHE:HA	1.84	0.77
1:AZ:298:TRP:CD1	1:AZ:312:VAL:HG13	2.18	0.77
1:AB:298:TRP:CD1	1:AB:312:VAL:HG13	2.16	0.77
1:AC:302:ASP:OD2	1:AC:305:ASN:HB3	1.84	0.77
1:BD:98:ILE:HG22	1:AW:91:ARG:NE	1.99	0.77
1:AO:314:TYR:HE1	1:AO:316:SER:CA	1.97	0.77
1:CQ:79:VAL:HG12	1:CQ:185:LEU:O	1.84	0.77
1:CT:151:LYS:NZ	1:Ba:153:TRP:O	2.17	0.77
1:CA:100:GLN:CG	1:CA:211:SER:OG	2.32	0.77
1:CB:101:ARG:NH1	1:CB:166:LEU:HD12	1.99	0.77
1:CC:100:GLN:CG	1:CC:211:SER:OG	2.32	0.77
1:AF:98:ILE:O	1:AF:211:SER:O	2.02	0.77
1:BH:98:ILE:HG22	1:Ad:91:ARG:NE	1.99	0.77
1:AI:314:TYR:HE1	1:AI:316:SER:CA	1.97	0.77
1:Aa:298:TRP:CD2	1:Aa:312:VAL:CG1	2.66	0.77
1:BU:122:GLY:C	1:BU:188:VAL:HG22	2.08	0.77
1:CZ:101:ARG:NH1	1:CZ:166:LEU:HD12	2.00	0.77
1:CI:141:LEU:CD2	1:CI:184:ILE:HD11	2.14	0.77
1:CN:101:ARG:NH1	1:CN:166:LEU:HD12	1.98	0.77
1:CX:101:ARG:NH1	1:CX:166:LEU:HD12	2.00	0.77
1:Ad:111:ILE:HG22	1:Ad:113:PRO:HD3	1.66	0.77
1:AD:298:TRP:CD2	1:AD:312:VAL:CG1	2.66	0.77
1:AE:314:TYR:HE1	1:AE:316:SER:CA	1.97	0.77
1:AG:72:THR:O	1:AG:191:ASN:ND2	2.18	0.77
1:CU:100:GLN:CG	1:CU:211:SER:OG	2.33	0.77
1:Ac:314:TYR:HE1	1:Ac:316:SER:CA	1.97	0.77
1:AE:298:TRP:CD2	1:AE:312:VAL:CG1	2.68	0.77
1:CH:101:ARG:NH1	1:CH:166:LEU:HD12	2.00	0.77
1:CV:100:GLN:CG	1:CV:211:SER:OG	2.32	0.77
1:AW:302:ASP:OD2	1:AW:305:ASN:HB3	1.83	0.77
1:CG:141:LEU:CD2	1:CG:184:ILE:HD11	2.15	0.77
1:AI:298:TRP:CD1	1:AI:312:VAL:HG13	2.18	0.77
1:BL:91:ARG:NH1	1:AU:98:ILE:HG23	1.99	0.77
1:BS:154:GLU:OE1	1:CS:43:SER:OG	2.02	0.77
1:AX:298:TRP:CD2	1:AX:312:VAL:CG1	2.67	0.77
1:AG:314:TYR:HE1	1:AG:316:SER:CA	1.98	0.77
1:AM:314:TYR:HE1	1:AM:316:SER:CA	1.96	0.77
1:AN:314:TYR:HE1	1:AN:316:SER:CA	1.98	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:302:ASP:OD2	1:AO:305:ASN:HB3	1.83	0.77
1:CU:101:ARG:NH1	1:CU:166:LEU:HD12	2.00	0.77
1:AA:298:TRP:CD1	1:AA:312:VAL:HG13	2.17	0.77
1:AS:314:TYR:HE1	1:AS:316:SER:CA	1.98	0.77
1:BU:114:MET:SD	1:CX:122:GLY:HA3	2.25	0.77
1:AU:298:TRP:CD1	1:AU:312:VAL:HG13	2.19	0.77
1:Ab:314:TYR:HE1	1:Ab:316:SER:CA	1.97	0.77
1:AA:314:TYR:HE1	1:AA:316:SER:CA	1.98	0.76
1:AE:298:TRP:CD1	1:AE:312:VAL:HG13	2.19	0.76
1:AI:72:THR:O	1:AI:191:ASN:ND2	2.18	0.76
1:AK:298:TRP:CD2	1:AK:312:VAL:CG1	2.63	0.76
1:CO:101:ARG:NH1	1:CO:166:LEU:HD12	1.98	0.76
1:CQ:101:ARG:NH1	1:CQ:166:LEU:HD12	2.00	0.76
1:Ac:302:ASP:OD2	1:Ac:305:ASN:HB3	1.84	0.76
1:CD:141:LEU:CD2	1:CD:184:ILE:HD11	2.13	0.76
1:AT:298:TRP:CD2	1:AT:312:VAL:CG1	2.66	0.76
1:AC:298:TRP:CD2	1:AC:312:VAL:CG1	2.67	0.76
1:Cb:141:LEU:HD21	1:Cb:184:ILE:CD1	2.14	0.76
1:CC:101:ARG:NH1	1:CC:166:LEU:HD12	1.99	0.76
1:CE:100:GLN:HG2	1:CE:211:SER:OG	1.85	0.76
1:CF:101:ARG:NH1	1:CF:166:LEU:HD12	1.99	0.76
1:AH:314:TYR:HE1	1:AH:316:SER:CA	1.97	0.76
1:BR:154:GLU:OE1	1:CR:43:SER:OG	2.03	0.76
1:AR:298:TRP:CD2	1:AR:312:VAL:CG1	2.65	0.76
1:CT:141:LEU:CD2	1:CT:184:ILE:HD11	2.12	0.76
1:Cb:101:ARG:NH1	1:Cb:166:LEU:HD12	2.00	0.76
1:Ad:298:TRP:CD1	1:Ad:312:VAL:HG13	2.18	0.76
1:BC:114:MET:SD	1:CY:122:GLY:HA3	2.26	0.76
1:CI:100:GLN:HG2	1:CI:213:GLU:OE2	1.85	0.76
1:CL:100:GLN:CG	1:CL:211:SER:OG	2.31	0.76
1:AQ:298:TRP:CD1	1:AQ:312:VAL:HG13	2.18	0.76
1:CW:101:ARG:NH1	1:CW:166:LEU:HD12	2.01	0.76
1:CD:101:ARG:NH1	1:CD:166:LEU:HD12	2.01	0.76
1:CL:99:PHE:HA	1:CL:209:VAL:O	1.86	0.76
1:AP:111:ILE:HG22	1:AP:113:PRO:HD3	1.66	0.76
1:AS:72:THR:O	1:AS:191:ASN:ND2	2.18	0.76
1:CT:100:GLN:HG3	1:CT:211:SER:OG	1.86	0.76
1:Aa:314:TYR:HE1	1:Aa:316:SER:CA	1.99	0.76
1:Ac:298:TRP:CD1	1:Ac:312:VAL:HG13	2.18	0.76
1:AD:105:GLU:O	1:AD:162:TYR:OH	2.03	0.76
1:BQ:154:GLU:OE1	1:CQ:43:SER:OG	2.03	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:298:TRP:CD2	1:AY:312:VAL:CG1	2.67	0.76
1:BB:98:ILE:HG22	1:AK:91:ARG:HE	1.51	0.76
1:CH:141:LEU:CD2	1:CH:184:ILE:HD11	2.15	0.76
1:CP:141:LEU:CD2	1:CP:184:ILE:HD11	2.14	0.76
1:BV:154:GLU:OE1	1:CV:43:SER:OG	2.03	0.76
1:BW:130:ASP:HB2	1:CW:100:GLN:HE22	1.49	0.76
1:CW:80:VAL:CG1	1:CW:185:LEU:CB	2.64	0.76
1:Ab:298:TRP:CD1	1:Ab:312:VAL:HG13	2.17	0.76
1:Cd:99:PHE:HA	1:Cd:209:VAL:O	1.86	0.76
1:CG:100:GLN:HG2	1:CG:213:GLU:OE2	1.84	0.76
1:AN:111:ILE:HG22	1:AN:113:PRO:HD3	1.67	0.76
1:CS:100:GLN:CG	1:CS:211:SER:OG	2.32	0.76
1:AV:298:TRP:CD2	1:AV:312:VAL:CG1	2.65	0.76
1:AY:302:ASP:HB3	1:AY:305:ASN:CG	2.11	0.76
1:Bc:101:ARG:HB3	1:Bc:166:LEU:HD11	1.68	0.76
1:CB:141:LEU:CD2	1:CB:184:ILE:HD11	2.13	0.75
1:BI:154:GLU:OE1	1:CI:43:SER:OG	2.03	0.75
1:AJ:314:TYR:HE1	1:AJ:316:SER:CA	1.99	0.75
1:AQ:314:TYR:HE1	1:AQ:316:SER:CA	1.98	0.75
1:CQ:80:VAL:CG1	1:CQ:185:LEU:HB3	2.15	0.75
1:CW:141:LEU:CD2	1:CW:184:ILE:HD11	2.14	0.75
1:BB:154:GLU:OE1	1:CB:43:SER:OG	2.03	0.75
1:BF:154:GLU:OE1	1:CF:43:SER:OG	2.03	0.75
1:CI:80:VAL:CG1	1:CI:185:LEU:HB3	2.15	0.75
1:BL:130:ASP:HB2	1:CL:100:GLN:HE22	1.51	0.75
1:CN:100:GLN:HG2	1:CN:213:GLU:OE2	1.86	0.75
1:AQ:298:TRP:CD2	1:AQ:312:VAL:CG1	2.67	0.75
1:CR:80:VAL:CG1	1:CR:185:LEU:HB3	2.16	0.75
1:Cb:100:GLN:HG2	1:Cb:211:SER:OG	1.85	0.75
1:Bd:130:ASP:HB2	1:Cd:100:GLN:HE22	1.51	0.75
1:CT:101:ARG:NH1	1:CT:166:LEU:HD12	2.01	0.75
1:AU:111:ILE:HG22	1:AU:113:PRO:HD3	1.67	0.75
1:CZ:100:GLN:HG2	1:CZ:213:GLU:OE2	1.87	0.75
1:CE:101:ARG:NH1	1:CE:166:LEU:HD12	2.01	0.75
1:CK:141:LEU:CD2	1:CK:184:ILE:HD11	2.13	0.75
1:BP:101:ARG:HB3	1:BP:166:LEU:HD11	1.69	0.75
1:AP:314:TYR:HE1	1:AP:316:SER:CA	1.98	0.75
1:CQ:99:PHE:HA	1:CQ:209:VAL:O	1.86	0.75
1:AR:298:TRP:CD1	1:AR:312:VAL:HG13	2.17	0.75
1:AY:314:TYR:HE1	1:AY:316:SER:CA	1.99	0.75
1:CB:100:GLN:HG2	1:CB:211:SER:OG	1.85	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:154:GLU:OE1	1:CC:43:SER:OG	2.04	0.75
1:CD:122:GLY:HA3	1:BF:114:MET:SD	2.26	0.75
1:AF:314:TYR:HE1	1:AF:316:SER:CA	1.98	0.75
1:CR:99:PHE:HA	1:CR:209:VAL:O	1.86	0.75
1:CX:141:LEU:CD2	1:CX:184:ILE:HD11	2.13	0.75
1:Cd:100:GLN:HG2	1:Cd:211:SER:OG	1.86	0.75
1:AA:298:TRP:CD2	1:AA:312:VAL:CG1	2.67	0.75
1:CA:101:ARG:NH1	1:CA:166:LEU:HD12	2.00	0.75
1:BJ:154:GLU:OE1	1:CJ:43:SER:OG	2.03	0.75
1:AK:105:GLU:O	1:AK:162:TYR:OH	2.03	0.75
1:CO:100:GLN:HG2	1:CO:211:SER:OG	1.85	0.75
1:CC:99:PHE:HA	1:CC:209:VAL:O	1.85	0.75
1:CD:100:GLN:HG2	1:CD:213:GLU:OE2	1.86	0.75
1:AE:302:ASP:HB3	1:AE:305:ASN:CG	2.11	0.75
1:AF:298:TRP:CD2	1:AF:312:VAL:CG1	2.69	0.75
1:CR:141:LEU:CD2	1:CR:184:ILE:HD11	2.13	0.75
1:CA:100:GLN:HG2	1:CA:213:GLU:OE2	1.87	0.75
1:AF:72:THR:O	1:AF:191:ASN:ND2	2.20	0.75
1:BM:154:GLU:OE1	1:CM:43:SER:OG	2.05	0.75
1:CW:100:GLN:HG2	1:CW:211:SER:OG	1.86	0.75
1:Ab:302:ASP:HB3	1:Ab:305:ASN:CG	2.12	0.75
1:AC:314:TYR:HE1	1:AC:316:SER:CA	1.99	0.74
1:AK:111:ILE:HG22	1:AK:113:PRO:HD3	1.69	0.74
1:CM:100:GLN:HG2	1:CM:211:SER:OG	1.87	0.74
1:CW:43:SER:HA	1:Cd:112:GLN:NE2	2.01	0.74
1:AL:111:ILE:HG22	1:AL:113:PRO:HD3	1.69	0.74
1:CN:100:GLN:HG3	1:CN:211:SER:OG	1.87	0.74
1:CT:99:PHE:HA	1:CT:209:VAL:O	1.87	0.74
1:AW:111:ILE:HG22	1:AW:113:PRO:HD3	1.69	0.74
1:AW:302:ASP:HB3	1:AW:305:ASN:CG	2.12	0.74
1:CY:101:ARG:NH1	1:CY:166:LEU:HD12	2.01	0.74
1:CB:80:VAL:CG1	1:CB:185:LEU:HB3	2.18	0.74
1:CH:100:GLN:HG2	1:CH:211:SER:OG	1.88	0.74
1:AJ:302:ASP:HB3	1:AJ:305:ASN:CG	2.12	0.74
1:BL:154:GLU:OE1	1:CL:43:SER:OG	2.04	0.74
1:AM:302:ASP:HB3	1:AM:305:ASN:CG	2.12	0.74
1:CT:80:VAL:CG1	1:CT:185:LEU:HB3	2.17	0.74
1:CU:122:GLY:O	1:CU:188:VAL:N	2.20	0.74
1:CX:62:ARG:NH1	1:Bc:75:ASP:OD2	2.20	0.74
1:Cc:63:ILE:HD12	1:Cc:88:LEU:HG	1.69	0.74
1:AL:314:TYR:HE1	1:AL:316:SER:CA	2.00	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:80:VAL:CG1	1:CL:185:LEU:HB3	2.18	0.74
1:AR:314:TYR:HE1	1:AR:316:SER:CA	2.00	0.74
1:AV:314:TYR:HE1	1:AV:316:SER:CA	2.00	0.74
1:CY:100:GLN:CG	1:CY:211:SER:OG	2.35	0.74
1:Ac:302:ASP:HB3	1:Ac:305:ASN:CG	2.11	0.74
1:AG:302:ASP:HB3	1:AG:305:ASN:CG	2.12	0.74
1:CI:80:VAL:CG1	1:CI:185:LEU:CB	2.65	0.74
1:AM:298:TRP:CD2	1:AM:312:VAL:CG1	2.69	0.74
1:AT:314:TYR:HE1	1:AT:316:SER:CA	2.00	0.74
1:Aa:302:ASP:HB3	1:Aa:305:ASN:CG	2.12	0.74
1:AD:302:ASP:HB3	1:AD:305:ASN:CG	2.13	0.74
1:AE:72:THR:O	1:AE:191:ASN:ND2	2.19	0.74
1:BH:91:ARG:NH1	1:Ad:98:ILE:HG23	2.03	0.74
1:CH:80:VAL:CG1	1:CH:185:LEU:HB3	2.17	0.74
1:AO:111:ILE:HG22	1:AO:113:PRO:HD3	1.70	0.74
1:AO:302:ASP:HB3	1:AO:305:ASN:CG	2.12	0.74
1:AW:72:THR:O	1:AW:191:ASN:ND2	2.21	0.74
1:CZ:80:VAL:CG1	1:CZ:185:LEU:CB	2.66	0.74
1:AF:302:ASP:HB3	1:AF:305:ASN:CG	2.11	0.74
1:CF:100:GLN:HG2	1:CF:213:GLU:OE2	1.88	0.74
1:AH:72:THR:O	1:AH:191:ASN:ND2	2.21	0.74
1:AT:302:ASP:HB3	1:AT:305:ASN:CG	2.12	0.74
1:AZ:302:ASP:HB3	1:AZ:305:ASN:CG	2.13	0.74
1:AB:302:ASP:HB3	1:AB:305:ASN:CG	2.12	0.74
1:AC:302:ASP:HB3	1:AC:305:ASN:CG	2.13	0.74
1:AD:314:TYR:HE1	1:AD:316:SER:CA	2.00	0.74
1:AK:72:THR:O	1:AK:191:ASN:ND2	2.20	0.74
1:AN:302:ASP:HB3	1:AN:305:ASN:CG	2.13	0.74
1:AP:72:THR:O	1:AP:191:ASN:ND2	2.20	0.74
1:AS:298:TRP:CD2	1:AS:312:VAL:CG1	2.69	0.74
1:AX:302:ASP:HB3	1:AX:305:ASN:CG	2.12	0.74
1:AK:302:ASP:HB3	1:AK:305:ASN:CG	2.13	0.74
1:CM:100:GLN:HG2	1:CM:213:GLU:OE2	1.88	0.74
1:AP:298:TRP:CD2	1:AP:312:VAL:CG1	2.67	0.74
1:BT:153:TRP:O	1:CV:151:LYS:NZ	2.21	0.74
1:AG:298:TRP:CD2	1:AG:312:VAL:CG1	2.69	0.74
1:CZ:100:GLN:HG3	1:CZ:211:SER:OG	1.88	0.74
1:Ca:100:GLN:HG2	1:Ca:213:GLU:OE2	1.87	0.74
1:Ca:101:ARG:NH1	1:Ca:166:LEU:HD12	2.02	0.74
1:Cc:100:GLN:HG3	1:Cc:211:SER:OG	1.88	0.74
1:AA:302:ASP:HB3	1:AA:305:ASN:CG	2.13	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:302:ASP:HB3	1:AP:305:ASN:CG	2.13	0.73
1:CQ:100:GLN:HG2	1:CQ:213:GLU:OE2	1.88	0.73
1:BU:130:ASP:HB2	1:CU:100:GLN:HE22	1.53	0.73
1:AZ:72:THR:O	1:AZ:191:ASN:ND2	2.21	0.73
1:Ac:298:TRP:CD2	1:Ac:312:VAL:CG1	2.69	0.73
1:AB:72:THR:O	1:AB:191:ASN:ND2	2.20	0.73
1:AB:298:TRP:CD2	1:AB:312:VAL:CG1	2.69	0.73
1:AF:265:ILE:CG2	1:AF:313:ALA:O	2.36	0.73
1:CF:99:PHE:HA	1:CF:209:VAL:O	1.88	0.73
1:CH:99:PHE:HA	1:CH:209:VAL:O	1.87	0.73
1:CH:122:GLY:O	1:CH:188:VAL:N	2.21	0.73
1:CI:100:GLN:HG3	1:CI:211:SER:OG	1.87	0.73
1:BK:154:GLU:OE1	1:CK:43:SER:OG	2.06	0.73
1:CK:45:VAL:HG23	1:CL:200:LEU:HD13	1.69	0.73
1:CO:100:GLN:HG2	1:CO:213:GLU:OE2	1.87	0.73
1:BQ:101:ARG:HB3	1:BQ:166:LEU:HD11	1.69	0.73
1:AU:298:TRP:CD2	1:AU:312:VAL:CG1	2.70	0.73
1:AU:302:ASP:HB3	1:AU:305:ASN:CG	2.12	0.73
1:CV:99:PHE:HA	1:CV:209:VAL:O	1.87	0.73
1:CZ:141:LEU:CD2	1:CZ:184:ILE:HD11	2.12	0.73
1:AH:298:TRP:CD2	1:AH:312:VAL:CG1	2.69	0.73
1:AH:299:GLY:CA	1:AH:310:ASP:O	2.36	0.73
1:AK:253:ASP:CG	1:AK:285:PHE:HA	2.13	0.73
1:AR:302:ASP:HB3	1:AR:305:ASN:CG	2.14	0.73
1:AT:72:THR:O	1:AT:191:ASN:ND2	2.21	0.73
1:AZ:314:TYR:HE1	1:AZ:316:SER:CA	2.00	0.73
1:Cb:100:GLN:HG3	1:Cb:211:SER:OG	1.87	0.73
1:Cb:122:GLY:O	1:Cb:188:VAL:N	2.21	0.73
1:Cc:100:GLN:HG2	1:Cc:211:SER:OG	1.88	0.73
1:CA:99:PHE:HA	1:CA:209:VAL:O	1.88	0.73
1:AD:72:THR:O	1:AD:191:ASN:ND2	2.21	0.73
1:CD:99:PHE:HA	1:CD:209:VAL:O	1.87	0.73
1:CK:80:VAL:CG1	1:CK:185:LEU:CB	2.67	0.73
1:AW:314:TYR:HE1	1:AW:316:SER:CA	2.01	0.73
1:AY:298:TRP:CD1	1:AY:312:VAL:HG13	2.20	0.73
1:CG:99:PHE:HA	1:CG:209:VAL:O	1.87	0.73
1:CJ:122:GLY:O	1:CJ:188:VAL:N	2.21	0.73
1:CQ:100:GLN:HG2	1:CQ:211:SER:OG	1.88	0.73
1:AX:111:ILE:HG22	1:AX:113:PRO:HD3	1.71	0.73
1:Bc:154:GLU:OE1	1:Cc:43:SER:OG	2.05	0.73
1:AE:253:ASP:CG	1:AE:285:PHE:HA	2.14	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:80:VAL:HG12	1:CI:185:LEU:CB	2.19	0.73
1:CP:99:PHE:HA	1:CP:209:VAL:O	1.88	0.73
1:CP:100:GLN:HG2	1:CP:211:SER:OG	1.87	0.73
1:CQ:141:LEU:CD2	1:CQ:184:ILE:HD11	2.15	0.73
1:CR:100:GLN:HG3	1:CR:211:SER:OG	1.88	0.73
1:AS:302:ASP:HB3	1:AS:305:ASN:CG	2.12	0.73
1:BV:130:ASP:HB2	1:CV:100:GLN:HE22	1.54	0.73
1:BX:154:GLU:OE1	1:CX:43:SER:OG	2.07	0.73
1:AY:111:ILE:HG22	1:AY:113:PRO:HD3	1.69	0.73
1:Ca:63:ILE:HD12	1:Ca:88:LEU:HG	1.71	0.73
1:Cc:99:PHE:HA	1:Cc:209:VAL:O	1.89	0.73
1:Ad:302:ASP:HB3	1:Ad:305:ASN:CG	2.13	0.73
1:Ad:314:TYR:HE1	1:Ad:316:SER:CA	2.02	0.73
1:CB:100:GLN:HG3	1:CB:211:SER:OG	1.88	0.73
1:CG:80:VAL:CG1	1:CG:185:LEU:HB3	2.17	0.73
1:BJ:130:ASP:HB2	1:CJ:100:GLN:HE22	1.53	0.73
1:CK:80:VAL:HG12	1:CK:185:LEU:CB	2.19	0.73
1:CL:141:LEU:CD2	1:CL:184:ILE:HD11	2.14	0.73
1:AO:72:THR:O	1:AO:191:ASN:ND2	2.22	0.73
1:AQ:302:ASP:HB3	1:AQ:305:ASN:CG	2.12	0.73
1:CU:100:GLN:HG2	1:CU:213:GLU:OE2	1.89	0.73
1:CB:122:GLY:O	1:CB:188:VAL:N	2.21	0.73
1:CH:100:GLN:HG2	1:CH:213:GLU:OE2	1.88	0.73
1:AJ:298:TRP:CD2	1:AJ:312:VAL:CG1	2.68	0.73
1:CM:141:LEU:CD2	1:CM:184:ILE:HD11	2.14	0.73
1:AN:298:TRP:CD2	1:AN:312:VAL:CG1	2.68	0.73
1:CN:141:LEU:CD2	1:CN:184:ILE:HD11	2.16	0.73
1:CX:100:GLN:HG3	1:CX:211:SER:OG	1.89	0.73
1:CB:99:PHE:HA	1:CB:209:VAL:O	1.89	0.73
1:CF:100:GLN:HG2	1:CF:211:SER:OG	1.88	0.73
1:AJ:72:THR:O	1:AJ:191:ASN:ND2	2.22	0.73
1:AO:265:ILE:CG2	1:AO:313:ALA:O	2.37	0.73
1:AU:265:ILE:CG2	1:AU:313:ALA:O	2.37	0.73
1:Ab:299:GLY:CA	1:Ab:310:ASP:O	2.37	0.73
1:Cd:100:GLN:HG3	1:Cd:211:SER:OG	1.88	0.73
1:AA:265:ILE:CG2	1:AA:313:ALA:O	2.36	0.73
1:CA:80:VAL:CG1	1:CA:185:LEU:HB3	2.18	0.73
1:CB:100:GLN:HG2	1:CB:213:GLU:OE2	1.88	0.73
1:CE:99:PHE:HA	1:CE:209:VAL:O	1.89	0.73
1:CF:63:ILE:HD12	1:CF:88:LEU:HG	1.71	0.73
1:AH:302:ASP:HB3	1:AH:305:ASN:CG	2.13	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:299:GLY:CA	1:AM:310:ASP:O	2.36	0.73
1:BN:154:GLU:OE1	1:CN:43:SER:OG	2.07	0.73
1:BR:130:ASP:HB2	1:CR:100:GLN:HE22	1.53	0.73
1:BT:130:ASP:HB2	1:CT:100:GLN:HE22	1.54	0.73
1:AV:302:ASP:HB3	1:AV:305:ASN:CG	2.12	0.73
1:CW:100:GLN:HG2	1:CW:213:GLU:OE2	1.89	0.73
1:CW:100:GLN:HG3	1:CW:211:SER:OG	1.88	0.73
1:CY:99:PHE:HA	1:CY:209:VAL:O	1.87	0.73
1:BZ:130:ASP:HB2	1:CZ:100:GLN:HE22	1.53	0.73
1:Cd:80:VAL:CG1	1:Cd:185:LEU:CB	2.67	0.73
1:BE:130:ASP:HB2	1:CE:100:GLN:HE22	1.54	0.72
1:AG:111:ILE:HG22	1:AG:113:PRO:HD3	1.71	0.72
1:CO:80:VAL:CG1	1:CO:185:LEU:HB3	2.19	0.72
1:BP:154:GLU:OE1	1:CP:43:SER:OG	2.07	0.72
1:CP:122:GLY:O	1:CP:188:VAL:N	2.22	0.72
1:AV:111:ILE:HG22	1:AV:113:PRO:HD3	1.71	0.72
1:BB:98:ILE:HG22	1:AK:91:ARG:NE	2.04	0.72
1:AC:299:GLY:CA	1:AC:310:ASP:O	2.37	0.72
1:AE:265:ILE:CG2	1:AE:313:ALA:O	2.37	0.72
1:BM:130:ASP:HB2	1:CM:100:GLN:HE22	1.53	0.72
1:CP:100:GLN:HG2	1:CP:213:GLU:OE2	1.89	0.72
1:AQ:253:ASP:CG	1:AQ:285:PHE:HA	2.14	0.72
1:CQ:100:GLN:HG3	1:CQ:211:SER:OG	1.88	0.72
1:AW:253:ASP:CG	1:AW:285:PHE:HA	2.14	0.72
1:Ca:99:PHE:HA	1:Ca:209:VAL:O	1.89	0.72
1:Ab:119:THR:HG23	1:Ab:193:ASP:HB2	1.71	0.72
1:Ac:119:THR:HG23	1:Ac:193:ASP:HB2	1.71	0.72
1:AC:265:ILE:CG2	1:AC:313:ALA:O	2.37	0.72
1:CE:122:GLY:O	1:CE:188:VAL:N	2.22	0.72
1:CG:100:GLN:HG3	1:CG:211:SER:OG	1.90	0.72
1:AI:302:ASP:HB3	1:AI:305:ASN:CG	2.13	0.72
1:BO:154:GLU:OE1	1:CO:43:SER:OG	2.06	0.72
1:CO:122:GLY:O	1:CO:188:VAL:N	2.22	0.72
1:CV:100:GLN:HG2	1:CV:213:GLU:OE2	1.89	0.72
1:Aa:265:ILE:CG2	1:Aa:313:ALA:O	2.37	0.72
1:Cb:80:VAL:CG1	1:Cb:185:LEU:HB3	2.18	0.72
1:Ac:111:ILE:HG22	1:Ac:113:PRO:HD3	1.71	0.72
1:BC:98:ILE:HG22	1:AY:91:ARG:HE	1.54	0.72
1:CK:200:LEU:HD13	1:CL:45:VAL:HG23	1.71	0.72
1:CP:80:VAL:CG1	1:CP:185:LEU:HB3	2.19	0.72
1:AQ:111:ILE:HG22	1:AQ:113:PRO:HD3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:299:GLY:CA	1:AV:310:ASP:O	2.37	0.72
1:BA:91:ARG:NH1	1:AI:98:ILE:HG23	2.04	0.72
1:AC:111:ILE:HG22	1:AC:113:PRO:HD3	1.71	0.72
1:CC:100:GLN:HG2	1:CC:213:GLU:OE2	1.89	0.72
1:BD:130:ASP:HB2	1:CD:100:GLN:HE22	1.54	0.72
1:CD:100:GLN:HG3	1:CD:211:SER:OG	1.88	0.72
1:BG:130:ASP:HB2	1:CG:100:GLN:HE22	1.54	0.72
1:BI:98:ILE:HG22	1:Aa:91:ARG:HE	1.54	0.72
1:BI:130:ASP:HB2	1:CI:100:GLN:HE22	1.55	0.72
1:CN:80:VAL:CG1	1:CN:185:LEU:HB3	2.19	0.72
1:CX:99:PHE:HA	1:CX:209:VAL:O	1.88	0.72
1:CZ:99:PHE:HA	1:CZ:209:VAL:O	1.89	0.72
1:Ab:72:THR:O	1:Ab:191:ASN:ND2	2.22	0.72
1:BK:130:ASP:HB2	1:CK:100:GLN:HE22	1.53	0.72
1:CK:100:GLN:HG3	1:CK:211:SER:OG	1.89	0.72
1:CL:100:GLN:HG2	1:CL:213:GLU:OE2	1.89	0.72
1:AM:72:THR:O	1:AM:191:ASN:ND2	2.21	0.72
1:CR:80:VAL:CG1	1:CR:185:LEU:CB	2.67	0.72
1:BW:154:GLU:OE1	1:CW:43:SER:OG	2.08	0.72
1:BB:130:ASP:HB2	1:CB:100:GLN:HE22	1.53	0.72
1:CD:80:VAL:CG1	1:CD:185:LEU:CB	2.68	0.72
1:AG:68:LEU:HB2	1:AG:195:VAL:HG22	1.71	0.72
1:AI:298:TRP:CD2	1:AI:312:VAL:CG1	2.68	0.72
1:CL:80:VAL:CG1	1:CL:185:LEU:CB	2.68	0.72
1:AN:72:THR:O	1:AN:191:ASN:ND2	2.23	0.72
1:CS:100:GLN:HG2	1:CS:213:GLU:OE2	1.89	0.72
1:AU:253:ASP:CG	1:AU:285:PHE:HA	2.14	0.72
1:CX:63:ILE:HD12	1:CX:88:LEU:HG	1.71	0.72
1:Ad:72:THR:O	1:Ad:191:ASN:ND2	2.23	0.72
1:BA:130:ASP:HB2	1:CA:100:GLN:HE22	1.55	0.72
1:AB:265:ILE:CG2	1:AB:313:ALA:O	2.38	0.72
1:BG:153:TRP:O	1:CP:151:LYS:NZ	2.22	0.72
1:CM:101:ARG:NH1	1:CM:166:LEU:HD12	2.05	0.72
1:AR:72:THR:O	1:AR:191:ASN:ND2	2.22	0.72
1:Bc:130:ASP:HB2	1:Cc:100:GLN:HE22	1.55	0.72
1:CG:80:VAL:CG1	1:CG:185:LEU:CB	2.68	0.72
1:CH:122:GLY:HA3	1:BN:114:MET:SD	2.30	0.72
1:BK:101:ARG:HB3	1:BK:166:LEU:HD11	1.70	0.72
1:AK:314:TYR:HE1	1:AK:316:SER:CA	2.03	0.72
1:CR:100:GLN:HG2	1:CR:211:SER:OG	1.90	0.72
1:CY:100:GLN:HG2	1:CY:213:GLU:OE2	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:111:ILE:HG22	1:AZ:113:PRO:HD3	1.72	0.72
1:AA:119:THR:HG23	1:AA:193:ASP:HB2	1.71	0.72
1:AB:299:GLY:CA	1:AB:310:ASP:O	2.37	0.72
1:AC:98:ILE:HG23	1:BS:91:ARG:NH1	2.03	0.72
1:CJ:100:GLN:HG2	1:CJ:211:SER:OG	1.88	0.72
1:CK:80:VAL:CG1	1:CK:185:LEU:HB3	2.20	0.72
1:CQ:80:VAL:CG1	1:CQ:185:LEU:CB	2.68	0.72
1:CR:100:GLN:HG2	1:CR:213:GLU:OE2	1.89	0.72
1:Aa:68:LEU:HB2	1:Aa:195:VAL:HG22	1.72	0.72
1:CD:43:SER:O	1:Cd:34:ARG:HD3	1.90	0.71
1:BH:130:ASP:HB2	1:CH:100:GLN:HE22	1.54	0.71
1:CK:63:ILE:HD12	1:CK:88:LEU:HG	1.71	0.71
1:CN:99:PHE:HA	1:CN:209:VAL:O	1.90	0.71
1:AU:72:THR:O	1:AU:191:ASN:ND2	2.23	0.71
1:AU:299:GLY:CA	1:AU:310:ASP:O	2.37	0.71
1:CZ:80:VAL:CG1	1:CZ:185:LEU:HB3	2.19	0.71
1:Ca:63:ILE:HD11	1:Ca:89:LEU:HD23	1.72	0.71
1:CD:100:GLN:HG2	1:CD:211:SER:OG	1.90	0.71
1:CG:100:GLN:HG2	1:CG:211:SER:OG	1.90	0.71
1:BI:98:ILE:HG22	1:Aa:91:ARG:NE	2.05	0.71
1:CJ:100:GLN:HG3	1:CJ:211:SER:OG	1.90	0.71
1:BQ:130:ASP:HB2	1:CQ:100:GLN:HE22	1.55	0.71
1:CS:100:GLN:HG2	1:CS:211:SER:OG	1.90	0.71
1:AW:314:TYR:CD1	1:AW:315:TYR:N	2.58	0.71
1:CI:99:PHE:HA	1:CI:209:VAL:O	1.90	0.71
1:CL:100:GLN:HG2	1:CL:211:SER:OG	1.90	0.71
1:CM:100:GLN:HG3	1:CM:211:SER:OG	1.90	0.71
1:BO:130:ASP:HB2	1:CO:100:GLN:HE22	1.55	0.71
1:AO:253:ASP:CG	1:AO:285:PHE:HA	2.15	0.71
1:CO:80:VAL:CG1	1:CO:185:LEU:CB	2.68	0.71
1:CT:80:VAL:CG1	1:CT:185:LEU:CB	2.68	0.71
1:AW:302:ASP:CB	1:AW:305:ASN:CG	2.64	0.71
1:CW:99:PHE:HA	1:CW:209:VAL:O	1.89	0.71
1:CX:100:GLN:HG2	1:CX:211:SER:OG	1.89	0.71
1:BE:72:THR:O	1:BE:191:ASN:ND2	2.24	0.71
1:AK:253:ASP:OD1	1:AK:285:PHE:CA	2.37	0.71
1:AT:91:ARG:HE	1:Ba:98:ILE:HG22	1.54	0.71
1:AV:265:ILE:CG2	1:AV:313:ALA:O	2.38	0.71
1:BX:130:ASP:HB2	1:CX:100:GLN:HE22	1.54	0.71
1:Ca:80:VAL:CG1	1:Ca:185:LEU:HB3	2.20	0.71
1:Cb:100:GLN:HG2	1:Cb:213:GLU:OE2	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:302:ASP:CB	1:AE:305:ASN:CG	2.64	0.71
1:CE:100:GLN:HG3	1:CE:211:SER:OG	1.89	0.71
1:AJ:302:ASP:CB	1:AJ:305:ASN:CG	2.64	0.71
1:AO:298:TRP:CD2	1:AO:312:VAL:CG1	2.68	0.71
1:AY:72:THR:O	1:AY:191:ASN:ND2	2.23	0.71
1:CY:122:GLY:O	1:CY:188:VAL:N	2.23	0.71
1:Ca:122:GLY:O	1:Ca:188:VAL:N	2.23	0.71
1:Bb:154:GLU:OE1	1:Cb:43:SER:OG	2.07	0.71
1:Ad:253:ASP:OD1	1:Ad:285:PHE:CA	2.38	0.71
1:AF:299:GLY:CA	1:AF:310:ASP:O	2.38	0.71
1:AX:253:ASP:CG	1:AX:285:PHE:HA	2.16	0.71
1:CX:100:GLN:HG2	1:CX:213:GLU:OE2	1.89	0.71
1:CZ:100:GLN:HG2	1:CZ:211:SER:OG	1.91	0.71
1:Ac:265:ILE:CG2	1:Ac:313:ALA:O	2.38	0.71
1:BA:98:ILE:HG22	1:AI:91:ARG:HE	1.54	0.71
1:CC:100:GLN:HG2	1:CC:211:SER:OG	1.89	0.71
1:BF:72:THR:O	1:BF:191:ASN:ND2	2.23	0.71
1:CG:101:ARG:NH1	1:CG:166:LEU:HD12	2.04	0.71
1:BH:101:ARG:HB3	1:BH:166:LEU:HD11	1.71	0.71
1:CH:80:VAL:CG1	1:CH:185:LEU:CB	2.69	0.71
1:BK:72:THR:O	1:BK:191:ASN:ND2	2.24	0.71
1:AR:299:GLY:CA	1:AR:310:ASP:O	2.38	0.71
1:CS:122:GLY:O	1:CS:188:VAL:N	2.24	0.71
1:Aa:72:THR:O	1:Aa:191:ASN:ND2	2.23	0.71
1:Ca:100:GLN:HG3	1:Ca:211:SER:OG	1.89	0.71
1:Ab:265:ILE:CG2	1:Ab:313:ALA:O	2.39	0.71
1:Ad:253:ASP:CG	1:Ad:285:PHE:HA	2.15	0.71
1:Cd:100:GLN:HG2	1:Cd:213:GLU:OE2	1.91	0.71
1:AB:91:ARG:HE	1:BY:98:ILE:HG22	1.56	0.71
1:AB:253:ASP:CG	1:AB:285:PHE:HA	2.15	0.71
1:AD:253:ASP:OD1	1:AD:285:PHE:CA	2.39	0.71
1:CK:99:PHE:HA	1:CK:209:VAL:O	1.90	0.71
1:AL:72:THR:O	1:AL:191:ASN:ND2	2.24	0.71
1:CM:99:PHE:HA	1:CM:209:VAL:O	1.89	0.71
1:AN:265:ILE:CG2	1:AN:313:ALA:O	2.39	0.71
1:AR:111:ILE:HG22	1:AR:113:PRO:HD3	1.72	0.71
1:CR:122:GLY:O	1:CR:188:VAL:N	2.23	0.71
1:AS:119:THR:HG23	1:AS:193:ASP:HB2	1.73	0.71
1:AY:119:THR:HG23	1:AY:193:ASP:HB2	1.73	0.71
1:Aa:302:ASP:CB	1:Aa:305:ASN:CG	2.64	0.71
1:Ac:72:THR:O	1:Ac:191:ASN:ND2	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bd:101:ARG:HB3	1:Bd:166:LEU:HD11	1.73	0.71
1:BA:101:ARG:HB3	1:BA:166:LEU:HD11	1.73	0.71
1:CB:80:VAL:CG1	1:CB:185:LEU:CB	2.69	0.71
1:BC:101:ARG:HB3	1:BC:166:LEU:HD11	1.72	0.71
1:BF:130:ASP:HB2	1:CF:100:GLN:HE22	1.56	0.71
1:AN:299:GLY:CA	1:AN:310:ASP:O	2.38	0.71
1:BQ:98:ILE:HG22	1:AZ:91:ARG:HE	1.55	0.71
1:AQ:299:GLY:CA	1:AQ:310:ASP:O	2.39	0.71
1:CR:63:ILE:HD12	1:CR:88:LEU:HG	1.73	0.71
1:CW:80:VAL:HG12	1:CW:185:LEU:CB	2.18	0.71
1:Aa:299:GLY:CA	1:Aa:310:ASP:O	2.36	0.71
1:Ca:141:LEU:CD2	1:Ca:184:ILE:HD11	2.17	0.71
1:Ab:298:TRP:CD2	1:Ab:312:VAL:CG1	2.69	0.71
1:Cc:80:VAL:CG1	1:Cc:185:LEU:HB3	2.21	0.71
1:CD:80:VAL:HG12	1:CD:185:LEU:CB	2.21	0.71
1:AH:118:ASN:O	1:Ad:116:PRO:HB3	1.91	0.71
1:AI:253:ASP:CG	1:AI:285:PHE:HA	2.16	0.71
1:AM:111:ILE:HG22	1:AM:113:PRO:HD3	1.72	0.71
1:AO:302:ASP:CB	1:AO:305:ASN:CG	2.64	0.71
1:AP:302:ASP:CB	1:AP:305:ASN:CG	2.64	0.71
1:AR:253:ASP:OD1	1:AR:285:PHE:CA	2.39	0.71
1:AV:72:THR:O	1:AV:191:ASN:ND2	2.23	0.71
1:AV:302:ASP:CB	1:AV:305:ASN:CG	2.64	0.71
1:AX:72:THR:O	1:AX:191:ASN:ND2	2.23	0.71
1:CY:100:GLN:HG2	1:CY:211:SER:OG	1.91	0.71
1:Ca:80:VAL:CG1	1:Ca:185:LEU:CB	2.69	0.71
1:Ab:253:ASP:CG	1:Ab:285:PHE:HA	2.16	0.71
1:Cb:99:PHE:HA	1:Cb:209:VAL:O	1.91	0.71
1:Ac:302:ASP:CB	1:Ac:305:ASN:CG	2.64	0.71
1:AA:72:THR:O	1:AA:191:ASN:ND2	2.24	0.70
1:AA:302:ASP:CB	1:AA:305:ASN:CG	2.64	0.70
1:CA:141:LEU:CD2	1:CA:184:ILE:HD11	2.19	0.70
1:AD:302:ASP:CB	1:AD:305:ASN:CG	2.64	0.70
1:AH:265:ILE:CG2	1:AH:313:ALA:O	2.39	0.70
1:AJ:119:THR:HG23	1:AJ:193:ASP:HB2	1.73	0.70
1:BL:139:ASP:HA	1:BL:142:GLN:HG2	1.72	0.70
1:AL:302:ASP:HB3	1:AL:305:ASN:CG	2.14	0.70
1:CL:100:GLN:HG3	1:CL:211:SER:OG	1.91	0.70
1:AQ:314:TYR:CD1	1:AQ:315:TYR:N	2.59	0.70
1:BT:154:GLU:OE1	1:CT:43:SER:OG	2.08	0.70
1:CU:99:PHE:HA	1:CU:209:VAL:O	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:265:ILE:CG2	1:AZ:313:ALA:O	2.39	0.70
1:Cd:80:VAL:CG1	1:Cd:185:LEU:HB3	2.19	0.70
1:AA:314:TYR:CD1	1:AA:315:TYR:N	2.59	0.70
1:CA:100:GLN:HG2	1:CA:211:SER:OG	1.91	0.70
1:AC:302:ASP:CB	1:AC:305:ASN:CG	2.65	0.70
1:AG:302:ASP:CB	1:AG:305:ASN:CG	2.64	0.70
1:BK:98:ILE:HG22	1:AS:91:ARG:HE	1.54	0.70
1:AK:302:ASP:CB	1:AK:305:ASN:CG	2.64	0.70
1:AK:314:TYR:CD1	1:AK:315:TYR:N	2.59	0.70
1:CK:117:ALA:CB	1:CL:38:PRO:O	2.39	0.70
1:AM:253:ASP:CG	1:AM:285:PHE:HA	2.15	0.70
1:AN:253:ASP:CG	1:AN:285:PHE:HA	2.15	0.70
1:AQ:302:ASP:CB	1:AQ:305:ASN:CG	2.64	0.70
1:CQ:122:GLY:O	1:CQ:188:VAL:N	2.24	0.70
1:AR:302:ASP:CB	1:AR:305:ASN:CG	2.64	0.70
1:BT:101:ARG:HB3	1:BT:166:LEU:HD11	1.73	0.70
1:BU:98:ILE:HG22	1:AX:91:ARG:HE	1.56	0.70
1:AZ:299:GLY:CA	1:AZ:310:ASP:O	2.36	0.70
1:Cc:141:LEU:CD2	1:Cc:184:ILE:HD11	2.18	0.70
1:AA:91:ARG:HE	1:BV:98:ILE:HG22	1.56	0.70
1:AF:68:LEU:HB2	1:AF:195:VAL:HG22	1.74	0.70
1:CF:100:GLN:HG3	1:CF:211:SER:OG	1.90	0.70
1:CH:80:VAL:HG12	1:CH:185:LEU:CB	2.22	0.70
1:AJ:68:LEU:HB2	1:AJ:195:VAL:HG22	1.73	0.70
1:AJ:314:TYR:CD1	1:AJ:315:TYR:N	2.59	0.70
1:AL:253:ASP:OD1	1:AL:285:PHE:CA	2.39	0.70
1:AM:314:TYR:CD1	1:AM:315:TYR:N	2.60	0.70
1:CM:122:GLY:O	1:CM:188:VAL:N	2.24	0.70
1:CO:99:PHE:HA	1:CO:209:VAL:O	1.90	0.70
1:CV:141:LEU:CD2	1:CV:184:ILE:HD11	2.17	0.70
1:BY:101:ARG:HB3	1:BY:166:LEU:HD11	1.73	0.70
1:AZ:253:ASP:OD1	1:AZ:285:PHE:CA	2.39	0.70
1:Cc:100:GLN:HG2	1:Cc:213:GLU:OE2	1.91	0.70
1:Cd:80:VAL:HG12	1:Cd:185:LEU:CB	2.20	0.70
1:AC:253:ASP:CG	1:AC:285:PHE:HA	2.15	0.70
1:CE:100:GLN:HG2	1:CE:213:GLU:OE2	1.91	0.70
1:AF:253:ASP:CG	1:AF:285:PHE:HA	2.16	0.70
1:CF:80:VAL:CG1	1:CF:185:LEU:HB3	2.21	0.70
1:AJ:299:GLY:CA	1:AJ:310:ASP:O	2.39	0.70
1:AQ:72:THR:O	1:AQ:191:ASN:ND2	2.24	0.70
1:CR:80:VAL:HG12	1:CR:185:LEU:CB	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:302:ASP:CB	1:AT:305:ASN:CG	2.64	0.70
1:AX:314:TYR:CD1	1:AX:315:TYR:N	2.60	0.70
1:AZ:302:ASP:CB	1:AZ:305:ASN:CG	2.65	0.70
1:Bd:72:THR:O	1:Bd:191:ASN:ND2	2.24	0.70
1:Ad:314:TYR:CD1	1:Ad:315:TYR:N	2.59	0.70
1:AA:299:GLY:CA	1:AA:310:ASP:O	2.38	0.70
1:AB:302:ASP:CB	1:AB:305:ASN:CG	2.65	0.70
1:CC:122:GLY:O	1:CC:188:VAL:N	2.24	0.70
1:CD:63:ILE:HD11	1:CD:89:LEU:HD23	1.73	0.70
1:BG:101:ARG:HB3	1:BG:166:LEU:HD11	1.73	0.70
1:CG:122:GLY:O	1:CG:188:VAL:N	2.24	0.70
1:AJ:253:ASP:OD1	1:AJ:285:PHE:CA	2.39	0.70
1:CK:100:GLN:HG2	1:CK:213:GLU:OE2	1.90	0.70
1:BL:101:ARG:HB3	1:BL:166:LEU:HD11	1.73	0.70
1:AM:314:TYR:CD1	1:AM:315:TYR:C	2.70	0.70
1:CM:80:VAL:CG1	1:CM:185:LEU:HB3	2.21	0.70
1:CV:122:GLY:O	1:CV:188:VAL:N	2.24	0.70
1:Cc:122:GLY:O	1:Cc:188:VAL:N	2.25	0.70
1:Ad:302:ASP:CB	1:Ad:305:ASN:CG	2.64	0.70
1:BA:101:ARG:CZ	1:BA:166:LEU:CD1	2.69	0.70
1:AA:253:ASP:CG	1:AA:285:PHE:HA	2.15	0.70
1:BE:101:ARG:HB3	1:BE:166:LEU:HD11	1.73	0.70
1:AF:302:ASP:CB	1:AF:305:ASN:CG	2.64	0.70
1:AH:253:ASP:CG	1:AH:285:PHE:HA	2.15	0.70
1:BI:101:ARG:HB3	1:BI:166:LEU:HD11	1.73	0.70
1:AI:111:ILE:HG22	1:AI:113:PRO:HD3	1.74	0.70
1:AI:299:GLY:CA	1:AI:310:ASP:O	2.37	0.70
1:CM:63:ILE:HD11	1:CM:89:LEU:HD23	1.74	0.70
1:AO:253:ASP:OD1	1:AO:285:PHE:CA	2.39	0.70
1:CO:63:ILE:HD12	1:CO:88:LEU:HG	1.74	0.70
1:BQ:72:THR:O	1:BQ:191:ASN:ND2	2.25	0.70
1:AS:314:TYR:CD1	1:AS:315:TYR:N	2.60	0.70
1:AT:314:TYR:CD1	1:AT:315:TYR:N	2.60	0.70
1:AW:299:GLY:CA	1:AW:310:ASP:O	2.39	0.70
1:CX:80:VAL:CG1	1:CX:185:LEU:HB3	2.21	0.70
1:AY:302:ASP:CB	1:AY:305:ASN:CG	2.64	0.70
1:CY:141:LEU:CD2	1:CY:184:ILE:HD11	2.18	0.70
1:AB:119:THR:HG23	1:AB:193:ASP:HB2	1.72	0.70
1:CG:63:ILE:HD12	1:CG:88:LEU:HG	1.71	0.70
1:AN:302:ASP:CB	1:AN:305:ASN:CG	2.64	0.70
1:AU:302:ASP:CB	1:AU:305:ASN:CG	2.64	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:119:THR:HG23	1:AW:193:ASP:HB2	1.74	0.70
1:CY:80:VAL:CG1	1:CY:185:LEU:HB3	2.20	0.70
1:BZ:154:GLU:OE1	1:CZ:43:SER:OG	2.09	0.70
1:CZ:80:VAL:HG12	1:CZ:185:LEU:CB	2.21	0.70
1:CA:100:GLN:HG3	1:CA:211:SER:OG	1.91	0.70
1:AB:253:ASP:OD1	1:AB:285:PHE:CA	2.39	0.70
1:CC:122:GLY:HA3	1:BS:114:MET:SD	2.31	0.70
1:AD:111:ILE:HG22	1:AD:113:PRO:HD3	1.73	0.70
1:BE:75:ASP:OD2	1:CH:62:ARG:NH1	2.20	0.70
1:AF:119:THR:HG23	1:AF:193:ASP:HB2	1.73	0.70
1:AF:314:TYR:CD1	1:AF:315:TYR:N	2.60	0.70
1:AH:302:ASP:CB	1:AH:305:ASN:CG	2.65	0.70
1:AL:314:TYR:CD1	1:AL:315:TYR:N	2.60	0.70
1:AM:253:ASP:OD1	1:AM:285:PHE:CA	2.39	0.70
1:AM:314:TYR:CE1	1:AM:316:SER:N	2.60	0.70
1:CP:100:GLN:HG3	1:CP:211:SER:OG	1.91	0.70
1:AS:302:ASP:CB	1:AS:305:ASN:CG	2.64	0.70
1:AX:253:ASP:OD1	1:AX:285:PHE:CA	2.40	0.70
1:AX:302:ASP:CB	1:AX:305:ASN:CG	2.64	0.70
1:AJ:91:ARG:NE	1:BR:98:ILE:CG2	2.55	0.70
1:BM:139:ASP:HA	1:BM:142:GLN:HG2	1.73	0.70
1:BN:130:ASP:HB2	1:CN:100:GLN:HE22	1.53	0.70
1:BQ:98:ILE:HG22	1:AZ:91:ARG:NE	2.06	0.70
1:CQ:63:ILE:HD11	1:CQ:89:LEU:HD23	1.74	0.70
1:CU:100:GLN:HG2	1:CU:211:SER:OG	1.92	0.70
1:AV:253:ASP:OD1	1:AV:285:PHE:CA	2.39	0.70
1:CV:100:GLN:HG2	1:CV:211:SER:OG	1.89	0.70
1:AX:299:GLY:CA	1:AX:310:ASP:O	2.38	0.70
1:CD:122:GLY:O	1:CD:188:VAL:N	2.25	0.70
1:AE:314:TYR:CD1	1:AE:315:TYR:N	2.60	0.70
1:AL:302:ASP:CB	1:AL:305:ASN:CG	2.65	0.70
1:AM:302:ASP:CB	1:AM:305:ASN:CG	2.64	0.70
1:BP:130:ASP:HB2	1:CP:100:GLN:HE22	1.56	0.70
1:AR:314:TYR:CD1	1:AR:315:TYR:N	2.60	0.70
1:AT:253:ASP:OD1	1:AT:285:PHE:CA	2.40	0.70
1:CT:100:GLN:HG2	1:CT:211:SER:OG	1.90	0.70
1:AZ:68:LEU:HB2	1:AZ:195:VAL:HG22	1.74	0.70
1:BI:139:ASP:HA	1:BI:142:GLN:HG2	1.74	0.69
1:AL:299:GLY:CA	1:AL:310:ASP:O	2.40	0.69
1:AP:299:GLY:CA	1:AP:310:ASP:O	2.38	0.69
1:CU:80:VAL:CG1	1:CU:185:LEU:HB3	2.20	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:253:ASP:CG	1:AV:285:PHE:HA	2.15	0.69
1:AV:314:TYR:CD1	1:AV:315:TYR:N	2.60	0.69
1:AX:265:ILE:CG2	1:AX:313:ALA:O	2.39	0.69
1:Aa:111:ILE:HG22	1:Aa:113:PRO:HD3	1.72	0.69
1:Ca:100:GLN:HG2	1:Ca:211:SER:OG	1.90	0.69
1:AA:253:ASP:OD1	1:AA:285:PHE:CA	2.39	0.69
1:AC:253:ASP:OD1	1:AC:285:PHE:CA	2.39	0.69
1:AF:111:ILE:HG22	1:AF:113:PRO:HD3	1.74	0.69
1:AH:253:ASP:OD1	1:AH:285:PHE:CA	2.40	0.69
1:CJ:80:VAL:CG1	1:CJ:185:LEU:HB3	2.21	0.69
1:AO:299:GLY:CA	1:AO:310:ASP:O	2.38	0.69
1:CQ:122:GLY:C	1:CQ:188:VAL:HB	2.16	0.69
1:CT:122:GLY:O	1:CT:188:VAL:N	2.23	0.69
1:CU:100:GLN:HG3	1:CU:211:SER:OG	1.92	0.69
1:Ab:302:ASP:CB	1:Ab:305:ASN:CG	2.64	0.69
1:Ac:253:ASP:OD1	1:Ac:285:PHE:CA	2.40	0.69
1:AA:111:ILE:HG22	1:AA:113:PRO:HD3	1.72	0.69
1:AA:141:LEU:O	1:AA:144:THR:CG2	2.37	0.69
1:CC:80:VAL:CG1	1:CC:185:LEU:HB3	2.22	0.69
1:AD:265:ILE:CG2	1:AD:313:ALA:O	2.40	0.69
1:CE:62:ARG:NH1	1:BH:75:ASP:OD2	2.24	0.69
1:AO:314:TYR:CD1	1:AO:315:TYR:N	2.60	0.69
1:AT:91:ARG:NE	1:Ba:98:ILE:HG22	2.06	0.69
1:AU:314:TYR:CD1	1:AU:315:TYR:N	2.60	0.69
1:CW:63:ILE:HD12	1:CW:88:LEU:HG	1.72	0.69
1:BZ:101:ARG:HB3	1:BZ:166:LEU:HD11	1.74	0.69
1:Ba:72:THR:O	1:Ba:191:ASN:ND2	2.25	0.69
1:CA:80:VAL:CG1	1:CA:185:LEU:CB	2.69	0.69
1:AD:119:THR:HG23	1:AD:193:ASP:HB2	1.74	0.69
1:AD:314:TYR:CD1	1:AD:315:TYR:N	2.60	0.69
1:CE:141:LEU:CD2	1:CE:184:ILE:HD11	2.18	0.69
1:AG:253:ASP:CG	1:AG:285:PHE:HA	2.16	0.69
1:BJ:72:THR:O	1:BJ:191:ASN:ND2	2.25	0.69
1:AN:253:ASP:OD1	1:AN:285:PHE:CA	2.39	0.69
1:BO:139:ASP:HA	1:BO:142:GLN:HG2	1.74	0.69
1:BQ:153:TRP:O	1:CZ:151:LYS:NZ	2.25	0.69
1:AQ:265:ILE:CG2	1:AQ:313:ALA:O	2.39	0.69
1:BS:130:ASP:HB2	1:CS:100:GLN:HE22	1.56	0.69
1:AU:253:ASP:OD1	1:AU:285:PHE:CA	2.39	0.69
1:AW:253:ASP:OD1	1:AW:285:PHE:CA	2.39	0.69
1:CY:63:ILE:HD12	1:CY:88:LEU:HG	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:122:GLY:O	1:CZ:188:VAL:N	2.25	0.69
1:Ac:314:TYR:CD1	1:Ac:315:TYR:N	2.60	0.69
1:AC:314:TYR:CD1	1:AC:315:TYR:N	2.60	0.69
1:AG:299:GLY:CA	1:AG:310:ASP:O	2.38	0.69
1:CG:122:GLY:O	1:CG:188:VAL:HB	1.93	0.69
1:AI:253:ASP:OD1	1:AI:285:PHE:CA	2.40	0.69
1:CO:80:VAL:HG12	1:CO:185:LEU:CB	2.22	0.69
1:AT:299:GLY:CA	1:AT:310:ASP:O	2.39	0.69
1:BV:318:GLU:N	1:BV:318:GLU:OE2	2.26	0.69
1:BX:101:ARG:HB3	1:BX:166:LEU:HD11	1.74	0.69
1:CA:122:GLY:O	1:CA:188:VAL:HB	1.93	0.69
1:BB:75:ASP:OD2	1:CF:62:ARG:NH1	2.24	0.69
1:AE:299:GLY:CA	1:AE:310:ASP:O	2.37	0.69
1:CJ:100:GLN:HG2	1:CJ:213:GLU:OE2	1.91	0.69
1:CK:117:ALA:HB2	1:CL:38:PRO:O	1.93	0.69
1:BN:101:ARG:HB3	1:BN:166:LEU:HD11	1.74	0.69
1:AN:314:TYR:CD1	1:AN:315:TYR:N	2.60	0.69
1:BQ:139:ASP:HA	1:BQ:142:GLN:HG2	1.75	0.69
1:BR:101:ARG:HB3	1:BR:166:LEU:HD11	1.75	0.69
1:CS:99:PHE:HA	1:CS:209:VAL:O	1.93	0.69
1:AX:314:TYR:CD1	1:AX:315:TYR:C	2.70	0.69
1:AZ:314:TYR:CD1	1:AZ:315:TYR:N	2.61	0.69
1:CA:122:GLY:O	1:CA:188:VAL:N	2.25	0.69
1:BC:130:ASP:HB2	1:CC:100:GLN:HE22	1.58	0.69
1:CE:63:ILE:HD12	1:CE:88:LEU:HG	1.74	0.69
1:AI:302:ASP:CB	1:AI:305:ASN:CG	2.65	0.69
1:AJ:111:ILE:HG22	1:AJ:113:PRO:HD3	1.73	0.69
1:AL:253:ASP:CG	1:AL:285:PHE:HA	2.16	0.69
1:CM:80:VAL:CG1	1:CM:185:LEU:CB	2.70	0.69
1:BS:101:ARG:HB3	1:BS:166:LEU:HD11	1.73	0.69
1:AS:253:ASP:OD1	1:AS:285:PHE:CA	2.40	0.69
1:CT:63:ILE:HD12	1:CT:88:LEU:HG	1.74	0.69
1:CY:80:VAL:CG1	1:CY:185:LEU:CB	2.70	0.69
1:Cb:63:ILE:HD11	1:Cb:89:LEU:HD23	1.73	0.69
1:CA:151:LYS:NZ	1:BV:153:TRP:O	2.24	0.69
1:AB:314:TYR:CD1	1:AB:315:TYR:N	2.60	0.69
1:CE:80:VAL:CG1	1:CE:185:LEU:HB3	2.23	0.69
1:CE:122:GLY:HA3	1:BM:114:MET:SD	2.33	0.69
1:AF:253:ASP:OD1	1:AF:285:PHE:CA	2.40	0.69
1:CF:80:VAL:CG1	1:CF:185:LEU:CB	2.71	0.69
1:AG:119:THR:HG23	1:AG:193:ASP:HB2	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:100:GLN:HG2	1:CI:211:SER:OG	1.91	0.69
1:AJ:253:ASP:CG	1:AJ:285:PHE:HA	2.15	0.69
1:BK:98:ILE:HG22	1:AS:91:ARG:NE	2.08	0.69
1:CL:141:LEU:N	1:CL:141:LEU:HD23	2.08	0.69
1:CP:63:ILE:HD12	1:CP:88:LEU:HG	1.72	0.69
1:CP:80:VAL:CG1	1:CP:185:LEU:CB	2.71	0.69
1:CQ:63:ILE:HD12	1:CQ:88:LEU:HG	1.74	0.69
1:BT:101:ARG:CZ	1:BT:166:LEU:CD1	2.71	0.69
1:Ab:253:ASP:OD1	1:Ab:285:PHE:CA	2.40	0.69
1:Ab:314:TYR:CD1	1:Ab:315:TYR:C	2.71	0.69
1:AC:72:THR:O	1:AC:191:ASN:ND2	2.25	0.69
1:AG:98:ILE:HG23	1:Bd:91:ARG:NH1	2.07	0.69
1:AL:265:ILE:CG2	1:AL:313:ALA:O	2.41	0.69
1:BM:101:ARG:HB3	1:BM:166:LEU:HD11	1.73	0.69
1:CN:80:VAL:CG1	1:CN:185:LEU:CB	2.71	0.69
1:AP:265:ILE:CG2	1:AP:313:ALA:O	2.41	0.69
1:CQ:80:VAL:HG12	1:CQ:185:LEU:CB	2.21	0.69
1:BS:318:GLU:N	1:BS:318:GLU:OE2	2.26	0.69
1:AS:299:GLY:CA	1:AS:310:ASP:O	2.39	0.69
1:AX:314:TYR:CE1	1:AX:316:SER:N	2.61	0.69
1:BZ:72:THR:O	1:BZ:191:ASN:ND2	2.26	0.69
1:AZ:68:LEU:HB2	1:AZ:195:VAL:CG2	2.23	0.69
1:AZ:119:THR:HG23	1:AZ:193:ASP:HB2	1.74	0.69
1:Aa:253:ASP:OD1	1:Aa:285:PHE:CA	2.40	0.69
1:CD:80:VAL:CG1	1:CD:185:LEU:HB3	2.23	0.69
1:AI:265:ILE:CG2	1:AI:313:ALA:O	2.40	0.69
1:AI:314:TYR:CD1	1:AI:315:TYR:C	2.71	0.69
1:BJ:101:ARG:HB3	1:BJ:166:LEU:HD11	1.74	0.69
1:AK:68:LEU:HB2	1:AK:195:VAL:CG2	2.22	0.69
1:BO:72:THR:O	1:BO:191:ASN:ND2	2.26	0.69
1:CQ:99:PHE:CA	1:CQ:209:VAL:O	2.41	0.69
1:CS:80:VAL:CG1	1:CS:185:LEU:HB3	2.23	0.69
1:CU:80:VAL:CG1	1:CU:185:LEU:CB	2.70	0.69
1:CW:122:GLY:O	1:CW:188:VAL:N	2.26	0.69
1:Ab:68:LEU:HB2	1:Ab:195:VAL:HG22	1.73	0.69
1:Ab:314:TYR:CD1	1:Ab:315:TYR:N	2.61	0.69
1:AA:314:TYR:CD1	1:AA:315:TYR:C	2.71	0.68
1:BC:91:ARG:NH1	1:AY:98:ILE:HG23	2.08	0.68
1:AG:265:ILE:CG2	1:AG:313:ALA:O	2.41	0.68
1:CI:63:ILE:HD12	1:CI:88:LEU:HG	1.75	0.68
1:CI:122:GLY:O	1:CI:188:VAL:HB	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:101:ARG:CZ	1:BN:166:LEU:CD1	2.71	0.68
1:AN:68:LEU:HB2	1:AN:195:VAL:HG22	1.75	0.68
1:AR:253:ASP:CG	1:AR:285:PHE:HA	2.16	0.68
1:AS:265:ILE:CG2	1:AS:313:ALA:O	2.41	0.68
1:AT:68:LEU:HB2	1:AT:195:VAL:HG22	1.75	0.68
1:BU:91:ARG:NH1	1:AX:98:ILE:HG23	2.08	0.68
1:CU:63:ILE:HD12	1:CU:88:LEU:HG	1.75	0.68
1:AX:119:THR:HG23	1:AX:193:ASP:HB2	1.75	0.68
1:CA:122:GLY:C	1:CA:188:VAL:HB	2.17	0.68
1:BC:101:ARG:CZ	1:BC:166:LEU:CD1	2.71	0.68
1:AC:91:ARG:HE	1:BS:98:ILE:HG22	1.58	0.68
1:BE:154:GLU:OE1	1:CE:43:SER:OG	2.11	0.68
1:AE:253:ASP:OD1	1:AE:285:PHE:CA	2.39	0.68
1:AG:314:TYR:CD1	1:AG:315:TYR:N	2.61	0.68
1:AI:314:TYR:CD1	1:AI:315:TYR:N	2.61	0.68
1:CM:62:ARG:NH1	1:BO:75:ASP:OD2	2.25	0.68
1:AQ:253:ASP:OD1	1:AQ:285:PHE:CA	2.40	0.68
1:CV:63:ILE:HD11	1:CV:89:LEU:HD23	1.75	0.68
1:CX:122:GLY:O	1:CX:188:VAL:N	2.25	0.68
1:CC:100:GLN:HG3	1:CC:211:SER:OG	1.92	0.68
1:AH:119:THR:HG23	1:AH:193:ASP:HB2	1.74	0.68
1:AH:314:TYR:CD1	1:AH:315:TYR:N	2.62	0.68
1:AJ:68:LEU:HB2	1:AJ:195:VAL:CG2	2.23	0.68
1:BL:98:ILE:HG22	1:AU:91:ARG:HE	1.57	0.68
1:CS:63:ILE:HD12	1:CS:88:LEU:HG	1.74	0.68
1:AU:314:TYR:CE1	1:AU:316:SER:N	2.61	0.68
1:Ba:101:ARG:HB3	1:Ba:166:LEU:HD11	1.73	0.68
1:Ba:130:ASP:HB2	1:Ca:100:GLN:HE22	1.56	0.68
1:Ba:318:GLU:N	1:Ba:318:GLU:OE2	2.26	0.68
1:Ab:111:ILE:HG22	1:Ab:113:PRO:HD3	1.76	0.68
1:CA:80:VAL:HG12	1:CA:185:LEU:CB	2.24	0.68
1:BF:318:GLU:N	1:BF:318:GLU:OE2	2.27	0.68
1:CF:63:ILE:HD11	1:CF:89:LEU:HD23	1.75	0.68
1:AG:253:ASP:OD1	1:AG:285:PHE:CA	2.40	0.68
1:CI:122:GLY:C	1:CI:188:VAL:HB	2.18	0.68
1:AJ:265:ILE:CG2	1:AJ:313:ALA:O	2.42	0.68
1:AN:119:THR:HG23	1:AN:193:ASP:HB2	1.74	0.68
1:AP:314:TYR:CD1	1:AP:315:TYR:N	2.61	0.68
1:AS:253:ASP:CG	1:AS:285:PHE:HA	2.15	0.68
1:BW:101:ARG:HB3	1:BW:166:LEU:HD11	1.75	0.68
1:Ac:299:GLY:CA	1:Ac:310:ASP:O	2.42	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cc:63:ILE:HD11	1:Cc:89:LEU:HD23	1.75	0.68
1:Ad:265:ILE:CG2	1:Ad:313:ALA:O	2.41	0.68
1:Cd:99:PHE:CA	1:Cd:209:VAL:O	2.42	0.68
1:BB:101:ARG:HB3	1:BB:166:LEU:HD11	1.74	0.68
1:AB:314:TYR:CD1	1:AB:315:TYR:C	2.71	0.68
1:AD:299:GLY:CA	1:AD:310:ASP:O	2.40	0.68
1:CG:63:ILE:HD11	1:CG:89:LEU:HD23	1.74	0.68
1:CG:80:VAL:HG12	1:CG:185:LEU:CB	2.22	0.68
1:BJ:318:GLU:OE2	1:BJ:318:GLU:N	2.27	0.68
1:CL:99:PHE:CA	1:CL:209:VAL:O	2.40	0.68
1:CO:141:LEU:CD2	1:CO:184:ILE:HD11	2.15	0.68
1:AP:253:ASP:OD1	1:AP:285:PHE:CA	2.41	0.68
1:CP:80:VAL:HG12	1:CP:185:LEU:CB	2.24	0.68
1:AU:314:TYR:CD1	1:AU:315:TYR:C	2.71	0.68
1:BW:72:THR:O	1:BW:191:ASN:ND2	2.27	0.68
1:Ac:314:TYR:CE1	1:Ac:316:SER:N	2.61	0.68
1:CB:80:VAL:HG12	1:CB:185:LEU:CB	2.23	0.68
1:BG:318:GLU:N	1:BG:318:GLU:OE2	2.27	0.68
1:AH:111:ILE:HG22	1:AH:113:PRO:HD3	1.74	0.68
1:CH:100:GLN:HG3	1:CH:211:SER:OG	1.92	0.68
1:AK:68:LEU:HB2	1:AK:195:VAL:HG22	1.75	0.68
1:AO:314:TYR:CE1	1:AO:316:SER:N	2.61	0.68
1:BX:318:GLU:OE2	1:BX:318:GLU:N	2.26	0.68
1:Aa:314:TYR:CD1	1:Aa:315:TYR:N	2.61	0.68
1:AB:111:ILE:HG22	1:AB:113:PRO:HD3	1.74	0.68
1:CJ:141:LEU:CD2	1:CJ:184:ILE:HD11	2.18	0.68
1:CS:100:GLN:HG3	1:CS:211:SER:OG	1.93	0.68
1:CU:63:ILE:HD11	1:CU:89:LEU:HD23	1.74	0.68
1:CY:99:PHE:CA	1:CY:209:VAL:O	2.42	0.68
1:CZ:122:GLY:O	1:CZ:188:VAL:HB	1.94	0.68
1:BA:98:ILE:HG22	1:AI:91:ARG:NE	2.09	0.68
1:BB:72:THR:O	1:BB:191:ASN:ND2	2.27	0.68
1:CC:141:LEU:N	1:CC:141:LEU:HD23	2.08	0.68
1:CE:80:VAL:CG1	1:CE:185:LEU:CB	2.72	0.68
1:CK:38:PRO:O	1:CL:117:ALA:HB2	1.94	0.68
1:AN:314:TYR:CE1	1:AN:316:SER:N	2.62	0.68
1:AO:314:TYR:CD1	1:AO:315:TYR:C	2.70	0.68
1:BR:72:THR:O	1:BR:191:ASN:ND2	2.27	0.68
1:BT:318:GLU:N	1:BT:318:GLU:OE2	2.27	0.68
1:CV:63:ILE:HD12	1:CV:88:LEU:HG	1.76	0.68
1:BY:318:GLU:N	1:BY:318:GLU:OE2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:63:ILE:HD12	1:CA:88:LEU:HG	1.75	0.68
1:CA:141:LEU:N	1:CA:141:LEU:HD23	2.08	0.68
1:CB:63:ILE:HD11	1:CB:89:LEU:HD23	1.75	0.68
1:BD:72:THR:O	1:BD:191:ASN:ND2	2.27	0.68
1:BD:318:GLU:N	1:BD:318:GLU:OE2	2.27	0.68
1:BI:153:TRP:O	1:Ca:151:LYS:NZ	2.27	0.68
1:CK:141:LEU:N	1:CK:141:LEU:HD23	2.09	0.68
1:CN:63:ILE:HD12	1:CN:88:LEU:HG	1.75	0.68
1:CQ:122:GLY:O	1:CQ:188:VAL:HB	1.94	0.68
1:AT:265:ILE:CG2	1:AT:313:ALA:O	2.42	0.68
1:Aa:62:ARG:HG2	1:Aa:62:ARG:HH11	1.59	0.68
1:CF:122:GLY:O	1:CF:188:VAL:N	2.27	0.68
1:AG:314:TYR:CD1	1:AG:315:TYR:C	2.72	0.68
1:AI:314:TYR:CE1	1:AI:316:SER:N	2.61	0.68
1:CJ:80:VAL:CG1	1:CJ:185:LEU:CB	2.72	0.68
1:AO:68:LEU:HB2	1:AO:195:VAL:HG22	1.75	0.68
1:AT:111:ILE:HG22	1:AT:113:PRO:HD3	1.73	0.68
1:CT:99:PHE:CA	1:CT:209:VAL:O	2.42	0.68
1:CX:99:PHE:CA	1:CX:209:VAL:O	2.42	0.68
1:AY:253:ASP:OD1	1:AY:285:PHE:CA	2.41	0.68
1:CB:122:GLY:HA3	1:BY:114:MET:SD	2.34	0.67
1:CC:151:LYS:NZ	1:BS:153:TRP:O	2.27	0.67
1:CM:80:VAL:HG12	1:CM:185:LEU:CB	2.24	0.67
1:CP:199:VAL:O	1:CP:199:VAL:HG13	1.94	0.67
1:AR:68:LEU:HB2	1:AR:195:VAL:HG22	1.76	0.67
1:CR:99:PHE:CA	1:CR:209:VAL:O	2.43	0.67
1:CS:80:VAL:CG1	1:CS:185:LEU:CB	2.71	0.67
1:BZ:318:GLU:N	1:BZ:318:GLU:OE2	2.26	0.67
1:AZ:314:TYR:CD1	1:AZ:315:TYR:C	2.72	0.67
1:Ab:68:LEU:HB2	1:Ab:195:VAL:CG2	2.25	0.67
1:CB:63:ILE:HD12	1:CB:88:LEU:HG	1.76	0.67
1:AD:68:LEU:HB2	1:AD:195:VAL:HG22	1.76	0.67
1:AF:314:TYR:CD1	1:AF:315:TYR:C	2.73	0.67
1:AI:141:LEU:O	1:AI:144:THR:CG2	2.38	0.67
1:AM:265:ILE:CG2	1:AM:313:ALA:O	2.41	0.67
1:BN:72:THR:O	1:BN:191:ASN:ND2	2.27	0.67
1:BV:101:ARG:HB3	1:BV:166:LEU:HD11	1.75	0.67
1:AY:253:ASP:CG	1:AY:285:PHE:HA	2.16	0.67
1:Cb:80:VAL:CG1	1:Cb:185:LEU:CB	2.72	0.67
1:Cc:199:VAL:HG13	1:Cc:199:VAL:O	1.94	0.67
1:AA:314:TYR:CE1	1:AA:316:SER:N	2.62	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:318:GLU:N	1:BE:318:GLU:OE2	2.27	0.67
1:AE:314:TYR:CD1	1:AE:315:TYR:C	2.72	0.67
1:CF:141:LEU:CD2	1:CF:184:ILE:HD11	2.19	0.67
1:AH:314:TYR:CE1	1:AH:316:SER:N	2.61	0.67
1:CI:122:GLY:O	1:CI:188:VAL:N	2.26	0.67
1:AJ:119:THR:O	1:AJ:192:THR:HB	1.95	0.67
1:AM:119:THR:HG23	1:AM:193:ASP:HB2	1.75	0.67
1:CN:122:GLY:O	1:CN:188:VAL:N	2.27	0.67
1:AP:253:ASP:CG	1:AP:285:PHE:HA	2.18	0.67
1:AR:265:ILE:CG2	1:AR:313:ALA:O	2.43	0.67
1:CR:200:LEU:HD13	1:CT:45:VAL:HG23	1.75	0.67
1:AS:314:TYR:CD1	1:AS:315:TYR:C	2.72	0.67
1:AT:253:ASP:CG	1:AT:285:PHE:HA	2.16	0.67
1:CV:80:VAL:CG1	1:CV:185:LEU:HB3	2.24	0.67
1:AZ:253:ASP:CG	1:AZ:285:PHE:HA	2.15	0.67
1:Bb:130:ASP:HB2	1:Cb:100:GLN:HE22	1.57	0.67
1:Bb:318:GLU:N	1:Bb:318:GLU:OE2	2.28	0.67
1:BC:318:GLU:N	1:BC:318:GLU:OE2	2.27	0.67
1:AC:119:THR:HG23	1:AC:193:ASP:HB2	1.76	0.67
1:CD:151:LYS:NZ	1:BF:153:TRP:O	2.28	0.67
1:BL:101:ARG:CZ	1:BL:166:LEU:CD1	2.73	0.67
1:BO:91:ARG:NH1	1:Ab:98:ILE:HG23	2.09	0.67
1:BQ:318:GLU:N	1:BQ:318:GLU:OE2	2.27	0.67
1:AV:314:TYR:CD1	1:AV:315:TYR:C	2.72	0.67
1:AB:314:TYR:CE1	1:AB:316:SER:N	2.62	0.67
1:AE:119:THR:HG23	1:AE:193:ASP:HB2	1.76	0.67
1:CJ:63:ILE:HD11	1:CJ:89:LEU:HD23	1.77	0.67
1:BP:72:THR:O	1:BP:191:ASN:ND2	2.28	0.67
1:CP:122:GLY:C	1:CP:188:VAL:HB	2.19	0.67
1:AQ:314:TYR:CE1	1:AQ:316:SER:N	2.63	0.67
1:AQ:314:TYR:CD1	1:AQ:315:TYR:C	2.72	0.67
1:CV:80:VAL:CG1	1:CV:185:LEU:CB	2.73	0.67
1:BW:101:ARG:CZ	1:BW:166:LEU:CD1	2.72	0.67
1:AY:314:TYR:CD1	1:AY:315:TYR:N	2.62	0.67
1:Aa:253:ASP:CG	1:Aa:285:PHE:HA	2.16	0.67
1:AA:98:ILE:HG23	1:BV:91:ARG:NH1	2.08	0.67
1:CF:34:ARG:HD3	1:CY:43:SER:O	1.95	0.67
1:CG:199:VAL:HG13	1:CG:199:VAL:O	1.94	0.67
1:CJ:99:PHE:HA	1:CJ:209:VAL:O	1.95	0.67
1:BL:98:ILE:HG22	1:AU:91:ARG:NE	2.08	0.67
1:AM:62:ARG:HG2	1:AM:62:ARG:HH11	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:265:ILE:CG2	1:AY:313:ALA:O	2.43	0.67
1:AY:299:GLY:CA	1:AY:310:ASP:O	2.41	0.67
1:CY:80:VAL:HG12	1:CY:185:LEU:CB	2.25	0.67
1:Aa:119:THR:HG23	1:Aa:193:ASP:HB2	1.75	0.67
1:Ad:119:THR:HG23	1:Ad:193:ASP:HB2	1.76	0.67
1:AE:314:TYR:CE1	1:AE:316:SER:N	2.62	0.67
1:AG:68:LEU:HB2	1:AG:195:VAL:CG2	2.25	0.67
1:BM:72:THR:O	1:BM:191:ASN:ND2	2.28	0.67
1:AM:114:MET:SD	1:Ac:122:GLY:HA3	2.34	0.67
1:BN:318:GLU:N	1:BN:318:GLU:OE2	2.28	0.67
1:BP:139:ASP:HA	1:BP:142:GLN:HG2	1.77	0.67
1:BQ:101:ARG:NH1	1:BQ:166:LEU:HD12	2.10	0.67
1:AS:111:ILE:HG22	1:AS:113:PRO:HD3	1.75	0.67
1:AT:314:TYR:CD1	1:AT:315:TYR:C	2.73	0.67
1:BU:101:ARG:HB3	1:BU:166:LEU:HD11	1.74	0.67
1:CX:80:VAL:CG1	1:CX:185:LEU:CB	2.73	0.67
1:Ca:99:PHE:CA	1:Ca:209:VAL:O	2.42	0.67
1:BA:72:THR:O	1:BA:191:ASN:ND2	2.27	0.67
1:AB:91:ARG:NE	1:BY:98:ILE:HG22	2.10	0.67
1:AC:91:ARG:NE	1:BS:98:ILE:HG22	2.10	0.67
1:CC:80:VAL:CG1	1:CC:185:LEU:CB	2.72	0.67
1:BD:101:ARG:HB3	1:BD:166:LEU:HD11	1.75	0.67
1:BG:72:THR:O	1:BG:191:ASN:ND2	2.28	0.67
1:BK:318:GLU:N	1:BK:318:GLU:OE2	2.27	0.67
1:BO:101:ARG:HB3	1:BO:166:LEU:HD11	1.77	0.67
1:BO:318:GLU:N	1:BO:318:GLU:OE2	2.27	0.67
1:AT:119:THR:HG23	1:AT:193:ASP:HB2	1.74	0.67
1:CU:80:VAL:HG12	1:CU:185:LEU:CB	2.23	0.67
1:BY:130:ASP:HB2	1:CY:100:GLN:HE22	1.58	0.67
1:BZ:139:ASP:HA	1:BZ:142:GLN:HG2	1.76	0.67
1:Bb:101:ARG:HB3	1:Bb:166:LEU:HD11	1.76	0.67
1:Ab:314:TYR:CE1	1:Ab:316:SER:N	2.61	0.67
1:Bd:318:GLU:N	1:Bd:318:GLU:OE2	2.28	0.67
1:BA:101:ARG:NH1	1:BA:166:LEU:HD12	2.09	0.67
1:AD:91:ARG:NE	1:BF:98:ILE:HG22	2.10	0.67
1:AE:141:LEU:O	1:AE:144:THR:CG2	2.41	0.67
1:AF:98:ILE:HG23	1:Bb:91:ARG:NH1	2.10	0.67
1:CJ:122:GLY:C	1:CJ:188:VAL:HB	2.19	0.67
1:CM:34:ARG:HD3	1:CW:43:SER:O	1.95	0.67
1:AO:119:THR:HG23	1:AO:193:ASP:HB2	1.76	0.67
1:BY:101:ARG:CZ	1:BY:166:LEU:CD1	2.73	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:314:TYR:CE1	1:AY:316:SER:N	2.63	0.67
1:Aa:314:TYR:CD1	1:Aa:315:TYR:C	2.73	0.67
1:AD:253:ASP:CG	1:AD:285:PHE:HA	2.15	0.67
1:CD:63:ILE:HD12	1:CD:88:LEU:HG	1.77	0.67
1:BH:318:GLU:N	1:BH:318:GLU:OE2	2.28	0.67
1:AJ:314:TYR:CE1	1:AJ:316:SER:N	2.63	0.67
1:CK:199:VAL:O	1:CK:199:VAL:HG13	1.94	0.67
1:AL:119:THR:HG23	1:AL:193:ASP:HB2	1.77	0.67
1:CM:151:LYS:NZ	1:Bc:153:TRP:O	2.27	0.67
1:BS:72:THR:O	1:BS:191:ASN:ND2	2.28	0.67
1:Ac:253:ASP:CG	1:Ac:285:PHE:HA	2.15	0.67
1:Ad:68:LEU:HB2	1:Ad:195:VAL:HG22	1.75	0.67
1:BD:139:ASP:HA	1:BD:142:GLN:HG2	1.75	0.66
1:AD:314:TYR:CD1	1:AD:315:TYR:C	2.73	0.66
1:AH:314:TYR:CD1	1:AH:315:TYR:C	2.72	0.66
1:BI:101:ARG:CZ	1:BI:166:LEU:CD1	2.72	0.66
1:BK:101:ARG:CZ	1:BK:166:LEU:CD1	2.73	0.66
1:AN:314:TYR:CD1	1:AN:315:TYR:C	2.71	0.66
1:CN:63:ILE:HD11	1:CN:89:LEU:HD23	1.76	0.66
1:CN:122:GLY:O	1:CN:188:VAL:HB	1.96	0.66
1:CA:63:ILE:HD11	1:CA:89:LEU:HD23	1.76	0.66
1:CC:141:LEU:CD2	1:CC:184:ILE:HD11	2.19	0.66
1:CH:99:PHE:CA	1:CH:209:VAL:O	2.43	0.66
1:BJ:101:ARG:CZ	1:BJ:166:LEU:CD1	2.71	0.66
1:CK:38:PRO:O	1:CL:117:ALA:CB	2.43	0.66
1:AS:314:TYR:CE1	1:AS:316:SER:N	2.63	0.66
1:BT:72:THR:O	1:BT:191:ASN:ND2	2.28	0.66
1:AV:119:THR:HG23	1:AV:193:ASP:HB2	1.76	0.66
1:CV:100:GLN:HG3	1:CV:211:SER:OG	1.93	0.66
1:CX:63:ILE:HD11	1:CX:89:LEU:HD23	1.76	0.66
1:CZ:99:PHE:CA	1:CZ:209:VAL:O	2.44	0.66
1:Bc:318:GLU:N	1:Bc:318:GLU:OE2	2.27	0.66
1:Ac:314:TYR:CD1	1:Ac:315:TYR:C	2.73	0.66
1:Ad:68:LEU:HB2	1:Ad:195:VAL:CG2	2.25	0.66
1:BA:101:ARG:NH1	1:BA:166:LEU:CD1	2.57	0.66
1:AB:68:LEU:HB2	1:AB:195:VAL:HG22	1.76	0.66
1:AB:98:ILE:HG23	1:BY:91:ARG:NH1	2.10	0.66
1:BK:91:ARG:NH1	1:AS:98:ILE:HG23	2.08	0.66
1:AP:119:THR:O	1:AP:192:THR:HB	1.96	0.66
1:AQ:119:THR:HG23	1:AQ:193:ASP:HB2	1.76	0.66
1:BT:139:ASP:HA	1:BT:142:GLN:HG2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BV:101:ARG:CZ	1:BV:166:LEU:CD1	2.74	0.66
1:BW:130:ASP:HB2	1:CW:100:GLN:NE2	2.11	0.66
1:AX:314:TYR:HE1	1:AX:316:SER:HA	1.61	0.66
1:Bb:139:ASP:HA	1:Bb:142:GLN:HG2	1.77	0.66
1:BA:166:LEU:HD13	1:BA:166:LEU:C	2.21	0.66
1:BA:318:GLU:N	1:BA:318:GLU:OE2	2.28	0.66
1:BB:318:GLU:N	1:BB:318:GLU:OE2	2.28	0.66
1:AC:314:TYR:CD1	1:AC:315:TYR:C	2.73	0.66
1:BF:101:ARG:HB3	1:BF:166:LEU:HD11	1.76	0.66
1:BG:98:ILE:HG22	1:AP:91:ARG:HE	1.60	0.66
1:AM:91:ARG:NH2	1:Bc:98:ILE:HG22	2.10	0.66
1:CO:63:ILE:HD11	1:CO:89:LEU:HD23	1.76	0.66
1:AP:119:THR:HG23	1:AP:193:ASP:HB2	1.76	0.66
1:CT:80:VAL:HG12	1:CT:185:LEU:CB	2.23	0.66
1:BU:101:ARG:CZ	1:BU:166:LEU:CD1	2.73	0.66
1:BU:318:GLU:N	1:BU:318:GLU:OE2	2.28	0.66
1:BV:72:THR:O	1:BV:191:ASN:ND2	2.27	0.66
1:BV:139:ASP:HA	1:BV:142:GLN:HG2	1.78	0.66
1:Aa:314:TYR:CE1	1:Aa:316:SER:N	2.64	0.66
1:Bd:101:ARG:NH1	1:Bd:166:LEU:HD12	2.10	0.66
1:Cd:63:ILE:HD12	1:Cd:88:LEU:HG	1.75	0.66
1:AA:91:ARG:NE	1:BV:98:ILE:HG22	2.09	0.66
1:CA:99:PHE:CA	1:CA:209:VAL:O	2.44	0.66
1:CB:43:SER:HA	1:CF:112:GLN:NE2	2.11	0.66
1:BC:98:ILE:HG22	1:AY:91:ARG:NE	2.10	0.66
1:AC:314:TYR:CE1	1:AC:316:SER:N	2.64	0.66
1:CD:99:PHE:CA	1:CD:209:VAL:O	2.43	0.66
1:CF:122:GLY:C	1:CF:188:VAL:HB	2.21	0.66
1:CK:63:ILE:HD11	1:CK:89:LEU:HD23	1.77	0.66
1:CL:63:ILE:HD11	1:CL:89:LEU:HD23	1.77	0.66
1:AM:91:ARG:NE	1:Bc:98:ILE:HG22	2.11	0.66
1:CM:63:ILE:HD12	1:CM:88:LEU:HG	1.76	0.66
1:AP:314:TYR:CD1	1:AP:315:TYR:C	2.73	0.66
1:CP:99:PHE:CA	1:CP:209:VAL:O	2.43	0.66
1:CV:317:ASP:HB3	1:CV:319:GLN:CD	2.21	0.66
1:CY:100:GLN:HG3	1:CY:211:SER:OG	1.96	0.66
1:Cc:80:VAL:CG1	1:Cc:185:LEU:CB	2.73	0.66
1:Cc:122:GLY:C	1:Cc:188:VAL:HB	2.20	0.66
1:CA:199:VAL:HG13	1:CA:199:VAL:O	1.95	0.66
1:CA:317:ASP:HB3	1:CA:319:GLN:CD	2.21	0.66
1:CC:317:ASP:HB3	1:CC:319:GLN:CD	2.20	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:314:TYR:CE1	1:AD:316:SER:N	2.64	0.66
1:AG:314:TYR:CE1	1:AG:316:SER:N	2.62	0.66
1:CL:122:GLY:O	1:CL:188:VAL:N	2.28	0.66
1:AM:68:LEU:HB2	1:AM:195:VAL:HG22	1.76	0.66
1:BQ:68:LEU:HD23	1:BQ:195:VAL:HG22	1.76	0.66
1:CS:317:ASP:HB3	1:CS:319:GLN:CD	2.21	0.66
1:CU:141:LEU:CD2	1:CU:184:ILE:HD11	2.19	0.66
1:AV:106:THR:HA	1:AV:162:TYR:OH	1.95	0.66
1:BW:318:GLU:N	1:BW:318:GLU:OE2	2.29	0.66
1:Ac:68:LEU:HB2	1:Ac:195:VAL:HG22	1.77	0.66
1:CD:122:GLY:C	1:CD:188:VAL:HB	2.20	0.66
1:AF:68:LEU:HB2	1:AF:195:VAL:CG2	2.26	0.66
1:BH:101:ARG:NH1	1:BH:166:LEU:HD12	2.10	0.66
1:CH:63:ILE:HD12	1:CH:88:LEU:HG	1.76	0.66
1:CJ:63:ILE:HD12	1:CJ:88:LEU:HG	1.76	0.66
1:CK:99:PHE:CA	1:CK:209:VAL:O	2.44	0.66
1:AN:68:LEU:HB2	1:AN:195:VAL:CG2	2.26	0.66
1:AP:314:TYR:CE1	1:AP:316:SER:N	2.63	0.66
1:CP:317:ASP:HB3	1:CP:319:GLN:CD	2.21	0.66
1:AQ:68:LEU:HB2	1:AQ:195:VAL:HG22	1.77	0.66
1:CT:122:GLY:C	1:CT:188:VAL:HB	2.20	0.66
1:BW:139:ASP:HA	1:BW:142:GLN:HG2	1.76	0.66
1:CW:99:PHE:CA	1:CW:209:VAL:O	2.43	0.66
1:AY:314:TYR:CD1	1:AY:315:TYR:C	2.74	0.66
1:Ca:80:VAL:HG12	1:Ca:185:LEU:CB	2.23	0.66
1:Bc:72:THR:O	1:Bc:191:ASN:ND2	2.29	0.66
1:Ad:314:TYR:CD1	1:Ad:315:TYR:C	2.73	0.66
1:CC:63:ILE:HD12	1:CC:88:LEU:HG	1.76	0.66
1:CC:80:VAL:HG12	1:CC:185:LEU:CB	2.26	0.66
1:CH:122:GLY:C	1:CH:188:VAL:HB	2.21	0.66
1:CI:63:ILE:HD11	1:CI:89:LEU:HD23	1.78	0.66
1:BK:98:ILE:C	1:BK:211:SER:O	2.39	0.66
1:BM:318:GLU:N	1:BM:318:GLU:OE2	2.28	0.66
1:CO:317:ASP:HB3	1:CO:319:GLN:CD	2.21	0.66
1:AV:68:LEU:HB2	1:AV:195:VAL:HG22	1.76	0.66
1:CV:99:PHE:CA	1:CV:209:VAL:O	2.43	0.66
1:CV:122:GLY:C	1:CV:188:VAL:HB	2.19	0.66
1:CZ:122:GLY:C	1:CZ:188:VAL:HB	2.20	0.66
1:Bd:139:ASP:HA	1:Bd:142:GLN:HG2	1.77	0.66
1:BB:316:SER:HB2	1:BB:319:GLN:OE1	1.95	0.66
1:BC:101:ARG:NH1	1:BC:166:LEU:HD12	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:199:VAL:O	1:CC:199:VAL:HG13	1.95	0.66
1:BF:101:ARG:CZ	1:BF:166:LEU:CD1	2.73	0.66
1:CG:99:PHE:CA	1:CG:209:VAL:O	2.43	0.66
1:CL:80:VAL:HG12	1:CL:185:LEU:CB	2.22	0.66
1:CN:99:PHE:CA	1:CN:209:VAL:O	2.43	0.66
1:CN:122:GLY:C	1:CN:188:VAL:HB	2.21	0.66
1:CP:63:ILE:HD11	1:CP:89:LEU:HD23	1.77	0.66
1:AT:314:TYR:CE1	1:AT:316:SER:N	2.64	0.66
1:CT:317:ASP:HB3	1:CT:319:GLN:CD	2.21	0.66
1:AU:119:THR:HG23	1:AU:193:ASP:HB2	1.78	0.66
1:CW:200:LEU:HD13	1:Cd:45:VAL:HG23	1.77	0.66
1:Bb:72:THR:O	1:Bb:191:ASN:ND2	2.28	0.66
1:Cb:63:ILE:HD12	1:Cb:88:LEU:HG	1.77	0.66
1:Bc:58:SER:HB3	1:Bc:204:SER:HB3	1.78	0.66
1:CC:109:PHE:HB2	1:CC:158:VAL:CG1	2.26	0.66
1:BD:91:ARG:NH1	1:AW:98:ILE:HG23	2.10	0.66
1:BD:101:ARG:CZ	1:BD:166:LEU:CD1	2.73	0.66
1:BH:101:ARG:CZ	1:BH:166:LEU:CD1	2.72	0.66
1:BH:139:ASP:HA	1:BH:142:GLN:HG2	1.77	0.66
1:AI:119:THR:HG23	1:AI:193:ASP:HB2	1.77	0.66
1:AN:141:LEU:O	1:AN:144:THR:CG2	2.41	0.66
1:AO:68:LEU:HB2	1:AO:195:VAL:CG2	2.26	0.66
1:BU:101:ARG:NH1	1:BU:166:LEU:HD12	2.09	0.66
1:AX:141:LEU:O	1:AX:144:THR:CG2	2.37	0.66
1:AF:314:TYR:CE1	1:AF:316:SER:N	2.62	0.65
1:CG:122:GLY:C	1:CG:188:VAL:HB	2.21	0.65
1:BI:101:ARG:NH1	1:BI:166:LEU:HD12	2.11	0.65
1:BL:101:ARG:NH1	1:BL:166:LEU:HD12	2.10	0.65
1:BL:318:GLU:N	1:BL:318:GLU:OE2	2.29	0.65
1:AL:314:TYR:CD1	1:AL:315:TYR:C	2.73	0.65
1:CN:317:ASP:HB3	1:CN:319:GLN:CD	2.21	0.65
1:AR:314:TYR:CD1	1:AR:315:TYR:C	2.74	0.65
1:CZ:63:ILE:HD11	1:CZ:89:LEU:HD23	1.78	0.65
1:Ca:58:SER:HA	1:Ca:203:TRP:CZ3	2.31	0.65
1:Ab:106:THR:HA	1:Ab:162:TYR:OH	1.96	0.65
1:Cb:141:LEU:N	1:Cb:141:LEU:HD23	2.09	0.65
1:Bc:98:ILE:O	1:Bc:211:SER:C	2.39	0.65
1:Cc:317:ASP:HB3	1:Cc:319:GLN:CD	2.20	0.65
1:AB:68:LEU:HB2	1:AB:195:VAL:CG2	2.26	0.65
1:CC:99:PHE:CA	1:CC:209:VAL:O	2.42	0.65
1:AE:68:LEU:HB2	1:AE:195:VAL:HG22	1.76	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:91:ARG:NE	1:Bd:98:ILE:HG22	2.11	0.65
1:AK:265:ILE:CG2	1:AK:313:ALA:O	2.44	0.65
1:AM:68:LEU:HB2	1:AM:195:VAL:CG2	2.26	0.65
1:CM:122:GLY:O	1:CM:188:VAL:HB	1.97	0.65
1:CN:80:VAL:HG12	1:CN:185:LEU:CB	2.26	0.65
1:BP:318:GLU:N	1:BP:318:GLU:OE2	2.29	0.65
1:CP:141:LEU:N	1:CP:141:LEU:HD23	2.10	0.65
1:BR:139:ASP:HA	1:BR:142:GLN:HG2	1.76	0.65
1:CY:317:ASP:HB3	1:CY:319:GLN:CD	2.22	0.65
1:Aa:106:THR:HA	1:Aa:162:TYR:OH	1.97	0.65
1:Cc:122:GLY:O	1:Cc:188:VAL:HB	1.95	0.65
1:Ad:299:GLY:CA	1:Ad:310:ASP:O	2.43	0.65
1:CF:122:GLY:O	1:CF:188:VAL:HB	1.95	0.65
1:AL:314:TYR:CE1	1:AL:316:SER:N	2.65	0.65
1:CL:63:ILE:HD12	1:CL:88:LEU:HG	1.78	0.65
1:BO:114:MET:SD	1:Cb:122:GLY:HA3	2.37	0.65
1:BP:98:ILE:C	1:BP:211:SER:O	2.39	0.65
1:CV:43:SER:HA	1:CZ:112:GLN:NE2	2.11	0.65
1:CV:141:LEU:N	1:CV:141:LEU:HD23	2.10	0.65
1:CW:75:ASP:OD1	1:CW:188:VAL:C	2.40	0.65
1:BX:139:ASP:HA	1:BX:142:GLN:HG2	1.78	0.65
1:BY:176:ARG:HD2	1:CY:168:TRP:CE2	2.31	0.65
1:BZ:101:ARG:NH1	1:BZ:166:LEU:HD12	2.11	0.65
1:Ad:106:THR:HA	1:Ad:162:TYR:OH	1.96	0.65
1:CB:199:VAL:O	1:CB:199:VAL:HG13	1.96	0.65
1:CD:122:GLY:O	1:CD:188:VAL:HB	1.97	0.65
1:AH:68:LEU:HB2	1:AH:195:VAL:HG22	1.76	0.65
1:CK:122:GLY:O	1:CK:188:VAL:N	2.28	0.65
1:CM:75:ASP:OD1	1:CM:188:VAL:C	2.40	0.65
1:BO:316:SER:HB2	1:BO:319:GLN:OE1	1.95	0.65
1:BQ:101:ARG:CZ	1:BQ:166:LEU:CD1	2.75	0.65
1:BQ:101:ARG:NH1	1:BQ:166:LEU:CD1	2.60	0.65
1:BR:318:GLU:N	1:BR:318:GLU:OE2	2.28	0.65
1:AT:68:LEU:HB2	1:AT:195:VAL:CG2	2.25	0.65
1:BV:111:ILE:HG21	1:BV:123:TYR:OH	1.96	0.65
1:AW:68:LEU:HB2	1:AW:195:VAL:HG22	1.77	0.65
1:Aa:68:LEU:HB2	1:Aa:195:VAL:CG2	2.26	0.65
1:Ca:199:VAL:O	1:Ca:199:VAL:HG13	1.96	0.65
1:Bc:101:ARG:NH1	1:Bc:166:LEU:HD12	2.11	0.65
1:BB:91:ARG:NH1	1:AK:98:ILE:HG23	2.10	0.65
1:AC:116:PRO:HB3	1:AS:118:ASN:O	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:317:ASP:HB3	1:CG:319:GLN:CD	2.21	0.65
1:CH:317:ASP:HB3	1:CH:319:GLN:CD	2.21	0.65
1:AM:106:THR:HA	1:AM:162:TYR:OH	1.96	0.65
1:BS:101:ARG:NH1	1:BS:166:LEU:HD12	2.12	0.65
1:CT:199:VAL:HG13	1:CT:199:VAL:O	1.96	0.65
1:AU:314:TYR:HE1	1:AU:316:SER:HA	1.61	0.65
1:AV:68:LEU:HB2	1:AV:195:VAL:CG2	2.25	0.65
1:AZ:106:THR:HA	1:AZ:162:TYR:OH	1.95	0.65
1:BB:101:ARG:CZ	1:BB:166:LEU:CD1	2.75	0.65
1:CB:122:GLY:C	1:CB:188:VAL:HB	2.22	0.65
1:CF:80:VAL:HG12	1:CF:185:LEU:CB	2.25	0.65
1:AG:91:ARG:HE	1:Bd:98:ILE:HG22	1.61	0.65
1:CI:141:LEU:N	1:CI:141:LEU:HD23	2.10	0.65
1:BM:98:ILE:O	1:BM:211:SER:C	2.39	0.65
1:AM:141:LEU:O	1:AM:144:THR:CG2	2.41	0.65
1:CM:99:PHE:CA	1:CM:209:VAL:O	2.45	0.65
1:BO:101:ARG:CZ	1:BO:166:LEU:CD1	2.74	0.65
1:CQ:141:LEU:N	1:CQ:141:LEU:HD23	2.12	0.65
1:CS:63:ILE:HD11	1:CS:89:LEU:HD23	1.78	0.65
1:BU:139:ASP:HA	1:BU:142:GLN:HG2	1.77	0.65
1:BY:101:ARG:NH1	1:BY:166:LEU:HD12	2.11	0.65
1:Cc:99:PHE:CA	1:Cc:209:VAL:O	2.43	0.65
1:BB:98:ILE:O	1:BB:211:SER:C	2.40	0.65
1:AB:118:ASN:O	1:AK:116:PRO:HB3	1.96	0.65
1:BC:139:ASP:HA	1:BC:142:GLN:HG2	1.78	0.65
1:AJ:314:TYR:CD1	1:AJ:315:TYR:C	2.74	0.65
1:BK:98:ILE:O	1:BK:211:SER:C	2.40	0.65
1:BK:139:ASP:HA	1:BK:142:GLN:HG2	1.78	0.65
1:AK:314:TYR:CD1	1:AK:315:TYR:C	2.75	0.65
1:BL:130:ASP:HB2	1:CL:100:GLN:NE2	2.12	0.65
1:CL:43:SER:O	1:Cb:34:ARG:HD3	1.97	0.65
1:AW:106:THR:HA	1:AW:162:TYR:OH	1.97	0.65
1:BX:101:ARG:CZ	1:BX:166:LEU:CD1	2.74	0.65
1:CY:63:ILE:HD11	1:CY:89:LEU:HD23	1.77	0.65
1:CA:109:PHE:HB2	1:CA:158:VAL:CG1	2.27	0.65
1:BC:101:ARG:NH1	1:BC:166:LEU:CD1	2.60	0.65
1:BF:98:ILE:C	1:BF:211:SER:O	2.40	0.65
1:AI:68:LEU:HB2	1:AI:195:VAL:HG22	1.78	0.65
1:BO:61:SER:CB	1:BO:90:PRO:HD2	2.22	0.65
1:CT:58:SER:HA	1:CT:203:TRP:CZ3	2.32	0.65
1:AY:119:THR:O	1:AY:192:THR:HB	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ca:75:ASP:OD1	1:Ca:188:VAL:C	2.40	0.65
1:AB:106:THR:HA	1:AB:162:TYR:OH	1.97	0.65
1:AB:314:TYR:HE1	1:AB:316:SER:HA	1.61	0.65
1:BD:58:SER:HB3	1:BD:204:SER:HB3	1.79	0.65
1:CF:317:ASP:HB3	1:CF:319:GLN:CD	2.20	0.65
1:BG:139:ASP:HA	1:BG:142:GLN:HG2	1.78	0.65
1:BI:72:THR:O	1:BI:191:ASN:ND2	2.29	0.65
1:BJ:98:ILE:O	1:BJ:211:SER:C	2.40	0.65
1:CJ:58:SER:HA	1:CJ:203:TRP:CZ3	2.32	0.65
1:CJ:141:LEU:HD23	1:CJ:141:LEU:N	2.10	0.65
1:CK:112:GLN:NE2	1:CL:43:SER:HA	2.11	0.65
1:BL:101:ARG:NH1	1:BL:166:LEU:CD1	2.60	0.65
1:AP:63:ILE:HB	1:AP:199:VAL:HG13	1.79	0.65
1:CP:111:ILE:O	1:CP:198:SER:O	2.15	0.65
1:BT:98:ILE:C	1:BT:211:SER:O	2.40	0.65
1:AW:314:TYR:CD1	1:AW:315:TYR:C	2.74	0.65
1:BD:176:ARG:HD2	1:CD:168:TRP:CE2	2.32	0.65
1:AI:302:ASP:CB	1:AI:305:ASN:ND2	2.60	0.65
1:BL:72:THR:O	1:BL:191:ASN:ND2	2.29	0.65
1:AL:144:THR:HG23	1:AL:147:ALA:HB2	1.79	0.65
1:AO:314:TYR:HE1	1:AO:316:SER:HA	1.61	0.65
1:BR:101:ARG:NH1	1:BR:166:LEU:HD12	2.11	0.65
1:CU:317:ASP:HB3	1:CU:319:GLN:CD	2.22	0.65
1:Ba:80:VAL:HG13	1:Ba:185:LEU:HB3	1.79	0.65
1:Ca:111:ILE:O	1:Ca:198:SER:O	2.15	0.65
1:Cb:317:ASP:HB3	1:Cb:319:GLN:CD	2.21	0.65
1:Ac:314:TYR:HE1	1:Ac:316:SER:HA	1.62	0.65
1:Bd:98:ILE:O	1:Bd:211:SER:C	2.40	0.65
1:CB:99:PHE:CA	1:CB:209:VAL:O	2.44	0.64
1:CB:317:ASP:HB3	1:CB:319:GLN:CD	2.22	0.64
1:BE:101:ARG:NH1	1:BE:166:LEU:HD12	2.12	0.64
1:CE:317:ASP:HB3	1:CE:319:GLN:CD	2.21	0.64
1:CH:63:ILE:HD11	1:CH:89:LEU:HD23	1.78	0.64
1:CI:163:THR:HG21	1:CI:167:LEU:HD11	1.79	0.64
1:CM:122:GLY:C	1:CM:188:VAL:HB	2.21	0.64
1:AQ:314:TYR:HE1	1:AQ:316:SER:HA	1.62	0.64
1:BU:72:THR:O	1:BU:191:ASN:ND2	2.31	0.64
1:CU:141:LEU:HD23	1:CU:141:LEU:N	2.09	0.64
1:Aa:119:THR:O	1:Aa:192:THR:HB	1.97	0.64
1:BB:98:ILE:C	1:BB:211:SER:O	2.41	0.64
1:AC:68:LEU:HB2	1:AC:195:VAL:HG22	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:119:THR:O	1:AE:192:THR:HB	1.97	0.64
1:BG:316:SER:HB2	1:BG:319:GLN:OE1	1.98	0.64
1:AH:106:THR:HA	1:AH:162:TYR:OH	1.97	0.64
1:BJ:58:SER:HB3	1:BJ:204:SER:HB3	1.80	0.64
1:AQ:106:THR:HA	1:AQ:162:TYR:OH	1.97	0.64
1:AR:68:LEU:HB2	1:AR:195:VAL:CG2	2.28	0.64
1:AR:106:THR:HA	1:AR:162:TYR:OH	1.98	0.64
1:BT:130:ASP:HB2	1:CT:100:GLN:NE2	2.12	0.64
1:CW:122:GLY:C	1:CW:188:VAL:HB	2.21	0.64
1:CX:111:ILE:O	1:CX:198:SER:O	2.15	0.64
1:CX:317:ASP:HB3	1:CX:319:GLN:CD	2.22	0.64
1:CD:43:SER:O	1:Cd:34:ARG:CD	2.45	0.64
1:CE:141:LEU:N	1:CE:141:LEU:HD23	2.11	0.64
1:AF:62:ARG:HG2	1:AF:62:ARG:HH11	1.63	0.64
1:CF:199:VAL:HG13	1:CF:199:VAL:O	1.96	0.64
1:BJ:166:LEU:HD13	1:BJ:166:LEU:C	2.23	0.64
1:CM:111:ILE:O	1:CM:198:SER:O	2.15	0.64
1:BN:139:ASP:HA	1:BN:142:GLN:HG2	1.78	0.64
1:BP:98:ILE:O	1:BP:211:SER:C	2.40	0.64
1:BP:101:ARG:NH1	1:BP:166:LEU:HD12	2.10	0.64
1:CQ:111:ILE:O	1:CQ:198:SER:O	2.16	0.64
1:BS:139:ASP:HA	1:BS:142:GLN:HG2	1.78	0.64
1:AU:68:LEU:HB2	1:AU:195:VAL:HG22	1.78	0.64
1:CW:122:GLY:O	1:CW:188:VAL:HB	1.97	0.64
1:CZ:63:ILE:HD12	1:CZ:88:LEU:HG	1.77	0.64
1:Ba:139:ASP:HA	1:Ba:142:GLN:HG2	1.79	0.64
1:Cb:99:PHE:CA	1:Cb:209:VAL:O	2.46	0.64
1:Bd:101:ARG:CZ	1:Bd:166:LEU:CD1	2.75	0.64
1:Ad:302:ASP:CB	1:Ad:305:ASN:ND2	2.60	0.64
1:Cd:111:ILE:O	1:Cd:198:SER:O	2.15	0.64
1:BA:139:ASP:HA	1:BA:142:GLN:HG2	1.78	0.64
1:BB:130:ASP:HB2	1:CB:100:GLN:NE2	2.13	0.64
1:BB:139:ASP:HA	1:BB:142:GLN:HG2	1.79	0.64
1:AD:91:ARG:HE	1:BF:98:ILE:HG22	1.62	0.64
1:CE:99:PHE:CA	1:CE:209:VAL:O	2.44	0.64
1:CF:99:PHE:CA	1:CF:209:VAL:O	2.45	0.64
1:CO:111:ILE:O	1:CO:198:SER:O	2.15	0.64
1:BP:101:ARG:CZ	1:BP:166:LEU:CD1	2.74	0.64
1:AR:119:THR:HG23	1:AR:193:ASP:HB2	1.80	0.64
1:AU:106:THR:HA	1:AU:162:TYR:OH	1.98	0.64
1:AV:314:TYR:CE1	1:AV:316:SER:N	2.64	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:199:VAL:HG13	1:CX:199:VAL:O	1.97	0.64
1:AY:62:ARG:HG2	1:AY:62:ARG:HH11	1.62	0.64
1:AY:106:THR:HA	1:AY:162:TYR:OH	1.98	0.64
1:AY:302:ASP:CB	1:AY:305:ASN:ND2	2.60	0.64
1:Bd:98:ILE:C	1:Bd:211:SER:O	2.39	0.64
1:CI:99:PHE:CA	1:CI:209:VAL:O	2.45	0.64
1:BJ:101:ARG:NH1	1:BJ:166:LEU:CD1	2.60	0.64
1:BM:98:ILE:C	1:BM:211:SER:O	2.39	0.64
1:AP:302:ASP:CB	1:AP:305:ASN:ND2	2.60	0.64
1:BR:130:ASP:HB2	1:CR:100:GLN:NE2	2.13	0.64
1:AS:106:THR:HA	1:AS:162:TYR:OH	1.97	0.64
1:AT:106:THR:HA	1:AT:162:TYR:OH	1.98	0.64
1:Bc:98:ILE:C	1:Bc:211:SER:O	2.40	0.64
1:Bc:101:ARG:CZ	1:Bc:166:LEU:CD1	2.76	0.64
1:Ac:106:THR:HA	1:Ac:162:TYR:OH	1.98	0.64
1:CH:141:LEU:N	1:CH:141:LEU:HD23	2.11	0.64
1:BJ:101:ARG:NH1	1:BJ:166:LEU:HD12	2.12	0.64
1:CJ:122:GLY:HA3	1:BR:114:MET:SD	2.38	0.64
1:CJ:317:ASP:HB3	1:CJ:319:GLN:CD	2.22	0.64
1:AM:302:ASP:CB	1:AM:305:ASN:ND2	2.60	0.64
1:AN:62:ARG:HG2	1:AN:62:ARG:HH11	1.62	0.64
1:BZ:130:ASP:HB2	1:CZ:100:GLN:NE2	2.13	0.64
1:BA:98:ILE:O	1:BA:211:SER:C	2.41	0.64
1:CC:43:SER:HA	1:CJ:112:GLN:NE2	2.12	0.64
1:BI:114:MET:SD	1:Ca:122:GLY:HA3	2.37	0.64
1:CI:317:ASP:HB3	1:CI:319:GLN:CD	2.23	0.64
1:AK:106:THR:HA	1:AK:162:TYR:OH	1.97	0.64
1:AK:302:ASP:CB	1:AK:305:ASN:ND2	2.61	0.64
1:BM:101:ARG:CZ	1:BM:166:LEU:CD1	2.75	0.64
1:BN:98:ILE:O	1:BN:211:SER:C	2.41	0.64
1:AN:314:TYR:HE1	1:AN:316:SER:HA	1.62	0.64
1:BR:101:ARG:CZ	1:BR:166:LEU:CD1	2.75	0.64
1:BR:166:LEU:HD13	1:BR:166:LEU:C	2.23	0.64
1:CS:80:VAL:HG12	1:CS:185:LEU:CB	2.26	0.64
1:CW:117:ALA:HB2	1:Cd:38:PRO:O	1.98	0.64
1:BY:72:THR:O	1:BY:191:ASN:ND2	2.30	0.64
1:Ba:101:ARG:CZ	1:Ba:166:LEU:CD1	2.76	0.64
1:Cd:63:ILE:HD11	1:Cd:89:LEU:HD23	1.78	0.64
1:BB:101:ARG:NH1	1:BB:166:LEU:CD1	2.61	0.64
1:CB:58:SER:HA	1:CB:203:TRP:CZ3	2.33	0.64
1:BD:130:ASP:HB2	1:CD:100:GLN:NE2	2.13	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:302:ASP:CB	1:AG:305:ASN:ND2	2.60	0.64
1:BH:101:ARG:NH1	1:BH:166:LEU:CD1	2.60	0.64
1:BJ:139:ASP:HA	1:BJ:142:GLN:HG2	1.80	0.64
1:CK:58:SER:HA	1:CK:203:TRP:CZ3	2.32	0.64
1:BM:316:SER:HB2	1:BM:319:GLN:OE1	1.98	0.64
1:BP:101:ARG:NH1	1:BP:166:LEU:CD1	2.60	0.64
1:CS:141:LEU:CD2	1:CS:184:ILE:HD11	2.20	0.64
1:BU:98:ILE:C	1:BU:211:SER:O	2.41	0.64
1:BU:101:ARG:NH1	1:BU:166:LEU:CD1	2.61	0.64
1:BV:98:ILE:C	1:BV:211:SER:O	2.40	0.64
1:BX:98:ILE:C	1:BX:211:SER:O	2.40	0.64
1:BZ:101:ARG:CZ	1:BZ:166:LEU:CD1	2.75	0.64
1:Bc:139:ASP:HA	1:Bc:142:GLN:HG2	1.80	0.64
1:Cd:199:VAL:O	1:Cd:199:VAL:HG13	1.97	0.64
1:AA:314:TYR:HE1	1:AA:316:SER:HA	1.62	0.64
1:AC:106:THR:HA	1:AC:162:TYR:OH	1.98	0.64
1:BD:98:ILE:CG2	1:AW:91:ARG:NE	2.60	0.64
1:AE:106:THR:HA	1:AE:162:TYR:OH	1.98	0.64
1:BH:72:THR:O	1:BH:191:ASN:ND2	2.31	0.64
1:AH:302:ASP:CB	1:AH:305:ASN:ND2	2.60	0.64
1:CH:199:VAL:O	1:CH:199:VAL:HG13	1.97	0.64
1:BI:91:ARG:NH1	1:Aa:98:ILE:HG23	2.13	0.64
1:BI:101:ARG:NH1	1:BI:166:LEU:CD1	2.60	0.64
1:AM:314:TYR:HE1	1:AM:316:SER:HA	1.61	0.64
1:BN:101:ARG:NH1	1:BN:166:LEU:HD12	2.13	0.64
1:CR:63:ILE:HD11	1:CR:89:LEU:HD23	1.78	0.64
1:CT:141:LEU:N	1:CT:141:LEU:HD23	2.12	0.64
1:Aa:302:ASP:CB	1:Aa:305:ASN:ND2	2.60	0.64
1:Ca:317:ASP:HB3	1:Ca:319:GLN:CD	2.23	0.64
1:CB:111:ILE:O	1:CB:198:SER:O	2.16	0.64
1:AC:314:TYR:HE1	1:AC:316:SER:HA	1.63	0.64
1:AD:106:THR:HA	1:AD:162:TYR:OH	1.98	0.64
1:AG:314:TYR:HE1	1:AG:316:SER:HA	1.63	0.64
1:CH:58:SER:HA	1:CH:203:TRP:CZ3	2.33	0.64
1:CH:79:VAL:CG1	1:CH:185:LEU:O	2.46	0.64
1:BI:318:GLU:N	1:BI:318:GLU:OE2	2.31	0.64
1:CJ:199:VAL:HG13	1:CJ:199:VAL:O	1.98	0.64
1:AL:68:LEU:HB2	1:AL:195:VAL:HG22	1.80	0.64
1:CM:317:ASP:HB3	1:CM:319:GLN:CD	2.22	0.64
1:CN:151:LYS:NZ	1:BP:153:TRP:O	2.31	0.64
1:CO:109:PHE:HB2	1:CO:158:VAL:CG1	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:122:GLY:C	1:CO:188:VAL:HB	2.23	0.64
1:AP:62:ARG:HG2	1:AP:62:ARG:HH11	1.63	0.64
1:AP:68:LEU:HB2	1:AP:195:VAL:HG22	1.78	0.64
1:CU:99:PHE:CA	1:CU:209:VAL:O	2.46	0.64
1:CY:122:GLY:C	1:CY:188:VAL:HB	2.23	0.64
1:AZ:314:TYR:HE1	1:AZ:316:SER:HA	1.63	0.64
1:Ba:111:ILE:HG21	1:Ba:123:TYR:OH	1.98	0.64
1:BB:101:ARG:NH1	1:BB:166:LEU:HD12	2.13	0.63
1:BE:139:ASP:HA	1:BE:142:GLN:HG2	1.80	0.63
1:BG:101:ARG:NH1	1:BG:166:LEU:HD12	2.12	0.63
1:AK:299:GLY:CA	1:AK:310:ASP:O	2.45	0.63
1:CK:185:LEU:C	1:CK:186:LEU:HD23	2.23	0.63
1:BP:80:VAL:HG13	1:BP:185:LEU:HB3	1.80	0.63
1:BQ:166:LEU:C	1:BQ:166:LEU:HD13	2.24	0.63
1:AT:314:TYR:HE1	1:AT:316:SER:HA	1.63	0.63
1:BV:130:ASP:HB2	1:CV:100:GLN:NE2	2.13	0.63
1:CV:80:VAL:HG12	1:CV:185:LEU:CB	2.27	0.63
1:BW:316:SER:HB2	1:BW:319:GLN:OE1	1.97	0.63
1:CX:163:THR:HG21	1:CX:167:LEU:HD11	1.80	0.63
1:AZ:314:TYR:CE1	1:AZ:316:SER:N	2.65	0.63
1:Cb:122:GLY:C	1:Cb:188:VAL:HB	2.22	0.63
1:Ad:314:TYR:HE1	1:Ad:316:SER:HA	1.63	0.63
1:Cd:317:ASP:HB3	1:Cd:319:GLN:CD	2.23	0.63
1:BC:75:ASP:OD2	1:CJ:62:ARG:NH1	2.26	0.63
1:CC:122:GLY:C	1:CC:188:VAL:HB	2.23	0.63
1:BD:98:ILE:O	1:BD:211:SER:C	2.41	0.63
1:BG:91:ARG:NH1	1:AP:98:ILE:HG23	2.13	0.63
1:BM:253:ASP:HB2	1:BM:286:ALA:HB2	1.81	0.63
1:BN:98:ILE:C	1:BN:211:SER:O	2.41	0.63
1:AO:302:ASP:CB	1:AO:305:ASN:ND2	2.60	0.63
1:CO:99:PHE:CA	1:CO:209:VAL:O	2.46	0.63
1:BP:68:LEU:HD23	1:BP:195:VAL:HG22	1.80	0.63
1:BR:127:PHE:HB3	1:BR:160:PRO:HB3	1.79	0.63
1:CR:317:ASP:HB3	1:CR:319:GLN:CD	2.24	0.63
1:BT:98:ILE:HG22	1:AV:91:ARG:NE	2.14	0.63
1:CT:63:ILE:HD11	1:CT:89:LEU:HD23	1.79	0.63
1:CW:112:GLN:NE2	1:Cd:43:SER:HA	2.13	0.63
1:BX:72:THR:O	1:BX:191:ASN:ND2	2.29	0.63
1:AX:106:THR:HA	1:AX:162:TYR:OH	1.98	0.63
1:CZ:79:VAL:CG1	1:CZ:185:LEU:O	2.47	0.63
1:Ca:122:GLY:C	1:Ca:188:VAL:HB	2.23	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:98:ILE:O	1:BF:211:SER:C	2.41	0.63
1:AF:91:ARG:NE	1:Bb:98:ILE:HG22	2.13	0.63
1:BG:98:ILE:O	1:BG:211:SER:C	2.42	0.63
1:AH:63:ILE:HB	1:AH:199:VAL:HG13	1.79	0.63
1:CI:109:PHE:HB2	1:CI:158:VAL:CG1	2.28	0.63
1:CJ:122:GLY:O	1:CJ:188:VAL:HB	1.99	0.63
1:CR:122:GLY:C	1:CR:188:VAL:HB	2.23	0.63
1:AS:68:LEU:HB2	1:AS:195:VAL:HG22	1.79	0.63
1:BT:68:LEU:HD23	1:BT:195:VAL:HG22	1.81	0.63
1:AW:302:ASP:CB	1:AW:305:ASN:ND2	2.60	0.63
1:AX:314:TYR:CZ	1:AX:315:TYR:O	2.52	0.63
1:Bb:101:ARG:CZ	1:Bb:166:LEU:CD1	2.76	0.63
1:Cc:141:LEU:HD23	1:Cc:141:LEU:N	2.14	0.63
1:BA:98:ILE:C	1:BA:211:SER:O	2.41	0.63
1:BF:139:ASP:HA	1:BF:142:GLN:HG2	1.80	0.63
1:AF:91:ARG:HE	1:Bb:98:ILE:HG22	1.62	0.63
1:BI:98:ILE:C	1:BI:211:SER:O	2.42	0.63
1:BJ:130:ASP:HB2	1:CJ:100:GLN:NE2	2.14	0.63
1:AJ:106:THR:HA	1:AJ:162:TYR:OH	1.99	0.63
1:AK:119:THR:HG23	1:AK:193:ASP:HB2	1.79	0.63
1:AM:144:THR:HG23	1:AM:147:ALA:HB2	1.81	0.63
1:AO:91:ARG:HE	1:BW:98:ILE:HG22	1.64	0.63
1:CO:58:SER:HA	1:CO:203:TRP:CZ3	2.34	0.63
1:CQ:58:SER:HA	1:CQ:203:TRP:CZ3	2.33	0.63
1:CS:99:PHE:CA	1:CS:209:VAL:O	2.47	0.63
1:BU:98:ILE:HG22	1:AX:91:ARG:NE	2.13	0.63
1:BU:316:SER:HB2	1:BU:319:GLN:OE1	1.98	0.63
1:AW:314:TYR:HE1	1:AW:316:SER:HA	1.64	0.63
1:Ba:176:ARG:HD2	1:Ca:168:TRP:CE2	2.34	0.63
1:Ad:314:TYR:CE1	1:Ad:316:SER:N	2.66	0.63
1:CD:79:VAL:CG1	1:CD:185:LEU:O	2.47	0.63
1:AE:111:ILE:HG22	1:AE:113:PRO:HD3	1.78	0.63
1:AF:302:ASP:CB	1:AF:305:ASN:ND2	2.60	0.63
1:BO:101:ARG:NH1	1:BO:166:LEU:HD12	2.14	0.63
1:CP:122:GLY:O	1:CP:188:VAL:HB	1.98	0.63
1:AR:314:TYR:CE1	1:AR:316:SER:N	2.66	0.63
1:BS:68:LEU:HD23	1:BS:195:VAL:HG22	1.79	0.63
1:AS:314:TYR:HE1	1:AS:316:SER:HA	1.63	0.63
1:AT:62:ARG:HG2	1:AT:62:ARG:HH11	1.64	0.63
1:AW:265:ILE:CG2	1:AW:313:ALA:O	2.46	0.63
1:Bb:316:SER:HB2	1:Bb:319:GLN:OE1	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ac:302:ASP:CB	1:Ac:305:ASN:ND2	2.60	0.63
1:Cd:122:GLY:O	1:Cd:188:VAL:N	2.31	0.63
1:BA:68:LEU:HD23	1:BA:195:VAL:HG22	1.79	0.63
1:CE:122:GLY:C	1:CE:188:VAL:HB	2.23	0.63
1:AF:106:THR:HA	1:AF:162:TYR:OH	1.98	0.63
1:CJ:99:PHE:CA	1:CJ:209:VAL:O	2.47	0.63
1:BN:101:ARG:NH1	1:BN:166:LEU:CD1	2.62	0.63
1:BP:253:ASP:HB2	1:BP:286:ALA:HB2	1.81	0.63
1:BV:98:ILE:O	1:BV:211:SER:C	2.41	0.63
1:CV:79:VAL:CG1	1:CV:185:LEU:O	2.45	0.63
1:BX:98:ILE:O	1:BX:211:SER:C	2.42	0.63
1:Ca:122:GLY:O	1:Ca:188:VAL:HB	1.99	0.63
1:Cc:80:VAL:HG12	1:Cc:185:LEU:CB	2.29	0.63
1:BA:316:SER:HB2	1:BA:319:GLN:OE1	1.99	0.63
1:BC:58:SER:HB3	1:BC:204:SER:HB3	1.80	0.63
1:CC:63:ILE:HD11	1:CC:89:LEU:HD23	1.79	0.63
1:AE:114:MET:SD	1:AM:122:GLY:HA3	2.38	0.63
1:BG:98:ILE:HG22	1:AP:91:ARG:NE	2.14	0.63
1:CG:141:LEU:HD23	1:CG:141:LEU:N	2.14	0.63
1:AH:114:MET:SD	1:AN:122:GLY:HA3	2.39	0.63
1:CH:122:GLY:O	1:CH:188:VAL:HB	1.98	0.63
1:CL:317:ASP:HB3	1:CL:319:GLN:CD	2.24	0.63
1:BM:166:LEU:C	1:BM:166:LEU:HD13	2.23	0.63
1:AN:91:ARG:NE	1:BP:98:ILE:HG22	2.14	0.63
1:BO:98:ILE:HG22	1:Ab:91:ARG:NE	2.14	0.63
1:AQ:302:ASP:CB	1:AQ:305:ASN:ND2	2.61	0.63
1:CQ:317:ASP:HB3	1:CQ:319:GLN:CD	2.22	0.63
1:BR:101:ARG:NH1	1:BR:166:LEU:CD1	2.61	0.63
1:BS:98:ILE:C	1:BS:211:SER:O	2.42	0.63
1:CS:199:VAL:O	1:CS:199:VAL:HG13	1.99	0.63
1:CW:63:ILE:HD11	1:CW:89:LEU:HD23	1.80	0.63
1:BZ:127:PHE:HB3	1:BZ:160:PRO:HB3	1.80	0.63
1:BA:75:ASP:OD2	1:CG:62:ARG:NH1	2.27	0.63
1:AA:68:LEU:HB2	1:AA:195:VAL:CG2	2.29	0.63
1:BC:166:LEU:C	1:BC:166:LEU:HD13	2.24	0.63
1:BD:101:ARG:NH1	1:BD:166:LEU:HD12	2.13	0.63
1:BD:111:ILE:HG21	1:BD:123:TYR:OH	1.99	0.63
1:AD:144:THR:HG23	1:AD:147:ALA:HB2	1.80	0.63
1:AG:106:THR:HA	1:AG:162:TYR:OH	1.99	0.63
1:BI:130:ASP:HB2	1:CI:100:GLN:NE2	2.13	0.63
1:AJ:62:ARG:HH11	1:AJ:62:ARG:HG2	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:317:ASP:HB3	1:CK:319:GLN:CD	2.23	0.63
1:AL:62:ARG:HG2	1:AL:62:ARG:HH11	1.62	0.63
1:BM:176:ARG:HD2	1:CM:168:TRP:CE2	2.34	0.63
1:BQ:114:MET:SD	1:CZ:122:GLY:HA3	2.38	0.63
1:AR:302:ASP:CB	1:AR:305:ASN:ND2	2.61	0.63
1:CR:79:VAL:CG1	1:CR:185:LEU:O	2.47	0.63
1:BS:316:SER:HB2	1:BS:319:GLN:OE1	1.99	0.63
1:BV:101:ARG:NH1	1:BV:166:LEU:HD12	2.14	0.63
1:BW:98:ILE:O	1:BW:211:SER:C	2.42	0.63
1:AW:314:TYR:CE1	1:AW:316:SER:N	2.65	0.63
1:AX:302:ASP:CB	1:AX:305:ASN:ND2	2.61	0.63
1:Ba:183:LEU:C	1:Ba:183:LEU:HD12	2.24	0.63
1:Cd:58:SER:HA	1:Cd:203:TRP:CZ3	2.34	0.63
1:CB:62:ARG:NH1	1:BF:75:ASP:OD2	2.29	0.63
1:BC:72:THR:O	1:BC:191:ASN:ND2	2.29	0.63
1:AE:68:LEU:HB2	1:AE:195:VAL:CG2	2.29	0.63
1:AE:302:ASP:CB	1:AE:305:ASN:ND2	2.60	0.63
1:CF:95:ALA:O	1:CF:98:ILE:HG12	1.98	0.63
1:BH:316:SER:HB2	1:BH:319:GLN:OE1	1.99	0.63
1:BI:68:LEU:HD23	1:BI:195:VAL:HG22	1.81	0.63
1:CK:111:ILE:O	1:CK:198:SER:O	2.17	0.63
1:AO:62:ARG:HG2	1:AO:62:ARG:HH11	1.64	0.63
1:AS:68:LEU:HB2	1:AS:195:VAL:CG2	2.28	0.63
1:BV:58:SER:HB3	1:BV:204:SER:HB3	1.80	0.63
1:BW:80:VAL:HG13	1:BW:185:LEU:HB3	1.81	0.63
1:AW:62:ARG:HG2	1:AW:62:ARG:HH11	1.64	0.63
1:CX:109:PHE:HB2	1:CX:158:VAL:CG1	2.29	0.63
1:AY:144:THR:HG23	1:AY:147:ALA:HB2	1.81	0.63
1:BZ:101:ARG:NH1	1:BZ:166:LEU:CD1	2.61	0.63
1:Ba:253:ASP:HB2	1:Ba:286:ALA:HB2	1.81	0.63
1:Bc:68:LEU:HD23	1:Bc:195:VAL:HG22	1.80	0.63
1:AA:106:THR:HA	1:AA:162:TYR:OH	1.99	0.62
1:BB:253:ASP:HB2	1:BB:286:ALA:HB2	1.81	0.62
1:AD:98:ILE:HG23	1:BF:91:ARG:NH1	2.14	0.62
1:BE:58:SER:HB3	1:BE:204:SER:HB3	1.81	0.62
1:AF:314:TYR:HE1	1:AF:316:SER:HA	1.64	0.62
1:BH:58:SER:HB3	1:BH:204:SER:HB3	1.81	0.62
1:BI:58:SER:HB3	1:BI:204:SER:HB3	1.81	0.62
1:CL:75:ASP:OD1	1:CL:188:VAL:C	2.40	0.62
1:AO:91:ARG:NE	1:BW:98:ILE:HG22	2.14	0.62
1:BP:166:LEU:C	1:BP:166:LEU:HD13	2.24	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:144:THR:HG23	1:AU:147:ALA:HB2	1.80	0.62
1:BY:139:ASP:HA	1:BY:142:GLN:HG2	1.79	0.62
1:Bb:176:ARG:HD2	1:Cb:168:TRP:CE2	2.34	0.62
1:CB:122:GLY:O	1:CB:188:VAL:HB	1.99	0.62
1:CF:75:ASP:OD1	1:CF:188:VAL:C	2.41	0.62
1:BH:114:MET:HE1	1:Cd:188:VAL:HG11	1.81	0.62
1:AH:314:TYR:HE1	1:AH:316:SER:HA	1.63	0.62
1:BI:316:SER:HB2	1:BI:319:GLN:OE1	1.99	0.62
1:CN:58:SER:HA	1:CN:203:TRP:CZ3	2.33	0.62
1:BO:98:ILE:O	1:BO:211:SER:C	2.42	0.62
1:BS:101:ARG:NH1	1:BS:166:LEU:CD1	2.62	0.62
1:BT:58:SER:HB3	1:BT:204:SER:HB3	1.80	0.62
1:BT:101:ARG:NH1	1:BT:166:LEU:HD12	2.13	0.62
1:AT:302:ASP:CB	1:AT:305:ASN:ND2	2.60	0.62
1:BU:130:ASP:HB2	1:CU:100:GLN:NE2	2.13	0.62
1:AV:314:TYR:HE1	1:AV:316:SER:HA	1.63	0.62
1:BX:316:SER:HB2	1:BX:319:GLN:OE1	1.99	0.62
1:AX:68:LEU:HB2	1:AX:195:VAL:HG22	1.81	0.62
1:BY:101:ARG:NH1	1:BY:166:LEU:CD1	2.62	0.62
1:AB:302:ASP:CB	1:AB:305:ASN:ND2	2.61	0.62
1:BD:68:LEU:HD23	1:BD:195:VAL:HG22	1.81	0.62
1:BD:101:ARG:NH1	1:BD:166:LEU:CD1	2.62	0.62
1:BK:130:ASP:HB2	1:CK:100:GLN:NE2	2.14	0.62
1:CL:58:SER:HA	1:CL:203:TRP:CZ3	2.34	0.62
1:BO:176:ARG:HD2	1:CO:168:TRP:CE2	2.34	0.62
1:AP:106:THR:HA	1:AP:162:TYR:OH	1.99	0.62
1:CP:58:SER:HA	1:CP:203:TRP:CZ3	2.32	0.62
1:CQ:109:PHE:HB2	1:CQ:158:VAL:CG1	2.28	0.62
1:CQ:185:LEU:C	1:CQ:186:LEU:HD23	2.24	0.62
1:AS:302:ASP:CB	1:AS:305:ASN:ND2	2.61	0.62
1:AU:302:ASP:CB	1:AU:305:ASN:ND2	2.60	0.62
1:BV:80:VAL:HG13	1:BV:185:LEU:HB3	1.81	0.62
1:AW:144:THR:HG23	1:AW:147:ALA:HB2	1.81	0.62
1:BZ:98:ILE:O	1:BZ:211:SER:C	2.42	0.62
1:Aa:314:TYR:HE1	1:Aa:316:SER:HA	1.63	0.62
1:Bc:101:ARG:NH1	1:Bc:166:LEU:CD1	2.62	0.62
1:Bd:130:ASP:HB2	1:Cd:100:GLN:NE2	2.12	0.62
1:CA:75:ASP:OD1	1:CA:188:VAL:C	2.42	0.62
1:AC:141:LEU:O	1:AC:144:THR:CG2	2.42	0.62
1:CC:163:THR:HG21	1:CC:167:LEU:HD11	1.82	0.62
1:CD:141:LEU:N	1:CD:141:LEU:HD23	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:144:THR:HG23	1:AE:147:ALA:HB2	1.81	0.62
1:CG:122:GLY:HA3	1:Bd:114:MET:SD	2.39	0.62
1:CI:75:ASP:OD1	1:CI:188:VAL:C	2.41	0.62
1:AM:91:ARG:HE	1:Bc:98:ILE:HG22	1.65	0.62
1:Ba:68:LEU:HD23	1:Ba:195:VAL:HG22	1.80	0.62
1:Ba:98:ILE:O	1:Ba:211:SER:C	2.42	0.62
1:Ad:141:LEU:O	1:Ad:144:THR:CG2	2.38	0.62
1:BC:80:VAL:HG13	1:BC:185:LEU:HB3	1.81	0.62
1:BC:176:ARG:HD2	1:CC:168:TRP:CE2	2.34	0.62
1:CE:63:ILE:HD11	1:CE:89:LEU:HD23	1.79	0.62
1:CG:58:SER:HA	1:CG:203:TRP:CZ3	2.34	0.62
1:BH:98:ILE:O	1:BH:211:SER:C	2.41	0.62
1:AH:62:ARG:HG2	1:AH:62:ARG:HH11	1.64	0.62
1:AH:138:PHE:CE2	1:Ad:62:ARG:CZ	2.82	0.62
1:AK:314:TYR:CE1	1:AK:316:SER:N	2.67	0.62
1:BN:316:SER:HB2	1:BN:319:GLN:OE1	2.00	0.62
1:CO:199:VAL:HG13	1:CO:199:VAL:O	1.98	0.62
1:BQ:98:ILE:O	1:BQ:211:SER:C	2.43	0.62
1:CR:58:SER:HA	1:CR:203:TRP:CZ3	2.34	0.62
1:CR:141:LEU:N	1:CR:141:LEU:HD23	2.13	0.62
1:BS:101:ARG:CZ	1:BS:166:LEU:CD1	2.76	0.62
1:BZ:316:SER:HB2	1:BZ:319:GLN:OE1	1.99	0.62
1:CZ:199:VAL:HG13	1:CZ:199:VAL:O	1.99	0.62
1:CZ:317:ASP:HB3	1:CZ:319:GLN:CD	2.23	0.62
1:Bb:101:ARG:NH1	1:Bb:166:LEU:HD12	2.14	0.62
1:Ab:314:TYR:HE1	1:Ab:316:SER:HA	1.63	0.62
1:AB:314:TYR:CZ	1:AB:315:TYR:O	2.53	0.62
1:BD:98:ILE:C	1:BD:211:SER:O	2.41	0.62
1:AE:314:TYR:HE1	1:AE:316:SER:HA	1.62	0.62
1:BH:98:ILE:HG23	1:Ad:91:ARG:HG2	1.80	0.62
1:BI:253:ASP:HB2	1:BI:286:ALA:HB2	1.80	0.62
1:BJ:98:ILE:C	1:BJ:211:SER:O	2.42	0.62
1:BL:98:ILE:O	1:BL:211:SER:C	2.42	0.62
1:AO:106:THR:HA	1:AO:162:TYR:OH	1.99	0.62
1:CO:141:LEU:N	1:CO:141:LEU:HD23	2.14	0.62
1:CR:112:GLN:NE2	1:CT:43:SER:HA	2.14	0.62
1:BU:98:ILE:O	1:BU:211:SER:C	2.43	0.62
1:CV:62:ARG:NH1	1:BZ:75:ASP:OD2	2.29	0.62
1:BW:58:SER:HB3	1:BW:204:SER:HB3	1.82	0.62
1:AZ:119:THR:O	1:AZ:192:THR:HB	2.00	0.62
1:Ba:166:LEU:C	1:Ba:166:LEU:HD13	2.25	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bb:166:LEU:HD13	1:Bb:166:LEU:C	2.25	0.62
1:Ab:63:ILE:HB	1:Ab:199:VAL:HG13	1.82	0.62
1:AB:144:THR:HG23	1:AB:147:ALA:HB2	1.82	0.62
1:CD:75:ASP:OD1	1:CD:188:VAL:C	2.42	0.62
1:AG:61:SER:CB	1:AG:90:PRO:HD2	2.28	0.62
1:CG:163:THR:HG21	1:CG:167:LEU:HD11	1.81	0.62
1:CJ:75:ASP:OD1	1:CJ:188:VAL:C	2.42	0.62
1:BK:316:SER:HB2	1:BK:319:GLN:OE1	1.99	0.62
1:CM:118:ASN:HA	1:Bc:116:PRO:CB	2.30	0.62
1:AO:314:TYR:CZ	1:AO:315:TYR:O	2.52	0.62
1:AQ:62:ARG:HG2	1:AQ:62:ARG:HH11	1.64	0.62
1:AT:141:LEU:O	1:AT:144:THR:CG2	2.41	0.62
1:BV:253:ASP:HB2	1:BV:286:ALA:HB2	1.81	0.62
1:CX:122:GLY:O	1:CX:188:VAL:HB	2.00	0.62
1:Bc:61:SER:CB	1:Bc:90:PRO:HD2	2.23	0.62
1:BA:127:PHE:HB3	1:BA:160:PRO:HB3	1.82	0.62
1:BA:153:TRP:O	1:CI:151:LYS:NZ	2.31	0.62
1:CB:75:ASP:OD1	1:CB:188:VAL:C	2.43	0.62
1:BC:98:ILE:C	1:BC:211:SER:O	2.42	0.62
1:AG:63:ILE:HB	1:AG:199:VAL:HG13	1.82	0.62
1:BL:58:SER:HB3	1:BL:204:SER:HB3	1.82	0.62
1:AL:68:LEU:HB2	1:AL:195:VAL:CG2	2.30	0.62
1:BM:130:ASP:HB2	1:CM:100:GLN:NE2	2.14	0.62
1:BN:130:ASP:HB2	1:CN:100:GLN:NE2	2.15	0.62
1:BS:58:SER:HB3	1:BS:204:SER:HB3	1.81	0.62
1:BT:111:ILE:HG21	1:BT:123:TYR:OH	2.00	0.62
1:CT:109:PHE:HB2	1:CT:158:VAL:CG1	2.30	0.62
1:CV:122:GLY:O	1:CV:188:VAL:HB	2.00	0.62
1:BW:98:ILE:C	1:BW:211:SER:O	2.42	0.62
1:BX:130:ASP:HB2	1:CX:100:GLN:NE2	2.14	0.62
1:CX:185:LEU:C	1:CX:186:LEU:HD23	2.24	0.62
1:CY:141:LEU:N	1:CY:141:LEU:HD23	2.14	0.62
1:Ba:101:ARG:NH1	1:Ba:166:LEU:HD12	2.14	0.62
1:Bb:253:ASP:HB2	1:Bb:286:ALA:HB2	1.81	0.62
1:Cb:141:LEU:CD2	1:Cb:184:ILE:HD11	2.25	0.62
1:Ac:144:THR:HG23	1:Ac:147:ALA:HB2	1.82	0.62
1:Ac:314:TYR:HE1	1:Ac:316:SER:N	1.97	0.62
1:Cc:58:SER:HA	1:Cc:203:TRP:CZ3	2.35	0.62
1:Cd:75:ASP:OD1	1:Cd:188:VAL:C	2.42	0.62
1:BC:98:ILE:O	1:BC:211:SER:C	2.42	0.62
1:CC:75:ASP:OD1	1:CC:188:VAL:C	2.43	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:68:LEU:HB2	1:AD:195:VAL:CG2	2.30	0.62
1:BG:130:ASP:HB2	1:CG:100:GLN:NE2	2.14	0.62
1:CG:79:VAL:CG1	1:CG:185:LEU:O	2.48	0.62
1:AJ:314:TYR:HE1	1:AJ:316:SER:HA	1.63	0.62
1:AL:106:THR:HA	1:AL:162:TYR:OH	1.99	0.62
1:AL:314:TYR:HE1	1:AL:316:SER:HA	1.63	0.62
1:CM:58:SER:HA	1:CM:203:TRP:CZ3	2.35	0.62
1:AO:122:GLY:HA3	1:Ab:114:MET:SD	2.39	0.62
1:CP:185:LEU:C	1:CP:186:LEU:HD23	2.25	0.62
1:CP:191:ASN:OD1	1:CP:191:ASN:N	2.32	0.62
1:AR:62:ARG:HG2	1:AR:62:ARG:HH11	1.65	0.62
1:BS:61:SER:CB	1:BS:90:PRO:HD2	2.23	0.62
1:AU:266:ASP:O	1:AU:314:TYR:HA	2.00	0.62
1:BV:316:SER:HB2	1:BV:319:GLN:OE1	2.00	0.62
1:Bb:58:SER:HB3	1:Bb:204:SER:HB3	1.81	0.62
1:Bb:98:ILE:C	1:Bb:211:SER:O	2.42	0.62
1:Cc:163:THR:HG21	1:Cc:167:LEU:HD11	1.81	0.62
1:Ad:320:PRO:O	1:Ad:322:GLN:HG3	2.00	0.62
1:AD:141:LEU:O	1:AD:144:THR:CG2	2.44	0.62
1:BG:101:ARG:CZ	1:BG:166:LEU:CD1	2.76	0.62
1:CJ:111:ILE:O	1:CJ:198:SER:O	2.17	0.62
1:BK:98:ILE:CG2	1:AS:91:ARG:NE	2.63	0.62
1:BN:80:VAL:HG13	1:BN:185:LEU:HB3	1.81	0.62
1:BN:166:LEU:C	1:BN:166:LEU:HD13	2.25	0.62
1:AR:144:THR:HG23	1:AR:147:ALA:HB2	1.80	0.62
1:CS:58:SER:HA	1:CS:203:TRP:CZ3	2.35	0.62
1:BW:101:ARG:NH1	1:BW:166:LEU:CD1	2.63	0.62
1:AX:144:THR:HG23	1:AX:147:ALA:HB2	1.81	0.62
1:Bd:316:SER:HB2	1:Bd:319:GLN:OE1	1.98	0.62
1:BA:130:ASP:HB2	1:CA:100:GLN:NE2	2.15	0.61
1:CB:95:ALA:O	1:CB:98:ILE:HG12	2.00	0.61
1:CD:58:SER:HA	1:CD:203:TRP:CZ3	2.34	0.61
1:BE:68:LEU:HD23	1:BE:195:VAL:HG22	1.82	0.61
1:BE:101:ARG:CZ	1:BE:166:LEU:CD1	2.77	0.61
1:BG:68:LEU:HD23	1:BG:195:VAL:HG22	1.81	0.61
1:BH:176:ARG:HD2	1:CH:168:TRP:CE2	2.35	0.61
1:CJ:80:VAL:HG12	1:CJ:185:LEU:CB	2.26	0.61
1:BK:101:ARG:NH1	1:BK:166:LEU:HD12	2.14	0.61
1:BK:114:MET:SD	1:CS:122:GLY:HA3	2.40	0.61
1:AK:63:ILE:HB	1:AK:199:VAL:HG13	1.82	0.61
1:CN:199:VAL:O	1:CN:199:VAL:HG13	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:314:TYR:HE1	1:AO:316:SER:N	1.98	0.61
1:BV:68:LEU:HD23	1:BV:195:VAL:HG22	1.81	0.61
1:CV:45:VAL:HG23	1:CZ:200:LEU:HD13	1.82	0.61
1:BW:68:LEU:HD23	1:BW:195:VAL:HG22	1.81	0.61
1:AY:63:ILE:HB	1:AY:199:VAL:HG13	1.82	0.61
1:AY:68:LEU:HB2	1:AY:195:VAL:HG22	1.82	0.61
1:AZ:63:ILE:HB	1:AZ:199:VAL:HG13	1.81	0.61
1:AA:68:LEU:HB2	1:AA:195:VAL:HG22	1.81	0.61
1:CB:141:LEU:N	1:CB:141:LEU:HD23	2.14	0.61
1:BH:98:ILE:C	1:BH:211:SER:O	2.43	0.61
1:AI:68:LEU:HB2	1:AI:195:VAL:CG2	2.30	0.61
1:CI:185:LEU:C	1:CI:186:LEU:HD23	2.24	0.61
1:BL:98:ILE:CG2	1:AU:91:ARG:NE	2.63	0.61
1:AQ:144:THR:HG23	1:AQ:147:ALA:HB2	1.82	0.61
1:BR:98:ILE:O	1:BR:211:SER:C	2.44	0.61
1:AT:91:ARG:NE	1:Ba:98:ILE:CG2	2.63	0.61
1:CY:75:ASP:OD1	1:CY:188:VAL:C	2.43	0.61
1:AZ:144:THR:HG23	1:AZ:147:ALA:HB2	1.82	0.61
1:Ca:141:LEU:N	1:Ca:141:LEU:HD23	2.14	0.61
1:Ab:141:LEU:O	1:Ab:144:THR:CG2	2.44	0.61
1:Bd:101:ARG:NH1	1:Bd:166:LEU:CD1	2.62	0.61
1:AB:141:LEU:O	1:AB:144:THR:CG2	2.43	0.61
1:CD:317:ASP:HB3	1:CD:319:GLN:CD	2.25	0.61
1:BE:101:ARG:NH1	1:BE:166:LEU:CD1	2.63	0.61
1:AE:91:ARG:HE	1:BM:98:ILE:HG22	1.65	0.61
1:CE:95:ALA:O	1:CE:98:ILE:HG12	1.99	0.61
1:AF:111:ILE:O	1:AF:198:SER:O	2.18	0.61
1:BG:101:ARG:NH1	1:BG:166:LEU:CD1	2.63	0.61
1:BI:166:LEU:HD13	1:BI:166:LEU:C	2.26	0.61
1:AI:314:TYR:HE1	1:AI:316:SER:N	1.98	0.61
1:AM:314:TYR:CZ	1:AM:315:TYR:O	2.52	0.61
1:BO:98:ILE:HG22	1:Ab:91:ARG:HE	1.64	0.61
1:CP:163:THR:HG21	1:CP:167:LEU:HD11	1.82	0.61
1:CQ:199:VAL:O	1:CQ:199:VAL:HG13	2.01	0.61
1:BW:176:ARG:HD2	1:CW:168:TRP:CE2	2.35	0.61
1:AW:68:LEU:HB2	1:AW:195:VAL:CG2	2.30	0.61
1:AW:320:PRO:O	1:AW:322:GLN:HG3	2.00	0.61
1:CX:122:GLY:C	1:CX:188:VAL:HB	2.24	0.61
1:Ad:144:THR:HG23	1:Ad:147:ALA:HB2	1.83	0.61
1:BB:58:SER:HB3	1:BB:204:SER:HB3	1.81	0.61
1:BB:114:MET:HE1	1:CK:188:VAL:HG11	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:80:VAL:HG13	1:BJ:185:LEU:HB3	1.83	0.61
1:BJ:111:ILE:HG21	1:BJ:123:TYR:OH	2.00	0.61
1:AJ:302:ASP:CB	1:AJ:305:ASN:ND2	2.60	0.61
1:CL:191:ASN:OD1	1:CL:191:ASN:N	2.33	0.61
1:BM:101:ARG:NH1	1:BM:166:LEU:CD1	2.64	0.61
1:BO:98:ILE:C	1:BO:211:SER:O	2.43	0.61
1:BO:130:ASP:HB2	1:CO:100:GLN:NE2	2.15	0.61
1:CT:95:ALA:O	1:CT:98:ILE:HG12	2.00	0.61
1:AU:314:TYR:CZ	1:AU:315:TYR:O	2.53	0.61
1:BY:98:ILE:O	1:BY:211:SER:C	2.42	0.61
1:BY:98:ILE:C	1:BY:211:SER:O	2.43	0.61
1:AZ:62:ARG:HG2	1:AZ:62:ARG:HH11	1.64	0.61
1:Ba:130:ASP:HB2	1:Ca:100:GLN:NE2	2.15	0.61
1:Ba:316:SER:HB2	1:Ba:319:GLN:OE1	2.01	0.61
1:BI:98:ILE:O	1:BI:211:SER:C	2.42	0.61
1:AI:144:THR:HG23	1:AI:147:ALA:HB2	1.83	0.61
1:AK:141:LEU:O	1:AK:144:THR:CG2	2.42	0.61
1:AL:302:ASP:CB	1:AL:305:ASN:ND2	2.62	0.61
1:AO:144:THR:HG23	1:AO:147:ALA:HB2	1.80	0.61
1:CR:75:ASP:OD1	1:CR:188:VAL:C	2.44	0.61
1:CR:163:THR:HG21	1:CR:167:LEU:HD11	1.83	0.61
1:BT:98:ILE:O	1:BT:211:SER:C	2.43	0.61
1:AT:98:ILE:HG23	1:Ba:91:ARG:NH1	2.15	0.61
1:CT:75:ASP:OD1	1:CT:188:VAL:C	2.44	0.61
1:BY:68:LEU:HD23	1:BY:195:VAL:HG22	1.82	0.61
1:Ab:266:ASP:O	1:Ab:314:TYR:HA	2.01	0.61
1:Bc:130:ASP:HB2	1:Cc:100:GLN:NE2	2.14	0.61
1:CD:185:LEU:C	1:CD:186:LEU:HD23	2.25	0.61
1:BJ:58:SER:HB3	1:BJ:204:SER:CB	2.31	0.61
1:BL:98:ILE:C	1:BL:211:SER:O	2.43	0.61
1:AN:106:THR:HA	1:AN:162:TYR:OH	1.99	0.61
1:AW:168:TRP:CE2	1:CW:176:ARG:HG2	2.36	0.61
1:CW:117:ALA:CB	1:Cd:38:PRO:O	2.49	0.61
1:BZ:98:ILE:C	1:BZ:211:SER:O	2.42	0.61
1:Ab:302:ASP:CB	1:Ab:305:ASN:ND2	2.61	0.61
1:Cb:111:ILE:O	1:Cb:198:SER:O	2.19	0.61
1:Ac:63:ILE:HB	1:Ac:199:VAL:HG13	1.83	0.61
1:Cc:109:PHE:HB2	1:Cc:158:VAL:CG1	2.30	0.61
1:Cd:122:GLY:C	1:Cd:188:VAL:HB	2.26	0.61
1:CA:58:SER:HA	1:CA:203:TRP:CZ3	2.35	0.61
1:BC:153:TRP:O	1:CY:151:LYS:NZ	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:302:ASP:CB	1:AD:305:ASN:ND2	2.61	0.61
1:AD:314:TYR:HE1	1:AD:316:SER:HA	1.64	0.61
1:BF:101:ARG:NH1	1:BF:166:LEU:HD12	2.16	0.61
1:BK:101:ARG:NH1	1:BK:166:LEU:CD1	2.63	0.61
1:CK:191:ASN:N	1:CK:191:ASN:OD1	2.31	0.61
1:AL:320:PRO:O	1:AL:322:GLN:HG3	2.00	0.61
1:BS:166:LEU:C	1:BS:166:LEU:HD13	2.25	0.61
1:AV:61:SER:CB	1:AV:90:PRO:HD2	2.27	0.61
1:BY:166:LEU:C	1:BY:166:LEU:HD13	2.26	0.61
1:Ba:98:ILE:C	1:Ba:211:SER:O	2.44	0.61
1:Bb:101:ARG:NH1	1:Bb:166:LEU:CD1	2.63	0.61
1:Ab:314:TYR:CZ	1:Ab:315:TYR:O	2.53	0.61
1:BB:166:LEU:C	1:BB:166:LEU:HD13	2.26	0.61
1:CB:109:PHE:HB2	1:CB:158:VAL:CG1	2.31	0.61
1:BC:98:ILE:CG2	1:AY:91:ARG:NE	2.64	0.61
1:BE:98:ILE:O	1:BE:211:SER:C	2.44	0.61
1:BE:130:ASP:HB2	1:CE:100:GLN:NE2	2.15	0.61
1:BG:98:ILE:C	1:BG:211:SER:O	2.43	0.61
1:AH:68:LEU:HB2	1:AH:195:VAL:CG2	2.31	0.61
1:BK:166:LEU:C	1:BK:166:LEU:HD13	2.26	0.61
1:AR:141:LEU:O	1:AR:144:THR:CG2	2.44	0.61
1:BS:253:ASP:HB2	1:BS:286:ALA:HB2	1.82	0.61
1:BT:101:ARG:NH1	1:BT:166:LEU:CD1	2.63	0.61
1:BU:166:LEU:HD13	1:BU:166:LEU:C	2.26	0.61
1:BU:253:ASP:HB2	1:BU:286:ALA:HB2	1.82	0.61
1:AU:314:TYR:HE1	1:AU:316:SER:N	1.98	0.61
1:CU:122:GLY:C	1:CU:188:VAL:HB	2.24	0.61
1:CW:317:ASP:HB3	1:CW:319:GLN:CD	2.24	0.61
1:CX:58:SER:HA	1:CX:203:TRP:CZ3	2.36	0.61
1:CX:141:LEU:HD23	1:CX:141:LEU:N	2.15	0.61
1:BZ:166:LEU:HD13	1:BZ:166:LEU:C	2.26	0.61
1:CZ:75:ASP:OD1	1:CZ:188:VAL:C	2.43	0.61
1:Ab:119:THR:O	1:Ab:192:THR:HB	2.00	0.61
1:Cb:58:SER:HA	1:Cb:203:TRP:CZ3	2.36	0.61
1:Cd:111:ILE:HG22	1:Cd:113:PRO:HD3	1.82	0.61
1:Cd:141:LEU:N	1:Cd:141:LEU:HD23	2.15	0.61
1:BA:176:ARG:HD2	1:CA:168:TRP:CE2	2.36	0.61
1:CA:111:ILE:O	1:CA:198:SER:O	2.19	0.61
1:AC:302:ASP:CB	1:AC:305:ASN:ND2	2.61	0.61
1:BD:166:LEU:HD13	1:BD:166:LEU:C	2.25	0.61
1:BI:176:ARG:HD2	1:CI:168:TRP:CE2	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:314:TYR:CZ	1:AI:315:TYR:O	2.53	0.61
1:AK:168:TRP:CE2	1:CK:176:ARG:HG2	2.36	0.61
1:CL:101:ARG:NH1	1:CL:166:LEU:CD1	2.62	0.61
1:BM:58:SER:HB3	1:BM:204:SER:HB3	1.83	0.61
1:AN:266:ASP:O	1:AN:314:TYR:HA	2.01	0.61
1:AN:314:TYR:CZ	1:AN:315:TYR:O	2.54	0.61
1:BO:101:ARG:NH1	1:BO:166:LEU:CD1	2.64	0.61
1:BQ:68:LEU:HD23	1:BQ:195:VAL:CG2	2.31	0.61
1:AR:320:PRO:O	1:AR:322:GLN:HG3	2.01	0.61
1:AT:119:THR:O	1:AT:192:THR:HB	2.01	0.61
1:BV:101:ARG:NH1	1:BV:166:LEU:CD1	2.64	0.61
1:BW:68:LEU:HD23	1:BW:195:VAL:CG2	2.30	0.61
1:BW:101:ARG:NH1	1:BW:166:LEU:HD12	2.15	0.61
1:BX:101:ARG:NH1	1:BX:166:LEU:HD12	2.15	0.61
1:AZ:302:ASP:CB	1:AZ:305:ASN:ND2	2.61	0.61
1:Ca:185:LEU:C	1:Ca:186:LEU:HD23	2.25	0.61
1:Cd:185:LEU:C	1:Cd:186:LEU:HD23	2.25	0.61
1:AA:303:ASN:N	1:AA:305:ASN:OD1	2.34	0.61
1:CB:151:LYS:NZ	1:BY:153:TRP:O	2.34	0.61
1:BD:316:SER:HB2	1:BD:319:GLN:OE1	2.01	0.61
1:BE:98:ILE:C	1:BE:211:SER:O	2.43	0.61
1:CE:163:THR:HG21	1:CE:167:LEU:HD11	1.83	0.61
1:CL:111:ILE:O	1:CL:198:SER:O	2.19	0.61
1:CL:122:GLY:C	1:CL:188:VAL:HB	2.26	0.61
1:CL:185:LEU:C	1:CL:186:LEU:HD23	2.25	0.61
1:AM:314:TYR:HE1	1:AM:316:SER:N	1.98	0.61
1:CM:141:LEU:HD23	1:CM:141:LEU:N	2.16	0.61
1:CM:191:ASN:N	1:CM:191:ASN:OD1	2.34	0.61
1:BO:80:VAL:HG13	1:BO:185:LEU:HB3	1.82	0.61
1:BO:253:ASP:HB2	1:BO:286:ALA:HB2	1.82	0.61
1:AQ:68:LEU:HB2	1:AQ:195:VAL:CG2	2.30	0.61
1:CT:122:GLY:O	1:CT:188:VAL:HB	2.00	0.61
1:AW:63:ILE:HB	1:AW:199:VAL:HG13	1.81	0.61
1:Bc:58:SER:HB3	1:Bc:204:SER:CB	2.31	0.61
1:Ac:68:LEU:HB2	1:Ac:195:VAL:CG2	2.31	0.61
1:Ad:303:ASN:N	1:Ad:305:ASN:OD1	2.32	0.61
1:CE:58:SER:HA	1:CE:203:TRP:CZ3	2.35	0.60
1:AI:106:THR:HA	1:AI:162:TYR:OH	2.01	0.60
1:CI:58:SER:HA	1:CI:203:TRP:CZ3	2.36	0.60
1:BJ:68:LEU:HD23	1:BJ:195:VAL:HG22	1.82	0.60
1:BM:101:ARG:NH1	1:BM:166:LEU:HD12	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:199:VAL:O	1:CM:199:VAL:HG13	2.01	0.60
1:CN:185:LEU:C	1:CN:186:LEU:HD23	2.26	0.60
1:BP:316:SER:HB2	1:BP:319:GLN:OE1	2.01	0.60
1:CQ:75:ASP:OD1	1:CQ:188:VAL:C	2.42	0.60
1:CR:122:GLY:O	1:CR:188:VAL:HB	2.01	0.60
1:AV:302:ASP:CB	1:AV:305:ASN:ND2	2.61	0.60
1:BY:80:VAL:HG13	1:BY:185:LEU:HB3	1.83	0.60
1:Ba:68:LEU:HD23	1:Ba:195:VAL:CG2	2.31	0.60
1:AB:114:MET:SD	1:AY:122:GLY:HA3	2.41	0.60
1:AB:314:TYR:HE1	1:AB:316:SER:N	1.99	0.60
1:AE:314:TYR:HE1	1:AE:316:SER:N	1.99	0.60
1:BH:98:ILE:CG2	1:Ad:91:ARG:NE	2.64	0.60
1:AK:111:ILE:O	1:AK:198:SER:O	2.18	0.60
1:AK:119:THR:O	1:AK:192:THR:HB	2.00	0.60
1:AK:320:PRO:O	1:AK:322:GLN:HG3	2.00	0.60
1:CK:75:ASP:OD1	1:CK:188:VAL:C	2.43	0.60
1:AN:302:ASP:CB	1:AN:305:ASN:ND2	2.60	0.60
1:BP:98:ILE:O	1:BP:211:SER:CA	2.49	0.60
1:BP:130:ASP:HB2	1:CP:100:GLN:NE2	2.16	0.60
1:BQ:130:ASP:HB2	1:CQ:100:GLN:NE2	2.15	0.60
1:CS:141:LEU:N	1:CS:141:LEU:HD23	2.15	0.60
1:AY:303:ASN:N	1:AY:305:ASN:OD1	2.34	0.60
1:Ba:58:SER:HB3	1:Ba:204:SER:HB3	1.82	0.60
1:Cc:95:ALA:O	1:Cc:98:ILE:HG12	2.01	0.60
1:Cd:163:THR:HG21	1:Cd:167:LEU:HD11	1.83	0.60
1:CC:122:GLY:O	1:CC:188:VAL:HB	2.01	0.60
1:AE:111:ILE:O	1:AE:198:SER:O	2.19	0.60
1:BG:253:ASP:HB2	1:BG:286:ALA:HB2	1.83	0.60
1:AH:314:TYR:CZ	1:AH:315:TYR:O	2.54	0.60
1:BI:98:ILE:CG2	1:Aa:91:ARG:NE	2.63	0.60
1:BP:58:SER:HB3	1:BP:204:SER:HB3	1.84	0.60
1:AP:68:LEU:HB2	1:AP:195:VAL:CG2	2.30	0.60
1:CP:75:ASP:OD1	1:CP:188:VAL:C	2.44	0.60
1:AQ:314:TYR:CZ	1:AQ:315:TYR:O	2.54	0.60
1:CU:163:THR:HG21	1:CU:167:LEU:HD11	1.83	0.60
1:AW:119:THR:O	1:AW:192:THR:HB	2.02	0.60
1:Cb:122:GLY:O	1:Cb:188:VAL:HB	2.01	0.60
1:AA:302:ASP:CB	1:AA:305:ASN:ND2	2.60	0.60
1:CA:79:VAL:CG1	1:CA:185:LEU:O	2.49	0.60
1:CC:58:SER:HA	1:CC:203:TRP:CZ3	2.36	0.60
1:AD:62:ARG:HG2	1:AD:62:ARG:HH11	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:58:SER:HB3	1:BG:204:SER:HB3	1.83	0.60
1:AK:144:THR:HG23	1:AK:147:ALA:HB2	1.83	0.60
1:AK:303:ASN:N	1:AK:305:ASN:OD1	2.32	0.60
1:BL:183:LEU:C	1:BL:183:LEU:HD12	2.27	0.60
1:CO:75:ASP:OD1	1:CO:188:VAL:C	2.43	0.60
1:CO:185:LEU:C	1:CO:186:LEU:HD23	2.25	0.60
1:AP:144:THR:HG23	1:AP:147:ALA:HB2	1.83	0.60
1:BQ:98:ILE:CG2	1:AZ:91:ARG:NE	2.63	0.60
1:AQ:63:ILE:HB	1:AQ:199:VAL:HG13	1.83	0.60
1:AR:119:THR:O	1:AR:192:THR:HB	2.01	0.60
1:AR:168:TRP:CE2	1:CR:176:ARG:HG2	2.36	0.60
1:AR:303:ASN:N	1:AR:305:ASN:OD1	2.34	0.60
1:BT:91:ARG:NH1	1:AV:98:ILE:HG23	2.15	0.60
1:BY:183:LEU:C	1:BY:183:LEU:HD12	2.26	0.60
1:Ab:314:TYR:HE1	1:Ab:316:SER:N	1.99	0.60
1:Ac:119:THR:O	1:Ac:192:THR:HB	2.01	0.60
1:AA:266:ASP:O	1:AA:314:TYR:HA	2.01	0.60
1:BF:101:ARG:NH1	1:BF:166:LEU:CD1	2.65	0.60
1:CF:58:SER:HA	1:CF:203:TRP:CZ3	2.36	0.60
1:BH:253:ASP:HB2	1:BH:286:ALA:HB2	1.82	0.60
1:AI:314:TYR:HE1	1:AI:316:SER:HA	1.65	0.60
1:AJ:144:THR:HG23	1:AJ:147:ALA:HB2	1.84	0.60
1:BL:316:SER:HB2	1:BL:319:GLN:OE1	2.01	0.60
1:CU:185:LEU:C	1:CU:186:LEU:HD23	2.27	0.60
1:BY:58:SER:HB3	1:BY:204:SER:HB3	1.82	0.60
1:AY:314:TYR:HE1	1:AY:316:SER:HA	1.65	0.60
1:CZ:111:ILE:O	1:CZ:198:SER:O	2.19	0.60
1:CZ:141:LEU:N	1:CZ:141:LEU:HD23	2.16	0.60
1:Bb:68:LEU:HD23	1:Bb:195:VAL:HG22	1.82	0.60
1:Bc:166:LEU:HD13	1:Bc:166:LEU:C	2.27	0.60
1:Bd:80:VAL:HG13	1:Bd:185:LEU:HB3	1.83	0.60
1:BA:68:LEU:HD23	1:BA:195:VAL:CG2	2.32	0.60
1:BC:183:LEU:C	1:BC:183:LEU:HD12	2.26	0.60
1:CE:75:ASP:OD1	1:CE:188:VAL:C	2.43	0.60
1:BG:166:LEU:HD13	1:BG:166:LEU:C	2.27	0.60
1:AG:119:THR:O	1:AG:192:THR:HB	2.01	0.60
1:BH:68:LEU:HD23	1:BH:195:VAL:HG22	1.84	0.60
1:CJ:79:VAL:CG1	1:CJ:185:LEU:O	2.49	0.60
1:BK:176:ARG:HD2	1:CK:168:TRP:CE2	2.37	0.60
1:BN:101:ARG:NH2	1:BN:166:LEU:HD12	2.16	0.60
1:BQ:58:SER:HB3	1:BQ:204:SER:HB3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:98:ILE:C	1:BQ:211:SER:O	2.44	0.60
1:CQ:191:ASN:N	1:CQ:191:ASN:OD1	2.34	0.60
1:BS:58:SER:HB3	1:BS:204:SER:CB	2.32	0.60
1:CT:111:ILE:O	1:CT:198:SER:O	2.19	0.60
1:CW:58:SER:HA	1:CW:203:TRP:CZ3	2.36	0.60
1:AX:119:THR:O	1:AX:192:THR:HB	2.00	0.60
1:BZ:176:ARG:HD2	1:CZ:168:TRP:CE2	2.36	0.60
1:Aa:314:TYR:CZ	1:Aa:315:TYR:O	2.55	0.60
1:BA:253:ASP:HB2	1:BA:286:ALA:HB2	1.83	0.60
1:AA:144:THR:HG23	1:AA:147:ALA:HB2	1.83	0.60
1:AC:303:ASN:N	1:AC:305:ASN:OD1	2.34	0.60
1:CC:185:LEU:C	1:CC:186:LEU:HD23	2.27	0.60
1:BH:58:SER:HB3	1:BH:204:SER:CB	2.32	0.60
1:AH:119:THR:O	1:AH:192:THR:HB	2.01	0.60
1:AH:122:GLY:HA3	1:Ad:114:MET:SD	2.42	0.60
1:AH:266:ASP:O	1:AH:314:TYR:HA	2.02	0.60
1:CH:75:ASP:OD1	1:CH:188:VAL:C	2.45	0.60
1:BI:80:VAL:HG13	1:BI:185:LEU:HB3	1.83	0.60
1:AJ:80:VAL:CG1	1:AJ:185:LEU:HB3	2.32	0.60
1:CP:101:ARG:NH1	1:CP:166:LEU:CD1	2.64	0.60
1:AQ:122:GLY:HA3	1:AZ:114:MET:SD	2.41	0.60
1:AU:68:LEU:HB2	1:AU:195:VAL:CG2	2.31	0.60
1:AU:111:ILE:O	1:AU:198:SER:O	2.20	0.60
1:Cb:75:ASP:OD1	1:Cb:188:VAL:C	2.44	0.60
1:BA:80:VAL:HG13	1:BA:185:LEU:HB3	1.83	0.60
1:BA:101:ARG:NH2	1:BA:166:LEU:HD12	2.16	0.60
1:AC:68:LEU:HB2	1:AC:195:VAL:CG2	2.32	0.60
1:BD:68:LEU:HD23	1:BD:195:VAL:CG2	2.32	0.60
1:AD:122:GLY:HA3	1:AW:114:MET:SD	2.42	0.60
1:AE:91:ARG:NE	1:BM:98:ILE:HG22	2.17	0.60
1:AE:266:ASP:O	1:AE:314:TYR:HA	2.02	0.60
1:CF:111:ILE:O	1:CF:198:SER:O	2.20	0.60
1:CG:75:ASP:OD1	1:CG:188:VAL:C	2.45	0.60
1:CK:79:VAL:CG1	1:CK:185:LEU:O	2.49	0.60
1:CM:122:GLY:HA3	1:Bc:114:MET:SD	2.42	0.60
1:AO:98:ILE:HG23	1:BW:91:ARG:NH1	2.16	0.60
1:CR:111:ILE:O	1:CR:198:SER:O	2.18	0.60
1:CR:185:LEU:C	1:CR:186:LEU:HD23	2.27	0.60
1:BS:98:ILE:O	1:BS:211:SER:C	2.44	0.60
1:BS:176:ARG:HD2	1:CS:168:TRP:CE2	2.36	0.60
1:AS:144:THR:HG23	1:AS:147:ALA:HB2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:168:TRP:CE2	1:CT:176:ARG:HG2	2.36	0.60
1:BU:68:LEU:HD23	1:BU:195:VAL:HG22	1.84	0.60
1:BU:111:ILE:HG22	1:BU:156:ARG:H	1.66	0.60
1:AV:303:ASN:N	1:AV:305:ASN:OD1	2.35	0.60
1:AV:314:TYR:CZ	1:AV:315:TYR:O	2.55	0.60
1:AW:111:ILE:O	1:AW:198:SER:O	2.20	0.60
1:CX:75:ASP:OD1	1:CX:188:VAL:C	2.44	0.60
1:CY:58:SER:HA	1:CY:203:TRP:CZ3	2.37	0.60
1:Bc:111:ILE:HG23	1:Bc:113:PRO:HD3	1.84	0.60
1:Bd:68:LEU:HD23	1:Bd:195:VAL:HG22	1.83	0.60
1:Bd:127:PHE:HB3	1:Bd:160:PRO:HB3	1.83	0.60
1:CC:112:GLN:NE2	1:CJ:43:SER:HA	2.17	0.60
1:BE:61:SER:CB	1:BE:90:PRO:HD2	2.25	0.60
1:BG:176:ARG:HD2	1:CG:168:TRP:CE2	2.36	0.60
1:AH:98:ILE:HG23	1:BN:91:ARG:NH1	2.16	0.60
1:AI:303:ASN:N	1:AI:305:ASN:OD1	2.34	0.60
1:BJ:316:SER:HB2	1:BJ:319:GLN:OE1	2.02	0.60
1:AK:314:TYR:HE1	1:AK:316:SER:HA	1.66	0.60
1:AL:168:TRP:CE2	1:CL:176:ARG:HG2	2.37	0.60
1:BM:80:VAL:HG13	1:BM:185:LEU:HB3	1.84	0.60
1:BN:253:ASP:HB2	1:BN:286:ALA:HB2	1.82	0.60
1:CN:163:THR:HG21	1:CN:167:LEU:HD11	1.83	0.60
1:AR:314:TYR:HE1	1:AR:316:SER:HA	1.64	0.60
1:CS:109:PHE:HB2	1:CS:158:VAL:CG1	2.32	0.60
1:CV:75:ASP:OD1	1:CV:188:VAL:C	2.45	0.60
1:AX:68:LEU:HB2	1:AX:195:VAL:CG2	2.30	0.60
1:AY:68:LEU:HB2	1:AY:195:VAL:CG2	2.32	0.60
1:CY:111:ILE:O	1:CY:198:SER:O	2.20	0.60
1:Bb:98:ILE:O	1:Bb:211:SER:C	2.44	0.60
1:Bc:316:SER:HB2	1:Bc:319:GLN:OE1	2.02	0.60
1:Ad:119:THR:O	1:Ad:192:THR:HB	2.02	0.60
1:AD:119:THR:O	1:AD:192:THR:HB	2.02	0.60
1:AG:122:GLY:HA3	1:AP:114:MET:SD	2.42	0.60
1:BK:183:LEU:C	1:BK:183:LEU:HD12	2.27	0.60
1:AM:91:ARG:HH21	1:Bc:98:ILE:HG22	1.66	0.60
1:AM:119:THR:O	1:AM:192:THR:HB	2.02	0.60
1:AM:303:ASN:N	1:AM:305:ASN:OD1	2.35	0.60
1:AN:91:ARG:HE	1:BP:98:ILE:HG22	1.67	0.60
1:BQ:80:VAL:HG13	1:BQ:185:LEU:HB3	1.84	0.60
1:CQ:163:THR:HG21	1:CQ:167:LEU:HD11	1.84	0.60
1:BT:68:LEU:HD23	1:BT:195:VAL:CG2	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BU:80:VAL:HG13	1:BU:185:LEU:HB3	1.84	0.60
1:BV:176:ARG:HD2	1:CV:168:TRP:CE2	2.37	0.60
1:CY:109:PHE:HB2	1:CY:158:VAL:CG1	2.31	0.60
1:CY:122:GLY:O	1:CY:188:VAL:HB	2.00	0.60
1:Aa:141:LEU:O	1:Aa:144:THR:CG2	2.44	0.60
1:Bd:176:ARG:HD2	1:Cd:168:TRP:CE2	2.37	0.60
1:AB:266:ASP:O	1:AB:314:TYR:HA	2.02	0.59
1:CD:109:PHE:HB2	1:CD:158:VAL:CG1	2.32	0.59
1:BF:80:VAL:HG13	1:BF:185:LEU:HB3	1.84	0.59
1:AG:114:MET:SD	1:Ad:122:GLY:HA3	2.41	0.59
1:AG:314:TYR:CZ	1:AG:315:TYR:O	2.54	0.59
1:CH:111:ILE:O	1:CH:198:SER:O	2.20	0.59
1:BR:253:ASP:HB2	1:BR:286:ALA:HB2	1.84	0.59
1:AU:63:ILE:HB	1:AU:199:VAL:HG13	1.84	0.59
1:AV:111:ILE:O	1:AV:198:SER:O	2.19	0.59
1:CW:95:ALA:O	1:CW:98:ILE:HG12	2.02	0.59
1:CW:163:THR:HG21	1:CW:167:LEU:HD11	1.83	0.59
1:AZ:314:TYR:CZ	1:AZ:315:TYR:O	2.55	0.59
1:Cb:109:PHE:HB2	1:Cb:158:VAL:CG1	2.32	0.59
1:Bc:253:ASP:HB2	1:Bc:286:ALA:HB2	1.84	0.59
1:Cc:75:ASP:OD1	1:Cc:188:VAL:C	2.45	0.59
1:CB:79:VAL:CG1	1:CB:185:LEU:O	2.48	0.59
1:BE:253:ASP:HB2	1:BE:286:ALA:HB2	1.84	0.59
1:CE:122:GLY:O	1:CE:188:VAL:HB	2.02	0.59
1:AG:111:ILE:O	1:AG:198:SER:O	2.20	0.59
1:BH:166:LEU:C	1:BH:166:LEU:HD13	2.27	0.59
1:AI:119:THR:O	1:AI:192:THR:HB	2.03	0.59
1:BK:68:LEU:HD23	1:BK:195:VAL:HG22	1.83	0.59
1:BO:58:SER:HB3	1:BO:204:SER:HB3	1.83	0.59
1:AO:109:PHE:HB2	1:AO:158:VAL:CG1	2.32	0.59
1:CO:79:VAL:CG1	1:CO:185:LEU:O	2.50	0.59
1:AP:314:TYR:HE1	1:AP:316:SER:HA	1.63	0.59
1:BR:68:LEU:HD23	1:BR:195:VAL:HG22	1.84	0.59
1:BU:58:SER:HB3	1:BU:204:SER:HB3	1.83	0.59
1:Aa:63:ILE:HB	1:Aa:199:VAL:HG13	1.83	0.59
1:Bd:166:LEU:C	1:Bd:166:LEU:HD13	2.27	0.59
1:AA:314:TYR:CZ	1:AA:315:TYR:O	2.54	0.59
1:CB:185:LEU:C	1:CB:186:LEU:HD23	2.26	0.59
1:CD:62:ARG:NH1	1:BI:75:ASP:OD2	2.31	0.59
1:CI:111:ILE:O	1:CI:198:SER:O	2.19	0.59
1:AJ:303:ASN:N	1:AJ:305:ASN:OD1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:127:PHE:HB3	1:BL:160:PRO:HB3	1.84	0.59
1:CN:141:LEU:N	1:CN:141:LEU:HD23	2.16	0.59
1:CO:34:ARG:HG3	1:Bc:156:ARG:NH2	2.16	0.59
1:CP:112:GLN:NE2	1:CQ:43:SER:HA	2.16	0.59
1:CS:79:VAL:CG1	1:CS:185:LEU:O	2.48	0.59
1:CS:111:ILE:O	1:CS:198:SER:O	2.20	0.59
1:BT:127:PHE:HB3	1:BT:160:PRO:HB3	1.83	0.59
1:AT:314:TYR:CZ	1:AT:315:TYR:O	2.56	0.59
1:BZ:253:ASP:HB2	1:BZ:286:ALA:HB2	1.84	0.59
1:CZ:58:SER:HA	1:CZ:203:TRP:CZ3	2.36	0.59
1:CZ:109:PHE:HB2	1:CZ:158:VAL:CG1	2.32	0.59
1:AD:314:TYR:HE1	1:AD:316:SER:N	2.01	0.59
1:BF:58:SER:HB3	1:BF:204:SER:HB3	1.84	0.59
1:BF:130:ASP:HB2	1:CF:100:GLN:NE2	2.17	0.59
1:AF:119:THR:O	1:AF:192:THR:HB	2.02	0.59
1:CG:109:PHE:HB2	1:CG:158:VAL:CG1	2.32	0.59
1:AI:63:ILE:HB	1:AI:199:VAL:HG13	1.84	0.59
1:CK:43:SER:HA	1:CL:112:GLN:NE2	2.17	0.59
1:CL:199:VAL:HG13	1:CL:199:VAL:O	2.02	0.59
1:AO:63:ILE:HB	1:AO:199:VAL:HG13	1.84	0.59
1:AO:303:ASN:N	1:AO:305:ASN:OD1	2.35	0.59
1:AQ:111:ILE:O	1:AQ:198:SER:O	2.20	0.59
1:AS:314:TYR:HE1	1:AS:316:SER:N	2.00	0.59
1:CS:122:GLY:C	1:CS:188:VAL:HB	2.26	0.59
1:AV:141:LEU:O	1:AV:144:THR:CG2	2.42	0.59
1:CW:185:LEU:C	1:CW:186:LEU:HD23	2.26	0.59
1:BA:112:GLN:HB2	1:BA:198:SER:O	2.02	0.59
1:AB:91:ARG:NE	1:BY:98:ILE:CG2	2.65	0.59
1:BE:166:LEU:C	1:BE:166:LEU:HD13	2.27	0.59
1:BF:176:ARG:HD2	1:CF:168:TRP:CE2	2.37	0.59
1:CF:122:GLY:HA3	1:Bb:114:MET:SD	2.42	0.59
1:CG:185:LEU:C	1:CG:186:LEU:HD23	2.27	0.59
1:BK:68:LEU:HD23	1:BK:195:VAL:CG2	2.33	0.59
1:BM:68:LEU:HD23	1:BM:195:VAL:HG22	1.85	0.59
1:BN:98:ILE:O	1:BN:211:SER:CA	2.51	0.59
1:CR:43:SER:HA	1:CT:112:GLN:NE2	2.18	0.59
1:CR:101:ARG:NH1	1:CR:166:LEU:CD1	2.66	0.59
1:CS:95:ALA:O	1:CS:98:ILE:HG12	2.03	0.59
1:BT:111:ILE:HG22	1:BT:156:ARG:H	1.68	0.59
1:CX:95:ALA:O	1:CX:98:ILE:HG12	2.02	0.59
1:BY:75:ASP:OD2	1:Ca:62:ARG:NH1	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:79:VAL:CG1	1:CY:185:LEU:O	2.47	0.59
1:Aa:80:VAL:CG1	1:Aa:185:LEU:HB3	2.33	0.59
1:Aa:144:THR:HG23	1:Aa:147:ALA:HB2	1.84	0.59
1:Aa:303:ASN:N	1:Aa:305:ASN:OD1	2.35	0.59
1:Cb:95:ALA:O	1:Cb:98:ILE:HG12	2.02	0.59
1:Ac:111:ILE:O	1:Ac:198:SER:O	2.21	0.59
1:CA:185:LEU:C	1:CA:186:LEU:HD23	2.28	0.59
1:BB:111:ILE:HG23	1:BB:113:PRO:HD3	1.85	0.59
1:AC:266:ASP:O	1:AC:314:TYR:HA	2.03	0.59
1:CD:80:VAL:CG1	1:CD:185:LEU:HB2	2.33	0.59
1:AJ:268:SER:HB3	1:AJ:273:ASP:O	2.03	0.59
1:BL:253:ASP:HB2	1:BL:286:ALA:HB2	1.85	0.59
1:AM:91:ARG:NE	1:Bc:98:ILE:CG2	2.65	0.59
1:AM:91:ARG:CZ	1:Bc:98:ILE:HG22	2.32	0.59
1:CN:95:ALA:O	1:CN:98:ILE:HG12	2.03	0.59
1:AO:111:ILE:O	1:AO:198:SER:O	2.20	0.59
1:AO:168:TRP:CE2	1:CO:176:ARG:HG2	2.38	0.59
1:CO:34:ARG:HD3	1:Cc:43:SER:O	2.01	0.59
1:CP:95:ALA:O	1:CP:98:ILE:HG12	2.03	0.59
1:BS:80:VAL:HG13	1:BS:185:LEU:HB3	1.85	0.59
1:CS:79:VAL:HG13	1:CS:80:VAL:N	2.16	0.59
1:BT:166:LEU:HD13	1:BT:166:LEU:C	2.27	0.59
1:AT:144:THR:HG23	1:AT:147:ALA:HB2	1.84	0.59
1:BU:75:ASP:OD2	1:Cb:62:ARG:NH1	2.31	0.59
1:BV:111:ILE:HG22	1:BV:156:ARG:H	1.68	0.59
1:BV:127:PHE:HB3	1:BV:160:PRO:HB3	1.84	0.59
1:AY:314:TYR:HE1	1:AY:316:SER:N	2.00	0.59
1:BZ:80:VAL:HG13	1:BZ:185:LEU:HB3	1.85	0.59
1:Cb:185:LEU:C	1:Cb:186:LEU:HD23	2.28	0.59
1:AD:111:ILE:O	1:AD:198:SER:O	2.20	0.59
1:AE:314:TYR:CZ	1:AE:315:TYR:O	2.55	0.59
1:CF:185:LEU:C	1:CF:186:LEU:HD23	2.27	0.59
1:BI:58:SER:HB3	1:BI:204:SER:CB	2.32	0.59
1:AK:62:ARG:HG2	1:AK:62:ARG:HH11	1.68	0.59
1:BN:112:GLN:HB2	1:BN:198:SER:O	2.02	0.59
1:AO:61:SER:CB	1:AO:90:PRO:HD2	2.30	0.59
1:AO:80:VAL:CG1	1:AO:185:LEU:HB3	2.33	0.59
1:AO:320:PRO:O	1:AO:322:GLN:HG3	2.03	0.59
1:AS:62:ARG:HG2	1:AS:62:ARG:HH11	1.67	0.59
1:AS:266:ASP:O	1:AS:314:TYR:HA	2.03	0.59
1:BT:316:SER:HB2	1:BT:319:GLN:OE1	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:101:ARG:NH1	1:BX:166:LEU:CD1	2.66	0.59
1:BY:253:ASP:HB2	1:BY:286:ALA:HB2	1.84	0.59
1:Ca:109:PHE:HB2	1:Ca:158:VAL:CG1	2.33	0.59
1:Cb:163:THR:HG21	1:Cb:167:LEU:HD11	1.85	0.59
1:Ac:62:ARG:HH11	1:Ac:62:ARG:HG2	1.66	0.59
1:AA:314:TYR:HE1	1:AA:316:SER:N	1.99	0.59
1:BB:111:ILE:HG22	1:BB:156:ARG:H	1.67	0.59
1:BE:111:ILE:HG23	1:BE:113:PRO:HD3	1.85	0.59
1:CE:185:LEU:C	1:CE:186:LEU:HD23	2.28	0.59
1:CK:101:ARG:NH1	1:CK:166:LEU:CD1	2.65	0.59
1:BL:112:GLN:HB2	1:BL:198:SER:O	2.03	0.59
1:AQ:314:TYR:HE1	1:AQ:316:SER:N	1.99	0.59
1:BR:316:SER:HB2	1:BR:319:GLN:OE1	2.02	0.59
1:AS:314:TYR:CZ	1:AS:315:TYR:O	2.55	0.59
1:CU:58:SER:HA	1:CU:203:TRP:CZ3	2.37	0.59
1:BV:61:SER:CB	1:BV:90:PRO:HD2	2.24	0.59
1:CV:163:THR:HG21	1:CV:167:LEU:HD11	1.84	0.59
1:CW:141:LEU:N	1:CW:141:LEU:HD23	2.18	0.59
1:AY:168:TRP:CE2	1:CY:176:ARG:HG2	2.38	0.59
1:Ba:127:PHE:HB3	1:Ba:160:PRO:HB3	1.83	0.59
1:Bc:127:PHE:HB3	1:Bc:160:PRO:HB3	1.85	0.59
1:Ac:80:VAL:CG1	1:Ac:185:LEU:HB3	2.33	0.59
1:Ad:62:ARG:HG2	1:Ad:62:ARG:HH11	1.67	0.59
1:AA:91:ARG:NE	1:BV:98:ILE:CG2	2.66	0.59
1:BB:98:ILE:O	1:BB:211:SER:CA	2.51	0.59
1:AC:314:TYR:CZ	1:AC:315:TYR:O	2.55	0.59
1:BD:80:VAL:HG13	1:BD:185:LEU:HB3	1.83	0.59
1:BD:112:GLN:HB2	1:BD:198:SER:O	2.03	0.59
1:CE:199:VAL:O	1:CE:199:VAL:HG13	2.02	0.59
1:BF:316:SER:HB2	1:BF:319:GLN:OE1	2.03	0.59
1:AF:168:TRP:CE2	1:CF:176:ARG:HG2	2.38	0.59
1:CF:141:LEU:N	1:CF:141:LEU:HD23	2.17	0.59
1:BG:68:LEU:HD23	1:BG:195:VAL:CG2	2.33	0.59
1:BG:127:PHE:HB3	1:BG:160:PRO:HB3	1.85	0.59
1:AG:266:ASP:O	1:AG:314:TYR:HA	2.03	0.59
1:AG:303:ASN:N	1:AG:305:ASN:OD1	2.34	0.59
1:AG:314:TYR:HE1	1:AG:316:SER:N	1.99	0.59
1:CH:109:PHE:HB2	1:CH:158:VAL:CG1	2.32	0.59
1:AJ:314:TYR:HE1	1:AJ:316:SER:N	1.99	0.59
1:CN:75:ASP:OD1	1:CN:188:VAL:C	2.46	0.59
1:BP:68:LEU:HD23	1:BP:195:VAL:CG2	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:176:ARG:HD2	1:CP:168:TRP:CE2	2.38	0.59
1:CS:75:ASP:OD1	1:CS:188:VAL:C	2.45	0.59
1:BT:253:ASP:HB2	1:BT:286:ALA:HB2	1.83	0.59
1:CT:79:VAL:CG1	1:CT:185:LEU:O	2.49	0.59
1:BW:166:LEU:HD13	1:BW:166:LEU:C	2.27	0.59
1:AX:314:TYR:HE1	1:AX:316:SER:N	1.98	0.59
1:Ca:163:THR:HG21	1:Ca:167:LEU:HD11	1.85	0.59
1:AA:320:PRO:O	1:AA:322:GLN:HG3	2.02	0.59
1:AB:168:TRP:CE2	1:CB:176:ARG:HG2	2.38	0.59
1:CB:163:THR:HG21	1:CB:167:LEU:HD11	1.84	0.59
1:AE:62:ARG:HG2	1:AE:62:ARG:HH11	1.68	0.59
1:CG:79:VAL:HG13	1:CG:80:VAL:N	2.18	0.59
1:BH:112:GLN:HB2	1:BH:198:SER:O	2.03	0.59
1:AH:314:TYR:HE1	1:AH:316:SER:N	1.99	0.59
1:CI:199:VAL:HG13	1:CI:199:VAL:O	2.02	0.59
1:AJ:63:ILE:HB	1:AJ:199:VAL:HG13	1.84	0.59
1:AN:144:THR:HG23	1:AN:147:ALA:HB2	1.84	0.59
1:AQ:303:ASN:N	1:AQ:305:ASN:OD1	2.35	0.59
1:BS:68:LEU:HD23	1:BS:195:VAL:CG2	2.33	0.59
1:AS:303:ASN:N	1:AS:305:ASN:OD1	2.35	0.59
1:BT:80:VAL:HG13	1:BT:185:LEU:HB3	1.84	0.59
1:BV:166:LEU:C	1:BV:166:LEU:HD13	2.28	0.59
1:AV:266:ASP:O	1:AV:314:TYR:HA	2.03	0.59
1:CW:199:VAL:HG13	1:CW:199:VAL:O	2.00	0.59
1:CZ:85:VAL:HG13	1:CZ:86:PRO:HD2	1.85	0.59
1:Ba:101:ARG:NH1	1:Ba:166:LEU:CD1	2.66	0.59
1:Bb:130:ASP:HB2	1:Cb:100:GLN:NE2	2.18	0.59
1:Bd:253:ASP:HB2	1:Bd:286:ALA:HB2	1.83	0.59
1:Cd:101:ARG:NH1	1:Cd:166:LEU:CD1	2.63	0.59
1:AA:63:ILE:HB	1:AA:199:VAL:HG13	1.85	0.58
1:AC:320:PRO:O	1:AC:322:GLN:HG3	2.04	0.58
1:BD:183:LEU:C	1:BD:183:LEU:HD12	2.28	0.58
1:BE:316:SER:HB2	1:BE:319:GLN:OE1	2.03	0.58
1:BF:183:LEU:C	1:BF:183:LEU:HD12	2.28	0.58
1:BH:80:VAL:HG13	1:BH:185:LEU:HB3	1.85	0.58
1:BH:130:ASP:HB2	1:CH:100:GLN:NE2	2.15	0.58
1:AH:91:ARG:NH2	1:BN:210:PRO:HB3	2.18	0.58
1:AK:253:ASP:CG	1:AK:285:PHE:CA	2.76	0.58
1:BO:166:LEU:HD13	1:BO:166:LEU:C	2.28	0.58
1:BP:111:ILE:HG21	1:BP:123:TYR:OH	2.03	0.58
1:CP:112:GLN:HE21	1:CQ:44:THR:H	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:111:ILE:HG22	1:BS:156:ARG:H	1.68	0.58
1:BU:153:TRP:O	1:CX:151:LYS:NZ	2.36	0.58
1:AV:314:TYR:HE1	1:AV:316:SER:N	2.01	0.58
1:CV:58:SER:HA	1:CV:203:TRP:CZ3	2.38	0.58
1:AX:303:ASN:N	1:AX:305:ASN:OD1	2.35	0.58
1:CY:199:VAL:O	1:CY:199:VAL:HG13	2.03	0.58
1:BZ:112:GLN:HB2	1:BZ:198:SER:O	2.03	0.58
1:Bc:80:VAL:HG13	1:Bc:185:LEU:HB3	1.85	0.58
1:Bc:98:ILE:O	1:Bc:211:SER:CA	2.50	0.58
1:Bd:98:ILE:O	1:Bd:211:SER:CA	2.51	0.58
1:Ad:314:TYR:CZ	1:Ad:315:TYR:O	2.56	0.58
1:Cd:122:GLY:O	1:Cd:188:VAL:HB	2.03	0.58
1:AB:63:ILE:HB	1:AB:199:VAL:HG13	1.85	0.58
1:BD:253:ASP:HB2	1:BD:286:ALA:HB2	1.83	0.58
1:AD:320:PRO:O	1:AD:322:GLN:HG3	2.03	0.58
1:AF:144:THR:HG23	1:AF:147:ALA:HB2	1.84	0.58
1:BR:80:VAL:HG13	1:BR:185:LEU:HB3	1.85	0.58
1:AS:141:LEU:O	1:AS:144:THR:CG2	2.44	0.58
1:BV:68:LEU:HD23	1:BV:195:VAL:CG2	2.33	0.58
1:AY:141:LEU:O	1:AY:144:THR:CG2	2.42	0.58
1:Bb:68:LEU:HD23	1:Bb:195:VAL:CG2	2.33	0.58
1:Ac:141:LEU:O	1:Ac:144:THR:CG2	2.44	0.58
1:Bd:58:SER:HB3	1:Bd:204:SER:HB3	1.84	0.58
1:BB:80:VAL:HG13	1:BB:185:LEU:HB3	1.84	0.58
1:AB:303:ASN:N	1:AB:305:ASN:OD1	2.35	0.58
1:BD:75:ASP:OD2	1:CI:62:ARG:NH1	2.33	0.58
1:CD:163:THR:HG21	1:CD:167:LEU:HD11	1.84	0.58
1:AF:314:TYR:HE1	1:AF:316:SER:N	1.99	0.58
1:CF:109:PHE:HB2	1:CF:158:VAL:CG1	2.34	0.58
1:CI:79:VAL:CG1	1:CI:185:LEU:O	2.51	0.58
1:BL:176:ARG:HD2	1:CL:168:TRP:CE2	2.38	0.58
1:BN:127:PHE:HB3	1:BN:160:PRO:HB3	1.85	0.58
1:BN:176:ARG:HD2	1:CN:168:TRP:CE2	2.38	0.58
1:CN:111:ILE:O	1:CN:198:SER:O	2.21	0.58
1:AO:266:ASP:O	1:AO:314:TYR:HA	2.03	0.58
1:BX:176:ARG:HD2	1:CX:168:TRP:CE2	2.38	0.58
1:BY:98:ILE:O	1:BY:211:SER:CA	2.50	0.58
1:CY:79:VAL:HG13	1:CY:80:VAL:N	2.17	0.58
1:AZ:168:TRP:CE2	1:CZ:176:ARG:HG2	2.37	0.58
1:Ba:115:CYS:HB2	1:Ba:116:PRO:HD2	1.85	0.58
1:BA:58:SER:HB3	1:BA:204:SER:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:68:LEU:HD23	1:BB:195:VAL:HG22	1.84	0.58
1:BB:112:GLN:HB2	1:BB:198:SER:O	2.03	0.58
1:AB:119:THR:O	1:AB:192:THR:HB	2.02	0.58
1:BC:253:ASP:HB2	1:BC:286:ALA:HB2	1.83	0.58
1:BE:176:ARG:HD2	1:CE:168:TRP:CE2	2.38	0.58
1:AF:63:ILE:HB	1:AF:199:VAL:HG13	1.84	0.58
1:CJ:185:LEU:C	1:CJ:186:LEU:HD23	2.28	0.58
1:BK:58:SER:HB3	1:BK:204:SER:HB3	1.84	0.58
1:AL:314:TYR:CZ	1:AL:315:TYR:O	2.56	0.58
1:CL:111:ILE:HG22	1:CL:113:PRO:HD3	1.84	0.58
1:BM:111:ILE:HG22	1:BM:156:ARG:H	1.68	0.58
1:AM:266:ASP:O	1:AM:314:TYR:HA	2.03	0.58
1:CM:185:LEU:C	1:CM:186:LEU:HD23	2.28	0.58
1:AN:119:THR:O	1:AN:192:THR:HB	2.03	0.58
1:AN:303:ASN:N	1:AN:305:ASN:OD1	2.35	0.58
1:CO:122:GLY:O	1:CO:188:VAL:HB	2.03	0.58
1:AP:314:TYR:CZ	1:AP:315:TYR:O	2.55	0.58
1:AU:141:LEU:O	1:AU:144:THR:CG2	2.42	0.58
1:CU:122:GLY:O	1:CU:188:VAL:HB	2.04	0.58
1:AV:62:ARG:HG2	1:AV:62:ARG:HH11	1.68	0.58
1:CV:185:LEU:C	1:CV:186:LEU:HD23	2.29	0.58
1:BY:68:LEU:HD23	1:BY:195:VAL:CG2	2.33	0.58
1:CY:163:THR:HG21	1:CY:167:LEU:HD11	1.84	0.58
1:Bc:111:ILE:HG21	1:Bc:123:TYR:OH	2.02	0.58
1:Bc:176:ARG:HD2	1:Cc:168:TRP:CE2	2.39	0.58
1:AA:62:ARG:HG2	1:AA:62:ARG:HH11	1.69	0.58
1:AG:62:ARG:HH11	1:AG:62:ARG:HG2	1.68	0.58
1:BI:101:ARG:NH2	1:BI:166:LEU:HD12	2.18	0.58
1:BI:127:PHE:HB3	1:BI:160:PRO:HB3	1.85	0.58
1:BJ:98:ILE:O	1:BJ:211:SER:CA	2.51	0.58
1:BJ:101:ARG:NH2	1:BJ:166:LEU:HD12	2.18	0.58
1:BL:58:SER:HB3	1:BL:204:SER:CB	2.34	0.58
1:CM:109:PHE:HB2	1:CM:158:VAL:CG1	2.34	0.58
1:AN:168:TRP:CE2	1:CN:176:ARG:HG2	2.39	0.58
1:BP:127:PHE:HB3	1:BP:160:PRO:HB3	1.85	0.58
1:CP:109:PHE:HB2	1:CP:158:VAL:CG1	2.33	0.58
1:CP:111:ILE:HG22	1:CP:113:PRO:HD3	1.84	0.58
1:BS:111:ILE:HG21	1:BS:123:TYR:OH	2.04	0.58
1:BT:176:ARG:HD2	1:CT:168:TRP:CE2	2.38	0.58
1:AT:122:GLY:HA3	1:AV:114:MET:SD	2.44	0.58
1:CT:185:LEU:C	1:CT:186:LEU:HD23	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:191:ASN:OD1	1:CV:191:ASN:N	2.34	0.58
1:BY:130:ASP:HB2	1:CY:100:GLN:NE2	2.18	0.58
1:Cb:80:VAL:HG12	1:Cb:185:LEU:CB	2.27	0.58
1:Ac:303:ASN:N	1:Ac:305:ASN:OD1	2.35	0.58
1:AD:266:ASP:O	1:AD:314:TYR:HA	2.03	0.58
1:AF:314:TYR:CZ	1:AF:315:TYR:O	2.56	0.58
1:CI:43:SER:O	1:CY:34:ARG:HD3	2.03	0.58
1:BM:98:ILE:O	1:BM:211:SER:CA	2.51	0.58
1:AT:303:ASN:N	1:AT:305:ASN:OD1	2.34	0.58
1:AV:168:TRP:CE2	1:CV:176:ARG:HG2	2.39	0.58
1:BX:68:LEU:HD23	1:BX:195:VAL:CG2	2.34	0.58
1:BX:253:ASP:HB2	1:BX:286:ALA:HB2	1.84	0.58
1:BY:111:ILE:HG23	1:BY:113:PRO:HD3	1.85	0.58
1:AY:111:ILE:O	1:AY:198:SER:O	2.22	0.58
1:BZ:98:ILE:O	1:BZ:211:SER:CA	2.52	0.58
1:AZ:314:TYR:HE1	1:AZ:316:SER:N	2.02	0.58
1:Bc:68:LEU:HD23	1:Bc:195:VAL:CG2	2.33	0.58
1:Bc:111:ILE:HG22	1:Bc:156:ARG:H	1.68	0.58
1:CA:95:ALA:O	1:CA:98:ILE:HG12	2.04	0.58
1:AC:144:THR:HG23	1:AC:147:ALA:HB2	1.84	0.58
1:CC:111:ILE:O	1:CC:198:SER:O	2.21	0.58
1:CD:111:ILE:O	1:CD:198:SER:O	2.22	0.58
1:BF:253:ASP:HB2	1:BF:286:ALA:HB2	1.86	0.58
1:AF:266:ASP:O	1:AF:314:TYR:HA	2.03	0.58
1:AG:91:ARG:NE	1:Bd:98:ILE:CG2	2.66	0.58
1:BK:98:ILE:O	1:BK:211:SER:CA	2.51	0.58
1:AL:303:ASN:N	1:AL:305:ASN:OD1	2.34	0.58
1:AM:320:PRO:O	1:AM:322:GLN:HG3	2.03	0.58
1:AN:63:ILE:HB	1:AN:199:VAL:HG13	1.84	0.58
1:BO:127:PHE:HB3	1:BO:160:PRO:HB3	1.84	0.58
1:BU:176:ARG:HD2	1:CU:168:TRP:CE2	2.37	0.58
1:Ab:62:ARG:HG2	1:Ab:62:ARG:HH11	1.69	0.58
1:BA:98:ILE:O	1:BA:211:SER:CA	2.52	0.58
1:AB:62:ARG:HG2	1:AB:62:ARG:HH11	1.68	0.58
1:BC:101:ARG:NH2	1:BC:166:LEU:HD12	2.18	0.58
1:CC:95:ALA:O	1:CC:98:ILE:HG12	2.04	0.58
1:AD:91:ARG:NE	1:BF:98:ILE:CG2	2.67	0.58
1:CD:95:ALA:O	1:CD:98:ILE:HG12	2.04	0.58
1:BE:98:ILE:O	1:BE:211:SER:CA	2.52	0.58
1:BF:111:ILE:HG22	1:BF:156:ARG:H	1.68	0.58
1:AF:320:PRO:O	1:AF:322:GLN:HG3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:111:ILE:HG21	1:BG:123:TYR:OH	2.03	0.58
1:BG:210:PRO:HB3	1:AP:91:ARG:NH2	2.19	0.58
1:CH:163:THR:HG21	1:CH:167:LEU:HD11	1.85	0.58
1:AI:320:PRO:O	1:AI:322:GLN:HG3	2.04	0.58
1:BN:58:SER:HB3	1:BN:204:SER:HB3	1.85	0.58
1:AP:111:ILE:O	1:AP:198:SER:O	2.21	0.58
1:AP:314:TYR:HE1	1:AP:316:SER:N	2.01	0.58
1:CT:163:THR:HG21	1:CT:167:LEU:HD11	1.85	0.58
1:CX:80:VAL:HG12	1:CX:185:LEU:CB	2.29	0.58
1:BY:111:ILE:HG22	1:BY:156:ARG:H	1.68	0.58
1:BZ:183:LEU:C	1:BZ:183:LEU:HD12	2.29	0.58
1:CZ:80:VAL:CG1	1:CZ:185:LEU:HB2	2.33	0.58
1:BB:98:ILE:CG2	1:AK:91:ARG:NE	2.67	0.58
1:BC:58:SER:HB3	1:BC:204:SER:CB	2.33	0.58
1:BC:68:LEU:HD23	1:BC:195:VAL:HG22	1.85	0.58
1:AD:314:TYR:CZ	1:AD:315:TYR:O	2.56	0.58
1:AH:111:ILE:O	1:AH:198:SER:O	2.21	0.58
1:AI:266:ASP:O	1:AI:314:TYR:HA	2.03	0.58
1:BJ:68:LEU:HD23	1:BJ:195:VAL:CG2	2.34	0.58
1:BK:80:VAL:HG13	1:BK:185:LEU:HB3	1.84	0.58
1:CK:80:VAL:CG1	1:CK:185:LEU:HB2	2.34	0.58
1:BM:112:GLN:HB2	1:BM:198:SER:O	2.04	0.58
1:BO:98:ILE:O	1:BO:211:SER:CA	2.52	0.58
1:CO:151:LYS:NZ	1:BW:153:TRP:O	2.37	0.58
1:BR:176:ARG:HD2	1:CR:168:TRP:CE2	2.39	0.58
1:BT:101:ARG:NH2	1:BT:166:LEU:HD12	2.18	0.58
1:CT:111:ILE:HD11	1:CT:125:ALA:CB	2.34	0.58
1:Bc:112:GLN:HB2	1:Bc:198:SER:O	2.04	0.58
1:BE:58:SER:HB3	1:BE:204:SER:CB	2.33	0.58
1:BF:166:LEU:HD13	1:BF:166:LEU:C	2.27	0.58
1:CF:191:ASN:OD1	1:CF:191:ASN:N	2.34	0.58
1:BI:112:GLN:HB2	1:BI:198:SER:O	2.03	0.58
1:BJ:111:ILE:HG22	1:BJ:156:ARG:H	1.69	0.58
1:BJ:176:ARG:HD2	1:CJ:168:TRP:CE2	2.38	0.58
1:AL:63:ILE:HB	1:AL:199:VAL:HG13	1.85	0.58
1:BN:68:LEU:HD23	1:BN:195:VAL:HG22	1.85	0.58
1:AQ:124:VAL:HG11	1:AQ:138:PHE:HD1	1.68	0.58
1:CV:109:PHE:HB2	1:CV:158:VAL:CG1	2.33	0.58
1:CY:191:ASN:N	1:CY:191:ASN:OD1	2.37	0.58
1:BZ:68:LEU:HD23	1:BZ:195:VAL:HG22	1.86	0.58
1:CZ:163:THR:HG21	1:CZ:167:LEU:HD11	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ad:253:ASP:CG	1:Ad:285:PHE:CA	2.77	0.58
1:AB:138:PHE:CE2	1:AK:62:ARG:CZ	2.87	0.57
1:BC:61:SER:CB	1:BC:90:PRO:HD2	2.28	0.57
1:AC:114:MET:SD	1:AS:122:GLY:HA3	2.44	0.57
1:AG:144:THR:HG23	1:AG:147:ALA:HB2	1.85	0.57
1:BI:111:ILE:HG22	1:BI:156:ARG:H	1.69	0.57
1:BJ:111:ILE:HG23	1:BJ:113:PRO:HD3	1.86	0.57
1:BO:68:LEU:HD23	1:BO:195:VAL:HG22	1.86	0.57
1:AP:266:ASP:O	1:AP:314:TYR:HA	2.04	0.57
1:BQ:111:ILE:HG22	1:BQ:156:ARG:H	1.68	0.57
1:BQ:127:PHE:HB3	1:BQ:160:PRO:HB3	1.86	0.57
1:BQ:176:ARG:HD2	1:CQ:168:TRP:CE2	2.38	0.57
1:BQ:253:ASP:HB2	1:BQ:286:ALA:HB2	1.85	0.57
1:BR:98:ILE:C	1:BR:211:SER:O	2.46	0.57
1:AS:168:TRP:CE2	1:CS:176:ARG:HG2	2.39	0.57
1:BT:98:ILE:HA	1:BT:211:SER:O	2.04	0.57
1:BT:115:CYS:HB2	1:BT:116:PRO:HD2	1.86	0.57
1:AU:303:ASN:N	1:AU:305:ASN:OD1	2.35	0.57
1:AU:320:PRO:O	1:AU:322:GLN:HG3	2.04	0.57
1:BV:183:LEU:C	1:BV:183:LEU:HD12	2.29	0.57
1:AV:119:THR:O	1:AV:192:THR:HB	2.04	0.57
1:AY:320:PRO:O	1:AY:322:GLN:HG3	2.03	0.57
1:BZ:58:SER:HB3	1:BZ:204:SER:HB3	1.86	0.57
1:AZ:141:LEU:O	1:AZ:144:THR:CG2	2.45	0.57
1:Cc:101:ARG:NH1	1:Cc:166:LEU:CD1	2.66	0.57
1:AA:111:ILE:O	1:AA:198:SER:O	2.22	0.57
1:BB:210:PRO:HB3	1:AK:91:ARG:NH2	2.19	0.57
1:CF:163:THR:HG21	1:CF:167:LEU:HD11	1.86	0.57
1:BH:98:ILE:O	1:BH:211:SER:CA	2.51	0.57
1:AH:91:ARG:HE	1:BN:98:ILE:HG22	1.69	0.57
1:AH:303:ASN:N	1:AH:305:ASN:OD1	2.35	0.57
1:AK:109:PHE:HB2	1:AK:158:VAL:CG1	2.34	0.57
1:CL:122:GLY:O	1:CL:188:VAL:HB	2.03	0.57
1:CN:109:PHE:HB2	1:CN:158:VAL:CG1	2.34	0.57
1:AP:303:ASN:N	1:AP:305:ASN:OD1	2.34	0.57
1:BR:58:SER:HB3	1:BR:204:SER:HB3	1.86	0.57
1:AR:314:TYR:CZ	1:AR:315:TYR:O	2.57	0.57
1:BX:127:PHE:HB3	1:BX:160:PRO:HB3	1.85	0.57
1:BZ:98:ILE:HA	1:BZ:211:SER:O	2.04	0.57
1:Ad:168:TRP:CE2	1:Cd:176:ARG:HG2	2.38	0.57
1:BG:58:SER:HB3	1:BG:204:SER:CB	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:115:CYS:C	1:Cd:120:GLY:HA2	2.29	0.57
1:AK:314:TYR:CZ	1:AK:315:TYR:O	2.58	0.57
1:AL:111:ILE:O	1:AL:198:SER:O	2.22	0.57
1:CR:109:PHE:HB2	1:CR:158:VAL:CG1	2.34	0.57
1:CS:191:ASN:OD1	1:CS:191:ASN:N	2.34	0.57
1:BT:98:ILE:HG22	1:AV:91:ARG:HE	1.69	0.57
1:BT:183:LEU:C	1:BT:183:LEU:HD12	2.29	0.57
1:CU:109:PHE:HB2	1:CU:158:VAL:CG1	2.35	0.57
1:CU:199:VAL:HG13	1:CU:199:VAL:O	2.03	0.57
1:AV:63:ILE:HB	1:AV:199:VAL:HG13	1.86	0.57
1:BX:58:SER:HB3	1:BX:204:SER:HB3	1.85	0.57
1:Aa:168:TRP:CE2	1:Ca:176:ARG:HG2	2.39	0.57
1:Bb:58:SER:HB3	1:Bb:204:SER:CB	2.34	0.57
1:Cd:95:ALA:O	1:Cd:98:ILE:HG12	2.04	0.57
1:CA:112:GLN:NE2	1:CG:43:SER:HA	2.20	0.57
1:AD:63:ILE:HB	1:AD:199:VAL:HG13	1.86	0.57
1:BE:111:ILE:HG22	1:BE:156:ARG:H	1.70	0.57
1:AH:141:LEU:O	1:AH:144:THR:CG2	2.45	0.57
1:BI:98:ILE:O	1:BI:211:SER:CA	2.52	0.57
1:BJ:253:ASP:HB2	1:BJ:286:ALA:HB2	1.87	0.57
1:AJ:98:ILE:CG2	1:BR:91:ARG:NH1	2.67	0.57
1:CJ:163:THR:HG21	1:CJ:167:LEU:HD11	1.85	0.57
1:BQ:316:SER:HB2	1:BQ:319:GLN:OE1	2.03	0.57
1:CQ:101:ARG:NH1	1:CQ:166:LEU:CD1	2.68	0.57
1:AT:314:TYR:HE1	1:AT:316:SER:N	2.01	0.57
1:BW:115:CYS:HB2	1:BW:116:PRO:HD2	1.86	0.57
1:BX:68:LEU:HD23	1:BX:195:VAL:HG22	1.85	0.57
1:AZ:266:ASP:O	1:AZ:314:TYR:HA	2.03	0.57
1:AZ:303:ASN:N	1:AZ:305:ASN:OD1	2.35	0.57
1:Aa:266:ASP:O	1:Aa:314:TYR:HA	2.04	0.57
1:Ab:303:ASN:N	1:Ab:305:ASN:OD1	2.35	0.57
1:Cc:185:LEU:C	1:Cc:186:LEU:HD23	2.28	0.57
1:Bd:58:SER:HB3	1:Bd:204:SER:CB	2.35	0.57
1:BC:127:PHE:HB3	1:BC:160:PRO:HB3	1.86	0.57
1:BC:130:ASP:HB2	1:CC:100:GLN:NE2	2.18	0.57
1:AC:168:TRP:CE2	1:CC:176:ARG:HG2	2.40	0.57
1:CC:191:ASN:N	1:CC:191:ASN:OD1	2.37	0.57
1:AO:119:THR:O	1:AO:192:THR:HB	2.05	0.57
1:AR:302:ASP:C	1:AR:305:ASN:ND2	2.63	0.57
1:CS:122:GLY:O	1:CS:188:VAL:HB	2.04	0.57
1:AT:320:PRO:O	1:AT:322:GLN:HG3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:168:TRP:CE2	1:CU:176:ARG:HG2	2.40	0.57
1:AX:111:ILE:O	1:AX:198:SER:O	2.22	0.57
1:AY:314:TYR:CZ	1:AY:315:TYR:O	2.57	0.57
1:Ba:111:ILE:HG23	1:Ba:113:PRO:HD3	1.86	0.57
1:BB:58:SER:HB3	1:BB:204:SER:CB	2.34	0.57
1:BB:176:ARG:HD2	1:CB:168:TRP:CE2	2.40	0.57
1:CB:118:ASN:HA	1:BY:116:PRO:CB	2.34	0.57
1:AC:119:THR:O	1:AC:192:THR:HB	2.03	0.57
1:BG:112:GLN:HB2	1:BG:198:SER:O	2.05	0.57
1:BH:127:PHE:HB3	1:BH:160:PRO:HB3	1.86	0.57
1:CM:163:THR:HG21	1:CM:167:LEU:HD11	1.86	0.57
1:AP:141:LEU:O	1:AP:144:THR:CG2	2.45	0.57
1:CP:79:VAL:CG1	1:CP:185:LEU:O	2.50	0.57
1:CQ:95:ALA:O	1:CQ:98:ILE:HG12	2.04	0.57
1:AR:266:ASP:O	1:AR:314:TYR:HA	2.05	0.57
1:AS:119:THR:O	1:AS:192:THR:HB	2.05	0.57
1:CW:79:VAL:CG1	1:CW:185:LEU:O	2.52	0.57
1:AZ:111:ILE:O	1:AZ:198:SER:O	2.22	0.57
1:Ac:168:TRP:CE2	1:Cc:176:ARG:HG2	2.40	0.57
1:Cd:85:VAL:HG13	1:Cd:86:PRO:HD2	1.87	0.57
1:AE:320:PRO:O	1:AE:322:GLN:HG3	2.04	0.57
1:CH:111:ILE:HG22	1:CH:113:PRO:HD3	1.86	0.57
1:AK:115:CYS:HB2	1:AK:116:PRO:HD2	1.86	0.57
1:CK:122:GLY:C	1:CK:188:VAL:HB	2.29	0.57
1:AL:119:THR:O	1:AL:192:THR:HB	2.04	0.57
1:CM:138:PHE:CD2	1:Bc:62:ARG:NH2	2.72	0.57
1:AN:253:ASP:CG	1:AN:285:PHE:CA	2.78	0.57
1:CP:43:SER:HA	1:CQ:112:GLN:NE2	2.19	0.57
1:CR:95:ALA:O	1:CR:98:ILE:HG12	2.04	0.57
1:CR:199:VAL:HG13	1:CR:199:VAL:O	2.04	0.57
1:BS:130:ASP:HB2	1:CS:100:GLN:NE2	2.17	0.57
1:AT:63:ILE:HB	1:AT:199:VAL:HG13	1.86	0.57
1:AT:80:VAL:CG1	1:AT:185:LEU:HB3	2.35	0.57
1:BU:112:GLN:HB2	1:BU:198:SER:O	2.05	0.57
1:AV:144:THR:HG23	1:AV:147:ALA:HB2	1.86	0.57
1:CV:101:ARG:NH1	1:CV:166:LEU:CD1	2.67	0.57
1:BX:75:ASP:OD2	1:Cc:62:ARG:NH1	2.32	0.57
1:BX:111:ILE:HG21	1:BX:123:TYR:OH	2.04	0.57
1:BY:316:SER:HB2	1:BY:319:GLN:OE1	2.04	0.57
1:CD:112:GLN:NE2	1:CI:43:SER:HA	2.19	0.57
1:BN:115:CYS:HB2	1:BN:116:PRO:HD2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:101:ARG:NH1	1:CO:166:LEU:CD1	2.67	0.57
1:BR:98:ILE:O	1:BR:211:SER:CA	2.53	0.57
1:CW:80:VAL:CG1	1:CW:185:LEU:HB2	2.35	0.57
1:AX:320:PRO:O	1:AX:322:GLN:HG3	2.05	0.57
1:Ba:98:ILE:O	1:Ba:211:SER:CA	2.52	0.57
1:Ac:314:TYR:CZ	1:Ac:315:TYR:O	2.57	0.57
1:Ad:63:ILE:HB	1:Ad:199:VAL:HG13	1.86	0.57
1:Ad:302:ASP:C	1:Ad:305:ASN:ND2	2.63	0.57
1:CA:111:ILE:HG22	1:CA:113:PRO:HD3	1.86	0.57
1:CC:79:VAL:CG1	1:CC:185:LEU:O	2.51	0.57
1:CE:111:ILE:O	1:CE:198:SER:O	2.23	0.57
1:AF:303:ASN:N	1:AF:305:ASN:OD1	2.35	0.57
1:BG:98:ILE:O	1:BG:211:SER:CA	2.53	0.57
1:AI:111:ILE:O	1:AI:198:SER:O	2.23	0.57
1:CL:112:GLN:NE2	1:CL:155:SER:OG	2.38	0.57
1:AM:253:ASP:CG	1:AM:285:PHE:CA	2.78	0.57
1:BO:58:SER:HB3	1:BO:204:SER:CB	2.35	0.57
1:BR:68:LEU:HD23	1:BR:195:VAL:CG2	2.35	0.57
1:CW:111:ILE:O	1:CW:198:SER:O	2.23	0.57
1:BX:101:ARG:NH2	1:BX:166:LEU:HD12	2.20	0.57
1:AX:266:ASP:O	1:AX:314:TYR:HA	2.04	0.57
1:AZ:320:PRO:O	1:AZ:322:GLN:HG3	2.04	0.57
1:Cc:79:VAL:CG1	1:Cc:185:LEU:O	2.51	0.57
1:AB:253:ASP:CG	1:AB:285:PHE:CA	2.78	0.57
1:CB:101:ARG:NH1	1:CB:166:LEU:CD1	2.67	0.57
1:BD:163:THR:OG1	1:BD:165:THR:CG2	2.53	0.57
1:CD:191:ASN:OD1	1:CD:191:ASN:N	2.34	0.57
1:AE:63:ILE:HB	1:AE:199:VAL:HG13	1.86	0.57
1:CE:202:ARG:HH12	1:CH:46:THR:HB	1.70	0.57
1:AH:80:VAL:CG1	1:AH:185:LEU:HB3	2.35	0.57
1:BI:183:LEU:C	1:BI:183:LEU:HD12	2.30	0.57
1:AJ:302:ASP:C	1:AJ:305:ASN:ND2	2.63	0.57
1:BL:68:LEU:HD23	1:BL:195:VAL:HG22	1.87	0.57
1:AN:320:PRO:O	1:AN:322:GLN:HG3	2.05	0.57
1:AS:63:ILE:HB	1:AS:199:VAL:HG13	1.87	0.57
1:BT:58:SER:HB3	1:BT:204:SER:CB	2.35	0.57
1:CT:191:ASN:N	1:CT:191:ASN:OD1	2.37	0.57
1:CU:101:ARG:NH1	1:CU:166:LEU:CD1	2.67	0.57
1:BW:127:PHE:HB3	1:BW:160:PRO:HB3	1.86	0.57
1:BW:253:ASP:HB2	1:BW:286:ALA:HB2	1.86	0.57
1:AX:62:ARG:HH11	1:AX:62:ARG:HG2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:98:ILE:HA	1:BY:211:SER:O	2.05	0.57
1:CZ:101:ARG:NH1	1:CZ:166:LEU:CD1	2.68	0.57
1:CZ:185:LEU:C	1:CZ:186:LEU:HD23	2.29	0.57
1:Aa:302:ASP:C	1:Aa:305:ASN:ND2	2.63	0.57
1:Bb:80:VAL:HG13	1:Bb:185:LEU:HB3	1.86	0.57
1:Ac:320:PRO:O	1:Ac:322:GLN:HG3	2.05	0.57
1:Cc:111:ILE:O	1:Cc:198:SER:O	2.22	0.57
1:Bd:183:LEU:C	1:Bd:183:LEU:HD12	2.29	0.57
1:BA:183:LEU:C	1:BA:183:LEU:HD12	2.30	0.56
1:AD:138:PHE:CE2	1:AW:62:ARG:CZ	2.87	0.56
1:BG:111:ILE:HG22	1:BG:156:ARG:H	1.69	0.56
1:BG:111:ILE:HG23	1:BG:113:PRO:HD3	1.86	0.56
1:CH:85:VAL:HG13	1:CH:86:PRO:HD2	1.87	0.56
1:CH:185:LEU:C	1:CH:186:LEU:HD23	2.30	0.56
1:BK:163:THR:OG1	1:BK:165:THR:CG2	2.53	0.56
1:CM:111:ILE:HG22	1:CM:113:PRO:HD3	1.87	0.56
1:AN:111:ILE:O	1:AN:198:SER:O	2.23	0.56
1:AP:302:ASP:C	1:AP:305:ASN:ND2	2.63	0.56
1:BQ:91:ARG:NH1	1:AZ:98:ILE:HG23	2.20	0.56
1:AR:253:ASP:CG	1:AR:285:PHE:CA	2.78	0.56
1:AU:119:THR:O	1:AU:192:THR:HB	2.05	0.56
1:AV:320:PRO:O	1:AV:322:GLN:HG3	2.04	0.56
1:BW:58:SER:HB3	1:BW:204:SER:CB	2.35	0.56
1:AW:142:GLN:NE2	1:AW:142:GLN:O	2.38	0.56
1:Ab:144:THR:HG23	1:Ab:147:ALA:HB2	1.87	0.56
1:Bd:111:ILE:HG21	1:Bd:123:TYR:OH	2.05	0.56
1:BA:98:ILE:CG2	1:AI:91:ARG:NE	2.68	0.56
1:AB:302:ASP:C	1:AB:305:ASN:ND2	2.63	0.56
1:AD:253:ASP:CG	1:AD:285:PHE:CA	2.78	0.56
1:CE:80:VAL:HG12	1:CE:185:LEU:CB	2.25	0.56
1:AH:320:PRO:O	1:AH:322:GLN:HG3	2.05	0.56
1:CH:191:ASN:OD1	1:CH:191:ASN:N	2.36	0.56
1:BI:68:LEU:HD23	1:BI:195:VAL:CG2	2.35	0.56
1:AI:253:ASP:CG	1:AI:285:PHE:CA	2.78	0.56
1:AJ:141:LEU:O	1:AJ:144:THR:CG2	2.45	0.56
1:AJ:320:PRO:O	1:AJ:322:GLN:HG3	2.05	0.56
1:BK:165:THR:OG1	1:BK:166:LEU:N	2.38	0.56
1:BL:166:LEU:HD13	1:BL:166:LEU:C	2.31	0.56
1:AL:253:ASP:CG	1:AL:285:PHE:CA	2.78	0.56
1:AL:302:ASP:C	1:AL:305:ASN:ND2	2.63	0.56
1:CM:111:ILE:HD11	1:CM:125:ALA:CB	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:91:ARG:NH2	1:BP:98:ILE:HG22	2.20	0.56
1:AN:302:ASP:C	1:AN:305:ASN:ND2	2.63	0.56
1:BO:111:ILE:HG22	1:BO:156:ARG:H	1.69	0.56
1:BQ:112:GLN:HB2	1:BQ:198:SER:O	2.06	0.56
1:AQ:80:VAL:CG1	1:AQ:185:LEU:HB3	2.35	0.56
1:AQ:115:CYS:HB2	1:AQ:116:PRO:HD2	1.86	0.56
1:BR:112:GLN:HB2	1:BR:198:SER:O	2.04	0.56
1:AR:115:CYS:HB2	1:AR:116:PRO:HD2	1.88	0.56
1:BU:61:SER:CB	1:BU:90:PRO:HD2	2.26	0.56
1:BV:58:SER:HB3	1:BV:204:SER:CB	2.35	0.56
1:BW:101:ARG:NH2	1:BW:166:LEU:HD12	2.19	0.56
1:AW:281:HIS:CE1	1:AW:301:TRP:HB3	2.40	0.56
1:BZ:111:ILE:HG21	1:BZ:123:TYR:OH	2.05	0.56
1:Aa:111:ILE:O	1:Aa:198:SER:O	2.22	0.56
1:Ca:79:VAL:CG1	1:Ca:185:LEU:O	2.50	0.56
1:Ac:268:SER:HB3	1:Ac:273:ASP:O	2.04	0.56
1:Cd:80:VAL:CG1	1:Cd:185:LEU:HB2	2.35	0.56
1:BA:98:ILE:HA	1:BA:211:SER:O	2.05	0.56
1:AA:253:ASP:CG	1:AA:285:PHE:CA	2.78	0.56
1:BC:316:SER:HB2	1:BC:319:GLN:OE1	2.05	0.56
1:AC:253:ASP:CG	1:AC:285:PHE:CA	2.78	0.56
1:BD:98:ILE:O	1:BD:211:SER:CA	2.52	0.56
1:BF:68:LEU:HD23	1:BF:195:VAL:HG22	1.87	0.56
1:AG:168:TRP:CE2	1:CG:176:ARG:HG2	2.38	0.56
1:BH:116:PRO:HD3	1:Cd:120:GLY:HA3	1.86	0.56
1:BH:183:LEU:C	1:BH:183:LEU:HD12	2.31	0.56
1:AJ:168:TRP:CE2	1:CJ:176:ARG:HG2	2.40	0.56
1:AJ:314:TYR:CZ	1:AJ:315:TYR:O	2.59	0.56
1:BK:253:ASP:HB2	1:BK:286:ALA:HB2	1.86	0.56
1:BL:74:THR:HA	1:BL:190:ASN:ND2	2.20	0.56
1:CL:163:THR:HG21	1:CL:167:LEU:HD11	1.87	0.56
1:BO:183:LEU:C	1:BO:183:LEU:HD12	2.31	0.56
1:AO:91:ARG:NE	1:BW:98:ILE:CG2	2.68	0.56
1:BP:111:ILE:HG22	1:BP:156:ARG:H	1.69	0.56
1:BQ:98:ILE:O	1:BQ:211:SER:CA	2.53	0.56
1:BQ:183:LEU:C	1:BQ:183:LEU:HD12	2.30	0.56
1:AQ:119:THR:O	1:AQ:192:THR:HB	2.06	0.56
1:BR:325:LEU:HD22	1:BR:329:THR:HG21	1.86	0.56
1:CS:163:THR:HG21	1:CS:167:LEU:HD11	1.87	0.56
1:AU:314:TYR:CE1	1:AU:316:SER:CA	2.85	0.56
1:CU:111:ILE:HD11	1:CU:125:ALA:CB	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:111:ILE:HG22	1:CU:113:PRO:HD3	1.88	0.56
1:CU:111:ILE:O	1:CU:198:SER:O	2.22	0.56
1:BV:98:ILE:O	1:BV:211:SER:CA	2.52	0.56
1:CV:98:ILE:HD11	1:CV:99:PHE:CE2	2.40	0.56
1:BW:111:ILE:HG22	1:BW:156:ARG:H	1.69	0.56
1:AW:253:ASP:CG	1:AW:285:PHE:CA	2.78	0.56
1:BX:111:ILE:HG22	1:BX:156:ARG:H	1.70	0.56
1:CY:95:ALA:O	1:CY:98:ILE:HG12	2.05	0.56
1:Bb:111:ILE:HG21	1:Bb:123:TYR:OH	2.06	0.56
1:Bb:165:THR:OG1	1:Bb:166:LEU:N	2.37	0.56
1:Ac:61:SER:CB	1:Ac:90:PRO:HD2	2.31	0.56
1:Ac:266:ASP:O	1:Ac:314:TYR:HA	2.05	0.56
1:CA:101:ARG:NH1	1:CA:166:LEU:CD1	2.69	0.56
1:AB:320:PRO:O	1:AB:322:GLN:HG3	2.05	0.56
1:AC:302:ASP:C	1:AC:305:ASN:ND2	2.63	0.56
1:CD:199:VAL:HG13	1:CD:199:VAL:O	2.03	0.56
1:AG:138:PHE:CE2	1:AP:62:ARG:CZ	2.89	0.56
1:AM:80:VAL:CG1	1:AM:185:LEU:HB3	2.35	0.56
1:AM:111:ILE:O	1:AM:198:SER:O	2.23	0.56
1:CN:111:ILE:HG22	1:CN:113:PRO:HD3	1.87	0.56
1:BP:183:LEU:HD12	1:BP:183:LEU:C	2.31	0.56
1:AR:314:TYR:HE1	1:AR:316:SER:N	2.03	0.56
1:Aa:115:CYS:HB2	1:Aa:116:PRO:HD2	1.86	0.56
1:Ab:168:TRP:CE2	1:Cb:176:ARG:HG2	2.40	0.56
1:Cb:199:VAL:HG13	1:Cb:199:VAL:O	2.05	0.56
1:AB:60:MET:HE2	1:AB:200:LEU:HB3	1.86	0.56
1:AC:314:TYR:HE1	1:AC:316:SER:N	2.00	0.56
1:CE:79:VAL:HG13	1:CE:80:VAL:N	2.21	0.56
1:AH:302:ASP:C	1:AH:305:ASN:ND2	2.63	0.56
1:AI:168:TRP:CE2	1:CI:176:ARG:HG2	2.40	0.56
1:AI:302:ASP:C	1:AI:305:ASN:ND2	2.63	0.56
1:CI:101:ARG:NH1	1:CI:166:LEU:CD1	2.68	0.56
1:BJ:127:PHE:HB3	1:BJ:160:PRO:HB3	1.87	0.56
1:CN:101:ARG:NH1	1:CN:166:LEU:CD1	2.67	0.56
1:AP:281:HIS:CE1	1:AP:301:TRP:HB3	2.41	0.56
1:CR:191:ASN:OD1	1:CR:191:ASN:N	2.33	0.56
1:BS:325:LEU:HD22	1:BS:329:THR:HG21	1.87	0.56
1:AT:61:SER:CB	1:AT:90:PRO:HD2	2.32	0.56
1:CU:75:ASP:OD1	1:CU:188:VAL:C	2.49	0.56
1:BW:74:THR:HA	1:BW:190:ASN:ND2	2.21	0.56
1:BW:112:GLN:HB2	1:BW:198:SER:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:101:ARG:NH1	1:CX:166:LEU:CD1	2.67	0.56
1:AZ:302:ASP:C	1:AZ:305:ASN:ND2	2.63	0.56
1:Ba:112:GLN:HB2	1:Ba:198:SER:O	2.06	0.56
1:CA:43:SER:O	1:CD:34:ARG:HD3	2.05	0.56
1:BB:127:PHE:HB3	1:BB:160:PRO:HB3	1.88	0.56
1:AB:80:VAL:CG1	1:AB:185:LEU:HB3	2.36	0.56
1:BD:58:SER:HB3	1:BD:204:SER:CB	2.34	0.56
1:BF:98:ILE:O	1:BF:211:SER:CA	2.53	0.56
1:BF:115:CYS:HB2	1:BF:116:PRO:HD2	1.88	0.56
1:CG:95:ALA:O	1:CG:98:ILE:HG12	2.05	0.56
1:CG:191:ASN:OD1	1:CG:191:ASN:N	2.39	0.56
1:CH:111:ILE:HD11	1:CH:125:ALA:CB	2.35	0.56
1:BJ:133:ASP:OD2	1:CJ:100:GLN:OE1	2.24	0.56
1:AJ:60:MET:HE2	1:AJ:200:LEU:HB3	1.88	0.56
1:CK:163:THR:OG1	1:CK:165:THR:HG23	2.04	0.56
1:AN:80:VAL:CG1	1:AN:185:LEU:HB3	2.36	0.56
1:BR:111:ILE:HG23	1:BR:113:PRO:HD3	1.88	0.56
1:AT:138:PHE:CE2	1:AV:62:ARG:CZ	2.89	0.56
1:AT:302:ASP:C	1:AT:305:ASN:ND2	2.63	0.56
1:BU:68:LEU:HD23	1:BU:195:VAL:CG2	2.36	0.56
1:BU:111:ILE:HG21	1:BU:123:TYR:OH	2.05	0.56
1:AU:281:HIS:CE1	1:AU:301:TRP:HB3	2.41	0.56
1:AV:302:ASP:C	1:AV:305:ASN:ND2	2.63	0.56
1:AW:314:TYR:CZ	1:AW:315:TYR:O	2.59	0.56
1:AX:109:PHE:HB2	1:AX:158:VAL:CG1	2.35	0.56
1:BY:115:CYS:HB2	1:BY:116:PRO:HD2	1.88	0.56
1:Ca:191:ASN:OD1	1:Ca:191:ASN:N	2.39	0.56
1:Bb:112:GLN:HB2	1:Bb:198:SER:O	2.05	0.56
1:Bc:115:CYS:HB2	1:Bc:116:PRO:HD2	1.87	0.56
1:Ac:302:ASP:C	1:Ac:305:ASN:ND2	2.64	0.56
1:CE:79:VAL:CG1	1:CE:185:LEU:O	2.52	0.56
1:BH:111:ILE:HG21	1:BH:123:TYR:OH	2.06	0.56
1:BK:127:PHE:HB3	1:BK:160:PRO:HB3	1.86	0.56
1:AK:302:ASP:C	1:AK:305:ASN:ND2	2.62	0.56
1:BO:115:CYS:HB2	1:BO:116:PRO:HD2	1.87	0.56
1:AQ:141:LEU:O	1:AQ:144:THR:CG2	2.41	0.56
1:AQ:320:PRO:O	1:AQ:322:GLN:HG3	2.04	0.56
1:BU:325:LEU:HD22	1:BU:329:THR:HG21	1.87	0.56
1:CV:111:ILE:O	1:CV:198:SER:O	2.23	0.56
1:CV:111:ILE:HG22	1:CV:113:PRO:HD3	1.86	0.56
1:AW:109:PHE:HB2	1:AW:158:VAL:CG1	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:80:VAL:HG13	1:BX:185:LEU:HB3	1.87	0.56
1:Bb:111:ILE:HG23	1:Bb:113:PRO:HD3	1.88	0.56
1:Ab:253:ASP:CG	1:Ab:285:PHE:CA	2.79	0.56
1:Bd:98:ILE:HA	1:Bd:211:SER:O	2.05	0.56
1:CA:163:THR:HG21	1:CA:167:LEU:HD11	1.87	0.56
1:CC:43:SER:O	1:Ca:34:ARG:HD3	2.06	0.56
1:CC:79:VAL:HG13	1:CC:80:VAL:N	2.20	0.56
1:AE:168:TRP:CE2	1:CE:176:ARG:HG2	2.41	0.56
1:BF:127:PHE:HB3	1:BF:160:PRO:HB3	1.86	0.56
1:AG:320:PRO:O	1:AG:322:GLN:HG3	2.06	0.56
1:CG:111:ILE:O	1:CG:198:SER:O	2.23	0.56
1:CM:79:VAL:CG1	1:CM:185:LEU:O	2.50	0.56
1:CN:79:VAL:CG1	1:CN:185:LEU:O	2.51	0.56
1:BO:112:GLN:HB2	1:BO:198:SER:O	2.06	0.56
1:CO:163:THR:HG21	1:CO:167:LEU:HD11	1.88	0.56
1:AQ:266:ASP:O	1:AQ:314:TYR:HA	2.04	0.56
1:BS:127:PHE:HB3	1:BS:160:PRO:HB3	1.88	0.56
1:CS:101:ARG:NH1	1:CS:166:LEU:CD1	2.67	0.56
1:AV:253:ASP:CG	1:AV:285:PHE:CA	2.78	0.56
1:BX:166:LEU:HD13	1:BX:166:LEU:C	2.31	0.56
1:Ba:111:ILE:HG22	1:Ba:156:ARG:H	1.70	0.56
1:Ab:111:ILE:O	1:Ab:198:SER:O	2.23	0.56
1:Ab:320:PRO:O	1:Ab:322:GLN:HG3	2.05	0.56
1:CA:191:ASN:OD1	1:CA:191:ASN:N	2.38	0.56
1:AB:111:ILE:O	1:AB:198:SER:O	2.24	0.56
1:AB:122:GLY:HA3	1:AK:114:MET:SD	2.46	0.56
1:BE:183:LEU:HD12	1:BE:183:LEU:C	2.30	0.56
1:CE:43:SER:HA	1:CH:112:GLN:NE2	2.21	0.56
1:CE:111:ILE:HG22	1:CE:113:PRO:HD3	1.87	0.56
1:AF:111:ILE:HG21	1:AF:123:TYR:CZ	2.41	0.56
1:BG:183:LEU:C	1:BG:183:LEU:HD12	2.31	0.56
1:CK:95:ALA:O	1:CK:98:ILE:HG12	2.06	0.56
1:BL:91:ARG:NH1	1:AU:98:ILE:CG2	2.68	0.56
1:CL:79:VAL:CG1	1:CL:185:LEU:O	2.52	0.56
1:AQ:253:ASP:CG	1:AQ:285:PHE:CA	2.78	0.56
1:BT:165:THR:OG1	1:BT:166:LEU:N	2.38	0.56
1:CU:191:ASN:OD1	1:CU:191:ASN:N	2.39	0.56
1:BY:127:PHE:HB3	1:BY:160:PRO:HB3	1.86	0.56
1:CY:62:ARG:NH1	1:Ba:75:ASP:OD2	2.31	0.56
1:CY:101:ARG:NH1	1:CY:166:LEU:CD1	2.68	0.56
1:Aa:253:ASP:CG	1:Aa:285:PHE:CA	2.79	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ab:310:ASP:HB3	1:Ab:312:VAL:HG22	1.88	0.56
1:Cb:111:ILE:HD11	1:Cb:125:ALA:CB	2.36	0.56
1:AB:268:SER:HB3	1:AB:273:ASP:O	2.06	0.56
1:BF:68:LEU:HD23	1:BF:195:VAL:CG2	2.36	0.56
1:BF:98:ILE:HA	1:BF:211:SER:O	2.06	0.56
1:AF:91:ARG:NE	1:Bb:98:ILE:CG2	2.69	0.56
1:AG:302:ASP:C	1:AG:305:ASN:ND2	2.63	0.56
1:AH:91:ARG:NE	1:BN:98:ILE:HG22	2.20	0.56
1:AH:109:PHE:HB2	1:AH:158:VAL:CG1	2.36	0.56
1:CH:101:ARG:NH1	1:CH:166:LEU:CD1	2.68	0.56
1:AI:62:ARG:HG2	1:AI:62:ARG:HH11	1.70	0.56
1:BL:74:THR:O	1:BL:75:ASP:C	2.49	0.56
1:AM:302:ASP:C	1:AM:305:ASN:ND2	2.63	0.56
1:BT:210:PRO:HB3	1:AV:91:ARG:NH2	2.21	0.56
1:AT:114:MET:SD	1:Aa:122:GLY:HA3	2.46	0.56
1:BU:74:THR:O	1:BU:75:ASP:C	2.49	0.56
1:BV:112:GLN:HB2	1:BV:198:SER:O	2.06	0.56
1:CV:95:ALA:O	1:CV:98:ILE:HG12	2.06	0.56
1:AW:80:VAL:CG1	1:AW:185:LEU:HB3	2.36	0.56
1:AW:141:LEU:O	1:AW:144:THR:CG2	2.45	0.56
1:BY:58:SER:HB3	1:BY:204:SER:CB	2.36	0.56
1:Cb:79:VAL:CG1	1:Cb:185:LEU:O	2.52	0.56
1:AA:168:TRP:CE2	1:CA:176:ARG:HG2	2.41	0.55
1:BD:101:ARG:NH2	1:BD:166:LEU:HD12	2.20	0.55
1:AF:80:VAL:CG1	1:AF:185:LEU:HB3	2.37	0.55
1:AF:114:MET:SD	1:Ab:122:GLY:HA3	2.46	0.55
1:CM:95:ALA:O	1:CM:98:ILE:HG12	2.07	0.55
1:BN:74:THR:O	1:BN:75:ASP:C	2.49	0.55
1:CO:111:ILE:HD11	1:CO:125:ALA:CB	2.36	0.55
1:AP:320:PRO:O	1:AP:322:GLN:HG3	2.05	0.55
1:BR:58:SER:HB3	1:BR:204:SER:CB	2.36	0.55
1:Ad:111:ILE:O	1:Ad:198:SER:O	2.24	0.55
1:BC:98:ILE:O	1:BC:211:SER:CA	2.53	0.55
1:AC:62:ARG:HG2	1:AC:62:ARG:HH11	1.69	0.55
1:AD:302:ASP:C	1:AD:305:ASN:ND2	2.63	0.55
1:BG:98:ILE:HA	1:BG:211:SER:O	2.06	0.55
1:AI:142:GLN:NE2	1:AI:142:GLN:O	2.39	0.55
1:CL:124:VAL:O	1:CL:124:VAL:HG13	2.06	0.55
1:AN:268:SER:HB3	1:AN:273:ASP:O	2.06	0.55
1:CP:79:VAL:HG13	1:CP:80:VAL:N	2.21	0.55
1:BQ:115:CYS:HB2	1:BQ:116:PRO:HD2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:111:ILE:O	1:AR:198:SER:O	2.25	0.55
1:BU:58:SER:HB3	1:BU:204:SER:CB	2.37	0.55
1:AY:101:ARG:CZ	1:AY:166:LEU:HD23	2.36	0.55
1:Aa:320:PRO:O	1:Aa:322:GLN:HG3	2.05	0.55
1:Cb:79:VAL:HG13	1:Cb:80:VAL:N	2.21	0.55
1:Cb:101:ARG:NH1	1:Cb:166:LEU:CD1	2.69	0.55
1:Cc:111:ILE:HG22	1:Cc:113:PRO:HD3	1.89	0.55
1:Cd:109:PHE:HB2	1:Cd:158:VAL:CG1	2.36	0.55
1:Cd:191:ASN:N	1:Cd:191:ASN:OD1	2.37	0.55
1:AA:114:MET:SD	1:AV:122:GLY:HA3	2.46	0.55
1:AA:119:THR:O	1:AA:192:THR:HB	2.07	0.55
1:BC:112:GLN:HB2	1:BC:198:SER:O	2.05	0.55
1:AC:63:ILE:HB	1:AC:199:VAL:HG13	1.86	0.55
1:BD:98:ILE:HA	1:BD:211:SER:O	2.06	0.55
1:AE:314:TYR:CE1	1:AE:316:SER:CA	2.87	0.55
1:AF:141:LEU:O	1:AF:144:THR:CG2	2.45	0.55
1:CF:151:LYS:NZ	1:Bb:153:TRP:O	2.39	0.55
1:AG:91:ARG:NH2	1:Bd:98:ILE:HG22	2.22	0.55
1:BM:68:LEU:HD23	1:BM:195:VAL:CG2	2.36	0.55
1:BM:111:ILE:HG21	1:BM:123:TYR:OH	2.06	0.55
1:CO:191:ASN:OD1	1:CO:191:ASN:N	2.40	0.55
1:BS:111:ILE:HG23	1:BS:113:PRO:HD3	1.87	0.55
1:BW:98:ILE:O	1:BW:211:SER:CA	2.53	0.55
1:Aa:109:PHE:HB2	1:Aa:158:VAL:CG1	2.36	0.55
1:Bb:74:THR:O	1:Bb:75:ASP:C	2.49	0.55
1:Ab:302:ASP:C	1:Ab:305:ASN:ND2	2.64	0.55
1:Bc:183:LEU:C	1:Bc:183:LEU:HD12	2.32	0.55
1:Cd:79:VAL:CG1	1:Cd:185:LEU:O	2.51	0.55
1:BA:111:ILE:HG22	1:BA:156:ARG:H	1.72	0.55
1:AC:281:HIS:CE1	1:AC:301:TRP:HB3	2.42	0.55
1:BE:98:ILE:HA	1:BE:211:SER:O	2.06	0.55
1:AE:303:ASN:N	1:AE:305:ASN:OD1	2.36	0.55
1:BL:98:ILE:O	1:BL:211:SER:CA	2.54	0.55
1:CL:109:PHE:HB2	1:CL:158:VAL:CG1	2.36	0.55
1:CR:111:ILE:HD11	1:CR:125:ALA:CB	2.37	0.55
1:AS:111:ILE:O	1:AS:198:SER:O	2.25	0.55
1:BU:98:ILE:O	1:BU:211:SER:CA	2.55	0.55
1:AU:109:PHE:HB2	1:AU:158:VAL:CG1	2.37	0.55
1:BV:98:ILE:HA	1:BV:211:SER:O	2.07	0.55
1:BW:163:THR:OG1	1:BW:165:THR:CG2	2.55	0.55
1:BX:183:LEU:C	1:BX:183:LEU:HD12	2.31	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:266:ASP:O	1:AY:314:TYR:HA	2.06	0.55
1:BZ:101:ARG:NH2	1:BZ:166:LEU:HD12	2.22	0.55
1:Cc:79:VAL:HG13	1:Cc:80:VAL:N	2.21	0.55
1:Bd:111:ILE:HG23	1:Bd:113:PRO:HD3	1.87	0.55
1:CA:111:ILE:HD11	1:CA:125:ALA:CB	2.37	0.55
1:BB:281:HIS:ND1	1:BB:301:TRP:HB3	2.22	0.55
1:BC:68:LEU:HD23	1:BC:195:VAL:CG2	2.37	0.55
1:CC:111:ILE:HD11	1:CC:125:ALA:CB	2.37	0.55
1:AE:115:CYS:HB2	1:AE:116:PRO:HD2	1.87	0.55
1:BK:58:SER:HB3	1:BK:204:SER:CB	2.37	0.55
1:BK:115:CYS:HB2	1:BK:116:PRO:HD2	1.89	0.55
1:BM:98:ILE:HA	1:BM:211:SER:O	2.06	0.55
1:BN:61:SER:CB	1:BN:90:PRO:HD2	2.25	0.55
1:AS:310:ASP:HB3	1:AS:312:VAL:HG22	1.86	0.55
1:AW:303:ASN:N	1:AW:305:ASN:OD1	2.34	0.55
1:AY:268:SER:HB3	1:AY:273:ASP:O	2.07	0.55
1:Ba:80:VAL:CG1	1:Ba:185:LEU:HB3	2.37	0.55
1:BF:58:SER:HB3	1:BF:204:SER:CB	2.37	0.55
1:BL:111:ILE:HG23	1:BL:113:PRO:HD3	1.89	0.55
1:AL:314:TYR:HE1	1:AL:316:SER:N	2.02	0.55
1:AM:91:ARG:HD2	1:Ac:143:ALA:HB1	1.89	0.55
1:BO:111:ILE:HG21	1:BO:123:TYR:OH	2.06	0.55
1:CO:34:ARG:CD	1:Cc:43:SER:O	2.55	0.55
1:BP:112:GLN:HB2	1:BP:198:SER:O	2.06	0.55
1:BQ:58:SER:HB3	1:BQ:204:SER:CB	2.37	0.55
1:AQ:109:PHE:HB2	1:AQ:158:VAL:CG1	2.36	0.55
1:AQ:168:TRP:CE2	1:CQ:176:ARG:HG2	2.41	0.55
1:AQ:281:HIS:CE1	1:AQ:301:TRP:HB3	2.41	0.55
1:CR:112:GLN:HE21	1:CT:44:THR:H	1.55	0.55
1:AS:109:PHE:HB2	1:AS:158:VAL:CG1	2.37	0.55
1:BU:101:ARG:NH2	1:BU:166:LEU:HD12	2.21	0.55
1:BZ:111:ILE:HG22	1:BZ:156:ARG:H	1.71	0.55
1:Ab:281:HIS:CE1	1:Ab:301:TRP:HB3	2.42	0.55
1:Ab:314:TYR:CE1	1:Ab:316:SER:CA	2.86	0.55
1:Cc:100:GLN:HA	1:Cc:213:GLU:OE2	2.06	0.55
1:AB:281:HIS:CE1	1:AB:301:TRP:HB3	2.42	0.55
1:BC:74:THR:O	1:BC:75:ASP:C	2.49	0.55
1:AF:281:HIS:CE1	1:AF:301:TRP:HB3	2.42	0.55
1:AF:302:ASP:C	1:AF:305:ASN:ND2	2.64	0.55
1:AH:168:TRP:CE2	1:CH:176:ARG:HG2	2.42	0.55
1:BI:325:LEU:HD22	1:BI:329:THR:HG21	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:79:VAL:HG13	1:CJ:80:VAL:N	2.21	0.55
1:BL:80:VAL:HG13	1:BL:185:LEU:HB3	1.88	0.55
1:BL:153:TRP:O	1:CU:151:LYS:NZ	2.40	0.55
1:BM:74:THR:O	1:BM:75:ASP:C	2.50	0.55
1:BM:75:ASP:OD2	1:CO:62:ARG:NH1	2.31	0.55
1:AM:91:ARG:CZ	1:Bc:98:ILE:CG2	2.84	0.55
1:AN:314:TYR:HE1	1:AN:316:SER:N	1.99	0.55
1:AP:253:ASP:CG	1:AP:285:PHE:CA	2.80	0.55
1:CP:44:THR:H	1:CQ:112:GLN:HE21	1.55	0.55
1:BR:115:CYS:HB2	1:BR:116:PRO:HD2	1.88	0.55
1:CR:79:VAL:HG13	1:CR:80:VAL:N	2.22	0.55
1:BS:101:ARG:NH2	1:BS:166:LEU:HD12	2.21	0.55
1:CS:185:LEU:C	1:CS:186:LEU:HD23	2.31	0.55
1:AU:302:ASP:C	1:AU:305:ASN:ND2	2.63	0.55
1:AX:302:ASP:C	1:AX:305:ASN:ND2	2.64	0.55
1:AX:314:TYR:CE1	1:AX:316:SER:HA	2.42	0.55
1:CX:163:THR:OG1	1:CX:165:THR:HG23	2.06	0.55
1:CY:185:LEU:C	1:CY:186:LEU:HD23	2.32	0.55
1:Cb:191:ASN:OD1	1:Cb:191:ASN:N	2.37	0.55
1:Ac:281:HIS:CE1	1:Ac:301:TRP:HB3	2.42	0.55
1:Bd:68:LEU:HD23	1:Bd:195:VAL:CG2	2.36	0.55
1:CA:98:ILE:HD11	1:CA:99:PHE:CE2	2.42	0.55
1:BD:156:ARG:NH2	1:Cd:34:ARG:HG3	2.22	0.55
1:AD:109:PHE:HB2	1:AD:158:VAL:CG1	2.37	0.55
1:AE:111:ILE:HG21	1:AE:123:TYR:CZ	2.42	0.55
1:BF:74:THR:O	1:BF:75:ASP:C	2.50	0.55
1:BG:80:VAL:HG13	1:BG:185:LEU:HB3	1.88	0.55
1:AG:141:LEU:O	1:AG:144:THR:CG2	2.44	0.55
1:BH:101:ARG:NH2	1:BH:166:LEU:HD12	2.21	0.55
1:AH:144:THR:HG23	1:AH:147:ALA:HB2	1.89	0.55
1:BI:281:HIS:ND1	1:BI:301:TRP:HB3	2.22	0.55
1:AK:314:TYR:HE1	1:AK:316:SER:N	2.04	0.55
1:BL:98:ILE:HG22	1:AU:91:ARG:NH2	2.22	0.55
1:AL:141:LEU:O	1:AL:144:THR:CG2	2.46	0.55
1:AL:266:ASP:O	1:AL:314:TYR:HA	2.07	0.55
1:BM:58:SER:HB3	1:BM:204:SER:CB	2.37	0.55
1:AN:91:ARG:NE	1:BP:98:ILE:CG2	2.69	0.55
1:CO:95:ALA:O	1:CO:98:ILE:HG12	2.07	0.55
1:BQ:74:THR:O	1:BQ:75:ASP:C	2.50	0.55
1:BR:74:THR:O	1:BR:75:ASP:C	2.49	0.55
1:BT:74:THR:HA	1:BT:190:ASN:ND2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ac:253:ASP:CG	1:Ac:285:PHE:CA	2.79	0.55
1:BA:74:THR:O	1:BA:75:ASP:C	2.50	0.55
1:AA:115:CYS:HB2	1:AA:116:PRO:HD2	1.89	0.55
1:BB:115:CYS:HB2	1:BB:116:PRO:HD2	1.89	0.55
1:CB:111:ILE:HD11	1:CB:125:ALA:CB	2.37	0.55
1:BF:163:THR:OG1	1:BF:165:THR:CG2	2.55	0.55
1:CF:79:VAL:HG13	1:CF:80:VAL:N	2.21	0.55
1:CF:101:ARG:NH1	1:CF:166:LEU:CD1	2.67	0.55
1:BH:210:PRO:HB3	1:Ad:91:ARG:NH2	2.22	0.55
1:CI:191:ASN:OD1	1:CI:191:ASN:N	2.39	0.55
1:AJ:109:PHE:HB2	1:AJ:158:VAL:CG1	2.37	0.55
1:CK:163:THR:HG21	1:CK:167:LEU:HD11	1.88	0.55
1:BM:183:LEU:C	1:BM:183:LEU:HD12	2.32	0.55
1:BO:74:THR:O	1:BO:75:ASP:C	2.50	0.55
1:AO:281:HIS:CE1	1:AO:301:TRP:HB3	2.42	0.55
1:BP:75:ASP:OD2	1:CQ:62:ARG:NH1	2.31	0.55
1:AQ:60:MET:HE2	1:AQ:200:LEU:HB3	1.89	0.55
1:AS:80:VAL:CG1	1:AS:185:LEU:HB3	2.37	0.55
1:AS:320:PRO:O	1:AS:322:GLN:HG3	2.06	0.55
1:BT:61:SER:CB	1:BT:90:PRO:HD2	2.28	0.55
1:AT:111:ILE:O	1:AT:198:SER:O	2.25	0.55
1:CT:79:VAL:HG13	1:CT:80:VAL:N	2.21	0.55
1:BU:98:ILE:CG2	1:AX:91:ARG:NE	2.70	0.55
1:BU:281:HIS:ND1	1:BU:301:TRP:HB3	2.21	0.55
1:CU:124:VAL:O	1:CU:124:VAL:HG13	2.07	0.55
1:AW:314:TYR:HE1	1:AW:316:SER:N	2.02	0.55
1:CW:112:GLN:NE2	1:CW:155:SER:OG	2.40	0.55
1:AX:168:TRP:CE2	1:CX:176:ARG:HG2	2.42	0.55
1:AY:302:ASP:C	1:AY:305:ASN:ND2	2.63	0.55
1:Ad:253:ASP:OD1	1:Ad:285:PHE:N	2.40	0.55
1:AD:303:ASN:N	1:AD:305:ASN:OD1	2.35	0.55
1:CD:101:ARG:NH1	1:CD:166:LEU:CD1	2.70	0.55
1:CE:109:PHE:HB2	1:CE:158:VAL:CG1	2.37	0.55
1:AF:268:SER:HB3	1:AF:273:ASP:O	2.07	0.55
1:AG:253:ASP:CG	1:AG:285:PHE:CA	2.79	0.55
1:BH:68:LEU:HD23	1:BH:195:VAL:CG2	2.37	0.55
1:CI:80:VAL:CG1	1:CI:185:LEU:HB2	2.36	0.55
1:CJ:101:ARG:NH1	1:CJ:166:LEU:CD1	2.70	0.55
1:BK:74:THR:HA	1:BK:190:ASN:ND2	2.22	0.55
1:CL:95:ALA:O	1:CL:98:ILE:HG12	2.07	0.55
1:BN:80:VAL:CG1	1:BN:185:LEU:HB3	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:111:ILE:HG23	1:BN:113:PRO:HD3	1.89	0.55
1:CO:80:VAL:CG1	1:CO:185:LEU:HB2	2.37	0.55
1:CO:111:ILE:HG22	1:CO:113:PRO:HD3	1.89	0.55
1:AT:109:PHE:HB2	1:AT:158:VAL:CG1	2.37	0.55
1:BW:111:ILE:HG21	1:BW:123:TYR:OH	2.06	0.55
1:CW:101:ARG:NH1	1:CW:166:LEU:CD1	2.68	0.55
1:CW:109:PHE:HB2	1:CW:158:VAL:CG1	2.37	0.55
1:BX:98:ILE:O	1:BX:211:SER:CA	2.54	0.55
1:AY:119:THR:HG23	1:AY:193:ASP:CB	2.37	0.55
1:Ba:163:THR:OG1	1:Ba:165:THR:CG2	2.55	0.55
1:BB:111:ILE:HG21	1:BB:123:TYR:OH	2.07	0.54
1:CB:111:ILE:HG22	1:CB:113:PRO:HD3	1.90	0.54
1:BC:98:ILE:HA	1:BC:211:SER:O	2.07	0.54
1:BC:111:ILE:HG21	1:BC:123:TYR:OH	2.08	0.54
1:AF:124:VAL:HG11	1:AF:138:PHE:HD1	1.72	0.54
1:AI:310:ASP:HB3	1:AI:312:VAL:HG22	1.89	0.54
1:CI:111:ILE:HG22	1:CI:113:PRO:HD3	1.88	0.54
1:BN:68:LEU:HD23	1:BN:195:VAL:CG2	2.37	0.54
1:BN:325:LEU:HD22	1:BN:329:THR:HG21	1.88	0.54
1:AP:142:GLN:NE2	1:AP:142:GLN:O	2.40	0.54
1:AS:302:ASP:C	1:AS:305:ASN:ND2	2.63	0.54
1:AX:281:HIS:CE1	1:AX:301:TRP:HB3	2.42	0.54
1:AY:80:VAL:CG1	1:AY:185:LEU:HB3	2.37	0.54
1:AY:109:PHE:HB2	1:AY:158:VAL:CG1	2.37	0.54
1:AY:253:ASP:CG	1:AY:285:PHE:CA	2.80	0.54
1:Ba:58:SER:HB3	1:Ba:204:SER:CB	2.36	0.54
1:Ba:74:THR:O	1:Ba:75:ASP:C	2.51	0.54
1:Ca:95:ALA:O	1:Ca:98:ILE:HG12	2.07	0.54
1:Bb:115:CYS:HB2	1:Bb:116:PRO:HD2	1.90	0.54
1:Ac:310:ASP:HB3	1:Ac:312:VAL:HG22	1.88	0.54
1:Ad:266:ASP:O	1:Ad:314:TYR:HA	2.07	0.54
1:BB:68:LEU:HD23	1:BB:195:VAL:CG2	2.36	0.54
1:AB:314:TYR:CE1	1:AB:316:SER:HA	2.41	0.54
1:AC:268:SER:HB3	1:AC:273:ASP:O	2.08	0.54
1:BD:150:ALA:HB2	1:BD:156:ARG:HD3	1.90	0.54
1:BF:101:ARG:NH2	1:BF:166:LEU:HD12	2.22	0.54
1:AG:115:CYS:HB2	1:AG:116:PRO:HD2	1.89	0.54
1:BJ:183:LEU:C	1:BJ:183:LEU:HD12	2.31	0.54
1:AJ:114:MET:SD	1:AR:122:GLY:HA3	2.48	0.54
1:CL:190:ASN:N	1:CL:190:ASN:HD22	2.04	0.54
1:BN:111:ILE:HG22	1:BN:156:ARG:H	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:80:VAL:CG1	1:BP:185:LEU:HB3	2.37	0.54
1:AR:279:TYR:CE2	1:AR:311:GLY:O	2.60	0.54
1:BX:112:GLN:HB2	1:BX:198:SER:O	2.07	0.54
1:Ba:281:HIS:ND1	1:Ba:301:TRP:HB3	2.23	0.54
1:Ac:124:VAL:HG11	1:Ac:138:PHE:HD1	1.72	0.54
1:BA:80:VAL:CG1	1:BA:185:LEU:HB3	2.38	0.54
1:AC:111:ILE:O	1:AC:198:SER:O	2.24	0.54
1:AD:168:TRP:CE2	1:CD:176:ARG:HG2	2.42	0.54
1:CD:79:VAL:HG13	1:CD:80:VAL:N	2.22	0.54
1:BE:68:LEU:HD23	1:BE:195:VAL:CG2	2.38	0.54
1:BE:127:PHE:HB3	1:BE:160:PRO:HB3	1.89	0.54
1:AE:109:PHE:HB2	1:AE:158:VAL:CG1	2.38	0.54
1:BF:112:GLN:HB2	1:BF:198:SER:O	2.06	0.54
1:CF:79:VAL:CG1	1:CF:185:LEU:O	2.52	0.54
1:AG:119:THR:HG23	1:AG:193:ASP:CB	2.37	0.54
1:BK:101:ARG:NH2	1:BK:166:LEU:HD12	2.21	0.54
1:CL:163:THR:OG1	1:CL:165:THR:HG23	2.06	0.54
1:BM:74:THR:HA	1:BM:190:ASN:ND2	2.22	0.54
1:BO:98:ILE:CG2	1:Ab:91:ARG:NE	2.70	0.54
1:BO:281:HIS:ND1	1:BO:301:TRP:HB3	2.22	0.54
1:AP:80:VAL:CG1	1:AP:185:LEU:HB3	2.37	0.54
1:BS:168:TRP:CE2	1:AS:176:ARG:HD2	2.43	0.54
1:BU:183:LEU:C	1:BU:183:LEU:HD12	2.32	0.54
1:CU:79:VAL:CG1	1:CU:185:LEU:O	2.53	0.54
1:CU:79:VAL:HG13	1:CU:80:VAL:N	2.21	0.54
1:CU:95:ALA:O	1:CU:98:ILE:HG12	2.08	0.54
1:BV:101:ARG:NH2	1:BV:166:LEU:HD12	2.21	0.54
1:CW:124:VAL:O	1:CW:124:VAL:HG13	2.06	0.54
1:CY:111:ILE:HG22	1:CY:113:PRO:HD3	1.89	0.54
1:AZ:109:PHE:HB2	1:AZ:158:VAL:CG1	2.36	0.54
1:AZ:115:CYS:HB2	1:AZ:116:PRO:HD2	1.88	0.54
1:Ab:115:CYS:HB2	1:Ab:116:PRO:HD2	1.88	0.54
1:BA:210:PRO:HB3	1:AI:91:ARG:NH2	2.23	0.54
1:CC:101:ARG:NH1	1:CC:166:LEU:CD1	2.68	0.54
1:BE:80:VAL:HG13	1:BE:185:LEU:HB3	1.88	0.54
1:BE:112:GLN:HB2	1:BE:198:SER:O	2.08	0.54
1:BE:325:LEU:HD22	1:BE:329:THR:HG21	1.89	0.54
1:CE:46:THR:HB	1:CH:202:ARG:HH12	1.72	0.54
1:CI:95:ALA:O	1:CI:98:ILE:HG12	2.06	0.54
1:AJ:61:SER:CB	1:AJ:90:PRO:HD2	2.35	0.54
1:AJ:266:ASP:O	1:AJ:314:TYR:HA	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:111:ILE:HG22	1:CK:113:PRO:HD3	1.88	0.54
1:BM:85:VAL:HG23	1:BM:86:PRO:HD2	1.89	0.54
1:AM:314:TYR:CE1	1:AM:316:SER:HA	2.41	0.54
1:CM:112:GLN:NE2	1:CO:43:SER:HA	2.22	0.54
1:BO:325:LEU:HD22	1:BO:329:THR:HG21	1.88	0.54
1:AP:124:VAL:HG11	1:AP:138:PHE:HD1	1.72	0.54
1:BQ:111:ILE:HG21	1:BQ:123:TYR:OH	2.07	0.54
1:CQ:111:ILE:HG22	1:CQ:113:PRO:HD3	1.89	0.54
1:CQ:163:THR:OG1	1:CQ:165:THR:HG23	2.08	0.54
1:AR:122:GLY:C	1:AR:188:VAL:HG22	2.32	0.54
1:AS:253:ASP:CG	1:AS:285:PHE:CA	2.79	0.54
1:CS:111:ILE:HD11	1:CS:125:ALA:CB	2.38	0.54
1:BT:98:ILE:O	1:BT:211:SER:CA	2.54	0.54
1:BU:98:ILE:HA	1:BU:211:SER:O	2.08	0.54
1:BZ:163:THR:OG1	1:BZ:165:THR:CG2	2.54	0.54
1:CZ:111:ILE:HG22	1:CZ:113:PRO:HD3	1.89	0.54
1:Ad:314:TYR:HE1	1:Ad:316:SER:N	2.03	0.54
1:BB:74:THR:O	1:BB:75:ASP:C	2.50	0.54
1:AC:124:VAL:HG11	1:AC:138:PHE:HD1	1.73	0.54
1:BD:127:PHE:HB3	1:BD:160:PRO:HB3	1.89	0.54
1:AE:310:ASP:HB3	1:AE:312:VAL:HG22	1.90	0.54
1:BH:325:LEU:HD22	1:BH:329:THR:HG21	1.89	0.54
1:AH:281:HIS:CE1	1:AH:301:TRP:HB3	2.42	0.54
1:CH:79:VAL:HG13	1:CH:80:VAL:N	2.22	0.54
1:AI:253:ASP:OD1	1:AI:285:PHE:N	2.41	0.54
1:BJ:165:THR:OG1	1:BJ:166:LEU:N	2.40	0.54
1:AK:61:SER:CB	1:AK:90:PRO:HD2	2.32	0.54
1:BL:68:LEU:HD23	1:BL:195:VAL:CG2	2.37	0.54
1:BM:101:ARG:NH2	1:BM:166:LEU:HD12	2.22	0.54
1:AM:109:PHE:HB2	1:AM:158:VAL:CG1	2.38	0.54
1:BN:98:ILE:HA	1:BN:211:SER:O	2.07	0.54
1:BO:165:THR:OG1	1:BO:166:LEU:N	2.41	0.54
1:BP:168:TRP:CE2	1:AP:176:ARG:HD2	2.43	0.54
1:AQ:61:SER:CB	1:AQ:90:PRO:HD2	2.34	0.54
1:AQ:268:SER:HB3	1:AQ:273:ASP:O	2.08	0.54
1:BR:111:ILE:HG22	1:BR:156:ARG:H	1.73	0.54
1:BU:80:VAL:CG1	1:BU:185:LEU:HB3	2.37	0.54
1:BW:74:THR:O	1:BW:75:ASP:C	2.50	0.54
1:BX:61:SER:CB	1:BX:90:PRO:HD2	2.27	0.54
1:AX:268:SER:HB3	1:AX:273:ASP:O	2.07	0.54
1:CX:111:ILE:HG22	1:CX:113:PRO:HD3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bc:74:THR:O	1:Bc:75:ASP:C	2.51	0.54
1:Ad:281:HIS:CE1	1:Ad:301:TRP:HB3	2.43	0.54
1:CA:34:ARG:HD3	1:Cd:43:SER:O	2.07	0.54
1:AD:61:SER:CB	1:AD:90:PRO:HD2	2.34	0.54
1:CE:101:ARG:NH1	1:CE:166:LEU:CD1	2.69	0.54
1:CE:112:GLN:NE2	1:CH:43:SER:HA	2.23	0.54
1:BF:111:ILE:HG21	1:BF:123:TYR:OH	2.08	0.54
1:AG:268:SER:HB3	1:AG:273:ASP:O	2.08	0.54
1:BH:74:THR:O	1:BH:75:ASP:C	2.50	0.54
1:AJ:119:THR:HG23	1:AJ:193:ASP:CB	2.38	0.54
1:AJ:281:HIS:CE1	1:AJ:301:TRP:HB3	2.42	0.54
1:CJ:95:ALA:O	1:CJ:98:ILE:HG12	2.07	0.54
1:BM:163:THR:OG1	1:BM:165:THR:CG2	2.56	0.54
1:BP:74:THR:O	1:BP:75:ASP:C	2.50	0.54
1:BP:281:HIS:ND1	1:BP:301:TRP:HB3	2.23	0.54
1:CR:111:ILE:HG22	1:CR:113:PRO:HD3	1.90	0.54
1:AW:302:ASP:C	1:AW:305:ASN:ND2	2.63	0.54
1:Ba:98:ILE:HA	1:Ba:211:SER:O	2.07	0.54
1:Aa:281:HIS:CE1	1:Aa:301:TRP:HB3	2.42	0.54
1:Bb:127:PHE:HB3	1:Bb:160:PRO:HB3	1.89	0.54
1:Ac:101:ARG:CZ	1:Ac:166:LEU:HD23	2.38	0.54
1:Cc:85:VAL:HG13	1:Cc:86:PRO:HD2	1.90	0.54
1:Cd:101:ARG:CZ	1:Cd:166:LEU:CD1	2.86	0.54
1:CD:43:SER:HA	1:CI:112:GLN:NE2	2.22	0.54
1:CD:46:THR:HB	1:CI:202:ARG:HH12	1.73	0.54
1:BI:165:THR:OG1	1:BI:166:LEU:N	2.39	0.54
1:BK:111:ILE:HG22	1:BK:156:ARG:H	1.73	0.54
1:AL:281:HIS:CE1	1:AL:301:TRP:HB3	2.42	0.54
1:BN:74:THR:HA	1:BN:190:ASN:ND2	2.23	0.54
1:BN:281:HIS:ND1	1:BN:301:TRP:HB3	2.22	0.54
1:AN:61:SER:HB2	1:AN:89:LEU:HD22	1.90	0.54
1:BP:61:SER:CB	1:BP:90:PRO:HD2	2.27	0.54
1:BP:115:CYS:HB2	1:BP:116:PRO:HD2	1.90	0.54
1:BR:99:PHE:N	1:BR:99:PHE:CD1	2.76	0.54
1:BT:74:THR:O	1:BT:75:ASP:C	2.50	0.54
1:AV:80:VAL:CG1	1:AV:185:LEU:HB3	2.38	0.54
1:BW:80:VAL:CG1	1:BW:185:LEU:HB3	2.38	0.54
1:BY:74:THR:O	1:BY:75:ASP:C	2.51	0.54
1:BY:101:ARG:NH2	1:BY:166:LEU:HD12	2.22	0.54
1:CY:112:GLN:NE2	1:Ca:43:SER:HA	2.23	0.54
1:CZ:80:VAL:HG11	1:CZ:185:LEU:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cb:98:ILE:HD11	1:Cb:99:PHE:CE2	2.43	0.54
1:Ad:61:SER:CB	1:Ad:90:PRO:HD2	2.33	0.54
1:BA:325:LEU:HD22	1:BA:329:THR:HG21	1.89	0.54
1:AA:314:TYR:CE1	1:AA:316:SER:HA	2.43	0.54
1:AF:314:TYR:CG	1:AF:315:TYR:N	2.76	0.54
1:AG:80:VAL:CG1	1:AG:185:LEU:HB3	2.37	0.54
1:AI:281:HIS:CE1	1:AI:301:TRP:HB3	2.42	0.54
1:BJ:74:THR:O	1:BJ:75:ASP:C	2.50	0.54
1:BK:111:ILE:HG21	1:BK:123:TYR:OH	2.06	0.54
1:AM:268:SER:HB3	1:AM:273:ASP:O	2.07	0.54
1:AM:314:TYR:CG	1:AM:315:TYR:N	2.76	0.54
1:BN:163:THR:OG1	1:BN:165:THR:CG2	2.56	0.54
1:AP:168:TRP:CE2	1:CP:176:ARG:HG2	2.42	0.54
1:CV:112:GLN:NE2	1:CZ:43:SER:HA	2.22	0.54
1:BW:183:LEU:C	1:BW:183:LEU:HD12	2.33	0.54
1:BY:123:TYR:HB2	1:BY:185:LEU:HD11	1.90	0.54
1:Bb:325:LEU:HD22	1:Bb:329:THR:HG21	1.89	0.54
1:Ad:124:VAL:HG11	1:Ad:138:PHE:HD1	1.72	0.54
1:BB:98:ILE:HG23	1:AK:91:ARG:HG2	1.90	0.54
1:AC:279:TYR:CE2	1:AC:311:GLY:O	2.60	0.54
1:AE:281:HIS:CE1	1:AE:301:TRP:HB3	2.43	0.54
1:AI:279:TYR:CE2	1:AI:311:GLY:O	2.60	0.54
1:BJ:98:ILE:HA	1:BJ:211:SER:O	2.08	0.54
1:BK:111:ILE:HG23	1:BK:113:PRO:HD3	1.89	0.54
1:BM:281:HIS:ND1	1:BM:301:TRP:HB3	2.23	0.54
1:CN:79:VAL:HG13	1:CN:80:VAL:N	2.23	0.54
1:CN:191:ASN:N	1:CN:191:ASN:OD1	2.37	0.54
1:BP:58:SER:HB3	1:BP:204:SER:CB	2.37	0.54
1:AQ:314:TYR:CE1	1:AQ:316:SER:HA	2.43	0.54
1:AU:80:VAL:CG1	1:AU:185:LEU:HB3	2.38	0.54
1:BV:74:THR:O	1:BV:75:ASP:C	2.51	0.54
1:CW:191:ASN:OD1	1:CW:191:ASN:N	2.37	0.54
1:BX:115:CYS:HB2	1:BX:116:PRO:HD2	1.90	0.54
1:Bc:163:THR:OG1	1:Bc:165:THR:CG2	2.56	0.54
1:BA:281:HIS:ND1	1:BA:301:TRP:HB3	2.23	0.54
1:AA:109:PHE:HB2	1:AA:158:VAL:CG1	2.38	0.54
1:CB:98:ILE:HD11	1:CB:99:PHE:CE2	2.43	0.54
1:BC:325:LEU:HD22	1:BC:329:THR:HG21	1.90	0.54
1:AE:98:ILE:HG23	1:BM:91:ARG:NH1	2.23	0.54
1:BF:111:ILE:HG23	1:BF:113:PRO:HD3	1.89	0.54
1:AG:281:HIS:CE1	1:AG:301:TRP:HB3	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:314:TYR:CE1	1:AH:316:SER:CA	2.87	0.54
1:BI:74:THR:O	1:BI:75:ASP:C	2.50	0.54
1:BI:111:ILE:HG23	1:BI:113:PRO:HD3	1.89	0.54
1:BL:163:THR:OG1	1:BL:165:THR:CG2	2.56	0.54
1:AM:101:ARG:CZ	1:AM:166:LEU:HD23	2.37	0.54
1:AM:279:TYR:CE2	1:AM:311:GLY:O	2.61	0.54
1:BN:58:SER:HB3	1:BN:204:SER:CB	2.38	0.54
1:BS:112:GLN:HB2	1:BS:198:SER:O	2.07	0.54
1:BS:183:LEU:HD12	1:BS:183:LEU:C	2.32	0.54
1:AT:281:HIS:CE1	1:AT:301:TRP:HB3	2.43	0.54
1:CV:111:ILE:HD11	1:CV:125:ALA:CB	2.38	0.54
1:AZ:162:TYR:N	1:AZ:162:TYR:CD1	2.76	0.54
1:CZ:79:VAL:HG13	1:CZ:80:VAL:N	2.23	0.54
1:CZ:191:ASN:OD1	1:CZ:191:ASN:N	2.37	0.54
1:Ca:80:VAL:CG1	1:Ca:185:LEU:HB2	2.38	0.54
1:Bb:183:LEU:C	1:Bb:183:LEU:HD12	2.33	0.54
1:Cd:124:VAL:HG13	1:Cd:124:VAL:O	2.08	0.54
1:AC:62:ARG:CZ	1:AS:138:PHE:CE2	2.91	0.53
1:CC:112:GLN:HE21	1:CJ:44:THR:H	1.55	0.53
1:CD:80:VAL:HG11	1:CD:185:LEU:HB2	1.91	0.53
1:CD:111:ILE:HG22	1:CD:113:PRO:HD3	1.90	0.53
1:BE:163:THR:OG1	1:BE:165:THR:CG2	2.55	0.53
1:CK:190:ASN:HD22	1:CK:190:ASN:N	2.06	0.53
1:CM:34:ARG:CD	1:CW:43:SER:O	2.56	0.53
1:BO:80:VAL:CG1	1:BO:185:LEU:HB3	2.37	0.53
1:AO:302:ASP:C	1:AO:305:ASN:ND2	2.64	0.53
1:AT:124:VAL:HG11	1:AT:138:PHE:HD1	1.74	0.53
1:BU:163:THR:OG1	1:BU:165:THR:CG2	2.56	0.53
1:Aa:253:ASP:OD1	1:Aa:285:PHE:N	2.41	0.53
1:Ab:80:VAL:CG1	1:Ab:185:LEU:HB3	2.38	0.53
1:BA:111:ILE:HG21	1:BA:123:TYR:OH	2.07	0.53
1:AA:302:ASP:C	1:AA:305:ASN:ND2	2.63	0.53
1:AA:314:TYR:CE1	1:AA:316:SER:CA	2.88	0.53
1:AB:310:ASP:HB3	1:AB:312:VAL:HG22	1.90	0.53
1:BC:281:HIS:ND1	1:BC:301:TRP:HB3	2.24	0.53
1:CC:124:VAL:O	1:CC:124:VAL:HG13	2.07	0.53
1:BD:281:HIS:ND1	1:BD:301:TRP:HB3	2.23	0.53
1:BF:165:THR:OG1	1:BF:166:LEU:N	2.39	0.53
1:BH:111:ILE:HG22	1:BH:156:ARG:H	1.74	0.53
1:AI:60:MET:HE2	1:AI:200:LEU:HB3	1.90	0.53
1:BL:99:PHE:N	1:BL:99:PHE:CD1	2.75	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:111:ILE:HD11	1:CL:125:ALA:CB	2.38	0.53
1:AM:63:ILE:HB	1:AM:199:VAL:HG13	1.89	0.53
1:BR:101:ARG:NH2	1:BR:166:LEU:HD12	2.23	0.53
1:BS:281:HIS:ND1	1:BS:301:TRP:HB3	2.23	0.53
1:AS:101:ARG:CZ	1:AS:166:LEU:HD23	2.38	0.53
1:AS:281:HIS:CE1	1:AS:301:TRP:HB3	2.44	0.53
1:AT:101:ARG:CZ	1:AT:166:LEU:HD23	2.38	0.53
1:AU:124:VAL:HG11	1:AU:138:PHE:HD1	1.74	0.53
1:AU:268:SER:HB3	1:AU:273:ASP:O	2.08	0.53
1:AV:281:HIS:CE1	1:AV:301:TRP:HB3	2.43	0.53
1:BX:58:SER:HB3	1:BX:204:SER:CB	2.38	0.53
1:CY:111:ILE:HD11	1:CY:125:ALA:CB	2.38	0.53
1:BZ:58:SER:HB3	1:BZ:204:SER:CB	2.37	0.53
1:Bb:98:ILE:O	1:Bb:211:SER:CA	2.56	0.53
1:Ab:314:TYR:CE1	1:Ab:316:SER:HA	2.43	0.53
1:Cb:111:ILE:HG22	1:Cb:113:PRO:HD3	1.89	0.53
1:Bc:325:LEU:HD22	1:Bc:329:THR:HG21	1.90	0.53
1:Cd:63:ILE:HD12	1:Cd:88:LEU:CD1	2.38	0.53
1:AA:119:THR:HG23	1:AA:193:ASP:CB	2.36	0.53
1:CA:109:PHE:HB2	1:CA:158:VAL:HG12	1.90	0.53
1:BB:183:LEU:HD12	1:BB:183:LEU:C	2.34	0.53
1:BC:111:ILE:HG23	1:BC:113:PRO:HD3	1.90	0.53
1:AC:91:ARG:NH2	1:BS:210:PRO:HB3	2.22	0.53
1:CD:112:GLN:NE2	1:CD:155:SER:OG	2.40	0.53
1:AF:305:ASN:OD1	1:AF:305:ASN:N	2.42	0.53
1:CH:95:ALA:O	1:CH:98:ILE:HG12	2.08	0.53
1:BI:115:CYS:HB2	1:BI:116:PRO:HD2	1.90	0.53
1:BJ:115:CYS:HB2	1:BJ:116:PRO:HD2	1.89	0.53
1:BM:99:PHE:N	1:BM:99:PHE:CD1	2.77	0.53
1:AM:168:TRP:CE2	1:CM:176:ARG:HG2	2.44	0.53
1:BN:183:LEU:C	1:BN:183:LEU:HD12	2.34	0.53
1:CN:111:ILE:HD11	1:CN:125:ALA:CB	2.38	0.53
1:BO:163:THR:OG1	1:BO:165:THR:CG2	2.56	0.53
1:BP:101:ARG:NH2	1:BP:166:LEU:HD12	2.24	0.53
1:BQ:98:ILE:HA	1:BQ:211:SER:O	2.09	0.53
1:AQ:314:TYR:CG	1:AQ:315:TYR:N	2.76	0.53
1:BR:98:ILE:HA	1:BR:211:SER:O	2.08	0.53
1:CU:112:GLN:HE21	1:Cb:44:THR:H	1.56	0.53
1:CU:130:ASP:OD2	1:CU:176:ARG:NH2	2.41	0.53
1:CX:98:ILE:HD11	1:CX:99:PHE:CE2	2.43	0.53
1:AZ:268:SER:HB3	1:AZ:273:ASP:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bb:101:ARG:NH2	1:Bb:166:LEU:HD12	2.23	0.53
1:Ab:60:MET:HE2	1:Ab:200:LEU:HB3	1.89	0.53
1:BA:166:LEU:HD13	1:BA:167:LEU:N	2.24	0.53
1:AA:138:PHE:CE2	1:AI:62:ARG:CZ	2.91	0.53
1:CB:191:ASN:OD1	1:CB:191:ASN:N	2.38	0.53
1:CC:34:ARG:HD3	1:CR:43:SER:O	2.08	0.53
1:AD:80:VAL:CG1	1:AD:185:LEU:HB3	2.38	0.53
1:AD:119:THR:HG23	1:AD:193:ASP:CB	2.37	0.53
1:AD:310:ASP:HB3	1:AD:312:VAL:HG22	1.90	0.53
1:CE:191:ASN:OD1	1:CE:191:ASN:N	2.38	0.53
1:AF:119:THR:HG23	1:AF:193:ASP:CB	2.39	0.53
1:BH:91:ARG:NH1	1:Ad:98:ILE:O	2.41	0.53
1:AI:268:SER:HB3	1:AI:273:ASP:O	2.09	0.53
1:CJ:109:PHE:HB2	1:CJ:158:VAL:CG1	2.37	0.53
1:CK:44:THR:H	1:CL:112:GLN:HE21	1.57	0.53
1:AM:281:HIS:CE1	1:AM:301:TRP:HB3	2.43	0.53
1:CM:91:ARG:HD2	1:CO:98:ILE:HB	1.91	0.53
1:AN:281:HIS:CE1	1:AN:301:TRP:HB3	2.43	0.53
1:BP:98:ILE:HA	1:BP:211:SER:O	2.08	0.53
1:BU:127:PHE:HB3	1:BU:160:PRO:HB3	1.90	0.53
1:AV:109:PHE:HB2	1:AV:158:VAL:CG1	2.39	0.53
1:AX:124:VAL:HG11	1:AX:138:PHE:HD1	1.73	0.53
1:Ba:61:SER:CB	1:Ba:90:PRO:HD2	2.27	0.53
1:Ca:101:ARG:NH1	1:Ca:166:LEU:CD1	2.71	0.53
1:Bb:281:HIS:ND1	1:Bb:301:TRP:HB3	2.22	0.53
1:Bd:115:CYS:HB2	1:Bd:116:PRO:HD2	1.89	0.53
1:AB:162:TYR:N	1:AB:162:TYR:CD1	2.77	0.53
1:AB:253:ASP:OD1	1:AB:285:PHE:N	2.41	0.53
1:CB:79:VAL:HG13	1:CB:80:VAL:N	2.23	0.53
1:BD:74:THR:O	1:BD:75:ASP:C	2.50	0.53
1:BE:281:HIS:ND1	1:BE:301:TRP:HB3	2.24	0.53
1:BF:168:TRP:CE2	1:AF:176:ARG:HD2	2.43	0.53
1:BH:281:HIS:ND1	1:BH:301:TRP:HB3	2.23	0.53
1:BJ:61:SER:CB	1:BJ:90:PRO:HD2	2.26	0.53
1:AM:111:ILE:HG21	1:AM:123:TYR:CZ	2.44	0.53
1:AM:253:ASP:OD1	1:AM:285:PHE:N	2.41	0.53
1:AO:314:TYR:CE1	1:AO:316:SER:HA	2.42	0.53
1:BP:111:ILE:HG23	1:BP:113:PRO:HD3	1.90	0.53
1:BR:183:LEU:C	1:BR:183:LEU:HD12	2.33	0.53
1:BT:111:ILE:HG23	1:BT:113:PRO:HD3	1.89	0.53
1:AT:60:MET:HE2	1:AT:200:LEU:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:266:ASP:O	1:AT:314:TYR:HA	2.07	0.53
1:AU:62:ARG:HH11	1:AU:62:ARG:HG2	1.72	0.53
1:BV:80:VAL:CG1	1:BV:185:LEU:HB3	2.38	0.53
1:BW:98:ILE:HA	1:BW:211:SER:O	2.09	0.53
1:BX:281:HIS:ND1	1:BX:301:TRP:HB3	2.23	0.53
1:AX:61:SER:CB	1:AX:90:PRO:HD2	2.35	0.53
1:BY:111:ILE:HG21	1:BY:123:TYR:OH	2.08	0.53
1:BY:112:GLN:HB2	1:BY:198:SER:O	2.08	0.53
1:BZ:99:PHE:N	1:BZ:99:PHE:CD1	2.77	0.53
1:AZ:119:THR:HG23	1:AZ:193:ASP:CB	2.39	0.53
1:AZ:253:ASP:OD1	1:AZ:285:PHE:N	2.42	0.53
1:Ac:115:CYS:HB2	1:Ac:116:PRO:HD2	1.91	0.53
1:AA:279:TYR:CE2	1:AA:311:GLY:O	2.61	0.53
1:AA:314:TYR:CG	1:AA:315:TYR:N	2.76	0.53
1:AB:115:CYS:HB2	1:AB:116:PRO:HD2	1.91	0.53
1:BC:74:THR:HA	1:BC:190:ASN:ND2	2.24	0.53
1:AF:314:TYR:CE1	1:AF:316:SER:HA	2.44	0.53
1:AH:115:CYS:HB2	1:AH:116:PRO:HD2	1.89	0.53
1:AI:80:VAL:CG1	1:AI:185:LEU:HB3	2.39	0.53
1:CJ:163:THR:OG1	1:CJ:165:THR:HG23	2.08	0.53
1:AM:142:GLN:O	1:AM:142:GLN:NE2	2.41	0.53
1:AN:314:TYR:CE1	1:AN:316:SER:HA	2.43	0.53
1:AQ:314:TYR:CE1	1:AQ:316:SER:CA	2.87	0.53
1:BS:74:THR:O	1:BS:75:ASP:C	2.51	0.53
1:AT:268:SER:HB3	1:AT:273:ASP:O	2.09	0.53
1:CU:98:ILE:HD11	1:CU:99:PHE:CE2	2.44	0.53
1:AV:253:ASP:OD1	1:AV:285:PHE:N	2.42	0.53
1:BX:98:ILE:HA	1:BX:211:SER:O	2.09	0.53
1:BZ:61:SER:CB	1:BZ:90:PRO:HD2	2.26	0.53
1:Ba:99:PHE:N	1:Ba:99:PHE:CD1	2.76	0.53
1:Bc:85:VAL:HG23	1:Bc:86:PRO:HD2	1.90	0.53
1:AA:110:GLU:HG2	1:AA:112:GLN:HG2	1.91	0.53
1:AA:281:HIS:CE1	1:AA:301:TRP:HB3	2.43	0.53
1:CA:100:GLN:HA	1:CA:213:GLU:OE2	2.09	0.53
1:BB:325:LEU:HD22	1:BB:329:THR:HG21	1.90	0.53
1:AB:109:PHE:HB2	1:AB:158:VAL:CG1	2.39	0.53
1:CC:111:ILE:HG22	1:CC:113:PRO:HD3	1.89	0.53
1:AE:268:SER:HB3	1:AE:273:ASP:O	2.09	0.53
1:AE:314:TYR:CG	1:AE:315:TYR:N	2.77	0.53
1:CE:91:ARG:HD2	1:CH:98:ILE:HB	1.91	0.53
1:BG:99:PHE:N	1:BG:99:PHE:CD1	2.76	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:111:ILE:HD11	1:CG:125:ALA:CB	2.38	0.53
1:AI:122:GLY:HA3	1:Aa:114:MET:SD	2.49	0.53
1:AI:162:TYR:N	1:AI:162:TYR:CD1	2.76	0.53
1:AJ:101:ARG:CZ	1:AJ:166:LEU:HD23	2.39	0.53
1:BK:74:THR:O	1:BK:75:ASP:C	2.51	0.53
1:CM:80:VAL:CG1	1:CM:185:LEU:HB2	2.37	0.53
1:AO:115:CYS:HB2	1:AO:116:PRO:HD2	1.91	0.53
1:AQ:101:ARG:CZ	1:AQ:166:LEU:HD23	2.39	0.53
1:CQ:43:SER:O	1:CV:34:ARG:HD3	2.09	0.53
1:AR:162:TYR:N	1:AR:162:TYR:CD1	2.76	0.53
1:AS:119:THR:HG23	1:AS:193:ASP:CB	2.38	0.53
1:AS:268:SER:HB3	1:AS:273:ASP:O	2.08	0.53
1:BV:115:CYS:HB2	1:BV:116:PRO:HD2	1.90	0.53
1:CW:163:THR:OG1	1:CW:165:THR:HG23	2.08	0.53
1:BX:325:LEU:HD22	1:BX:329:THR:HG21	1.91	0.53
1:CX:79:VAL:HG13	1:CX:80:VAL:N	2.22	0.53
1:BZ:115:CYS:HB2	1:BZ:116:PRO:HD2	1.91	0.53
1:CZ:95:ALA:O	1:CZ:98:ILE:HG12	2.09	0.53
1:Ba:101:ARG:NH2	1:Ba:166:LEU:HD12	2.24	0.53
1:Aa:314:TYR:HE1	1:Aa:316:SER:N	2.01	0.53
1:Ca:111:ILE:HG22	1:Ca:113:PRO:HD3	1.90	0.53
1:Bb:98:ILE:HA	1:Bb:211:SER:O	2.09	0.53
1:Bb:111:ILE:HG22	1:Bb:156:ARG:H	1.73	0.53
1:Bd:112:GLN:HB2	1:Bd:198:SER:O	2.08	0.53
1:Ad:109:PHE:HB2	1:Ad:158:VAL:CG1	2.39	0.53
1:AA:268:SER:HB3	1:AA:273:ASP:O	2.08	0.53
1:BC:165:THR:OG1	1:BC:166:LEU:N	2.42	0.53
1:BE:74:THR:O	1:BE:75:ASP:C	2.50	0.53
1:AE:302:ASP:C	1:AE:305:ASN:ND2	2.64	0.53
1:AH:162:TYR:CD1	1:AH:162:TYR:N	2.76	0.53
1:AI:305:ASN:OD1	1:AI:305:ASN:N	2.42	0.53
1:AJ:111:ILE:O	1:AJ:198:SER:O	2.27	0.53
1:BK:98:ILE:HA	1:BK:211:SER:O	2.09	0.53
1:AK:80:VAL:CG1	1:AK:185:LEU:HB3	2.39	0.53
1:AK:142:GLN:NE2	1:AK:142:GLN:O	2.42	0.53
1:CM:118:ASN:HA	1:Bc:116:PRO:HB3	1.91	0.53
1:BN:111:ILE:HG21	1:BN:123:TYR:OH	2.08	0.53
1:AR:109:PHE:HB2	1:AR:158:VAL:CG1	2.39	0.53
1:AT:116:PRO:HB3	1:Aa:118:ASN:O	2.09	0.53
1:AT:305:ASN:OD1	1:AT:305:ASN:N	2.42	0.53
1:BV:111:ILE:HG23	1:BV:113:PRO:HD3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:119:THR:HG23	1:AW:193:ASP:CB	2.39	0.53
1:BZ:74:THR:O	1:BZ:75:ASP:C	2.50	0.53
1:BZ:325:LEU:HD22	1:BZ:329:THR:HG21	1.90	0.53
1:Ab:111:ILE:HG21	1:Ab:123:TYR:CZ	2.44	0.53
1:Bc:98:ILE:HA	1:Bc:211:SER:O	2.08	0.53
1:Ad:80:VAL:CG1	1:Ad:185:LEU:HB3	2.39	0.53
1:BA:99:PHE:N	1:BA:99:PHE:CD1	2.77	0.53
1:AA:310:ASP:HB3	1:AA:312:VAL:HG22	1.91	0.53
1:CA:79:VAL:HG13	1:CA:80:VAL:N	2.23	0.53
1:CA:223:MET:HE2	1:CA:328:GLY:HA2	1.91	0.53
1:BB:98:ILE:HA	1:BB:211:SER:O	2.08	0.53
1:BC:111:ILE:HG22	1:BC:156:ARG:H	1.72	0.53
1:CF:100:GLN:HA	1:CF:213:GLU:OE2	2.09	0.53
1:BI:98:ILE:HG22	1:Aa:91:ARG:CZ	2.38	0.53
1:BI:163:THR:OG1	1:BI:165:THR:CG2	2.57	0.53
1:CI:79:VAL:HG13	1:CI:80:VAL:N	2.22	0.53
1:AJ:115:CYS:HB2	1:AJ:116:PRO:HD2	1.90	0.53
1:CJ:191:ASN:OD1	1:CJ:191:ASN:N	2.36	0.53
1:AL:111:ILE:HG21	1:AL:123:TYR:CZ	2.43	0.53
1:AL:253:ASP:OD1	1:AL:285:PHE:N	2.42	0.53
1:BN:85:VAL:HG23	1:BN:86:PRO:HD2	1.91	0.53
1:AO:314:TYR:CG	1:AO:315:TYR:N	2.77	0.53
1:AP:101:ARG:CZ	1:AP:166:LEU:HD23	2.39	0.53
1:BR:75:ASP:OD2	1:CT:62:ARG:NH1	2.37	0.53
1:AR:63:ILE:HB	1:AR:199:VAL:HG13	1.89	0.53
1:AR:80:VAL:CG1	1:AR:185:LEU:HB3	2.38	0.53
1:CS:63:ILE:HD12	1:CS:88:LEU:CD1	2.39	0.53
1:AU:314:TYR:CG	1:AU:315:TYR:N	2.77	0.53
1:AA:61:SER:CB	1:AA:90:PRO:HD2	2.32	0.53
1:BB:80:VAL:CG1	1:BB:185:LEU:HB3	2.39	0.53
1:BH:80:VAL:CG1	1:BH:185:LEU:HB3	2.39	0.53
1:BJ:80:VAL:CG1	1:BJ:185:LEU:HB3	2.39	0.53
1:BJ:163:THR:OG1	1:BJ:165:THR:CG2	2.57	0.53
1:AJ:162:TYR:N	1:AJ:162:TYR:CD1	2.77	0.53
1:BK:153:TRP:O	1:CS:151:LYS:NZ	2.41	0.53
1:BL:123:TYR:HB2	1:BL:185:LEU:HD11	1.91	0.53
1:CL:80:VAL:CG1	1:CL:185:LEU:HB2	2.38	0.53
1:AM:60:MET:HE2	1:AM:200:LEU:HB3	1.90	0.53
1:AN:115:CYS:HB2	1:AN:116:PRO:HD2	1.90	0.53
1:BO:123:TYR:HB2	1:BO:185:LEU:HD11	1.91	0.53
1:CP:63:ILE:HD12	1:CP:88:LEU:CG	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:85:VAL:HG13	1:CQ:86:PRO:HD2	1.91	0.53
1:CR:80:VAL:CG1	1:CR:185:LEU:HB2	2.38	0.53
1:BS:99:PHE:N	1:BS:99:PHE:CD1	2.76	0.53
1:BT:163:THR:OG1	1:BT:165:THR:CG2	2.57	0.53
1:AT:115:CYS:HB2	1:AT:116:PRO:HD2	1.89	0.53
1:AT:253:ASP:OD1	1:AT:285:PHE:N	2.42	0.53
1:CT:111:ILE:HG22	1:CT:113:PRO:HD3	1.90	0.53
1:BV:74:THR:HA	1:BV:190:ASN:ND2	2.24	0.53
1:AX:253:ASP:OD1	1:AX:285:PHE:N	2.42	0.53
1:AY:124:VAL:HG11	1:AY:138:PHE:HD1	1.74	0.53
1:AY:142:GLN:NE2	1:AY:142:GLN:O	2.42	0.53
1:Ab:314:TYR:CG	1:Ab:315:TYR:N	2.77	0.53
1:AA:162:TYR:N	1:AA:162:TYR:CD1	2.77	0.52
1:BG:74:THR:O	1:BG:75:ASP:C	2.51	0.52
1:AG:110:GLU:HG2	1:AG:112:GLN:HG2	1.91	0.52
1:AG:142:GLN:O	1:AG:142:GLN:NE2	2.41	0.52
1:AG:314:TYR:CE1	1:AG:316:SER:CA	2.88	0.52
1:BH:99:PHE:N	1:BH:99:PHE:CD1	2.77	0.52
1:BH:165:THR:OG1	1:BH:166:LEU:N	2.42	0.52
1:AH:314:TYR:CE1	1:AH:316:SER:HA	2.43	0.52
1:BM:111:ILE:HG23	1:BM:113:PRO:HD3	1.90	0.52
1:AN:91:ARG:CZ	1:BP:98:ILE:HG22	2.38	0.52
1:AN:253:ASP:OD1	1:AN:285:PHE:N	2.41	0.52
1:BO:101:ARG:NH2	1:BO:166:LEU:HD12	2.22	0.52
1:AO:101:ARG:CZ	1:AO:166:LEU:HD23	2.38	0.52
1:CO:34:ARG:CD	1:Bc:156:ARG:HH22	2.22	0.52
1:CP:101:ARG:CZ	1:CP:166:LEU:CD1	2.87	0.52
1:BQ:61:SER:CB	1:BQ:90:PRO:HD2	2.27	0.52
1:AQ:124:VAL:HG11	1:AQ:138:PHE:CD1	2.43	0.52
1:AQ:302:ASP:C	1:AQ:305:ASN:ND2	2.63	0.52
1:AS:314:TYR:CE1	1:AS:316:SER:HA	2.43	0.52
1:AY:111:ILE:HG21	1:AY:123:TYR:CZ	2.43	0.52
1:Ba:85:VAL:HG23	1:Ba:86:PRO:HD2	1.91	0.52
1:Bc:99:PHE:N	1:Bc:99:PHE:CD1	2.77	0.52
1:Ac:314:TYR:CG	1:Ac:315:TYR:N	2.77	0.52
1:BA:58:SER:HB3	1:BA:204:SER:CB	2.39	0.52
1:AC:91:ARG:NE	1:BS:98:ILE:CG2	2.71	0.52
1:CC:85:VAL:HG13	1:CC:86:PRO:HD2	1.91	0.52
1:BE:101:ARG:NH2	1:BE:166:LEU:HD12	2.24	0.52
1:BJ:112:GLN:HB2	1:BJ:198:SER:O	2.10	0.52
1:AL:85:VAL:HG22	1:AL:86:PRO:HD2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:115:CYS:HB2	1:BM:116:PRO:HD2	1.91	0.52
1:BM:325:LEU:HD22	1:BM:329:THR:HG21	1.89	0.52
1:AM:314:TYR:CE1	1:AM:316:SER:CA	2.85	0.52
1:CM:85:VAL:HG13	1:CM:86:PRO:HD2	1.92	0.52
1:AN:305:ASN:OD1	1:AN:305:ASN:N	2.42	0.52
1:AO:91:ARG:NH2	1:BW:98:ILE:HG22	2.24	0.52
1:BQ:111:ILE:HG23	1:BQ:113:PRO:HD3	1.91	0.52
1:AS:142:GLN:NE2	1:AS:142:GLN:O	2.42	0.52
1:BT:325:LEU:HD22	1:BT:329:THR:HG21	1.92	0.52
1:AT:253:ASP:CG	1:AT:285:PHE:CA	2.79	0.52
1:CT:43:SER:O	1:CZ:34:ARG:HD3	2.09	0.52
1:AU:142:GLN:O	1:AU:142:GLN:NE2	2.42	0.52
1:CU:100:GLN:HA	1:CU:213:GLU:OE2	2.10	0.52
1:CU:112:GLN:NE2	1:Cb:43:SER:HA	2.24	0.52
1:AX:80:VAL:CG1	1:AX:185:LEU:HB3	2.39	0.52
1:AX:162:TYR:N	1:AX:162:TYR:CD1	2.77	0.52
1:AX:314:TYR:CG	1:AX:315:TYR:N	2.77	0.52
1:Ba:166:LEU:HD13	1:Ba:167:LEU:N	2.24	0.52
1:Aa:268:SER:HB3	1:Aa:273:ASP:O	2.09	0.52
1:Ab:109:PHE:HB2	1:Ab:158:VAL:CG1	2.39	0.52
1:Cc:111:ILE:HD11	1:Cc:125:ALA:CB	2.38	0.52
1:Bd:99:PHE:N	1:Bd:99:PHE:CD1	2.77	0.52
1:BB:85:VAL:HG23	1:BB:86:PRO:HD2	1.92	0.52
1:BF:281:HIS:ND1	1:BF:301:TRP:HB3	2.23	0.52
1:AF:61:SER:CB	1:AF:90:PRO:HD2	2.37	0.52
1:BG:101:ARG:NH2	1:BG:166:LEU:HD12	2.23	0.52
1:BH:98:ILE:HA	1:BH:211:SER:O	2.09	0.52
1:AH:279:TYR:CE2	1:AH:311:GLY:O	2.61	0.52
1:BI:98:ILE:HA	1:BI:211:SER:O	2.08	0.52
1:AI:314:TYR:CE1	1:AI:316:SER:CA	2.87	0.52
1:AJ:310:ASP:HB3	1:AJ:312:VAL:HG22	1.90	0.52
1:CK:109:PHE:HB2	1:CK:158:VAL:CG1	2.40	0.52
1:AN:98:ILE:HG23	1:BP:91:ARG:NH1	2.25	0.52
1:AN:162:TYR:N	1:AN:162:TYR:CD1	2.76	0.52
1:AN:314:TYR:CG	1:AN:315:TYR:N	2.77	0.52
1:AP:305:ASN:OD1	1:AP:305:ASN:N	2.42	0.52
1:CQ:79:VAL:HG13	1:CQ:80:VAL:N	2.24	0.52
1:CS:80:VAL:CG1	1:CS:185:LEU:HB2	2.39	0.52
1:AX:63:ILE:HB	1:AX:199:VAL:HG13	1.90	0.52
1:Ab:119:THR:HG23	1:Ab:193:ASP:CB	2.38	0.52
1:Ab:268:SER:HB3	1:Ab:273:ASP:O	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cb:85:VAL:HG13	1:Cb:86:PRO:HD2	1.91	0.52
1:Ac:314:TYR:CE1	1:Ac:316:SER:HA	2.43	0.52
1:Bd:281:HIS:ND1	1:Bd:301:TRP:HB3	2.25	0.52
1:AC:253:ASP:OD1	1:AC:285:PHE:N	2.42	0.52
1:AE:80:VAL:CG1	1:AE:185:LEU:HB3	2.40	0.52
1:AE:314:TYR:CE1	1:AE:316:SER:HA	2.42	0.52
1:CF:111:ILE:HD11	1:CF:125:ALA:CB	2.38	0.52
1:BG:281:HIS:ND1	1:BG:301:TRP:HB3	2.24	0.52
1:AG:305:ASN:OD1	1:AG:305:ASN:N	2.42	0.52
1:AH:268:SER:HB3	1:AH:273:ASP:O	2.09	0.52
1:AI:101:ARG:CZ	1:AI:166:LEU:HD23	2.40	0.52
1:AO:253:ASP:OD1	1:AO:285:PHE:N	2.42	0.52
1:AP:279:TYR:CE2	1:AP:311:GLY:O	2.61	0.52
1:CP:63:ILE:HD12	1:CP:88:LEU:CD1	2.39	0.52
1:CP:190:ASN:HD22	1:CP:190:ASN:N	2.06	0.52
1:BQ:123:TYR:HB2	1:BQ:185:LEU:HD11	1.91	0.52
1:BR:163:THR:OG1	1:BR:165:THR:CG2	2.57	0.52
1:AR:111:ILE:HG21	1:AR:123:TYR:CZ	2.44	0.52
1:CR:34:ARG:HD3	1:Ca:43:SER:O	2.09	0.52
1:CR:100:GLN:HA	1:CR:213:GLU:OE2	2.10	0.52
1:BT:112:GLN:HB2	1:BT:198:SER:O	2.09	0.52
1:AT:162:TYR:N	1:AT:162:TYR:CD1	2.78	0.52
1:AV:305:ASN:OD1	1:AV:305:ASN:N	2.42	0.52
1:CW:111:ILE:HG22	1:CW:113:PRO:HD3	1.90	0.52
1:CW:111:ILE:HD11	1:CW:125:ALA:CB	2.40	0.52
1:BZ:68:LEU:HD23	1:BZ:195:VAL:CG2	2.39	0.52
1:Ba:325:LEU:HD22	1:Ba:329:THR:HG21	1.92	0.52
1:Ac:119:THR:HG23	1:Ac:193:ASP:CB	2.38	0.52
1:Ad:60:MET:HE2	1:Ad:200:LEU:HB3	1.92	0.52
1:Ad:111:ILE:HG21	1:Ad:123:TYR:CZ	2.45	0.52
1:BA:163:THR:OG1	1:BA:165:THR:CG2	2.57	0.52
1:BC:163:THR:OG1	1:BC:165:THR:CG2	2.58	0.52
1:BD:99:PHE:N	1:BD:99:PHE:CD1	2.77	0.52
1:AE:305:ASN:OD1	1:AE:305:ASN:N	2.42	0.52
1:CG:111:ILE:HG22	1:CG:113:PRO:HD3	1.90	0.52
1:AH:142:GLN:NE2	1:AH:142:GLN:O	2.43	0.52
1:CH:80:VAL:CG1	1:CH:185:LEU:HB2	2.40	0.52
1:BK:281:HIS:ND1	1:BK:301:TRP:HB3	2.25	0.52
1:AK:305:ASN:OD1	1:AK:305:ASN:N	2.43	0.52
1:AN:109:PHE:HB2	1:AN:158:VAL:CG1	2.40	0.52
1:BO:205:VAL:HG22	1:BO:206:ARG:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:268:SER:HB3	1:AO:273:ASP:O	2.08	0.52
1:AR:305:ASN:OD1	1:AR:305:ASN:N	2.43	0.52
1:CS:63:ILE:HD12	1:CS:88:LEU:CG	2.40	0.52
1:CV:81:ASP:C	1:CV:81:ASP:OD1	2.53	0.52
1:AW:314:TYR:CG	1:AW:315:TYR:N	2.78	0.52
1:AX:253:ASP:CG	1:AX:285:PHE:CA	2.79	0.52
1:Cc:191:ASN:OD1	1:Cc:191:ASN:N	2.38	0.52
1:Bd:74:THR:O	1:Bd:75:ASP:C	2.51	0.52
1:Bd:325:LEU:HD22	1:Bd:329:THR:HG21	1.92	0.52
1:BA:61:SER:CB	1:BA:90:PRO:HD2	2.28	0.52
1:AA:118:ASN:O	1:AI:116:PRO:HB3	2.09	0.52
1:CH:138:PHE:CD1	1:CH:138:PHE:C	2.88	0.52
1:AK:266:ASP:O	1:AK:314:TYR:HA	2.10	0.52
1:BL:98:ILE:CG2	1:AU:91:ARG:CZ	2.88	0.52
1:BL:101:ARG:NH2	1:BL:166:LEU:HD12	2.23	0.52
1:BL:115:CYS:HB2	1:BL:116:PRO:HD2	1.90	0.52
1:AM:162:TYR:N	1:AM:162:TYR:CD1	2.78	0.52
1:AQ:305:ASN:OD1	1:AQ:305:ASN:N	2.43	0.52
1:AR:281:HIS:CE1	1:AR:301:TRP:HB3	2.45	0.52
1:AT:142:GLN:NE2	1:AT:142:GLN:O	2.43	0.52
1:AU:310:ASP:HB3	1:AU:312:VAL:HG22	1.91	0.52
1:CU:98:ILE:HB	1:Cb:91:ARG:HD2	1.91	0.52
1:BV:281:HIS:ND1	1:BV:301:TRP:HB3	2.25	0.52
1:AV:119:THR:HG23	1:AV:193:ASP:CB	2.40	0.52
1:AW:266:ASP:O	1:AW:314:TYR:HA	2.09	0.52
1:CW:47:GLY:H	1:Cd:60:MET:HE1	1.74	0.52
1:CW:80:VAL:HG11	1:CW:185:LEU:HB2	1.91	0.52
1:AX:60:MET:HE2	1:AX:200:LEU:HB3	1.91	0.52
1:AY:305:ASN:OD1	1:AY:305:ASN:N	2.42	0.52
1:Aa:310:ASP:HB3	1:Aa:312:VAL:HG22	1.91	0.52
1:BA:85:VAL:HG23	1:BA:86:PRO:HD2	1.91	0.52
1:BD:325:LEU:HD22	1:BD:329:THR:HG21	1.92	0.52
1:AD:305:ASN:OD1	1:AD:305:ASN:N	2.42	0.52
1:CE:81:ASP:OD2	1:CE:136:HIS:NE2	2.41	0.52
1:AF:115:CYS:HB2	1:AF:116:PRO:HD2	1.92	0.52
1:CF:63:ILE:HD12	1:CF:88:LEU:CD1	2.39	0.52
1:AH:310:ASP:HB3	1:AH:312:VAL:HG22	1.90	0.52
1:AN:119:THR:HG23	1:AN:193:ASP:CB	2.40	0.52
1:CQ:79:VAL:CG1	1:CQ:185:LEU:O	2.56	0.52
1:AS:314:TYR:CG	1:AS:315:TYR:N	2.77	0.52
1:BT:281:HIS:ND1	1:BT:301:TRP:HB3	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CT:80:VAL:CG1	1:CT:185:LEU:HB2	2.39	0.52
1:CT:101:ARG:NH1	1:CT:166:LEU:CD1	2.71	0.52
1:CV:79:VAL:HG13	1:CV:80:VAL:N	2.24	0.52
1:AW:124:VAL:HG11	1:AW:138:PHE:HD1	1.74	0.52
1:BX:74:THR:O	1:BX:75:ASP:C	2.50	0.52
1:CX:101:ARG:CZ	1:CX:166:LEU:CD1	2.88	0.52
1:BZ:74:THR:HA	1:BZ:190:ASN:ND2	2.24	0.52
1:CZ:111:ILE:HD11	1:CZ:125:ALA:CB	2.40	0.52
1:Ac:305:ASN:OD1	1:Ac:305:ASN:N	2.42	0.52
1:Bd:101:ARG:NH2	1:Bd:166:LEU:HD12	2.23	0.52
1:BA:111:ILE:HG23	1:BA:113:PRO:HD3	1.91	0.52
1:CC:190:ASN:HD22	1:CC:190:ASN:N	2.08	0.52
1:AD:314:TYR:CG	1:AD:315:TYR:N	2.77	0.52
1:AF:310:ASP:HB3	1:AF:312:VAL:HG22	1.91	0.52
1:CF:63:ILE:HD12	1:CF:88:LEU:CG	2.38	0.52
1:AM:91:ARG:NH2	1:Bc:98:ILE:CG2	2.72	0.52
1:CM:101:ARG:NH1	1:CM:166:LEU:CD1	2.73	0.52
1:BR:165:THR:OG1	1:BR:166:LEU:N	2.43	0.52
1:CU:62:ARG:NH1	1:Bb:75:ASP:OD2	2.35	0.52
1:BV:163:THR:OG1	1:BV:165:THR:CG2	2.58	0.52
1:BW:111:ILE:HG23	1:BW:113:PRO:HD3	1.92	0.52
1:AW:111:ILE:HG21	1:AW:123:TYR:CZ	2.45	0.52
1:AX:305:ASN:OD1	1:AX:305:ASN:N	2.42	0.52
1:Cb:112:GLN:NE2	1:Cb:155:SER:OG	2.43	0.52
1:Cd:77:TYR:CD1	1:Cd:77:TYR:C	2.86	0.52
1:BC:80:VAL:CG1	1:BC:185:LEU:HB3	2.39	0.52
1:AE:116:PRO:HB3	1:AM:118:ASN:O	2.10	0.52
1:CF:57:LEU:HD23	1:CF:203:TRP:CH2	2.45	0.52
1:AG:109:PHE:HB2	1:AG:158:VAL:CG1	2.40	0.52
1:AH:124:VAL:HG11	1:AH:138:PHE:HD1	1.75	0.52
1:AH:305:ASN:OD1	1:AH:305:ASN:N	2.42	0.52
1:AI:314:TYR:CG	1:AI:315:TYR:N	2.78	0.52
1:CI:111:ILE:HD11	1:CI:125:ALA:CB	2.40	0.52
1:AJ:124:VAL:HG11	1:AJ:138:PHE:HD1	1.75	0.52
1:AJ:314:TYR:CG	1:AJ:315:TYR:N	2.77	0.52
1:CJ:111:ILE:HG22	1:CJ:113:PRO:HD3	1.92	0.52
1:BK:98:ILE:HG22	1:AS:91:ARG:NH2	2.24	0.52
1:AL:60:MET:HE2	1:AL:200:LEU:HB3	1.92	0.52
1:BM:127:PHE:HB3	1:BM:160:PRO:HB3	1.91	0.52
1:AM:124:VAL:HG11	1:AM:138:PHE:HD1	1.74	0.52
1:BO:68:LEU:HD23	1:BO:195:VAL:CG2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:111:ILE:HG23	1:BO:113:PRO:HD3	1.92	0.52
1:BO:123:TYR:HB2	1:BO:185:LEU:CD1	2.40	0.52
1:CO:190:ASN:N	1:CO:190:ASN:HD22	2.08	0.52
1:AP:109:PHE:HB2	1:AP:158:VAL:CG1	2.39	0.52
1:CP:62:ARG:NH1	1:BQ:75:ASP:OD2	2.35	0.52
1:AQ:118:ASN:O	1:AZ:116:PRO:HB3	2.09	0.52
1:AQ:310:ASP:HB3	1:AQ:312:VAL:HG22	1.91	0.52
1:CQ:190:ASN:HD22	1:CQ:190:ASN:N	2.08	0.52
1:AS:124:VAL:HG11	1:AS:138:PHE:HD1	1.75	0.52
1:CU:85:VAL:HG13	1:CU:86:PRO:HD2	1.92	0.52
1:AV:268:SER:HB3	1:AV:273:ASP:O	2.10	0.52
1:CV:199:VAL:O	1:CV:199:VAL:HG13	2.08	0.52
1:BX:123:TYR:HB2	1:BX:185:LEU:HD11	1.92	0.52
1:BX:165:THR:OG1	1:BX:166:LEU:N	2.42	0.52
1:AY:310:ASP:HB3	1:AY:312:VAL:HG22	1.92	0.52
1:AZ:314:TYR:CG	1:AZ:315:TYR:N	2.78	0.52
1:Cd:100:GLN:HA	1:Cd:213:GLU:OE2	2.10	0.52
1:AC:115:CYS:HB2	1:AC:116:PRO:HD2	1.91	0.52
1:CC:62:ARG:NH1	1:BJ:75:ASP:OD2	2.36	0.52
1:CC:109:PHE:HB2	1:CC:158:VAL:HG12	1.92	0.52
1:BG:115:CYS:HB2	1:BG:116:PRO:HD2	1.92	0.52
1:AG:61:SER:HB2	1:AG:89:LEU:HD22	1.92	0.52
1:AG:91:ARG:CZ	1:Bd:98:ILE:HG22	2.40	0.52
1:AG:162:TYR:N	1:AG:162:TYR:CD1	2.77	0.52
1:AG:314:TYR:CG	1:AG:315:TYR:N	2.78	0.52
1:CG:80:VAL:CG1	1:CG:185:LEU:HB2	2.39	0.52
1:AH:60:MET:HE2	1:AH:200:LEU:HB3	1.90	0.52
1:CH:151:LYS:NZ	1:BN:153:TRP:O	2.43	0.52
1:BI:98:ILE:HG22	1:Aa:91:ARG:NH2	2.25	0.52
1:AJ:111:ILE:HG21	1:AJ:123:TYR:CZ	2.45	0.52
1:BL:98:ILE:HA	1:BL:211:SER:O	2.09	0.52
1:BN:123:TYR:HB2	1:BN:185:LEU:HD11	1.92	0.52
1:AO:162:TYR:N	1:AO:162:TYR:CD1	2.78	0.52
1:CO:122:GLY:HA3	1:BW:114:MET:SD	2.50	0.52
1:BP:325:LEU:HD22	1:BP:329:THR:HG21	1.92	0.52
1:CQ:99:PHE:CB	1:CQ:209:VAL:O	2.59	0.52
1:AU:60:MET:HE2	1:AU:200:LEU:HB3	1.92	0.52
1:AU:314:TYR:CE1	1:AU:316:SER:HA	2.41	0.52
1:AV:142:GLN:NE2	1:AV:142:GLN:O	2.43	0.52
1:AX:101:ARG:CZ	1:AX:166:LEU:HD23	2.39	0.52
1:CY:80:VAL:CG1	1:CY:185:LEU:HB2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:288:ASN:N	1:CZ:288:ASN:OD1	2.44	0.52
1:Aa:314:TYR:CE1	1:Aa:316:SER:HA	2.44	0.52
1:Ab:61:SER:CB	1:Ab:90:PRO:HD2	2.34	0.52
1:AA:305:ASN:OD1	1:AA:305:ASN:N	2.43	0.51
1:CB:237:ASP:HB3	1:CB:297:ARG:HG2	1.92	0.51
1:AC:119:THR:HG23	1:AC:193:ASP:CB	2.40	0.51
1:AC:162:TYR:N	1:AC:162:TYR:CD1	2.77	0.51
1:BE:123:TYR:HB2	1:BE:185:LEU:HD11	1.92	0.51
1:BH:205:VAL:HG22	1:BH:206:ARG:N	2.25	0.51
1:CH:43:SER:O	1:CW:34:ARG:HD3	2.09	0.51
1:CH:98:ILE:HD11	1:CH:99:PHE:CE2	2.45	0.51
1:BI:80:VAL:CG1	1:BI:185:LEU:HB3	2.39	0.51
1:BJ:150:ALA:HB2	1:BJ:156:ARG:HD3	1.92	0.51
1:AK:315:TYR:CE2	1:AK:317:ASP:OD2	2.63	0.51
1:AM:115:CYS:HB2	1:AM:116:PRO:HD2	1.90	0.51
1:CM:237:ASP:HB3	1:CM:297:ARG:HG2	1.92	0.51
1:CO:43:SER:O	1:CU:34:ARG:HD3	2.10	0.51
1:AP:310:ASP:HB3	1:AP:312:VAL:HG22	1.92	0.51
1:BR:161:GLN:NE2	1:CR:210:PRO:HD2	2.26	0.51
1:AR:253:ASP:OD1	1:AR:285:PHE:N	2.42	0.51
1:BS:98:ILE:O	1:BS:211:SER:CA	2.58	0.51
1:AV:314:TYR:CE1	1:AV:316:SER:HA	2.44	0.51
1:CW:85:VAL:HG13	1:CW:86:PRO:HD2	1.92	0.51
1:CX:43:SER:HA	1:Cc:112:GLN:NE2	2.26	0.51
1:BY:80:VAL:CG1	1:BY:185:LEU:HB3	2.39	0.51
1:AY:115:CYS:HB2	1:AY:116:PRO:HD2	1.91	0.51
1:CY:223:MET:HE2	1:CY:328:GLY:HA2	1.92	0.51
1:Aa:61:SER:CB	1:Aa:90:PRO:HD2	2.32	0.51
1:Bc:101:ARG:NH2	1:Bc:166:LEU:HD12	2.25	0.51
1:Ac:142:GLN:O	1:Ac:142:GLN:NE2	2.43	0.51
1:CB:81:ASP:C	1:CB:81:ASP:OD1	2.53	0.51
1:BD:111:ILE:HG23	1:BD:113:PRO:HD3	1.92	0.51
1:AD:101:ARG:CZ	1:AD:166:LEU:HD23	2.40	0.51
1:AD:268:SER:HB3	1:AD:273:ASP:O	2.10	0.51
1:CF:80:VAL:CG1	1:CF:185:LEU:HB2	2.40	0.51
1:CF:124:VAL:O	1:CF:124:VAL:HG13	2.10	0.51
1:AH:314:TYR:CG	1:AH:315:TYR:N	2.77	0.51
1:BI:254:GLY:CA	1:BI:283:LYS:HE3	2.27	0.51
1:BJ:166:LEU:HD13	1:BJ:167:LEU:N	2.25	0.51
1:AJ:314:TYR:CE1	1:AJ:316:SER:HA	2.45	0.51
1:AK:281:HIS:CE1	1:AK:301:TRP:HB3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:305:ASN:OD1	1:AM:305:ASN:N	2.42	0.51
1:AN:61:SER:CB	1:AN:90:PRO:HD2	2.33	0.51
1:CN:81:ASP:C	1:CN:81:ASP:OD1	2.53	0.51
1:AO:119:THR:HG23	1:AO:193:ASP:CB	2.40	0.51
1:CO:163:THR:OG1	1:CO:165:THR:HG23	2.10	0.51
1:BP:99:PHE:N	1:BP:99:PHE:CD1	2.78	0.51
1:AP:253:ASP:OD1	1:AP:285:PHE:N	2.43	0.51
1:BQ:325:LEU:HD22	1:BQ:329:THR:HG21	1.91	0.51
1:CQ:109:PHE:HB2	1:CQ:158:VAL:HG12	1.92	0.51
1:AR:314:TYR:CE1	1:AR:316:SER:CA	2.90	0.51
1:CS:163:THR:OG1	1:CS:165:THR:HG23	2.10	0.51
1:AV:115:CYS:HB2	1:AV:116:PRO:HD2	1.92	0.51
1:BZ:281:HIS:ND1	1:BZ:301:TRP:HB3	2.25	0.51
1:AZ:122:GLY:C	1:AZ:188:VAL:HG22	2.35	0.51
1:AZ:305:ASN:OD1	1:AZ:305:ASN:N	2.43	0.51
1:Ab:162:TYR:N	1:Ab:162:TYR:CD1	2.78	0.51
1:Ac:162:TYR:N	1:Ac:162:TYR:CD1	2.78	0.51
1:Ad:119:THR:HG23	1:Ad:193:ASP:CB	2.41	0.51
1:CB:81:ASP:OD2	1:CB:136:HIS:NE2	2.40	0.51
1:BD:115:CYS:HB2	1:BD:116:PRO:HD2	1.91	0.51
1:BD:116:PRO:HD3	1:CW:120:GLY:HA3	1.92	0.51
1:AD:253:ASP:OD1	1:AD:285:PHE:N	2.42	0.51
1:CD:124:VAL:O	1:CD:124:VAL:HG13	2.10	0.51
1:AE:91:ARG:NE	1:BM:98:ILE:CG2	2.74	0.51
1:AH:119:THR:HG23	1:AH:193:ASP:CB	2.40	0.51
1:AH:253:ASP:OD1	1:AH:285:PHE:N	2.42	0.51
1:AI:111:ILE:HG21	1:AI:123:TYR:CZ	2.45	0.51
1:BJ:325:LEU:HD22	1:BJ:329:THR:HG21	1.92	0.51
1:BK:98:ILE:HG22	1:AS:91:ARG:CZ	2.40	0.51
1:CK:77:TYR:CD1	1:CK:77:TYR:C	2.86	0.51
1:AO:310:ASP:HB3	1:AO:312:VAL:HG22	1.92	0.51
1:CO:79:VAL:HG13	1:CO:80:VAL:N	2.25	0.51
1:BQ:281:HIS:ND1	1:BQ:301:TRP:HB3	2.25	0.51
1:BS:98:ILE:HA	1:BS:211:SER:O	2.09	0.51
1:AS:305:ASN:OD1	1:AS:305:ASN:N	2.42	0.51
1:CU:80:VAL:CG1	1:CU:185:LEU:HB2	2.39	0.51
1:AV:162:TYR:CD1	1:AV:162:TYR:N	2.78	0.51
1:AX:119:THR:HG23	1:AX:193:ASP:CB	2.41	0.51
1:CX:99:PHE:CB	1:CX:209:VAL:O	2.58	0.51
1:AZ:60:MET:HE2	1:AZ:200:LEU:HB3	1.93	0.51
1:AZ:80:VAL:CG1	1:AZ:185:LEU:HB3	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:124:VAL:HG11	1:BA:138:PHE:CD2	2.46	0.51
1:AB:119:THR:HG23	1:AB:193:ASP:CB	2.38	0.51
1:BC:115:CYS:HB2	1:BC:116:PRO:HD2	1.93	0.51
1:AC:110:GLU:HG2	1:AC:112:GLN:HG2	1.90	0.51
1:CC:81:ASP:C	1:CC:81:ASP:OD1	2.54	0.51
1:AD:281:HIS:CE1	1:AD:301:TRP:HB3	2.45	0.51
1:CD:81:ASP:C	1:CD:81:ASP:OD1	2.52	0.51
1:BG:165:THR:OG1	1:BG:166:LEU:N	2.44	0.51
1:AG:101:ARG:CZ	1:AG:166:LEU:HD23	2.40	0.51
1:CH:100:GLN:HA	1:CH:213:GLU:OE2	2.11	0.51
1:CJ:85:VAL:O	1:CJ:86:PRO:C	2.54	0.51
1:CL:79:VAL:HG13	1:CL:80:VAL:N	2.24	0.51
1:BO:98:ILE:HA	1:BO:211:SER:O	2.09	0.51
1:BP:276:ARG:O	1:AP:276:ARG:NH2	2.44	0.51
1:CQ:80:VAL:CG1	1:CQ:185:LEU:HB2	2.40	0.51
1:AT:118:ASN:O	1:AV:116:PRO:HB3	2.10	0.51
1:AV:279:TYR:CE2	1:AV:311:GLY:O	2.63	0.51
1:AW:253:ASP:OD1	1:AW:285:PHE:N	2.42	0.51
1:AY:61:SER:CB	1:AY:90:PRO:HD2	2.35	0.51
1:AY:314:TYR:CG	1:AY:315:TYR:N	2.79	0.51
1:AZ:142:GLN:O	1:AZ:142:GLN:NE2	2.43	0.51
1:Bb:80:VAL:CG1	1:Bb:185:LEU:HB3	2.40	0.51
1:Ac:314:TYR:CE1	1:Ac:316:SER:CA	2.87	0.51
1:AA:80:VAL:CG1	1:AA:185:LEU:HB3	2.40	0.51
1:AD:110:GLU:HG2	1:AD:112:GLN:HG2	1.93	0.51
1:CD:98:ILE:HD11	1:CD:99:PHE:CE2	2.45	0.51
1:AF:279:TYR:CE2	1:AF:311:GLY:O	2.63	0.51
1:BG:123:TYR:HB2	1:BG:185:LEU:HD11	1.92	0.51
1:BI:99:PHE:N	1:BI:99:PHE:CD1	2.79	0.51
1:BI:210:PRO:HB3	1:Aa:91:ARG:NH2	2.26	0.51
1:BL:150:ALA:HB2	1:BL:156:ARG:HD3	1.92	0.51
1:BM:80:VAL:CG1	1:BM:185:LEU:HB3	2.40	0.51
1:AN:110:GLU:HG2	1:AN:112:GLN:HG2	1.92	0.51
1:AP:246:THR:N	1:AP:247:PRO:CD	2.74	0.51
1:AP:314:TYR:CG	1:AP:315:TYR:N	2.78	0.51
1:BR:281:HIS:ND1	1:BR:301:TRP:HB3	2.25	0.51
1:CV:57:LEU:HD23	1:CV:203:TRP:CH2	2.45	0.51
1:BW:161:GLN:NE2	1:CW:210:PRO:HD2	2.25	0.51
1:BX:80:VAL:CG1	1:BX:185:LEU:HB3	2.40	0.51
1:CX:191:ASN:OD1	1:CX:191:ASN:N	2.41	0.51
1:Bb:85:VAL:HG23	1:Bb:86:PRO:HD2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ab:101:ARG:CZ	1:Ab:166:LEU:HD23	2.40	0.51
1:Cb:124:VAL:O	1:Cb:124:VAL:HG13	2.11	0.51
1:AB:314:TYR:CG	1:AB:315:TYR:N	2.78	0.51
1:CC:80:VAL:CG1	1:CC:185:LEU:HB2	2.41	0.51
1:CE:111:ILE:HD11	1:CE:125:ALA:CB	2.41	0.51
1:BG:325:LEU:HD22	1:BG:329:THR:HG21	1.91	0.51
1:BK:325:LEU:HD22	1:BK:329:THR:HG21	1.93	0.51
1:AK:111:ILE:HG21	1:AK:123:TYR:CZ	2.46	0.51
1:BL:98:ILE:HG22	1:AU:91:ARG:HH21	1.75	0.51
1:AL:115:CYS:HB2	1:AL:116:PRO:HD2	1.91	0.51
1:CM:112:GLN:NE2	1:CM:155:SER:OG	2.43	0.51
1:CM:163:THR:OG1	1:CM:165:THR:HG23	2.11	0.51
1:AO:141:LEU:O	1:AO:144:THR:CG2	2.45	0.51
1:CQ:62:ARG:HA	1:CQ:200:LEU:HD23	1.93	0.51
1:BR:111:ILE:HG21	1:BR:123:TYR:OH	2.10	0.51
1:CS:190:ASN:HD22	1:CS:190:ASN:N	2.09	0.51
1:AT:111:ILE:HG21	1:AT:123:TYR:CZ	2.46	0.51
1:BV:85:VAL:HG23	1:BV:86:PRO:HD2	1.91	0.51
1:CW:190:ASN:HD22	1:CW:190:ASN:N	2.09	0.51
1:AX:64:SER:OG	1:AX:80:VAL:HG21	2.11	0.51
1:CX:85:VAL:HG13	1:CX:86:PRO:HD2	1.92	0.51
1:CX:112:GLN:NE2	1:Cc:43:SER:HA	2.26	0.51
1:BY:163:THR:OG1	1:BY:165:THR:CG2	2.59	0.51
1:BZ:111:ILE:HG23	1:BZ:113:PRO:HD3	1.92	0.51
1:AZ:281:HIS:CE1	1:AZ:301:TRP:HB3	2.45	0.51
1:Aa:305:ASN:OD1	1:Aa:305:ASN:N	2.42	0.51
1:Cb:130:ASP:OD2	1:Cb:176:ARG:NH2	2.43	0.51
1:CC:63:ILE:HD12	1:CC:88:LEU:CD1	2.41	0.51
1:AD:91:ARG:CZ	1:BF:98:ILE:HG22	2.41	0.51
1:AE:61:SER:CB	1:AE:90:PRO:HD2	2.35	0.51
1:CG:62:ARG:HA	1:CG:200:LEU:HD23	1.91	0.51
1:CI:124:VAL:O	1:CI:124:VAL:HG13	2.09	0.51
1:CJ:111:ILE:HD11	1:CJ:125:ALA:CB	2.40	0.51
1:AL:109:PHE:HB2	1:AL:158:VAL:CG1	2.40	0.51
1:AO:124:VAL:HG11	1:AO:138:PHE:HD1	1.74	0.51
1:AP:60:MET:HE2	1:AP:200:LEU:HB3	1.91	0.51
1:BQ:156:ARG:NH2	1:CV:34:ARG:HG3	2.26	0.51
1:BQ:163:THR:OG1	1:BQ:165:THR:CG2	2.59	0.51
1:BQ:168:TRP:CE2	1:AQ:176:ARG:HD2	2.46	0.51
1:AQ:279:TYR:CE2	1:AQ:311:GLY:O	2.63	0.51
1:AR:314:TYR:CG	1:AR:315:TYR:N	2.78	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:123:TYR:HB2	1:BS:185:LEU:HD11	1.93	0.51
1:CS:98:ILE:HD11	1:CS:99:PHE:CE2	2.46	0.51
1:CS:111:ILE:HG22	1:CS:113:PRO:HD3	1.93	0.51
1:AU:305:ASN:OD1	1:AU:305:ASN:N	2.42	0.51
1:CV:112:GLN:NE2	1:CV:155:SER:OG	2.44	0.51
1:AW:101:ARG:CZ	1:AW:166:LEU:HD23	2.41	0.51
1:BX:168:TRP:CE2	1:AX:176:ARG:HD2	2.46	0.51
1:BY:281:HIS:ND1	1:BY:301:TRP:HB3	2.26	0.51
1:Ca:124:VAL:HG13	1:Ca:124:VAL:O	2.10	0.51
1:Ab:253:ASP:OD1	1:Ab:285:PHE:N	2.42	0.51
1:CA:85:VAL:HG13	1:CA:86:PRO:HD2	1.93	0.51
1:AB:111:ILE:HG21	1:AB:123:TYR:CZ	2.46	0.51
1:AB:305:ASN:OD1	1:AB:305:ASN:N	2.42	0.51
1:AB:314:TYR:CE1	1:AB:316:SER:CA	2.85	0.51
1:CB:100:GLN:HA	1:CB:213:GLU:OE2	2.11	0.51
1:AD:124:VAL:HG11	1:AD:138:PHE:HD1	1.75	0.51
1:AD:162:TYR:N	1:AD:162:TYR:CD1	2.79	0.51
1:CE:85:VAL:HG13	1:CE:86:PRO:HD2	1.93	0.51
1:BG:98:ILE:CG2	1:AP:91:ARG:NE	2.74	0.51
1:BH:115:CYS:C	1:Cd:120:GLY:CA	2.84	0.51
1:CH:237:ASP:HB3	1:CH:297:ARG:HG2	1.91	0.51
1:AI:314:TYR:CE1	1:AI:316:SER:HA	2.45	0.51
1:BK:112:GLN:HB2	1:BK:198:SER:O	2.11	0.51
1:AK:101:ARG:CZ	1:AK:166:LEU:HD23	2.40	0.51
1:BL:98:ILE:HG22	1:AU:91:ARG:CZ	2.40	0.51
1:AL:305:ASN:OD1	1:AL:305:ASN:N	2.44	0.51
1:CL:101:ARG:CZ	1:CL:166:LEU:CD1	2.89	0.51
1:BM:166:LEU:HD13	1:BM:167:LEU:N	2.26	0.51
1:AM:310:ASP:HB3	1:AM:312:VAL:HG22	1.92	0.51
1:BN:165:THR:OG1	1:BN:166:LEU:N	2.44	0.51
1:BP:166:LEU:HD13	1:BP:167:LEU:N	2.25	0.51
1:BQ:85:VAL:HG23	1:BQ:86:PRO:HD2	1.93	0.51
1:AQ:162:TYR:N	1:AQ:162:TYR:CD1	2.78	0.51
1:AR:124:VAL:HG11	1:AR:138:PHE:HD1	1.75	0.51
1:BS:80:VAL:CG1	1:BS:185:LEU:HB3	2.41	0.51
1:BT:98:ILE:CA	1:BT:211:SER:O	2.59	0.51
1:CW:101:ARG:CZ	1:CW:166:LEU:CD1	2.89	0.51
1:CX:190:ASN:HD22	1:CX:190:ASN:N	2.09	0.51
1:AZ:314:TYR:CE1	1:AZ:316:SER:HA	2.44	0.51
1:Ac:111:ILE:HG21	1:Ac:123:TYR:CZ	2.46	0.51
1:Cc:101:ARG:CZ	1:Cc:166:LEU:CD1	2.87	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ad:305:ASN:OD1	1:Ad:305:ASN:N	2.42	0.51
1:Cd:78:VAL:HG13	1:Cd:78:VAL:O	2.10	0.51
1:BA:74:THR:HA	1:BA:190:ASN:ND2	2.26	0.51
1:BA:115:CYS:HB2	1:BA:116:PRO:HD2	1.93	0.51
1:AA:122:GLY:C	1:AA:188:VAL:HG22	2.36	0.51
1:AA:253:ASP:OD1	1:AA:285:PHE:N	2.42	0.51
1:AC:101:ARG:CZ	1:AC:166:LEU:HD23	2.40	0.51
1:AC:305:ASN:OD1	1:AC:305:ASN:N	2.42	0.51
1:CC:63:ILE:HD12	1:CC:88:LEU:CG	2.41	0.51
1:AD:142:GLN:O	1:AD:142:GLN:NE2	2.43	0.51
1:BE:99:PHE:N	1:BE:99:PHE:CD1	2.78	0.51
1:CE:112:GLN:HE21	1:CH:44:THR:H	1.58	0.51
1:CF:34:ARG:CD	1:CY:43:SER:O	2.59	0.51
1:AG:253:ASP:OD1	1:AG:285:PHE:N	2.42	0.51
1:BH:111:ILE:HG23	1:BH:113:PRO:HD3	1.91	0.51
1:CJ:190:ASN:HD22	1:CJ:190:ASN:N	2.09	0.51
1:AK:253:ASP:OD1	1:AK:285:PHE:N	2.41	0.51
1:CK:111:ILE:HD11	1:CK:125:ALA:CB	2.41	0.51
1:BL:111:ILE:HG22	1:BL:156:ARG:H	1.75	0.51
1:BL:276:ARG:O	1:AL:276:ARG:NH2	2.44	0.51
1:AM:119:THR:HG23	1:AM:193:ASP:CB	2.39	0.51
1:AN:124:VAL:HG11	1:AN:138:PHE:HD1	1.76	0.51
1:CP:85:VAL:HG13	1:CP:86:PRO:HD2	1.92	0.51
1:CQ:101:ARG:CZ	1:CQ:166:LEU:CD1	2.89	0.51
1:AR:268:SER:HB3	1:AR:273:ASP:O	2.10	0.51
1:AR:310:ASP:HB3	1:AR:312:VAL:HG22	1.93	0.51
1:BS:205:VAL:HG22	1:BS:206:ARG:N	2.26	0.51
1:AV:110:GLU:HG2	1:AV:112:GLN:HG2	1.93	0.51
1:BX:111:ILE:HG23	1:BX:113:PRO:HD3	1.91	0.51
1:AY:281:HIS:CE1	1:AY:301:TRP:HB3	2.46	0.51
1:CZ:237:ASP:HB3	1:CZ:297:ARG:HG2	1.93	0.51
1:AA:246:THR:N	1:AA:247:PRO:CD	2.74	0.51
1:CA:81:ASP:C	1:CA:81:ASP:OD1	2.54	0.51
1:AB:142:GLN:O	1:AB:142:GLN:NE2	2.44	0.51
1:AC:80:VAL:CG1	1:AC:185:LEU:HB3	2.41	0.51
1:AC:310:ASP:HB3	1:AC:312:VAL:HG22	1.93	0.51
1:AC:314:TYR:CG	1:AC:315:TYR:N	2.79	0.51
1:BD:80:VAL:CG1	1:BD:185:LEU:HB3	2.40	0.51
1:CE:80:VAL:CG1	1:CE:185:LEU:HB2	2.40	0.51
1:BF:325:LEU:HD22	1:BF:329:THR:HG21	1.92	0.51
1:AG:310:ASP:HB3	1:AG:312:VAL:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:314:TYR:CE1	1:AG:316:SER:HA	2.44	0.51
1:CI:112:GLN:NE2	1:CI:155:SER:OG	2.44	0.51
1:CK:60:MET:HE1	1:CL:47:GLY:H	1.76	0.51
1:AL:315:TYR:CE2	1:AL:317:ASP:OD2	2.64	0.51
1:AM:315:TYR:CE2	1:AM:317:ASP:OD2	2.64	0.51
1:BN:168:TRP:CE2	1:AN:176:ARG:HD2	2.46	0.51
1:AO:305:ASN:OD1	1:AO:305:ASN:N	2.42	0.51
1:BP:124:VAL:HG11	1:BP:138:PHE:CD2	2.46	0.51
1:AS:110:GLU:HG2	1:AS:112:GLN:HG2	1.93	0.51
1:CU:43:SER:HA	1:Cb:112:GLN:NE2	2.26	0.51
1:AV:101:ARG:CZ	1:AV:166:LEU:HD23	2.41	0.51
1:BW:85:VAL:HG23	1:BW:86:PRO:HD2	1.93	0.51
1:AW:115:CYS:HB2	1:AW:116:PRO:HD2	1.92	0.51
1:CY:112:GLN:NE2	1:CY:155:SER:OG	2.44	0.51
1:AZ:124:VAL:HG11	1:AZ:138:PHE:HD1	1.76	0.51
1:CZ:124:VAL:O	1:CZ:124:VAL:HG13	2.11	0.51
1:Ca:81:ASP:C	1:Ca:81:ASP:OD1	2.54	0.51
1:Ca:111:ILE:HD11	1:Ca:125:ALA:CB	2.41	0.51
1:Cc:163:THR:OG1	1:Cc:165:THR:HG23	2.11	0.51
1:Ad:85:VAL:HG22	1:Ad:86:PRO:HD2	1.93	0.51
1:Cd:111:ILE:HD11	1:Cd:125:ALA:CB	2.41	0.51
1:CA:101:ARG:CZ	1:CA:166:LEU:CD1	2.89	0.50
1:CB:57:LEU:HD23	1:CB:203:TRP:CH2	2.46	0.50
1:CB:80:VAL:CG1	1:CB:185:LEU:HB2	2.40	0.50
1:CB:112:GLN:HE21	1:CF:44:THR:H	1.59	0.50
1:BJ:281:HIS:ND1	1:BJ:301:TRP:HB3	2.26	0.50
1:CK:122:GLY:O	1:CK:188:VAL:HB	2.10	0.50
1:AM:110:GLU:HG2	1:AM:112:GLN:HG2	1.94	0.50
1:CM:79:VAL:HG13	1:CM:80:VAL:N	2.25	0.50
1:CM:103:ALA:HB2	1:CM:166:LEU:HB3	1.92	0.50
1:BN:99:PHE:CD1	1:BN:99:PHE:N	2.78	0.50
1:CN:133:ASP:O	1:CN:182:ARG:NH2	2.45	0.50
1:BQ:166:LEU:HD13	1:BQ:167:LEU:N	2.27	0.50
1:AT:314:TYR:CE1	1:AT:316:SER:HA	2.45	0.50
1:CT:99:PHE:CB	1:CT:209:VAL:O	2.59	0.50
1:BV:165:THR:OG1	1:BV:166:LEU:N	2.44	0.50
1:Ca:99:PHE:CB	1:Ca:209:VAL:O	2.58	0.50
1:Ca:99:PHE:HB3	1:Ca:209:VAL:O	2.10	0.50
1:Bb:214:ASN:HD22	1:Bb:215:PRO:HD2	1.76	0.50
1:Bc:166:LEU:HD13	1:Bc:167:LEU:N	2.25	0.50
1:BA:165:THR:OG1	1:BA:166:LEU:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:101:ARG:NH2	1:BB:166:LEU:HD12	2.25	0.50
1:BB:165:THR:OG1	1:BB:166:LEU:N	2.44	0.50
1:CC:100:GLN:HA	1:CC:213:GLU:OE2	2.11	0.50
1:CD:100:GLN:HA	1:CD:213:GLU:OE2	2.11	0.50
1:AF:162:TYR:N	1:AF:162:TYR:CD1	2.79	0.50
1:CF:237:ASP:HB3	1:CF:297:ARG:HG2	1.92	0.50
1:CI:80:VAL:HG11	1:CI:185:LEU:HB2	1.93	0.50
1:CK:80:VAL:HG11	1:CK:185:LEU:HB2	1.92	0.50
1:AM:114:MET:SD	1:Ac:188:VAL:HG23	2.51	0.50
1:BP:85:VAL:HG23	1:BP:86:PRO:HD2	1.93	0.50
1:AQ:111:ILE:HG21	1:AQ:123:TYR:CZ	2.47	0.50
1:AQ:119:THR:HG23	1:AQ:193:ASP:CB	2.40	0.50
1:CR:117:ALA:HB2	1:CT:38:PRO:O	2.11	0.50
1:AT:119:THR:HG23	1:AT:193:ASP:CB	2.39	0.50
1:BU:99:PHE:N	1:BU:99:PHE:CD1	2.78	0.50
1:CV:80:VAL:CG1	1:CV:185:LEU:HB2	2.41	0.50
1:AY:315:TYR:CE2	1:AY:317:ASP:OD2	2.65	0.50
1:Ab:142:GLN:NE2	1:Ab:142:GLN:O	2.44	0.50
1:BA:276:ARG:O	1:AA:276:ARG:NH2	2.44	0.50
1:CA:77:TYR:C	1:CA:77:TYR:CD1	2.89	0.50
1:BD:123:TYR:HB2	1:BD:185:LEU:HD11	1.93	0.50
1:AF:142:GLN:NE2	1:AF:142:GLN:O	2.44	0.50
1:BI:166:LEU:HD13	1:BI:167:LEU:N	2.26	0.50
1:CI:237:ASP:HB3	1:CI:297:ARG:HG2	1.93	0.50
1:CJ:100:GLN:HA	1:CJ:213:GLU:OE2	2.11	0.50
1:BN:124:VAL:HG11	1:BN:138:PHE:CD2	2.46	0.50
1:CP:237:ASP:HB3	1:CP:297:ARG:HG2	1.93	0.50
1:CR:190:ASN:HD22	1:CR:190:ASN:N	2.09	0.50
1:BS:166:LEU:HD13	1:BS:167:LEU:N	2.27	0.50
1:AS:60:MET:HE2	1:AS:200:LEU:HB3	1.94	0.50
1:AS:61:SER:CB	1:AS:90:PRO:HD2	2.36	0.50
1:AS:314:TYR:CE1	1:AS:316:SER:CA	2.87	0.50
1:AT:314:TYR:CG	1:AT:315:TYR:N	2.79	0.50
1:AU:279:TYR:CE2	1:AU:311:GLY:O	2.63	0.50
1:BV:325:LEU:HD22	1:BV:329:THR:HG21	1.94	0.50
1:AX:115:CYS:HB2	1:AX:116:PRO:HD2	1.92	0.50
1:AX:310:ASP:HB3	1:AX:312:VAL:HG22	1.93	0.50
1:CY:99:PHE:CB	1:CY:209:VAL:O	2.59	0.50
1:CY:288:ASN:OD1	1:CY:288:ASN:N	2.45	0.50
1:Aa:124:VAL:HG11	1:Aa:138:PHE:HD1	1.76	0.50
1:Cb:237:ASP:HB3	1:Cb:297:ARG:HG2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ad:315:TYR:CE2	1:Ad:317:ASP:OD2	2.64	0.50
1:Cd:79:VAL:HG13	1:Cd:80:VAL:N	2.26	0.50
1:CC:223:MET:HE2	1:CC:328:GLY:HA2	1.93	0.50
1:AD:91:ARG:NH2	1:BF:98:ILE:HG22	2.26	0.50
1:BE:124:VAL:HG11	1:BE:138:PHE:CD2	2.46	0.50
1:AE:162:TYR:CD1	1:AE:162:TYR:N	2.80	0.50
1:AH:315:TYR:CE2	1:AH:317:ASP:OD2	2.64	0.50
1:AJ:305:ASN:OD1	1:AJ:305:ASN:N	2.42	0.50
1:BL:114:MET:SD	1:CU:122:GLY:HA3	2.52	0.50
1:AL:80:VAL:CG1	1:AL:185:LEU:HB3	2.41	0.50
1:AL:314:TYR:CG	1:AL:315:TYR:N	2.79	0.50
1:BM:168:TRP:CE2	1:AM:176:ARG:HD2	2.46	0.50
1:CP:199:VAL:O	1:CP:199:VAL:CG1	2.60	0.50
1:BQ:101:ARG:NH2	1:BQ:166:LEU:HD12	2.25	0.50
1:BR:74:THR:HA	1:BR:190:ASN:ND2	2.26	0.50
1:AR:60:MET:HE2	1:AR:200:LEU:HB3	1.92	0.50
1:CR:123:TYR:CD1	1:CR:185:LEU:HD21	2.47	0.50
1:AS:162:TYR:CD1	1:AS:162:TYR:N	2.80	0.50
1:BT:98:ILE:CG2	1:AV:91:ARG:NE	2.74	0.50
1:BV:99:PHE:N	1:BV:99:PHE:CD1	2.80	0.50
1:AV:85:VAL:HG22	1:AV:86:PRO:HD2	1.94	0.50
1:AX:142:GLN:O	1:AX:142:GLN:NE2	2.44	0.50
1:CX:111:ILE:HD11	1:CX:125:ALA:CB	2.41	0.50
1:AY:162:TYR:N	1:AY:162:TYR:CD1	2.79	0.50
1:AZ:279:TYR:CE2	1:AZ:311:GLY:O	2.62	0.50
1:Ad:279:TYR:CE2	1:Ad:311:GLY:O	2.63	0.50
1:Ad:302:ASP:CA	1:Ad:305:ASN:ND2	2.75	0.50
1:Cd:190:ASN:HD22	1:Cd:190:ASN:N	2.09	0.50
1:BD:111:ILE:HG22	1:BD:156:ARG:H	1.76	0.50
1:AD:114:MET:SD	1:AF:122:GLY:HA3	2.51	0.50
1:AD:279:TYR:CE2	1:AD:311:GLY:O	2.63	0.50
1:BE:166:LEU:HD13	1:BE:167:LEU:N	2.27	0.50
1:BF:74:THR:HA	1:BF:190:ASN:ND2	2.27	0.50
1:AF:109:PHE:HB2	1:AF:158:VAL:CG1	2.41	0.50
1:CF:111:ILE:HG22	1:CF:113:PRO:HD3	1.94	0.50
1:BH:61:SER:CB	1:BH:90:PRO:HD2	2.25	0.50
1:AJ:91:ARG:CZ	1:BR:98:ILE:HG22	2.41	0.50
1:AK:119:THR:HG23	1:AK:193:ASP:CB	2.41	0.50
1:AK:302:ASP:CA	1:AK:305:ASN:ND2	2.74	0.50
1:BL:165:THR:OG1	1:BL:166:LEU:N	2.45	0.50
1:AL:314:TYR:CE1	1:AL:316:SER:HA	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:116:PRO:HB3	1:Ac:118:ASN:O	2.11	0.50
1:CP:111:ILE:HD11	1:CP:125:ALA:CB	2.41	0.50
1:AQ:246:THR:N	1:AQ:247:PRO:CD	2.74	0.50
1:CQ:288:ASN:OD1	1:CQ:288:ASN:N	2.45	0.50
1:AS:115:CYS:HB2	1:AS:116:PRO:HD2	1.93	0.50
1:BT:85:VAL:HG23	1:BT:86:PRO:HD2	1.92	0.50
1:CT:121:GLY:C	1:CT:152:TRP:CD1	2.89	0.50
1:CX:100:GLN:HA	1:CX:213:GLU:OE2	2.11	0.50
1:CY:237:ASP:HB3	1:CY:297:ARG:HG2	1.94	0.50
1:BZ:166:LEU:HD13	1:BZ:167:LEU:N	2.27	0.50
1:Aa:246:THR:N	1:Aa:247:PRO:CD	2.74	0.50
1:Ab:305:ASN:OD1	1:Ab:305:ASN:N	2.42	0.50
1:Cb:163:THR:OG1	1:Cb:165:THR:HG23	2.11	0.50
1:Bd:111:ILE:HG22	1:Bd:156:ARG:H	1.75	0.50
1:Ad:115:CYS:HB2	1:Ad:116:PRO:HD2	1.93	0.50
1:BA:98:ILE:CA	1:BA:211:SER:O	2.60	0.50
1:BA:122:GLY:C	1:BA:188:VAL:CG2	2.83	0.50
1:CA:112:GLN:NE2	1:CA:155:SER:OG	2.45	0.50
1:AE:60:MET:HE2	1:AE:200:LEU:HB3	1.92	0.50
1:AF:314:TYR:CE1	1:AF:316:SER:CA	2.87	0.50
1:BI:74:THR:HA	1:BI:190:ASN:ND2	2.27	0.50
1:AK:310:ASP:HB3	1:AK:312:VAL:HG22	1.94	0.50
1:CK:85:VAL:HG13	1:CK:86:PRO:HD2	1.92	0.50
1:CK:101:ARG:CZ	1:CK:166:LEU:CD1	2.90	0.50
1:AL:119:THR:HG23	1:AL:193:ASP:CB	2.41	0.50
1:BM:61:SER:CB	1:BM:90:PRO:HD2	2.27	0.50
1:CP:80:VAL:CG1	1:CP:185:LEU:HB2	2.42	0.50
1:CP:81:ASP:C	1:CP:81:ASP:OD1	2.55	0.50
1:CR:80:VAL:HG11	1:CR:185:LEU:HB2	1.94	0.50
1:CT:100:GLN:HA	1:CT:213:GLU:OE2	2.11	0.50
1:AV:314:TYR:CG	1:AV:315:TYR:N	2.79	0.50
1:AY:253:ASP:OD1	1:AY:285:PHE:N	2.44	0.50
1:Cc:99:PHE:CB	1:Cc:209:VAL:O	2.60	0.50
1:Bd:150:ALA:HB2	1:Bd:156:ARG:HD3	1.93	0.50
1:Ad:314:TYR:CD1	1:Ad:314:TYR:C	2.90	0.50
1:BF:161:GLN:NE2	1:CF:210:PRO:HD2	2.26	0.50
1:AF:101:ARG:CZ	1:AF:166:LEU:HD23	2.42	0.50
1:AF:124:VAL:HG11	1:AF:138:PHE:CD1	2.47	0.50
1:CF:98:ILE:HD11	1:CF:99:PHE:CE2	2.47	0.50
1:AH:80:VAL:HG13	1:AH:185:LEU:HB3	1.93	0.50
1:CH:34:ARG:HD3	1:CM:43:SER:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:81:ASP:OD2	1:CH:136:HIS:NE2	2.43	0.50
1:BJ:99:PHE:N	1:BJ:99:PHE:CD1	2.79	0.50
1:AJ:268:SER:CB	1:AJ:273:ASP:O	2.60	0.50
1:AK:124:VAL:HG11	1:AK:138:PHE:HD1	1.76	0.50
1:AL:310:ASP:HB3	1:AL:312:VAL:HG22	1.93	0.50
1:BM:98:ILE:CA	1:BM:211:SER:O	2.59	0.50
1:CM:81:ASP:HA	1:CM:184:ILE:HG22	1.94	0.50
1:BO:153:TRP:O	1:Cb:151:LYS:NZ	2.44	0.50
1:AP:314:TYR:CE1	1:AP:316:SER:HA	2.44	0.50
1:AR:119:THR:HG23	1:AR:193:ASP:CB	2.42	0.50
1:CR:45:VAL:HG23	1:CT:200:LEU:HD13	1.93	0.50
1:CR:99:PHE:CD2	1:CR:207:LEU:HB3	2.47	0.50
1:CR:223:MET:HE2	1:CR:328:GLY:HA2	1.94	0.50
1:BT:161:GLN:NE2	1:CT:210:PRO:HD2	2.27	0.50
1:CT:163:THR:OG1	1:CT:165:THR:HG23	2.12	0.50
1:BU:111:ILE:HG23	1:BU:113:PRO:HD3	1.94	0.50
1:CX:99:PHE:HB3	1:CX:209:VAL:O	2.11	0.50
1:CY:101:ARG:CZ	1:CY:166:LEU:CD1	2.90	0.50
1:CZ:63:ILE:HD12	1:CZ:88:LEU:CD1	2.41	0.50
1:CZ:190:ASN:N	1:CZ:190:ASN:HD22	2.10	0.50
1:Aa:314:TYR:CG	1:Aa:315:TYR:N	2.78	0.50
1:Bb:99:PHE:N	1:Bb:99:PHE:CD1	2.79	0.50
1:Ac:253:ASP:OD1	1:Ac:285:PHE:N	2.44	0.50
1:Bd:80:VAL:CG1	1:Bd:185:LEU:HB3	2.40	0.50
1:Ad:314:TYR:CG	1:Ad:315:TYR:N	2.79	0.50
1:CA:62:ARG:NH1	1:BG:75:ASP:OD2	2.42	0.50
1:AB:101:ARG:CZ	1:AB:166:LEU:HD23	2.41	0.50
1:CD:62:ARG:HA	1:CD:200:LEU:HD23	1.94	0.50
1:CE:98:ILE:HD11	1:CE:99:PHE:CE2	2.47	0.50
1:AF:253:ASP:OD1	1:AF:285:PHE:N	2.43	0.50
1:AG:60:MET:HE2	1:AG:200:LEU:HB3	1.94	0.50
1:CG:100:GLN:HA	1:CG:213:GLU:OE2	2.12	0.50
1:BJ:85:VAL:HG23	1:BJ:86:PRO:HD2	1.93	0.50
1:AJ:142:GLN:O	1:AJ:142:GLN:NE2	2.44	0.50
1:AJ:279:TYR:CE2	1:AJ:311:GLY:O	2.65	0.50
1:CJ:62:ARG:HA	1:CJ:200:LEU:HD23	1.94	0.50
1:BK:161:GLN:NE2	1:CK:210:PRO:HD2	2.27	0.50
1:AK:314:TYR:CG	1:AK:315:TYR:N	2.79	0.50
1:BL:325:LEU:HD22	1:BL:329:THR:HG21	1.94	0.50
1:BM:165:THR:OG1	1:BM:166:LEU:N	2.43	0.50
1:CN:101:ARG:CZ	1:CN:166:LEU:CD1	2.90	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CN:163:THR:OG1	1:CN:165:THR:HG23	2.12	0.50
1:CP:45:VAL:HG23	1:CQ:200:LEU:HD13	1.94	0.50
1:AQ:253:ASP:OD1	1:AQ:285:PHE:N	2.43	0.50
1:CR:101:ARG:CZ	1:CR:166:LEU:CD1	2.90	0.50
1:CS:81:ASP:C	1:CS:81:ASP:OD1	2.55	0.50
1:BT:99:PHE:CD1	1:BT:99:PHE:N	2.79	0.50
1:AT:279:TYR:CE2	1:AT:311:GLY:O	2.63	0.50
1:AU:253:ASP:OD1	1:AU:285:PHE:N	2.42	0.50
1:CU:81:ASP:HA	1:CU:184:ILE:HG22	1.94	0.50
1:BX:85:VAL:HG23	1:BX:86:PRO:HD2	1.94	0.50
1:CX:63:ILE:HD12	1:CX:88:LEU:CG	2.41	0.50
1:CX:79:VAL:CG1	1:CX:185:LEU:O	2.53	0.50
1:Aa:119:THR:HG23	1:Aa:193:ASP:CB	2.40	0.50
1:Aa:142:GLN:NE2	1:Aa:142:GLN:O	2.45	0.50
1:Ac:109:PHE:HB2	1:Ac:158:VAL:CG1	2.42	0.50
1:BB:99:PHE:N	1:BB:99:PHE:CD1	2.80	0.50
1:BC:99:PHE:CD1	1:BC:99:PHE:N	2.79	0.50
1:AE:101:ARG:CZ	1:AE:166:LEU:HD23	2.41	0.50
1:AE:119:THR:HG23	1:AE:193:ASP:CB	2.41	0.50
1:CE:101:ARG:CZ	1:CE:166:LEU:CD1	2.90	0.50
1:CI:101:ARG:CZ	1:CI:166:LEU:CD1	2.90	0.50
1:AJ:246:THR:N	1:AJ:247:PRO:CD	2.75	0.50
1:CK:63:ILE:HD12	1:CK:88:LEU:CG	2.40	0.50
1:CL:63:ILE:HD12	1:CL:88:LEU:CD1	2.42	0.50
1:AM:114:MET:SD	1:Ac:188:VAL:CG2	3.00	0.50
1:CM:190:ASN:HD22	1:CM:190:ASN:N	2.10	0.50
1:BS:165:THR:OG1	1:BS:166:LEU:N	2.45	0.50
1:BT:214:ASN:HD22	1:BT:215:PRO:HD2	1.77	0.50
1:CU:81:ASP:C	1:CU:81:ASP:OD1	2.54	0.50
1:AV:310:ASP:HB3	1:AV:312:VAL:HG22	1.94	0.50
1:AW:310:ASP:HB3	1:AW:312:VAL:HG22	1.93	0.50
1:AY:246:THR:N	1:AY:247:PRO:CD	2.74	0.50
1:Aa:110:GLU:HG2	1:Aa:112:GLN:HG2	1.93	0.50
1:Ca:163:THR:OG1	1:Ca:165:THR:HG23	2.12	0.50
1:Cb:138:PHE:C	1:Cb:138:PHE:CD1	2.89	0.50
1:Bc:281:HIS:ND1	1:Bc:301:TRP:HB3	2.27	0.50
1:Cc:199:VAL:O	1:Cc:199:VAL:CG1	2.60	0.50
1:Cd:98:ILE:HD11	1:Cd:99:PHE:CE2	2.47	0.50
1:BC:85:VAL:HG23	1:BC:86:PRO:HD2	1.94	0.49
1:BC:168:TRP:CE2	1:AC:176:ARG:HD2	2.47	0.49
1:AC:315:TYR:CE2	1:AC:317:ASP:OD2	2.65	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:98:ILE:HG23	1:AW:91:ARG:HG2	1.94	0.49
1:AD:115:CYS:HB2	1:AD:116:PRO:HD2	1.94	0.49
1:CE:288:ASN:OD1	1:CE:288:ASN:N	2.45	0.49
1:BG:166:LEU:HD13	1:BG:167:LEU:N	2.26	0.49
1:CG:288:ASN:N	1:CG:288:ASN:OD1	2.45	0.49
1:AH:61:SER:CB	1:AH:90:PRO:HD2	2.34	0.49
1:CH:163:THR:OG1	1:CH:165:THR:HG23	2.12	0.49
1:BI:205:VAL:HG22	1:BI:206:ARG:N	2.27	0.49
1:AI:110:GLU:HG2	1:AI:112:GLN:HG2	1.94	0.49
1:AK:246:THR:N	1:AK:247:PRO:CD	2.74	0.49
1:CK:79:VAL:HG13	1:CK:80:VAL:N	2.26	0.49
1:CM:98:ILE:HB	1:CO:91:ARG:HD2	1.93	0.49
1:BO:210:PRO:HB3	1:Ab:91:ARG:NH2	2.27	0.49
1:CO:57:LEU:HD23	1:CO:203:TRP:CH2	2.47	0.49
1:CO:81:ASP:C	1:CO:81:ASP:OD1	2.55	0.49
1:CQ:111:ILE:HD11	1:CQ:125:ALA:CB	2.41	0.49
1:BR:85:VAL:HG23	1:BR:86:PRO:HD2	1.93	0.49
1:AR:246:THR:N	1:AR:247:PRO:CD	2.75	0.49
1:CU:119:THR:O	1:CU:120:GLY:C	2.55	0.49
1:AV:122:GLY:C	1:AV:188:VAL:HG22	2.37	0.49
1:BW:123:TYR:HB2	1:BW:185:LEU:HD11	1.92	0.49
1:AW:279:TYR:CE2	1:AW:311:GLY:O	2.63	0.49
1:CW:79:VAL:HG13	1:CW:80:VAL:N	2.27	0.49
1:BY:276:ARG:O	1:AY:276:ARG:NH2	2.45	0.49
1:BY:325:LEU:HD22	1:BY:329:THR:HG21	1.92	0.49
1:Ba:150:ALA:HB2	1:Ba:156:ARG:HD3	1.94	0.49
1:Aa:314:TYR:CE1	1:Aa:316:SER:CA	2.88	0.49
1:Ca:79:VAL:HG13	1:Ca:80:VAL:N	2.25	0.49
1:Bc:168:TRP:CE2	1:Ac:176:ARG:HD2	2.46	0.49
1:BB:163:THR:OG1	1:BB:165:THR:CG2	2.61	0.49
1:CB:77:TYR:CD1	1:CB:77:TYR:C	2.89	0.49
1:BC:166:LEU:HD13	1:BC:167:LEU:N	2.27	0.49
1:CC:163:THR:OG1	1:CC:165:THR:HG23	2.12	0.49
1:CD:190:ASN:N	1:CD:190:ASN:HD22	2.10	0.49
1:CE:100:GLN:HA	1:CE:213:GLU:OE2	2.12	0.49
1:BF:99:PHE:CD1	1:BF:99:PHE:N	2.80	0.49
1:CF:199:VAL:O	1:CF:199:VAL:CG1	2.61	0.49
1:BG:161:GLN:NE2	1:CG:210:PRO:HD2	2.28	0.49
1:AG:91:ARG:HH21	1:Bd:98:ILE:HG22	1.76	0.49
1:BH:168:TRP:CE2	1:AH:176:ARG:HD2	2.47	0.49
1:AI:118:ASN:O	1:Aa:116:PRO:HB3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:122:GLY:C	1:AI:188:VAL:HG22	2.37	0.49
1:BK:166:LEU:HD13	1:BK:167:LEU:N	2.27	0.49
1:BL:85:VAL:HG23	1:BL:86:PRO:HD2	1.94	0.49
1:AL:122:GLY:HA3	1:AU:114:MET:SD	2.52	0.49
1:AN:246:THR:N	1:AN:247:PRO:CD	2.75	0.49
1:AN:310:ASP:HB3	1:AN:312:VAL:HG22	1.93	0.49
1:AO:85:VAL:HG22	1:AO:86:PRO:HD2	1.92	0.49
1:BR:166:LEU:HD13	1:BR:167:LEU:N	2.27	0.49
1:AS:111:ILE:HG21	1:AS:123:TYR:CZ	2.48	0.49
1:BU:276:ARG:O	1:AU:276:ARG:NH2	2.45	0.49
1:AU:111:ILE:HG21	1:AU:123:TYR:CZ	2.47	0.49
1:CU:163:THR:OG1	1:CU:165:THR:HG23	2.11	0.49
1:CV:46:THR:HB	1:CZ:202:ARG:HH12	1.76	0.49
1:AW:305:ASN:OD1	1:AW:305:ASN:N	2.43	0.49
1:CX:237:ASP:HB3	1:CX:297:ARG:HG2	1.95	0.49
1:CY:99:PHE:HB3	1:CY:209:VAL:O	2.12	0.49
1:Aa:60:MET:HE2	1:Aa:200:LEU:HB3	1.94	0.49
1:Ca:288:ASN:OD1	1:Ca:288:ASN:N	2.45	0.49
1:AA:60:MET:HE2	1:AA:200:LEU:HB3	1.95	0.49
1:AC:142:GLN:NE2	1:AC:142:GLN:O	2.45	0.49
1:CD:81:ASP:HA	1:CD:184:ILE:HG22	1.94	0.49
1:CD:101:ARG:CZ	1:CD:166:LEU:CD1	2.91	0.49
1:BE:85:VAL:HG23	1:BE:86:PRO:HD2	1.93	0.49
1:BE:111:ILE:HG21	1:BE:123:TYR:OH	2.13	0.49
1:CG:34:ARG:HD3	1:CV:43:SER:O	2.12	0.49
1:CG:63:ILE:HD12	1:CG:88:LEU:CG	2.42	0.49
1:BH:166:LEU:HD13	1:BH:167:LEU:N	2.26	0.49
1:AI:109:PHE:HB2	1:AI:158:VAL:CG1	2.41	0.49
1:BJ:168:TRP:CE2	1:AJ:176:ARG:HD2	2.47	0.49
1:AL:110:GLU:HG2	1:AL:112:GLN:HG2	1.95	0.49
1:CL:80:VAL:HG22	1:CL:81:ASP:N	2.26	0.49
1:CM:98:ILE:HD11	1:CM:99:PHE:CE2	2.48	0.49
1:BN:123:TYR:HB2	1:BN:185:LEU:CD1	2.42	0.49
1:AN:91:ARG:NH2	1:BP:210:PRO:HB3	2.27	0.49
1:BP:161:GLN:NE2	1:CP:210:PRO:HD2	2.27	0.49
1:CR:85:VAL:HG13	1:CR:86:PRO:HD2	1.94	0.49
1:BS:163:THR:OG1	1:BS:165:THR:CG2	2.60	0.49
1:AS:253:ASP:OD1	1:AS:285:PHE:N	2.42	0.49
1:CS:288:ASN:OD1	1:CS:288:ASN:N	2.45	0.49
1:BW:166:LEU:HD13	1:BW:167:LEU:N	2.26	0.49
1:BX:99:PHE:N	1:BX:99:PHE:CD1	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:298:TRP:NE1	1:AZ:312:VAL:CB	2.75	0.49
1:Ba:161:GLN:NE2	1:Ca:210:PRO:HD2	2.26	0.49
1:Aa:162:TYR:CD1	1:Aa:162:TYR:N	2.79	0.49
1:Bb:163:THR:OG1	1:Bb:165:THR:CG2	2.59	0.49
1:Bc:165:THR:OG1	1:Bc:166:LEU:N	2.43	0.49
1:Ad:110:GLU:HG2	1:Ad:112:GLN:HG2	1.94	0.49
1:BA:254:GLY:CA	1:BA:283:LYS:HE3	2.28	0.49
1:AB:124:VAL:HG11	1:AB:138:PHE:HD1	1.77	0.49
1:BC:142:GLN:HB2	1:CC:48:PHE:CE1	2.48	0.49
1:AC:64:SER:OG	1:AC:80:VAL:HG21	2.13	0.49
1:CC:77:TYR:CD1	1:CC:77:TYR:C	2.89	0.49
1:AD:118:ASN:O	1:AW:116:PRO:HB3	2.12	0.49
1:CD:111:ILE:HD11	1:CD:125:ALA:CB	2.42	0.49
1:CD:163:THR:OG1	1:CD:165:THR:HG23	2.12	0.49
1:BF:98:ILE:CA	1:BF:211:SER:O	2.61	0.49
1:AF:298:TRP:NE1	1:AF:312:VAL:CB	2.76	0.49
1:CG:101:ARG:NH1	1:CG:166:LEU:CD1	2.74	0.49
1:BI:85:VAL:HG23	1:BI:86:PRO:HD2	1.93	0.49
1:AI:115:CYS:HB2	1:AI:116:PRO:HD2	1.94	0.49
1:CK:63:ILE:HD12	1:CK:88:LEU:CD1	2.42	0.49
1:CL:85:VAL:HG13	1:CL:86:PRO:HD2	1.93	0.49
1:BN:214:ASN:HD22	1:BN:215:PRO:HD2	1.76	0.49
1:AP:61:SER:HB2	1:AP:89:LEU:HD22	1.94	0.49
1:CP:133:ASP:O	1:CP:182:ARG:NH2	2.45	0.49
1:BQ:98:ILE:HG22	1:AZ:91:ARG:CZ	2.43	0.49
1:CQ:99:PHE:HB3	1:CQ:209:VAL:O	2.12	0.49
1:BR:123:TYR:HB2	1:BR:185:LEU:HD11	1.95	0.49
1:CS:101:ARG:CZ	1:CS:166:LEU:CD1	2.90	0.49
1:AT:302:ASP:CA	1:AT:305:ASN:ND2	2.76	0.49
1:BU:165:THR:OG1	1:BU:166:LEU:N	2.44	0.49
1:BV:168:TRP:CE2	1:AV:176:ARG:HD2	2.47	0.49
1:BW:142:GLN:HB2	1:CW:48:PHE:HE1	1.78	0.49
1:CW:81:ASP:C	1:CW:81:ASP:OD1	2.55	0.49
1:BZ:98:ILE:CA	1:BZ:211:SER:O	2.60	0.49
1:AZ:310:ASP:HB3	1:AZ:312:VAL:HG22	1.94	0.49
1:Ba:74:THR:HA	1:Ba:190:ASN:ND2	2.27	0.49
1:Ca:98:ILE:HD11	1:Ca:99:PHE:CE2	2.47	0.49
1:Ca:112:GLN:NE2	1:Ca:155:SER:OG	2.44	0.49
1:Cc:237:ASP:HB3	1:Cc:297:ARG:HG2	1.94	0.49
1:Cd:119:THR:O	1:Cd:120:GLY:C	2.55	0.49
1:CC:199:VAL:O	1:CC:199:VAL:CG1	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:74:THR:HA	1:BD:190:ASN:ND2	2.27	0.49
1:AD:122:GLY:C	1:AD:188:VAL:HG22	2.37	0.49
1:AD:314:TYR:CE1	1:AD:316:SER:HA	2.45	0.49
1:CD:69:PRO:O	1:CD:72:THR:OG1	2.25	0.49
1:CD:237:ASP:HB3	1:CD:297:ARG:HG2	1.93	0.49
1:BF:85:VAL:HG23	1:BF:86:PRO:HD2	1.94	0.49
1:BG:85:VAL:HG23	1:BG:86:PRO:HD2	1.94	0.49
1:CG:151:LYS:NZ	1:Bd:153:TRP:O	2.46	0.49
1:BH:74:THR:HA	1:BH:190:ASN:ND2	2.27	0.49
1:BI:214:ASN:HD22	1:BI:215:PRO:HD2	1.76	0.49
1:CN:80:VAL:CG1	1:CN:185:LEU:HB2	2.42	0.49
1:BO:85:VAL:HG23	1:BO:86:PRO:HD2	1.94	0.49
1:AO:110:GLU:HG2	1:AO:112:GLN:HG2	1.93	0.49
1:AO:279:TYR:CE2	1:AO:311:GLY:O	2.63	0.49
1:AQ:122:GLY:C	1:AQ:188:VAL:HG22	2.37	0.49
1:AR:314:TYR:CE1	1:AR:316:SER:HA	2.46	0.49
1:BT:80:VAL:CG1	1:BT:185:LEU:HB3	2.42	0.49
1:CT:85:VAL:HG13	1:CT:86:PRO:HD2	1.94	0.49
1:BV:98:ILE:CA	1:BV:211:SER:O	2.60	0.49
1:CV:101:ARG:CZ	1:CV:166:LEU:CD1	2.90	0.49
1:CV:288:ASN:OD1	1:CV:288:ASN:N	2.45	0.49
1:Bc:150:ALA:HB2	1:Bc:156:ARG:HD3	1.95	0.49
1:Bc:276:ARG:O	1:Ac:276:ARG:NH2	2.46	0.49
1:Ad:61:SER:HB2	1:Ad:89:LEU:HD22	1.93	0.49
1:Cd:80:VAL:HG11	1:Cd:185:LEU:HB2	1.93	0.49
1:BA:114:MET:HE1	1:CI:188:VAL:HG11	1.94	0.49
1:AA:302:ASP:CA	1:AA:305:ASN:ND2	2.76	0.49
1:AC:60:MET:HE2	1:AC:200:LEU:HB3	1.95	0.49
1:AC:314:TYR:CE1	1:AC:316:SER:HA	2.45	0.49
1:CF:163:THR:OG1	1:CF:165:THR:HG23	2.13	0.49
1:BG:124:VAL:HG11	1:BG:138:PHE:CD2	2.47	0.49
1:AG:111:ILE:HG21	1:AG:123:TYR:CZ	2.48	0.49
1:BI:111:ILE:HG21	1:BI:123:TYR:OH	2.13	0.49
1:AI:263:LEU:HB3	1:AI:279:TYR:O	2.12	0.49
1:CI:57:LEU:HD23	1:CI:203:TRP:CH2	2.47	0.49
1:CJ:77:TYR:C	1:CJ:77:TYR:CD1	2.91	0.49
1:CM:80:VAL:HG11	1:CM:185:LEU:HB2	1.94	0.49
1:AN:101:ARG:CZ	1:AN:166:LEU:HD23	2.42	0.49
1:BO:99:PHE:N	1:BO:99:PHE:CD1	2.79	0.49
1:CO:288:ASN:N	1:CO:288:ASN:OD1	2.45	0.49
1:AP:268:SER:HB3	1:AP:273:ASP:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:315:TYR:CE2	1:AP:317:ASP:OD2	2.66	0.49
1:BQ:99:PHE:CD1	1:BQ:99:PHE:N	2.80	0.49
1:CS:85:VAL:HG13	1:CS:86:PRO:HD2	1.94	0.49
1:BT:123:TYR:HB2	1:BT:185:LEU:HD11	1.95	0.49
1:BU:166:LEU:HD13	1:BU:167:LEU:N	2.27	0.49
1:BW:99:PHE:N	1:BW:99:PHE:CD1	2.80	0.49
1:BW:109:PHE:HB2	1:BW:158:VAL:CG1	2.42	0.49
1:AW:298:TRP:NE1	1:AW:312:VAL:CB	2.75	0.49
1:CX:57:LEU:HD23	1:CX:203:TRP:CH2	2.48	0.49
1:BZ:123:TYR:HB2	1:BZ:185:LEU:HD11	1.95	0.49
1:Ba:214:ASN:HD22	1:Ba:215:PRO:HD2	1.78	0.49
1:Ad:268:SER:HB3	1:Ad:273:ASP:O	2.12	0.49
1:CA:99:PHE:CB	1:CA:209:VAL:O	2.61	0.49
1:AC:122:GLY:HA3	1:AY:114:MET:SD	2.52	0.49
1:AC:124:VAL:HG11	1:AC:138:PHE:CD1	2.48	0.49
1:CD:77:TYR:C	1:CD:77:TYR:CD1	2.91	0.49
1:CF:190:ASN:HD22	1:CF:190:ASN:N	2.10	0.49
1:CJ:151:LYS:NZ	1:BR:153:TRP:O	2.46	0.49
1:BK:205:VAL:HG22	1:BK:206:ARG:N	2.28	0.49
1:CK:112:GLN:HE21	1:CL:44:THR:N	2.10	0.49
1:AN:122:GLY:C	1:AN:188:VAL:HG22	2.38	0.49
1:CN:288:ASN:OD1	1:CN:288:ASN:N	2.45	0.49
1:AO:80:VAL:HG13	1:AO:185:LEU:HB3	1.95	0.49
1:BP:165:THR:OG1	1:BP:166:LEU:N	2.44	0.49
1:AP:61:SER:CB	1:AP:90:PRO:HD2	2.37	0.49
1:CP:81:ASP:OD2	1:CP:136:HIS:NE2	2.45	0.49
1:BQ:74:THR:HA	1:BQ:190:ASN:ND2	2.28	0.49
1:CS:124:VAL:HG13	1:CS:124:VAL:O	2.12	0.49
1:BT:166:LEU:HD13	1:BT:167:LEU:N	2.28	0.49
1:AT:124:VAL:HG11	1:AT:138:PHE:CD1	2.48	0.49
1:AU:122:GLY:HA3	1:AX:114:MET:SD	2.52	0.49
1:AU:315:TYR:CE2	1:AU:317:ASP:OD2	2.66	0.49
1:AW:122:GLY:C	1:AW:188:VAL:HG22	2.38	0.49
1:AW:314:TYR:CD1	1:AW:314:TYR:C	2.91	0.49
1:AX:111:ILE:HG21	1:AX:123:TYR:CZ	2.48	0.49
1:AX:124:VAL:HG11	1:AX:138:PHE:CD1	2.48	0.49
1:BY:61:SER:CB	1:BY:90:PRO:HD2	2.28	0.49
1:CY:124:VAL:HG13	1:CY:124:VAL:O	2.12	0.49
1:CZ:81:ASP:C	1:CZ:81:ASP:OD1	2.54	0.49
1:Bc:161:GLN:NE2	1:Cc:210:PRO:HD2	2.27	0.49
1:Cc:288:ASN:N	1:Cc:288:ASN:OD1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bd:98:ILE:CA	1:Bd:211:SER:O	2.60	0.49
1:Cd:99:PHE:CB	1:Cd:209:VAL:O	2.61	0.49
1:AA:111:ILE:HG21	1:AA:123:TYR:CZ	2.47	0.49
1:AA:315:TYR:CE2	1:AA:317:ASP:OD2	2.66	0.49
1:CB:62:ARG:HA	1:CB:200:LEU:HD23	1.95	0.49
1:BC:142:GLN:HB2	1:CC:48:PHE:HE1	1.77	0.49
1:CC:200:LEU:HD13	1:CJ:45:VAL:HG23	1.94	0.49
1:BE:276:ARG:O	1:AE:276:ARG:NH2	2.45	0.49
1:AE:127:PHE:O	1:AE:144:THR:OG1	2.30	0.49
1:AE:279:TYR:CE2	1:AE:311:GLY:O	2.64	0.49
1:CG:77:TYR:C	1:CG:77:TYR:CD1	2.91	0.49
1:AH:110:GLU:HG2	1:AH:112:GLN:HG2	1.95	0.49
1:BI:150:ALA:HB2	1:BI:156:ARG:HD3	1.95	0.49
1:AJ:122:GLY:C	1:AJ:188:VAL:HG22	2.38	0.49
1:CJ:63:ILE:HD12	1:CJ:88:LEU:CD1	2.42	0.49
1:CJ:123:TYR:HA	1:CJ:188:VAL:HG23	1.95	0.49
1:CJ:288:ASN:N	1:CJ:288:ASN:OD1	2.45	0.49
1:CK:81:ASP:C	1:CK:81:ASP:OD1	2.56	0.49
1:CM:43:SER:HA	1:CO:112:GLN:NE2	2.28	0.49
1:CO:80:VAL:HG11	1:CO:185:LEU:HB2	1.94	0.49
1:CO:85:VAL:HG13	1:CO:86:PRO:HD2	1.95	0.49
1:AQ:315:TYR:CE2	1:AQ:317:ASP:OD2	2.66	0.49
1:CQ:100:GLN:HA	1:CQ:213:GLU:OE2	2.13	0.49
1:BR:142:GLN:HB2	1:CR:48:PHE:HE1	1.77	0.49
1:AR:61:SER:CB	1:AR:90:PRO:HD2	2.34	0.49
1:CT:99:PHE:HB3	1:CT:209:VAL:O	2.13	0.49
1:CT:237:ASP:HB3	1:CT:297:ARG:HG2	1.94	0.49
1:AU:101:ARG:CZ	1:AU:166:LEU:HD23	2.43	0.49
1:BW:276:ARG:O	1:AW:276:ARG:NH2	2.46	0.49
1:CW:99:PHE:CB	1:CW:209:VAL:O	2.60	0.49
1:BZ:80:VAL:CG1	1:BZ:185:LEU:HB3	2.43	0.49
1:Bc:80:VAL:CG1	1:Bc:185:LEU:HB3	2.43	0.49
1:Cd:237:ASP:HB3	1:Cd:297:ARG:HG2	1.94	0.49
1:AA:101:ARG:CZ	1:AA:166:LEU:HD23	2.42	0.49
1:CA:80:VAL:CG1	1:CA:185:LEU:HB2	2.40	0.49
1:AB:122:GLY:C	1:AB:188:VAL:HG22	2.38	0.49
1:AB:279:TYR:CE2	1:AB:311:GLY:O	2.62	0.49
1:BC:163:THR:C	1:BC:165:THR:HG22	2.38	0.49
1:BC:205:VAL:HG22	1:BC:206:ARG:N	2.28	0.49
1:AC:298:TRP:NE1	1:AC:312:VAL:HA	2.28	0.49
1:CC:112:GLN:NE2	1:CC:155:SER:OG	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:85:VAL:HG23	1:BD:86:PRO:HD2	1.95	0.49
1:BD:98:ILE:CA	1:BD:211:SER:O	2.61	0.49
1:AD:111:ILE:HG21	1:AD:123:TYR:CZ	2.48	0.49
1:AF:246:THR:N	1:AF:247:PRO:CD	2.75	0.49
1:CF:123:TYR:HA	1:CF:188:VAL:HG23	1.95	0.49
1:AG:118:ASN:O	1:AP:116:PRO:HB3	2.12	0.49
1:CH:124:VAL:HG13	1:CH:124:VAL:O	2.11	0.49
1:CH:288:ASN:OD1	1:CH:288:ASN:N	2.45	0.49
1:CK:133:ASP:O	1:CK:182:ARG:NH2	2.46	0.49
1:CL:98:ILE:HD11	1:CL:99:PHE:CE2	2.48	0.49
1:CN:190:ASN:HD22	1:CN:190:ASN:N	2.10	0.49
1:CO:34:ARG:CG	1:Bc:156:ARG:NH2	2.76	0.49
1:CO:63:ILE:HD12	1:CO:88:LEU:CG	2.41	0.49
1:BQ:116:PRO:CB	1:CZ:118:ASN:HA	2.43	0.49
1:AQ:188:VAL:CG2	1:AZ:114:MET:SD	3.01	0.49
1:CQ:81:ASP:C	1:CQ:81:ASP:OD1	2.55	0.49
1:CQ:81:ASP:OD2	1:CQ:136:HIS:NE2	2.45	0.49
1:AR:298:TRP:NE1	1:AR:312:VAL:CB	2.76	0.49
1:AT:91:ARG:CZ	1:Ba:98:ILE:HG22	2.42	0.49
1:AU:110:GLU:HG2	1:AU:112:GLN:HG2	1.95	0.49
1:BV:205:VAL:HG22	1:BV:206:ARG:N	2.27	0.49
1:CV:44:THR:H	1:CZ:112:GLN:HE21	1.59	0.49
1:BX:205:VAL:HG22	1:BX:206:ARG:N	2.28	0.49
1:AX:110:GLU:HG2	1:AX:112:GLN:HG2	1.94	0.49
1:AZ:101:ARG:CZ	1:AZ:166:LEU:HD23	2.42	0.49
1:CZ:81:ASP:HA	1:CZ:184:ILE:HG22	1.95	0.49
1:Aa:122:GLY:C	1:Aa:188:VAL:HG22	2.38	0.49
1:Aa:279:TYR:CE2	1:Aa:311:GLY:O	2.62	0.49
1:Ac:124:VAL:HG11	1:Ac:138:PHE:CD1	2.47	0.49
1:Bd:85:VAL:HG23	1:Bd:86:PRO:HD2	1.95	0.49
1:Cd:63:ILE:HD12	1:Cd:88:LEU:CG	2.42	0.49
1:CA:112:GLN:HE21	1:CG:44:THR:H	1.61	0.49
1:AC:302:ASP:CA	1:AC:305:ASN:ND2	2.76	0.49
1:BD:114:MET:HE1	1:CW:188:VAL:HG11	1.95	0.49
1:BE:98:ILE:CA	1:BE:211:SER:O	2.61	0.49
1:BE:150:ALA:HB2	1:BE:156:ARG:HD3	1.95	0.49
1:CE:99:PHE:CB	1:CE:209:VAL:O	2.61	0.49
1:BH:62:ARG:HB2	1:Cd:138:PHE:CE1	2.47	0.49
1:BH:276:ARG:O	1:AH:276:ARG:NH2	2.46	0.49
1:CJ:101:ARG:CZ	1:CJ:166:LEU:CD1	2.90	0.49
1:CK:124:VAL:HG13	1:CK:124:VAL:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:80:VAL:CG1	1:BL:185:LEU:HB3	2.43	0.49
1:AL:302:ASP:CA	1:AL:305:ASN:ND2	2.76	0.49
1:AP:314:TYR:CE1	1:AP:316:SER:CA	2.88	0.49
1:CQ:124:VAL:O	1:CQ:124:VAL:HG13	2.13	0.49
1:AR:101:ARG:CZ	1:AR:166:LEU:HD23	2.42	0.49
1:BS:85:VAL:HG23	1:BS:86:PRO:HD2	1.94	0.49
1:BS:163:THR:C	1:BS:165:THR:HG22	2.38	0.49
1:CU:101:ARG:CZ	1:CU:166:LEU:CD1	2.91	0.49
1:CV:99:PHE:CB	1:CV:209:VAL:O	2.61	0.49
1:CV:133:ASP:O	1:CV:182:ARG:NH2	2.46	0.49
1:Ca:130:ASP:OD2	1:Ca:176:ARG:NH2	2.46	0.49
1:Bb:168:TRP:CE2	1:Ab:176:ARG:HD2	2.48	0.49
1:Ac:63:ILE:CD1	1:Ac:89:LEU:HD21	2.43	0.49
1:AC:298:TRP:NE1	1:AC:312:VAL:CB	2.75	0.48
1:BD:214:ASN:HD22	1:BD:215:PRO:HD2	1.78	0.48
1:AD:60:MET:HE2	1:AD:200:LEU:HB3	1.94	0.48
1:BE:80:VAL:CG1	1:BE:185:LEU:HB3	2.42	0.48
1:BE:214:ASN:HD22	1:BE:215:PRO:HD2	1.78	0.48
1:AE:61:SER:HB2	1:AE:89:LEU:HD22	1.95	0.48
1:AE:246:THR:N	1:AE:247:PRO:CD	2.76	0.48
1:BG:150:ALA:HB2	1:BG:156:ARG:HD3	1.95	0.48
1:CH:101:ARG:CZ	1:CH:166:LEU:CD1	2.90	0.48
1:BI:123:TYR:HB2	1:BI:185:LEU:HD11	1.95	0.48
1:BJ:205:VAL:HG22	1:BJ:206:ARG:N	2.28	0.48
1:BK:74:THR:HA	1:BK:190:ASN:HD22	1.77	0.48
1:AK:162:TYR:N	1:AK:162:TYR:CD1	2.80	0.48
1:BL:260:ASP:HA	1:AL:261:ARG:NH2	2.28	0.48
1:AL:314:TYR:CD1	1:AL:314:TYR:C	2.91	0.48
1:BM:234:SER:HB3	1:BM:237:ASP:OD1	2.13	0.48
1:AN:91:ARG:HH21	1:BP:98:ILE:HG22	1.77	0.48
1:CN:124:VAL:HG13	1:CN:124:VAL:O	2.13	0.48
1:BP:98:ILE:CA	1:BP:211:SER:O	2.61	0.48
1:AR:302:ASP:CA	1:AR:305:ASN:ND2	2.75	0.48
1:CR:288:ASN:N	1:CR:288:ASN:OD1	2.46	0.48
1:CT:109:PHE:HB2	1:CT:158:VAL:HG12	1.94	0.48
1:CT:190:ASN:HD22	1:CT:190:ASN:N	2.11	0.48
1:CU:288:ASN:N	1:CU:288:ASN:OD1	2.45	0.48
1:AV:61:SER:HB2	1:AV:89:LEU:HD22	1.95	0.48
1:CV:100:GLN:HA	1:CV:213:GLU:OE2	2.12	0.48
1:CV:138:PHE:CD1	1:CV:138:PHE:C	2.92	0.48
1:BW:74:THR:HA	1:BW:190:ASN:HD22	1.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:168:TRP:CE2	1:AW:176:ARG:HD2	2.48	0.48
1:CW:288:ASN:N	1:CW:288:ASN:OD1	2.46	0.48
1:CX:288:ASN:N	1:CX:288:ASN:OD1	2.45	0.48
1:BY:166:LEU:HD13	1:BY:167:LEU:N	2.28	0.48
1:BY:168:TRP:CE2	1:AY:176:ARG:HD2	2.48	0.48
1:CZ:98:ILE:HD11	1:CZ:99:PHE:CE2	2.48	0.48
1:Ca:100:GLN:HA	1:Ca:213:GLU:OE2	2.12	0.48
1:Ab:110:GLU:HG2	1:Ab:112:GLN:HG2	1.95	0.48
1:Ac:246:THR:N	1:Ac:247:PRO:CD	2.75	0.48
1:Cc:85:VAL:O	1:Cc:86:PRO:C	2.55	0.48
1:Ad:314:TYR:CE1	1:Ad:316:SER:HA	2.45	0.48
1:Cd:81:ASP:C	1:Cd:81:ASP:OD1	2.55	0.48
1:AA:142:GLN:O	1:AA:142:GLN:NE2	2.46	0.48
1:CA:237:ASP:HB3	1:CA:297:ARG:HG2	1.94	0.48
1:CB:103:ALA:HB2	1:CB:166:LEU:HB3	1.95	0.48
1:BD:117:ALA:HB2	1:CW:117:ALA:HB1	1.95	0.48
1:CE:237:ASP:HB3	1:CE:297:ARG:HG2	1.94	0.48
1:CF:81:ASP:OD2	1:CF:136:HIS:NE2	2.44	0.48
1:AG:124:VAL:HG11	1:AG:138:PHE:HD1	1.77	0.48
1:AH:101:ARG:CZ	1:AH:166:LEU:HD23	2.43	0.48
1:AJ:116:PRO:HB3	1:AR:118:ASN:O	2.13	0.48
1:AK:60:MET:HE2	1:AK:200:LEU:HB3	1.95	0.48
1:CK:288:ASN:OD1	1:CK:288:ASN:N	2.46	0.48
1:AL:246:THR:N	1:AL:247:PRO:CD	2.75	0.48
1:AN:279:TYR:CE2	1:AN:311:GLY:O	2.63	0.48
1:AN:302:ASP:CA	1:AN:305:ASN:ND2	2.76	0.48
1:BO:168:TRP:CE2	1:AO:176:ARG:HD2	2.48	0.48
1:AO:91:ARG:CZ	1:BW:98:ILE:CG2	2.91	0.48
1:AP:162:TYR:N	1:AP:162:TYR:CD1	2.81	0.48
1:BQ:142:GLN:HB2	1:CQ:48:PHE:HE1	1.78	0.48
1:BS:276:ARG:O	1:AS:276:ARG:NH2	2.46	0.48
1:AU:124:VAL:HG11	1:AU:138:PHE:CD1	2.48	0.48
1:AU:246:THR:N	1:AU:247:PRO:CD	2.76	0.48
1:CU:44:THR:H	1:Cb:112:GLN:HE21	1.59	0.48
1:CV:237:ASP:HB3	1:CV:297:ARG:HG2	1.94	0.48
1:AW:110:GLU:HG2	1:AW:112:GLN:HG2	1.95	0.48
1:CX:81:ASP:OD2	1:CX:136:HIS:NE2	2.44	0.48
1:CX:109:PHE:HB2	1:CX:158:VAL:HG12	1.96	0.48
1:BY:98:ILE:CA	1:BY:211:SER:O	2.61	0.48
1:CY:138:PHE:CD1	1:CY:138:PHE:C	2.92	0.48
1:Bb:166:LEU:HD13	1:Bb:167:LEU:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ad:101:ARG:CZ	1:Ad:166:LEU:HD23	2.43	0.48
1:BA:150:ALA:HB2	1:BA:156:ARG:HD3	1.95	0.48
1:AA:124:VAL:HG11	1:AA:138:PHE:HD1	1.77	0.48
1:BB:98:ILE:CA	1:BB:211:SER:O	2.61	0.48
1:BB:276:ARG:O	1:AB:276:ARG:NH2	2.46	0.48
1:CF:43:SER:O	1:CI:34:ARG:HD3	2.12	0.48
1:CG:80:VAL:HG11	1:CG:185:LEU:HB2	1.95	0.48
1:BH:234:SER:HB3	1:BH:237:ASP:OD1	2.12	0.48
1:AI:302:ASP:CA	1:AI:305:ASN:ND2	2.76	0.48
1:CJ:99:PHE:HB3	1:CJ:209:VAL:O	2.13	0.48
1:BK:98:ILE:CG2	1:AS:91:ARG:CZ	2.92	0.48
1:CK:199:VAL:O	1:CK:199:VAL:CG1	2.61	0.48
1:BL:281:HIS:ND1	1:BL:301:TRP:HB3	2.28	0.48
1:BM:205:VAL:HG22	1:BM:206:ARG:N	2.28	0.48
1:CM:288:ASN:N	1:CM:288:ASN:OD1	2.46	0.48
1:CO:81:ASP:HA	1:CO:184:ILE:HG22	1.96	0.48
1:CO:101:ARG:CZ	1:CO:166:LEU:CD1	2.90	0.48
1:AP:115:CYS:HB2	1:AP:116:PRO:HD2	1.95	0.48
1:AP:124:VAL:HG11	1:AP:138:PHE:CD1	2.47	0.48
1:CP:77:TYR:CD1	1:CP:77:TYR:C	2.89	0.48
1:BQ:123:TYR:HB2	1:BQ:185:LEU:CD1	2.43	0.48
1:BQ:276:ARG:O	1:AQ:276:ARG:NH2	2.46	0.48
1:BR:276:ARG:O	1:AR:276:ARG:NH2	2.46	0.48
1:AU:162:TYR:N	1:AU:162:TYR:CD1	2.81	0.48
1:AV:60:MET:HE2	1:AV:200:LEU:HB3	1.95	0.48
1:BW:142:GLN:HB2	1:CW:48:PHE:CE1	2.48	0.48
1:CW:123:TYR:CD1	1:CW:185:LEU:HD21	2.49	0.48
1:BY:99:PHE:N	1:BY:99:PHE:CD1	2.81	0.48
1:Ba:276:ARG:O	1:Aa:276:ARG:NH2	2.46	0.48
1:Ca:81:ASP:HA	1:Ca:184:ILE:HG22	1.96	0.48
1:Bd:163:THR:OG1	1:Bd:165:THR:CG2	2.61	0.48
1:Ad:142:GLN:NE2	1:Ad:142:GLN:O	2.46	0.48
1:Ad:162:TYR:CD1	1:Ad:162:TYR:N	2.81	0.48
1:CD:85:VAL:O	1:CD:86:PRO:C	2.57	0.48
1:CD:99:PHE:CB	1:CD:209:VAL:O	2.61	0.48
1:AE:302:ASP:CA	1:AE:305:ASN:ND2	2.77	0.48
1:BF:80:VAL:CG1	1:BF:185:LEU:HB3	2.43	0.48
1:CF:109:PHE:HB2	1:CF:158:VAL:HG12	1.95	0.48
1:BG:123:TYR:HB2	1:BG:185:LEU:CD1	2.43	0.48
1:AG:246:THR:N	1:AG:247:PRO:CD	2.77	0.48
1:AG:302:ASP:CA	1:AG:305:ASN:ND2	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:161:GLN:NE2	1:CH:210:PRO:HD2	2.28	0.48
1:BH:163:THR:OG1	1:BH:165:THR:CG2	2.62	0.48
1:CH:81:ASP:HA	1:CH:184:ILE:HG22	1.95	0.48
1:BI:234:SER:HB3	1:BI:237:ASP:OD1	2.13	0.48
1:CI:122:GLY:O	1:CI:188:VAL:CB	2.62	0.48
1:CJ:130:ASP:OD2	1:CJ:176:ARG:NH2	2.47	0.48
1:AK:314:TYR:CD1	1:AK:314:TYR:C	2.91	0.48
1:CK:112:GLN:HE21	1:CL:44:THR:H	1.61	0.48
1:BL:111:ILE:HG21	1:BL:123:TYR:OH	2.13	0.48
1:AN:91:ARG:CZ	1:BP:98:ILE:CG2	2.91	0.48
1:AN:142:GLN:NE2	1:AN:142:GLN:O	2.46	0.48
1:CN:85:VAL:HG13	1:CN:86:PRO:HD2	1.95	0.48
1:BQ:150:ALA:HB2	1:BQ:156:ARG:HD3	1.96	0.48
1:AQ:110:GLU:HG2	1:AQ:112:GLN:HG2	1.95	0.48
1:AR:142:GLN:O	1:AR:142:GLN:NE2	2.46	0.48
1:AS:127:PHE:O	1:AS:144:THR:OG1	2.28	0.48
1:BT:98:ILE:HG22	1:AV:91:ARG:CZ	2.43	0.48
1:AT:110:GLU:HG2	1:AT:112:GLN:HG2	1.95	0.48
1:AT:315:TYR:CE2	1:AT:317:ASP:OD2	2.67	0.48
1:BW:325:LEU:HD22	1:BW:329:THR:HG21	1.95	0.48
1:CX:81:ASP:C	1:CX:81:ASP:OD1	2.56	0.48
1:AY:63:ILE:CD1	1:AY:89:LEU:HD21	2.42	0.48
1:CZ:100:GLN:HA	1:CZ:213:GLU:OE2	2.13	0.48
1:Bb:123:TYR:HB2	1:Bb:185:LEU:HD11	1.94	0.48
1:Cc:109:PHE:HB2	1:Cc:158:VAL:HG12	1.96	0.48
1:Bd:165:THR:OG1	1:Bd:166:LEU:N	2.44	0.48
1:Ad:124:VAL:HG11	1:Ad:138:PHE:CD1	2.48	0.48
1:BA:214:ASN:HD22	1:BA:215:PRO:HD2	1.78	0.48
1:BA:234:SER:HB3	1:BA:237:ASP:OD1	2.13	0.48
1:CA:190:ASN:N	1:CA:190:ASN:HD22	2.11	0.48
1:AC:314:TYR:CE1	1:AC:316:SER:CA	2.89	0.48
1:AD:288:ASN:O	1:AD:289:ALA:C	2.56	0.48
1:AD:314:TYR:CE1	1:AD:316:SER:CA	2.89	0.48
1:CF:288:ASN:OD1	1:CF:288:ASN:N	2.46	0.48
1:CG:98:ILE:HD11	1:CG:99:PHE:CE2	2.49	0.48
1:CG:237:ASP:HB3	1:CG:297:ARG:HG2	1.94	0.48
1:BH:91:ARG:NH1	1:Ad:98:ILE:CG2	2.76	0.48
1:CH:119:THR:O	1:CH:120:GLY:C	2.56	0.48
1:BI:276:ARG:O	1:AI:276:ARG:NH2	2.46	0.48
1:CI:100:GLN:HA	1:CI:213:GLU:OE2	2.13	0.48
1:CI:288:ASN:OD1	1:CI:288:ASN:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:122:GLY:C	1:AK:188:VAL:HG22	2.39	0.48
1:BL:205:VAL:HG22	1:BL:206:ARG:N	2.29	0.48
1:BL:214:ASN:HD22	1:BL:215:PRO:HD2	1.77	0.48
1:AL:268:SER:HB3	1:AL:273:ASP:O	2.13	0.48
1:BN:98:ILE:CA	1:BN:211:SER:O	2.62	0.48
1:BN:161:GLN:NE2	1:CN:210:PRO:HD2	2.28	0.48
1:AN:111:ILE:HG21	1:AN:123:TYR:CZ	2.48	0.48
1:CN:112:GLN:NE2	1:CN:155:SER:OG	2.47	0.48
1:BO:161:GLN:NE2	1:CO:210:PRO:HD2	2.28	0.48
1:BO:276:ARG:O	1:AO:276:ARG:NH2	2.47	0.48
1:AO:91:ARG:CZ	1:BW:98:ILE:HG22	2.43	0.48
1:AO:314:TYR:CE1	1:AO:316:SER:CA	2.86	0.48
1:AP:110:GLU:HG2	1:AP:112:GLN:HG2	1.96	0.48
1:AP:298:TRP:NE1	1:AP:312:VAL:CB	2.75	0.48
1:AP:302:ASP:CA	1:AP:305:ASN:ND2	2.76	0.48
1:CP:100:GLN:HA	1:CP:213:GLU:OE2	2.13	0.48
1:CP:163:THR:OG1	1:CP:165:THR:HG23	2.13	0.48
1:CP:200:LEU:HD13	1:CQ:45:VAL:HG23	1.96	0.48
1:AQ:64:SER:OG	1:AQ:80:VAL:HG21	2.13	0.48
1:AQ:142:GLN:NE2	1:AQ:142:GLN:O	2.46	0.48
1:CQ:98:ILE:HD11	1:CQ:99:PHE:CE2	2.48	0.48
1:CQ:130:ASP:OD2	1:CQ:176:ARG:NH2	2.47	0.48
1:CR:62:ARG:NH1	1:BT:75:ASP:OD2	2.40	0.48
1:CR:81:ASP:OD2	1:CR:136:HIS:NE2	2.43	0.48
1:CS:81:ASP:HA	1:CS:184:ILE:HG22	1.95	0.48
1:BT:260:ASP:HA	1:AT:261:ARG:NH2	2.29	0.48
1:BU:123:TYR:HB2	1:BU:185:LEU:HD11	1.94	0.48
1:AU:119:THR:HG23	1:AU:193:ASP:CB	2.42	0.48
1:AV:302:ASP:CA	1:AV:305:ASN:ND2	2.77	0.48
1:CV:223:MET:HE2	1:CV:328:GLY:HA2	1.96	0.48
1:BW:61:SER:CB	1:BW:90:PRO:HD2	2.28	0.48
1:AW:162:TYR:N	1:AW:162:TYR:CD1	2.82	0.48
1:AW:314:TYR:CE1	1:AW:316:SER:HA	2.46	0.48
1:BY:123:TYR:HB2	1:BY:185:LEU:CD1	2.43	0.48
1:AY:110:GLU:HG2	1:AY:112:GLN:HG2	1.95	0.48
1:CY:81:ASP:C	1:CY:81:ASP:OD1	2.57	0.48
1:Aa:111:ILE:HG21	1:Aa:123:TYR:CZ	2.48	0.48
1:Aa:315:TYR:CE2	1:Aa:317:ASP:OD2	2.66	0.48
1:Bb:232:SER:HB3	1:Bb:242:LEU:HD11	1.94	0.48
1:Ab:279:TYR:CE2	1:Ab:311:GLY:O	2.62	0.48
1:Cb:190:ASN:HD22	1:Cb:190:ASN:N	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ad:122:GLY:C	1:Ad:188:VAL:HG22	2.38	0.48
1:AA:314:TYR:CD1	1:AA:314:TYR:C	2.92	0.48
1:CA:103:ALA:HB2	1:CA:166:LEU:HB3	1.95	0.48
1:AB:110:GLU:HG2	1:AB:112:GLN:HG2	1.96	0.48
1:AC:85:VAL:HG22	1:AC:86:PRO:HD2	1.95	0.48
1:CC:46:THR:HB	1:CJ:202:ARG:HH12	1.78	0.48
1:CD:288:ASN:N	1:CD:288:ASN:OD1	2.46	0.48
1:AE:142:GLN:NE2	1:AE:142:GLN:O	2.46	0.48
1:AG:279:TYR:CE2	1:AG:311:GLY:O	2.63	0.48
1:AG:315:TYR:CE2	1:AG:317:ASP:OD2	2.66	0.48
1:BH:115:CYS:HB2	1:BH:116:PRO:HD2	1.94	0.48
1:BH:123:TYR:HB2	1:BH:185:LEU:HD11	1.96	0.48
1:AH:111:ILE:HG21	1:AH:123:TYR:CZ	2.49	0.48
1:AH:122:GLY:C	1:AH:188:VAL:HG22	2.39	0.48
1:AH:302:ASP:CA	1:AH:305:ASN:ND2	2.77	0.48
1:AI:63:ILE:CD1	1:AI:89:LEU:HD21	2.44	0.48
1:CI:109:PHE:HB2	1:CI:158:VAL:HG12	1.94	0.48
1:AJ:253:ASP:OD1	1:AJ:285:PHE:N	2.43	0.48
1:AL:101:ARG:CZ	1:AL:166:LEU:HD23	2.43	0.48
1:AM:122:GLY:C	1:AM:188:VAL:HG22	2.38	0.48
1:BN:166:LEU:HD13	1:BN:167:LEU:N	2.28	0.48
1:CN:103:ALA:HB2	1:CN:166:LEU:HB3	1.96	0.48
1:CN:237:ASP:HB3	1:CN:297:ARG:HG2	1.96	0.48
1:CO:121:GLY:C	1:CO:152:TRP:CD1	2.92	0.48
1:CP:288:ASN:N	1:CP:288:ASN:OD1	2.46	0.48
1:CQ:237:ASP:HB3	1:CQ:297:ARG:HG2	1.95	0.48
1:AR:315:TYR:CE2	1:AR:317:ASP:OD2	2.66	0.48
1:CR:63:ILE:HD12	1:CR:88:LEU:CD1	2.43	0.48
1:CR:78:VAL:O	1:CR:78:VAL:HG13	2.13	0.48
1:BS:161:GLN:NE2	1:CS:210:PRO:HD2	2.28	0.48
1:CT:80:VAL:HG11	1:CT:185:LEU:HB2	1.95	0.48
1:BU:150:ALA:HB2	1:BU:156:ARG:HD3	1.95	0.48
1:CU:123:TYR:HA	1:CU:188:VAL:HG23	1.95	0.48
1:BW:281:HIS:ND1	1:BW:301:TRP:HB3	2.27	0.48
1:BX:234:SER:HB3	1:BX:237:ASP:OD1	2.14	0.48
1:AX:85:VAL:HG22	1:AX:86:PRO:HD2	1.95	0.48
1:CY:103:ALA:HB2	1:CY:166:LEU:HB3	1.96	0.48
1:AZ:298:TRP:NE1	1:AZ:312:VAL:HA	2.28	0.48
1:CZ:101:ARG:CZ	1:CZ:166:LEU:CD1	2.92	0.48
1:Aa:302:ASP:CA	1:Aa:305:ASN:ND2	2.76	0.48
1:Bb:161:GLN:NE2	1:Cb:210:PRO:HD2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cb:288:ASN:OD1	1:Cb:288:ASN:N	2.45	0.48
1:Ac:279:TYR:CE2	1:Ac:311:GLY:O	2.63	0.48
1:Ad:246:THR:N	1:Ad:247:PRO:CD	2.76	0.48
1:Cd:123:TYR:HB2	1:Cd:185:LEU:HD21	1.96	0.48
1:BD:168:TRP:CE2	1:AD:176:ARG:HD2	2.48	0.48
1:CD:54:ASP:N	1:CD:54:ASP:OD1	2.46	0.48
1:BG:98:ILE:CA	1:BG:211:SER:O	2.61	0.48
1:CH:57:LEU:HD23	1:CH:203:TRP:CH2	2.49	0.48
1:CH:99:PHE:CB	1:CH:209:VAL:O	2.62	0.48
1:BI:225:GLN:HG3	1:BI:244:GLY:O	2.14	0.48
1:CJ:63:ILE:HD12	1:CJ:88:LEU:CG	2.42	0.48
1:CJ:99:PHE:CB	1:CJ:209:VAL:O	2.62	0.48
1:BK:80:VAL:CG1	1:BK:185:LEU:HB3	2.44	0.48
1:CK:112:GLN:NE2	1:CK:155:SER:OG	2.46	0.48
1:BL:168:TRP:CE2	1:AL:176:ARG:HD2	2.48	0.48
1:AM:302:ASP:CA	1:AM:305:ASN:ND2	2.77	0.48
1:BR:142:GLN:HB2	1:CR:48:PHE:CE1	2.48	0.48
1:CR:112:GLN:NE2	1:CR:155:SER:OG	2.47	0.48
1:CT:77:TYR:CD1	1:CT:77:TYR:C	2.90	0.48
1:AV:298:TRP:NE1	1:AV:312:VAL:HA	2.28	0.48
1:CV:109:PHE:HB2	1:CV:158:VAL:HG12	1.95	0.48
1:AW:60:MET:HE2	1:AW:200:LEU:HB3	1.95	0.48
1:AW:302:ASP:CA	1:AW:305:ASN:ND2	2.76	0.48
1:CW:99:PHE:HB3	1:CW:209:VAL:O	2.13	0.48
1:CY:100:GLN:HA	1:CY:213:GLU:OE2	2.14	0.48
1:BZ:85:VAL:HG23	1:BZ:86:PRO:HD2	1.96	0.48
1:AZ:110:GLU:HG2	1:AZ:112:GLN:HG2	1.95	0.48
1:CZ:79:VAL:HG13	1:CZ:80:VAL:HG12	1.94	0.48
1:Aa:80:VAL:HG13	1:Aa:185:LEU:HB3	1.95	0.48
1:Ca:80:VAL:HG11	1:Ca:185:LEU:HB2	1.95	0.48
1:Bb:250:ILE:O	1:Bb:250:ILE:HG22	2.14	0.48
1:Cc:99:PHE:HB3	1:Cc:209:VAL:O	2.13	0.48
1:Bd:168:TRP:CE2	1:Ad:176:ARG:HD2	2.49	0.48
1:BA:123:TYR:HB2	1:BA:185:LEU:HD11	1.96	0.48
1:CA:63:ILE:HD12	1:CA:88:LEU:CD1	2.44	0.48
1:CB:112:GLN:NE2	1:CF:43:SER:HA	2.28	0.48
1:CB:190:ASN:HD22	1:CB:190:ASN:N	2.11	0.48
1:CC:79:VAL:HG13	1:CC:80:VAL:HG12	1.96	0.48
1:CC:101:ARG:CZ	1:CC:166:LEU:CD1	2.91	0.48
1:BD:61:SER:CB	1:BD:90:PRO:HD2	2.29	0.48
1:BD:165:THR:OG1	1:BD:166:LEU:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:276:ARG:O	1:AD:276:ARG:NH2	2.46	0.48
1:BE:115:CYS:HB2	1:BE:116:PRO:HD2	1.94	0.48
1:AE:124:VAL:HG11	1:AE:138:PHE:HD1	1.79	0.48
1:BG:142:GLN:HB2	1:CG:48:PHE:HE1	1.79	0.48
1:AG:268:SER:CB	1:AG:273:ASP:O	2.62	0.48
1:BI:61:SER:CB	1:BI:90:PRO:HD2	2.26	0.48
1:CI:163:THR:OG1	1:CI:165:THR:HG23	2.14	0.48
1:BJ:184:ILE:HD13	1:BJ:184:ILE:N	2.28	0.48
1:CJ:80:VAL:CG1	1:CJ:185:LEU:HB2	2.42	0.48
1:CL:288:ASN:N	1:CL:288:ASN:OD1	2.46	0.48
1:AN:268:SER:CB	1:AN:273:ASP:O	2.61	0.48
1:AN:298:TRP:NE1	1:AN:312:VAL:CB	2.77	0.48
1:CO:39:VAL:HA	1:Cc:39:VAL:HG21	1.95	0.48
1:CO:100:GLN:HA	1:CO:213:GLU:OE2	2.13	0.48
1:CO:124:VAL:O	1:CO:124:VAL:HG13	2.13	0.48
1:CQ:80:VAL:HG11	1:CQ:185:LEU:HB2	1.96	0.48
1:BS:150:ALA:HB2	1:BS:156:ARG:HD3	1.96	0.48
1:CS:138:PHE:CD1	1:CS:138:PHE:C	2.91	0.48
1:AT:298:TRP:NE1	1:AT:312:VAL:CB	2.75	0.48
1:AT:310:ASP:HB3	1:AT:312:VAL:HG22	1.95	0.48
1:AU:302:ASP:CA	1:AU:305:ASN:ND2	2.76	0.48
1:BV:123:TYR:HB2	1:BV:185:LEU:CD1	2.44	0.48
1:CW:133:ASP:O	1:CW:182:ARG:NH2	2.46	0.48
1:CX:124:VAL:HG13	1:CX:124:VAL:O	2.13	0.48
1:BY:74:THR:HA	1:BY:190:ASN:ND2	2.28	0.48
1:CY:43:SER:HA	1:Ca:112:GLN:NE2	2.29	0.48
1:CY:85:VAL:HG13	1:CY:86:PRO:HD2	1.95	0.48
1:Ca:63:ILE:HD12	1:Ca:88:LEU:CG	2.41	0.48
1:Bc:98:ILE:CA	1:Bc:211:SER:O	2.62	0.48
1:AB:268:SER:CB	1:AB:273:ASP:O	2.62	0.48
1:AB:302:ASP:CA	1:AB:305:ASN:ND2	2.77	0.48
1:CB:85:VAL:O	1:CB:86:PRO:C	2.57	0.48
1:AC:122:GLY:C	1:AC:188:VAL:HG22	2.39	0.48
1:AC:298:TRP:HE1	1:AC:312:VAL:HA	1.79	0.48
1:CF:77:TYR:CD1	1:CF:77:TYR:C	2.91	0.48
1:BG:142:GLN:HB2	1:CG:48:PHE:CE1	2.49	0.48
1:BG:163:THR:OG1	1:BG:165:THR:CG2	2.61	0.48
1:CH:190:ASN:HD22	1:CH:190:ASN:N	2.11	0.48
1:AI:119:THR:HG23	1:AI:193:ASP:CB	2.42	0.48
1:AJ:64:SER:OG	1:AJ:80:VAL:HG21	2.14	0.48
1:AJ:91:ARG:CZ	1:BR:98:ILE:CG2	2.91	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:75:ASP:OD2	1:CL:62:ARG:NH1	2.42	0.48
1:AK:85:VAL:HG22	1:AK:86:PRO:HD2	1.95	0.48
1:BL:74:THR:HA	1:BL:190:ASN:HD22	1.77	0.48
1:BL:161:GLN:NE2	1:CL:210:PRO:HD2	2.29	0.48
1:CL:77:TYR:CD1	1:CL:77:TYR:C	2.89	0.48
1:CL:138:PHE:C	1:CL:138:PHE:CD1	2.92	0.48
1:BM:254:GLY:CA	1:BM:283:LYS:HE3	2.30	0.48
1:CN:81:ASP:HA	1:CN:184:ILE:HG22	1.94	0.48
1:BO:214:ASN:HD22	1:BO:215:PRO:HD2	1.78	0.48
1:AO:91:ARG:HH21	1:BW:98:ILE:HG22	1.79	0.48
1:BU:115:CYS:HB2	1:BU:116:PRO:HD2	1.94	0.48
1:BU:214:ASN:HD22	1:BU:215:PRO:HD2	1.79	0.48
1:CU:202:ARG:HH12	1:Cb:46:THR:HB	1.77	0.48
1:BV:276:ARG:O	1:AV:276:ARG:NH2	2.47	0.48
1:AV:315:TYR:CE2	1:AV:317:ASP:OD2	2.67	0.48
1:Ba:123:TYR:HB2	1:Ba:185:LEU:HD11	1.96	0.48
1:Ca:237:ASP:HB3	1:Ca:297:ARG:HG2	1.95	0.48
1:Bb:150:ALA:HB2	1:Bb:156:ARG:HD3	1.95	0.48
1:Bb:276:ARG:O	1:Ab:276:ARG:NH2	2.47	0.48
1:Cb:81:ASP:C	1:Cb:81:ASP:OD1	2.57	0.48
1:Cb:100:GLN:HA	1:Cb:213:GLU:OE2	2.13	0.48
1:Cd:79:VAL:HG13	1:Cd:80:VAL:HG12	1.95	0.48
1:AA:64:SER:OG	1:AA:80:VAL:HG21	2.13	0.48
1:CB:138:PHE:CD1	1:CB:138:PHE:C	2.91	0.48
1:AC:246:THR:N	1:AC:247:PRO:CD	2.77	0.48
1:AD:298:TRP:NE1	1:AD:312:VAL:CB	2.76	0.48
1:BE:165:THR:OG1	1:BE:166:LEU:N	2.46	0.48
1:BE:168:TRP:CE2	1:AE:176:ARG:HD2	2.48	0.48
1:AE:315:TYR:CE2	1:AE:317:ASP:OD2	2.67	0.48
1:CE:45:VAL:O	1:CE:45:VAL:HG13	2.14	0.48
1:BF:150:ALA:HB2	1:BF:156:ARG:HD3	1.95	0.48
1:AI:124:VAL:HG11	1:AI:138:PHE:HD1	1.78	0.48
1:CI:81:ASP:C	1:CI:81:ASP:OD1	2.57	0.48
1:BJ:124:VAL:HG11	1:BJ:138:PHE:CD2	2.48	0.48
1:BL:98:ILE:CG2	1:AU:91:ARG:NH2	2.77	0.48
1:BP:142:GLN:HB2	1:CP:48:PHE:CE1	2.49	0.48
1:CQ:112:GLN:NE2	1:CQ:155:SER:OG	2.47	0.48
1:CS:99:PHE:CB	1:CS:209:VAL:O	2.62	0.48
1:CS:237:ASP:HB3	1:CS:297:ARG:HG2	1.94	0.48
1:CT:78:VAL:HG13	1:CT:78:VAL:O	2.13	0.48
1:BU:74:THR:HA	1:BU:190:ASN:ND2	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:190:ASN:HD22	1:CU:190:ASN:N	2.12	0.48
1:CU:223:MET:HE2	1:CU:328:GLY:HA2	1.94	0.48
1:AW:61:SER:CB	1:AW:90:PRO:HD2	2.35	0.48
1:AW:268:SER:HB3	1:AW:273:ASP:O	2.13	0.48
1:AZ:268:SER:CB	1:AZ:273:ASP:O	2.62	0.48
1:AZ:302:ASP:CA	1:AZ:305:ASN:ND2	2.77	0.48
1:Ac:60:MET:HE2	1:Ac:200:LEU:HB3	1.96	0.48
1:Ac:85:VAL:HG22	1:Ac:86:PRO:HD2	1.96	0.48
1:CA:99:PHE:HB3	1:CA:209:VAL:O	2.14	0.47
1:CC:250:ILE:O	1:CC:250:ILE:HG22	2.13	0.47
1:BE:205:VAL:HG22	1:BE:206:ARG:N	2.29	0.47
1:AE:85:VAL:HG22	1:AE:86:PRO:HD2	1.95	0.47
1:BF:276:ARG:O	1:AF:276:ARG:NH2	2.47	0.47
1:BG:168:TRP:CE2	1:AG:176:ARG:HD2	2.48	0.47
1:CG:43:SER:O	1:CQ:34:ARG:HD3	2.14	0.47
1:AH:69:PRO:C	1:AH:72:THR:HG1	2.21	0.47
1:CI:77:TYR:CD1	1:CI:77:TYR:C	2.90	0.47
1:BJ:74:THR:HA	1:BJ:190:ASN:ND2	2.30	0.47
1:CJ:81:ASP:C	1:CJ:81:ASP:OD1	2.57	0.47
1:BK:260:ASP:HA	1:AK:261:ARG:NH2	2.29	0.47
1:BM:276:ARG:O	1:AM:276:ARG:NH2	2.47	0.47
1:CO:89:LEU:HD13	1:CO:203:TRP:CG	2.49	0.47
1:CO:112:GLN:NE2	1:CO:155:SER:OG	2.47	0.47
1:BP:74:THR:HA	1:BP:190:ASN:ND2	2.29	0.47
1:BP:163:THR:OG1	1:BP:165:THR:CG2	2.62	0.47
1:AP:127:PHE:O	1:AP:144:THR:OG1	2.30	0.47
1:BQ:80:VAL:CG1	1:BQ:185:LEU:HB3	2.43	0.47
1:AR:298:TRP:NE1	1:AR:312:VAL:HA	2.29	0.47
1:CR:79:VAL:HG13	1:CR:80:VAL:HG12	1.95	0.47
1:AS:302:ASP:CA	1:AS:305:ASN:ND2	2.77	0.47
1:AT:298:TRP:NE1	1:AT:312:VAL:HA	2.29	0.47
1:CV:85:VAL:HG13	1:CV:86:PRO:HD2	1.96	0.47
1:CV:190:ASN:HD22	1:CV:190:ASN:N	2.12	0.47
1:AY:302:ASP:CA	1:AY:305:ASN:ND2	2.76	0.47
1:AY:314:TYR:CE1	1:AY:316:SER:CA	2.89	0.47
1:CZ:99:PHE:CB	1:CZ:209:VAL:O	2.61	0.47
1:Aa:61:SER:HB2	1:Aa:89:LEU:HD22	1.94	0.47
1:Ab:63:ILE:CD1	1:Ab:89:LEU:HD21	2.44	0.47
1:Ab:315:TYR:CE2	1:Ab:317:ASP:OD2	2.66	0.47
1:Cb:77:TYR:CD1	1:Cb:77:TYR:C	2.92	0.47
1:Cb:99:PHE:HB3	1:Cb:209:VAL:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ac:61:SER:HB2	1:Ac:89:LEU:HD22	1.95	0.47
1:Ac:298:TRP:NE1	1:Ac:312:VAL:CB	2.76	0.47
1:Ac:302:ASP:CA	1:Ac:305:ASN:ND2	2.77	0.47
1:Cc:98:ILE:HD11	1:Cc:99:PHE:CE2	2.48	0.47
1:Cc:190:ASN:HD22	1:Cc:190:ASN:N	2.12	0.47
1:Bd:74:THR:HA	1:Bd:190:ASN:ND2	2.28	0.47
1:Bd:142:GLN:HB2	1:Cd:48:PHE:HE1	1.79	0.47
1:Cd:199:VAL:O	1:Cd:199:VAL:CG1	2.62	0.47
1:BA:91:ARG:NH1	1:AI:98:ILE:CG2	2.75	0.47
1:BB:166:LEU:HD13	1:BB:167:LEU:N	2.29	0.47
1:BB:225:GLN:HG3	1:BB:244:GLY:O	2.15	0.47
1:AB:61:SER:CB	1:AB:90:PRO:HD2	2.38	0.47
1:CC:99:PHE:CB	1:CC:209:VAL:O	2.62	0.47
1:BD:161:GLN:NE2	1:CD:210:PRO:HD2	2.29	0.47
1:BD:166:LEU:HD13	1:BD:167:LEU:N	2.29	0.47
1:AD:302:ASP:CA	1:AD:305:ASN:ND2	2.77	0.47
1:AD:315:TYR:CE2	1:AD:317:ASP:OD2	2.67	0.47
1:CE:138:PHE:CD1	1:CE:138:PHE:C	2.92	0.47
1:BF:123:TYR:HB2	1:BF:185:LEU:HD11	1.96	0.47
1:BF:156:ARG:NH2	1:CI:34:ARG:HG3	2.29	0.47
1:AF:64:SER:OG	1:AF:80:VAL:HG21	2.15	0.47
1:AF:302:ASP:CA	1:AF:305:ASN:ND2	2.77	0.47
1:BG:276:ARG:O	1:AG:276:ARG:NH2	2.47	0.47
1:CI:81:ASP:OD2	1:CI:136:HIS:NE2	2.45	0.47
1:BJ:276:ARG:O	1:AJ:276:ARG:NH2	2.47	0.47
1:AJ:302:ASP:CA	1:AJ:305:ASN:ND2	2.77	0.47
1:AJ:314:TYR:CD1	1:AJ:314:TYR:C	2.91	0.47
1:CK:121:GLY:C	1:CK:152:TRP:CD1	2.91	0.47
1:CM:100:GLN:HA	1:CM:213:GLU:OE2	2.13	0.47
1:CN:109:PHE:HB2	1:CN:158:VAL:HG12	1.96	0.47
1:CO:98:ILE:HD11	1:CO:99:PHE:CE2	2.49	0.47
1:BP:234:SER:HB3	1:BP:237:ASP:OD1	2.14	0.47
1:AP:119:THR:HG23	1:AP:193:ASP:CB	2.41	0.47
1:BQ:225:GLN:HG3	1:BQ:244:GLY:O	2.13	0.47
1:CQ:123:TYR:HB2	1:CQ:185:LEU:HD21	1.95	0.47
1:CS:54:ASP:OD1	1:CS:54:ASP:N	2.47	0.47
1:AT:64:SER:OG	1:AT:80:VAL:HG21	2.14	0.47
1:AT:69:PRO:C	1:AT:72:THR:HG1	2.21	0.47
1:CU:138:PHE:CD1	1:CU:138:PHE:C	2.92	0.47
1:CW:54:ASP:N	1:CW:54:ASP:OD1	2.46	0.47
1:CW:100:GLN:HA	1:CW:213:GLU:OE2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ca:77:TYR:CD1	1:Ca:77:TYR:C	2.92	0.47
1:Cc:138:PHE:CD1	1:Cc:138:PHE:C	2.91	0.47
1:Bd:123:TYR:HB2	1:Bd:185:LEU:CD1	2.44	0.47
1:CA:43:SER:HA	1:CG:112:GLN:NE2	2.28	0.47
1:AB:315:TYR:CE2	1:AB:317:ASP:OD2	2.66	0.47
1:AD:314:TYR:CD1	1:AD:314:TYR:C	2.92	0.47
1:CD:158:VAL:O	1:CD:158:VAL:HG13	2.13	0.47
1:CE:99:PHE:HB3	1:CE:209:VAL:O	2.14	0.47
1:CF:62:ARG:HA	1:CF:200:LEU:HD23	1.96	0.47
1:CF:85:VAL:HG13	1:CF:86:PRO:HD2	1.97	0.47
1:BG:80:VAL:CG1	1:BG:185:LEU:HB3	2.44	0.47
1:AH:116:PRO:HB3	1:AN:118:ASN:O	2.14	0.47
1:AJ:80:VAL:HG13	1:AJ:185:LEU:HB3	1.96	0.47
1:BK:234:SER:HB3	1:BK:237:ASP:OD1	2.14	0.47
1:BL:142:GLN:HB2	1:CL:48:PHE:CE1	2.50	0.47
1:CL:80:VAL:HG11	1:CL:185:LEU:HB2	1.95	0.47
1:BM:161:GLN:NE2	1:CM:210:PRO:HD2	2.29	0.47
1:AM:268:SER:CB	1:AM:273:ASP:O	2.62	0.47
1:BO:142:GLN:HB2	1:CO:48:PHE:HE1	1.80	0.47
1:AP:224:THR:HG22	1:AP:329:THR:N	2.30	0.47
1:CP:79:VAL:HG13	1:CP:80:VAL:HG12	1.97	0.47
1:CQ:81:ASP:HA	1:CQ:184:ILE:HG22	1.96	0.47
1:CR:77:TYR:C	1:CR:77:TYR:CD1	2.90	0.47
1:BT:74:THR:HA	1:BT:190:ASN:HD22	1.79	0.47
1:AT:91:ARG:NH2	1:Ba:98:ILE:HG22	2.29	0.47
1:AT:268:SER:CB	1:AT:273:ASP:O	2.62	0.47
1:AT:314:TYR:CD1	1:AT:314:TYR:C	2.93	0.47
1:CT:112:GLN:NE2	1:CT:155:SER:OG	2.48	0.47
1:AU:85:VAL:HG22	1:AU:86:PRO:HD2	1.95	0.47
1:CU:158:VAL:HG13	1:CU:158:VAL:O	2.15	0.47
1:AV:64:SER:OG	1:AV:80:VAL:HG21	2.14	0.47
1:AV:314:TYR:CD1	1:AV:314:TYR:C	2.92	0.47
1:CW:58:SER:HB3	1:CW:204:SER:HB2	1.96	0.47
1:Bb:61:SER:CB	1:Bb:90:PRO:HD2	2.28	0.47
1:Ab:302:ASP:CA	1:Ab:305:ASN:ND2	2.78	0.47
1:Ad:64:SER:OG	1:Ad:80:VAL:HG21	2.14	0.47
1:Ad:314:TYR:CE1	1:Ad:316:SER:CA	2.91	0.47
1:BA:98:ILE:HG23	1:AI:91:ARG:HG2	1.97	0.47
1:AC:268:SER:CB	1:AC:273:ASP:O	2.62	0.47
1:AC:314:TYR:CD1	1:AC:314:TYR:C	2.93	0.47
1:CC:123:TYR:HA	1:CC:188:VAL:HG23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:98:ILE:HG22	1:AW:91:ARG:CZ	2.43	0.47
1:CD:85:VAL:HG13	1:CD:86:PRO:HD2	1.95	0.47
1:AE:314:TYR:CD1	1:AE:314:TYR:C	2.93	0.47
1:AF:122:GLY:C	1:AF:188:VAL:HG22	2.40	0.47
1:CG:81:ASP:C	1:CG:81:ASP:OD1	2.58	0.47
1:CG:99:PHE:CB	1:CG:209:VAL:O	2.63	0.47
1:CG:112:GLN:NE2	1:CG:155:SER:OG	2.47	0.47
1:BI:124:VAL:HG11	1:BI:138:PHE:CD2	2.49	0.47
1:BK:99:PHE:N	1:BK:99:PHE:CD1	2.81	0.47
1:AL:122:GLY:C	1:AL:188:VAL:HG22	2.39	0.47
1:CL:81:ASP:C	1:CL:81:ASP:OD1	2.58	0.47
1:CM:81:ASP:C	1:CM:81:ASP:OD1	2.57	0.47
1:AN:302:ASP:C	1:AN:305:ASN:HD21	2.23	0.47
1:CN:99:PHE:CB	1:CN:209:VAL:O	2.61	0.47
1:CN:99:PHE:HB3	1:CN:209:VAL:O	2.14	0.47
1:BO:74:THR:HA	1:BO:190:ASN:ND2	2.29	0.47
1:CO:63:ILE:HD12	1:CO:88:LEU:CD1	2.44	0.47
1:AP:298:TRP:NE1	1:AP:312:VAL:HA	2.30	0.47
1:CP:99:PHE:CB	1:CP:209:VAL:O	2.62	0.47
1:AQ:302:ASP:CA	1:AQ:305:ASN:ND2	2.77	0.47
1:CR:81:ASP:C	1:CR:81:ASP:OD1	2.58	0.47
1:BS:115:CYS:HB2	1:BS:116:PRO:HD2	1.96	0.47
1:CT:63:ILE:HD12	1:CT:88:LEU:CD1	2.44	0.47
1:CT:199:VAL:O	1:CT:199:VAL:CG1	2.62	0.47
1:BU:98:ILE:CA	1:BU:211:SER:O	2.61	0.47
1:BU:210:PRO:HB3	1:AX:91:ARG:NH2	2.29	0.47
1:BV:75:ASP:OD2	1:CZ:62:ARG:NH1	2.42	0.47
1:BV:123:TYR:HB2	1:BV:185:LEU:HD11	1.96	0.47
1:BV:150:ALA:HB2	1:BV:156:ARG:HD3	1.96	0.47
1:CW:62:ARG:NH1	1:Bd:75:ASP:OD2	2.43	0.47
1:CW:77:TYR:CD1	1:CW:77:TYR:C	2.91	0.47
1:BX:276:ARG:O	1:AX:276:ARG:NH2	2.47	0.47
1:CX:81:ASP:HA	1:CX:184:ILE:HG22	1.96	0.47
1:CX:123:TYR:HB2	1:CX:185:LEU:HD21	1.95	0.47
1:CY:109:PHE:HB2	1:CY:158:VAL:HG12	1.96	0.47
1:BZ:161:GLN:NE2	1:CZ:210:PRO:HD2	2.29	0.47
1:Cb:81:ASP:HA	1:Cb:184:ILE:HG22	1.97	0.47
1:Ac:268:SER:CB	1:Ac:273:ASP:O	2.62	0.47
1:Bd:166:LEU:HD13	1:Bd:167:LEU:N	2.29	0.47
1:AA:91:ARG:CZ	1:BV:98:ILE:HG22	2.44	0.47
1:CA:122:GLY:O	1:CA:188:VAL:CB	2.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:112:GLN:NE2	1:CB:155:SER:OG	2.48	0.47
1:AE:110:GLU:HG2	1:AE:112:GLN:HG2	1.96	0.47
1:CE:77:TYR:CD1	1:CE:77:TYR:C	2.90	0.47
1:AF:314:TYR:CD1	1:AF:314:TYR:C	2.92	0.47
1:CF:34:ARG:HG3	1:BY:156:ARG:NH2	2.29	0.47
1:CG:199:VAL:O	1:CG:199:VAL:CG1	2.60	0.47
1:CH:77:TYR:CD1	1:CH:77:TYR:C	2.93	0.47
1:BI:123:TYR:HB2	1:BI:185:LEU:CD1	2.44	0.47
1:BI:161:GLN:NE2	1:CI:210:PRO:HD2	2.29	0.47
1:CJ:124:VAL:HG13	1:CJ:124:VAL:O	2.13	0.47
1:CL:99:PHE:CB	1:CL:209:VAL:O	2.62	0.47
1:BN:234:SER:HB3	1:BN:237:ASP:OD1	2.15	0.47
1:CN:138:PHE:CD1	1:CN:138:PHE:C	2.93	0.47
1:BO:166:LEU:HD13	1:BO:167:LEU:N	2.29	0.47
1:BO:254:GLY:CA	1:BO:283:LYS:HE3	2.30	0.47
1:AO:246:THR:N	1:AO:247:PRO:CD	2.77	0.47
1:AP:111:ILE:HG21	1:AP:123:TYR:CZ	2.50	0.47
1:CP:250:ILE:HG22	1:CP:250:ILE:O	2.13	0.47
1:BR:225:GLN:HG3	1:BR:244:GLY:O	2.14	0.47
1:AU:61:SER:CB	1:AU:90:PRO:HD2	2.33	0.47
1:CU:109:PHE:HB2	1:CU:158:VAL:HG12	1.96	0.47
1:AV:124:VAL:HG11	1:AV:138:PHE:HD1	1.79	0.47
1:BY:85:VAL:HG23	1:BY:86:PRO:HD2	1.96	0.47
1:CY:63:ILE:HD12	1:CY:88:LEU:CG	2.43	0.47
1:BZ:168:TRP:CE2	1:AZ:176:ARG:HD2	2.50	0.47
1:CZ:63:ILE:HD12	1:CZ:88:LEU:CG	2.43	0.47
1:Cc:124:VAL:HG13	1:Cc:124:VAL:O	2.14	0.47
1:Ad:224:THR:HG22	1:Ad:329:THR:N	2.30	0.47
1:BB:74:THR:HA	1:BB:190:ASN:ND2	2.30	0.47
1:BB:214:ASN:HD22	1:BB:215:PRO:HD2	1.79	0.47
1:AB:91:ARG:NH2	1:BY:98:ILE:HG22	2.29	0.47
1:AB:98:ILE:CG2	1:BY:91:ARG:NH1	2.77	0.47
1:CC:288:ASN:OD1	1:CC:288:ASN:N	2.48	0.47
1:CF:101:ARG:CZ	1:CF:166:LEU:CD1	2.92	0.47
1:BG:98:ILE:HG23	1:AP:91:ARG:HG2	1.97	0.47
1:BG:234:SER:HB3	1:BG:237:ASP:OD1	2.15	0.47
1:CH:81:ASP:C	1:CH:81:ASP:OD1	2.57	0.47
1:CI:89:LEU:HD13	1:CI:203:TRP:CG	2.49	0.47
1:BJ:98:ILE:CA	1:BJ:211:SER:O	2.63	0.47
1:BK:85:VAL:HG23	1:BK:86:PRO:HD2	1.96	0.47
1:AK:64:SER:OG	1:AK:80:VAL:HG21	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:123:TYR:HB2	1:CL:185:LEU:HD21	1.97	0.47
1:CM:46:THR:HB	1:CO:202:ARG:HH12	1.80	0.47
1:AN:314:TYR:CD1	1:AN:314:TYR:C	2.93	0.47
1:AN:315:TYR:CE2	1:AN:317:ASP:OD2	2.68	0.47
1:CN:98:ILE:HD11	1:CN:99:PHE:CE2	2.50	0.47
1:BO:260:ASP:HA	1:AO:261:ARG:NH2	2.30	0.47
1:CP:123:TYR:HB2	1:CP:185:LEU:HD21	1.96	0.47
1:CP:124:VAL:HG13	1:CP:124:VAL:O	2.14	0.47
1:CQ:77:TYR:CD1	1:CQ:77:TYR:C	2.92	0.47
1:CR:63:ILE:HD12	1:CR:88:LEU:CG	2.42	0.47
1:AS:314:TYR:CD1	1:AS:314:TYR:C	2.92	0.47
1:CS:80:VAL:HG11	1:CS:185:LEU:HB2	1.95	0.47
1:BT:276:ARG:O	1:AT:276:ARG:NH2	2.47	0.47
1:CT:57:LEU:HD23	1:CT:203:TRP:CH2	2.49	0.47
1:BU:136:HIS:O	1:BU:186:LEU:HD11	2.14	0.47
1:AV:298:TRP:NE1	1:AV:312:VAL:CB	2.75	0.47
1:AX:302:ASP:CA	1:AX:305:ASN:ND2	2.77	0.47
1:AY:60:MET:HE2	1:AY:200:LEU:HB3	1.97	0.47
1:AY:100:GLN:HA	1:AY:169:THR:OG1	2.15	0.47
1:AY:279:TYR:CE2	1:AY:311:GLY:O	2.66	0.47
1:CY:123:TYR:HA	1:CY:188:VAL:HG23	1.97	0.47
1:AZ:111:ILE:HG21	1:AZ:123:TYR:CZ	2.50	0.47
1:AZ:253:ASP:CG	1:AZ:285:PHE:CA	2.78	0.47
1:CZ:223:MET:HE2	1:CZ:328:GLY:HA2	1.96	0.47
1:Ba:74:THR:HA	1:Ba:190:ASN:HD22	1.79	0.47
1:Ba:98:ILE:CA	1:Ba:211:SER:O	2.62	0.47
1:Cb:99:PHE:CB	1:Cb:209:VAL:O	2.62	0.47
1:Bc:74:THR:HA	1:Bc:190:ASN:ND2	2.30	0.47
1:Cc:79:VAL:HG13	1:Cc:80:VAL:HG12	1.97	0.47
1:CA:288:ASN:N	1:CA:288:ASN:OD1	2.47	0.47
1:AB:298:TRP:NE1	1:AB:312:VAL:CB	2.77	0.47
1:CB:99:PHE:CB	1:CB:209:VAL:O	2.62	0.47
1:CB:124:VAL:HG13	1:CB:124:VAL:O	2.15	0.47
1:CB:199:VAL:O	1:CB:199:VAL:CG1	2.62	0.47
1:CB:288:ASN:N	1:CB:288:ASN:OD1	2.46	0.47
1:BC:91:ARG:NH1	1:AY:98:ILE:CG2	2.76	0.47
1:BC:98:ILE:CA	1:BC:211:SER:O	2.63	0.47
1:AC:98:ILE:CG2	1:BS:91:ARG:NH1	2.75	0.47
1:AD:124:VAL:HG11	1:AD:138:PHE:CD1	2.50	0.47
1:BE:123:TYR:HB2	1:BE:185:LEU:CD1	2.44	0.47
1:CE:63:ILE:HD12	1:CE:88:LEU:CG	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:81:ASP:C	1:CE:81:ASP:OD1	2.57	0.47
1:AF:85:VAL:HG22	1:AF:86:PRO:HD2	1.96	0.47
1:BG:61:SER:CB	1:BG:90:PRO:HD2	2.26	0.47
1:CG:138:PHE:CD1	1:CG:138:PHE:C	2.92	0.47
1:BH:124:VAL:HG11	1:BH:138:PHE:CD2	2.49	0.47
1:AI:85:VAL:HG22	1:AI:86:PRO:HD2	1.97	0.47
1:AI:314:TYR:CD1	1:AI:314:TYR:C	2.92	0.47
1:AI:315:TYR:CE2	1:AI:317:ASP:OD2	2.68	0.47
1:CI:63:ILE:HD12	1:CI:88:LEU:CD1	2.45	0.47
1:CJ:78:VAL:O	1:CJ:78:VAL:HG13	2.14	0.47
1:CJ:119:THR:O	1:CJ:120:GLY:C	2.56	0.47
1:BL:61:SER:CB	1:BL:90:PRO:HD2	2.28	0.47
1:AL:124:VAL:HG11	1:AL:138:PHE:HD1	1.79	0.47
1:CL:119:THR:O	1:CL:120:GLY:C	2.57	0.47
1:CL:121:GLY:C	1:CL:152:TRP:CD1	2.93	0.47
1:BM:142:GLN:HB2	1:CM:48:PHE:CE1	2.50	0.47
1:BM:142:GLN:HB2	1:CM:48:PHE:HE1	1.79	0.47
1:CN:80:VAL:HG11	1:CN:185:LEU:HB2	1.97	0.47
1:BO:232:SER:HB3	1:BO:242:LEU:HD11	1.97	0.47
1:AO:122:GLY:C	1:AO:188:VAL:HG22	2.40	0.47
1:CO:119:THR:O	1:CO:120:GLY:C	2.57	0.47
1:CO:237:ASP:HB3	1:CO:297:ARG:HG2	1.95	0.47
1:BP:254:GLY:CA	1:BP:283:LYS:HE3	2.30	0.47
1:AP:85:VAL:HG22	1:AP:86:PRO:HD2	1.96	0.47
1:BQ:161:GLN:NE2	1:CQ:210:PRO:HD2	2.29	0.47
1:AQ:63:ILE:CD1	1:AQ:89:LEU:HD21	2.45	0.47
1:CR:117:ALA:CB	1:CT:38:PRO:O	2.63	0.47
1:BS:214:ASN:HD22	1:BS:215:PRO:HD2	1.79	0.47
1:AS:246:THR:N	1:AS:247:PRO:CD	2.77	0.47
1:CT:133:ASP:O	1:CT:182:ARG:NH2	2.48	0.47
1:BU:124:VAL:HG11	1:BU:138:PHE:CD2	2.50	0.47
1:BU:161:GLN:NE2	1:CU:210:PRO:HD2	2.29	0.47
1:BU:168:TRP:CE2	1:AU:176:ARG:HD2	2.50	0.47
1:AU:268:SER:CB	1:AU:273:ASP:O	2.63	0.47
1:BW:205:VAL:HG22	1:BW:206:ARG:N	2.30	0.47
1:AW:124:VAL:HG11	1:AW:138:PHE:CD1	2.48	0.47
1:AW:315:TYR:CE2	1:AW:317:ASP:OD2	2.67	0.47
1:BX:98:ILE:CA	1:BX:211:SER:O	2.63	0.47
1:BX:161:GLN:NE2	1:CX:210:PRO:HD2	2.29	0.47
1:CX:79:VAL:HG13	1:CX:80:VAL:HG12	1.96	0.47
1:CY:202:ARG:HH12	1:Ca:46:THR:HB	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:276:ARG:O	1:AZ:276:ARG:NH2	2.48	0.47
1:AZ:315:TYR:CE2	1:AZ:317:ASP:OD2	2.67	0.47
1:CZ:99:PHE:HB3	1:CZ:209:VAL:O	2.15	0.47
1:Ba:165:THR:OG1	1:Ba:166:LEU:N	2.48	0.47
1:Ba:168:TRP:CE2	1:Aa:176:ARG:HD2	2.50	0.47
1:Ca:57:LEU:HD23	1:Ca:203:TRP:CH2	2.50	0.47
1:Ca:138:PHE:CD1	1:Ca:138:PHE:C	2.92	0.47
1:Ab:122:GLY:C	1:Ab:188:VAL:HG22	2.38	0.47
1:Cb:57:LEU:HD23	1:Cb:203:TRP:CH2	2.49	0.47
1:Ac:122:GLY:C	1:Ac:188:VAL:HG22	2.40	0.47
1:BA:163:THR:C	1:BA:165:THR:HG22	2.39	0.47
1:CA:119:THR:O	1:CA:120:GLY:C	2.58	0.47
1:AB:91:ARG:CZ	1:BY:98:ILE:HG22	2.45	0.47
1:CB:101:ARG:CZ	1:CB:166:LEU:CD1	2.92	0.47
1:CB:121:GLY:C	1:CB:152:TRP:CD1	2.92	0.47
1:AD:85:VAL:HG22	1:AD:86:PRO:HD2	1.96	0.47
1:AE:253:ASP:CG	1:AE:285:PHE:CA	2.78	0.47
1:BF:142:GLN:HB2	1:CF:48:PHE:HE1	1.79	0.47
1:BF:166:LEU:HD13	1:BF:167:LEU:N	2.30	0.47
1:AF:268:SER:CB	1:AF:273:ASP:O	2.63	0.47
1:AH:127:PHE:O	1:AH:144:THR:OG1	2.28	0.47
1:AI:61:SER:HB2	1:AI:89:LEU:HD22	1.97	0.47
1:AJ:110:GLU:HG2	1:AJ:112:GLN:HG2	1.97	0.47
1:CJ:54:ASP:N	1:CJ:54:ASP:OD1	2.46	0.47
1:BK:98:ILE:HG22	1:AS:91:ARG:HH21	1.79	0.47
1:BK:98:ILE:CA	1:BK:211:SER:O	2.62	0.47
1:BK:168:TRP:CE2	1:AK:176:ARG:HD2	2.49	0.47
1:CM:63:ILE:HD12	1:CM:88:LEU:CG	2.44	0.47
1:CM:99:PHE:CD2	1:CM:207:LEU:HB3	2.50	0.47
1:AN:314:TYR:CE1	1:AN:316:SER:CA	2.87	0.47
1:AO:111:ILE:HG21	1:AO:123:TYR:CZ	2.49	0.47
1:AO:114:MET:SD	1:AW:122:GLY:HA3	2.55	0.47
1:AO:268:SER:CB	1:AO:273:ASP:O	2.63	0.47
1:AP:314:TYR:CD1	1:AP:314:TYR:C	2.92	0.47
1:CP:98:ILE:HD11	1:CP:99:PHE:CE2	2.49	0.47
1:CR:99:PHE:CB	1:CR:209:VAL:O	2.63	0.47
1:AS:268:SER:CB	1:AS:273:ASP:O	2.63	0.47
1:CS:100:GLN:HA	1:CS:213:GLU:OE2	2.14	0.47
1:CU:112:GLN:NE2	1:CU:155:SER:OG	2.48	0.47
1:BW:123:TYR:HB2	1:BW:185:LEU:CD1	2.44	0.47
1:CY:62:ARG:HA	1:CY:200:LEU:HD23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:314:TYR:CE1	1:AZ:316:SER:CA	2.89	0.47
1:Aa:268:SER:CB	1:Aa:273:ASP:O	2.63	0.47
1:Aa:314:TYR:CD1	1:Aa:314:TYR:C	2.93	0.47
1:Cb:81:ASP:OD2	1:Cb:136:HIS:NE2	2.43	0.47
1:Bc:124:VAL:HG11	1:Bc:138:PHE:CD2	2.50	0.47
1:Ac:80:VAL:HG13	1:Ac:185:LEU:HB3	1.97	0.47
1:AA:263:LEU:HB3	1:AA:279:TYR:O	2.14	0.47
1:BB:123:TYR:HB2	1:BB:185:LEU:HD11	1.97	0.47
1:BB:250:ILE:O	1:BB:250:ILE:HG22	2.15	0.47
1:CB:123:TYR:HA	1:CB:188:VAL:HG23	1.96	0.47
1:AC:69:PRO:C	1:AC:72:THR:HG1	2.22	0.47
1:AF:110:GLU:HG2	1:AF:112:GLN:HG2	1.96	0.47
1:BH:123:TYR:HB2	1:BH:185:LEU:CD1	2.45	0.47
1:BI:168:TRP:CE2	1:AI:176:ARG:HD2	2.50	0.47
1:AI:302:ASP:C	1:AI:305:ASN:HD21	2.22	0.47
1:BM:250:ILE:O	1:BM:250:ILE:HG22	2.14	0.47
1:AM:98:ILE:HG23	1:Bc:91:ARG:NH1	2.29	0.47
1:AM:314:TYR:CD1	1:AM:314:TYR:C	2.92	0.47
1:CM:250:ILE:HG22	1:CM:250:ILE:O	2.15	0.47
1:AP:298:TRP:HE1	1:AP:312:VAL:HA	1.80	0.47
1:CR:124:VAL:O	1:CR:124:VAL:HG13	2.15	0.47
1:CR:138:PHE:CD1	1:CR:138:PHE:C	2.92	0.47
1:BS:122:GLY:C	1:BS:188:VAL:CG2	2.84	0.47
1:BS:123:TYR:HB2	1:BS:185:LEU:CD1	2.45	0.47
1:AT:91:ARG:CZ	1:Ba:98:ILE:CG2	2.93	0.47
1:CT:79:VAL:HG13	1:CT:80:VAL:HG12	1.97	0.47
1:CT:288:ASN:OD1	1:CT:288:ASN:N	2.47	0.47
1:CU:80:VAL:HG11	1:CU:185:LEU:HB2	1.97	0.47
1:CV:103:ALA:HB2	1:CV:166:LEU:HB3	1.97	0.47
1:BW:234:SER:HB3	1:BW:237:ASP:OD1	2.14	0.47
1:CX:199:VAL:O	1:CX:199:VAL:CG1	2.63	0.47
1:BY:124:VAL:HG11	1:BY:138:PHE:CD2	2.50	0.47
1:AY:85:VAL:HG22	1:AY:86:PRO:HD2	1.96	0.47
1:AY:314:TYR:CE1	1:AY:316:SER:HA	2.46	0.47
1:AZ:103:ALA:HB2	1:AZ:166:LEU:HA	1.97	0.47
1:AZ:246:THR:N	1:AZ:247:PRO:CD	2.78	0.47
1:Ca:133:ASP:O	1:Ca:182:ARG:NH2	2.47	0.47
1:Bb:74:THR:HA	1:Bb:190:ASN:ND2	2.29	0.47
1:Ab:263:LEU:HB3	1:Ab:279:TYR:O	2.15	0.47
1:Bc:234:SER:HB3	1:Bc:237:ASP:OD1	2.15	0.47
1:Ac:110:GLU:HG2	1:Ac:112:GLN:HG2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ac:314:TYR:CD1	1:Ac:314:TYR:C	2.93	0.47
1:Cc:122:GLY:O	1:Cc:188:VAL:CB	2.63	0.47
1:Bd:276:ARG:O	1:Ad:276:ARG:NH2	2.48	0.47
1:Cd:85:VAL:O	1:Cd:86:PRO:C	2.56	0.47
1:CA:63:ILE:HD12	1:CA:88:LEU:CG	2.43	0.47
1:CB:79:VAL:HG13	1:CB:80:VAL:HG12	1.97	0.47
1:CB:80:VAL:HG11	1:CB:185:LEU:HB2	1.97	0.47
1:AF:60:MET:HE2	1:AF:200:LEU:HB3	1.97	0.47
1:BG:250:ILE:O	1:BG:250:ILE:HG22	2.15	0.47
1:BH:184:ILE:HD13	1:BH:184:ILE:N	2.29	0.47
1:BH:225:GLN:HG3	1:BH:244:GLY:O	2.15	0.47
1:CJ:223:MET:HE2	1:CJ:328:GLY:HA2	1.97	0.47
1:CK:130:ASP:OD2	1:CK:176:ARG:NH2	2.48	0.47
1:CL:99:PHE:CD2	1:CL:207:LEU:HB3	2.50	0.47
1:BQ:165:THR:OG1	1:BQ:166:LEU:N	2.48	0.47
1:BQ:232:SER:HB3	1:BQ:242:LEU:HD11	1.97	0.47
1:AQ:127:PHE:O	1:AQ:144:THR:OG1	2.30	0.47
1:AR:61:SER:HB2	1:AR:89:LEU:HD22	1.96	0.47
1:AR:110:GLU:HG2	1:AR:112:GLN:HG2	1.96	0.47
1:CR:163:THR:OG1	1:CR:165:THR:HG23	2.15	0.47
1:CS:109:PHE:HB2	1:CS:158:VAL:HG12	1.97	0.47
1:AU:115:CYS:HB2	1:AU:116:PRO:HD2	1.96	0.47
1:CU:77:TYR:C	1:CU:77:TYR:CD1	2.90	0.47
1:CU:103:ALA:HB2	1:CU:166:LEU:HB3	1.97	0.47
1:BV:161:GLN:NE2	1:CV:210:PRO:HD2	2.30	0.47
1:AW:61:SER:HB2	1:AW:89:LEU:HD22	1.96	0.47
1:AW:224:THR:HG22	1:AW:329:THR:N	2.30	0.47
1:BX:163:THR:OG1	1:BX:165:THR:CG2	2.62	0.47
1:AX:314:TYR:CE1	1:AX:316:SER:CA	2.86	0.47
1:CX:89:LEU:HD13	1:CX:203:TRP:CG	2.50	0.47
1:AY:268:SER:CB	1:AY:273:ASP:O	2.63	0.47
1:CY:79:VAL:HG13	1:CY:80:VAL:HG12	1.96	0.47
1:AZ:298:TRP:HE1	1:AZ:312:VAL:HA	1.79	0.47
1:CZ:109:PHE:HB2	1:CZ:158:VAL:HG12	1.97	0.47
1:Ba:205:VAL:HG22	1:Ba:206:ARG:N	2.30	0.47
1:Aa:101:ARG:CZ	1:Aa:166:LEU:HD23	2.44	0.47
1:Ca:199:VAL:O	1:Ca:199:VAL:CG1	2.63	0.47
1:Ab:85:VAL:HG22	1:Ab:86:PRO:HD2	1.97	0.47
1:Ab:124:VAL:HG11	1:Ab:138:PHE:HD1	1.79	0.47
1:Bc:123:TYR:HB2	1:Bc:185:LEU:HD11	1.96	0.47
1:Bc:142:GLN:HB2	1:Cc:48:PHE:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cc:130:ASP:OD2	1:Cc:176:ARG:NH2	2.48	0.47
1:Bd:142:GLN:HB2	1:Cd:48:PHE:CE1	2.49	0.47
1:CA:89:LEU:HD13	1:CA:203:TRP:CG	2.50	0.46
1:CA:200:LEU:HD13	1:CG:45:VAL:HG23	1.96	0.46
1:CC:57:LEU:HD23	1:CC:203:TRP:CH2	2.50	0.46
1:AD:91:ARG:NH2	1:BF:210:PRO:HB3	2.29	0.46
1:AD:246:THR:N	1:AD:247:PRO:CD	2.79	0.46
1:BG:232:SER:HB3	1:BG:242:LEU:HD11	1.96	0.46
1:CG:85:VAL:HG13	1:CG:86:PRO:HD2	1.96	0.46
1:BH:85:VAL:HG23	1:BH:86:PRO:HD2	1.97	0.46
1:AH:263:LEU:HB3	1:AH:279:TYR:O	2.15	0.46
1:BI:98:ILE:CG2	1:Aa:91:ARG:CZ	2.93	0.46
1:CI:63:ILE:HD12	1:CI:88:LEU:CG	2.43	0.46
1:CI:190:ASN:HD22	1:CI:190:ASN:N	2.13	0.46
1:BK:142:GLN:HB2	1:CK:48:PHE:CE1	2.50	0.46
1:BK:142:GLN:HB2	1:CK:48:PHE:HE1	1.80	0.46
1:CK:99:PHE:CB	1:CK:209:VAL:O	2.63	0.46
1:CL:79:VAL:HG13	1:CL:80:VAL:HG12	1.97	0.46
1:CO:38:PRO:C	1:Cc:39:VAL:HG23	2.40	0.46
1:BS:74:THR:HA	1:BS:190:ASN:ND2	2.29	0.46
1:CS:79:VAL:HG13	1:CS:80:VAL:HG12	1.96	0.46
1:CS:112:GLN:NE2	1:CS:155:SER:OG	2.48	0.46
1:CT:63:ILE:HD12	1:CT:88:LEU:CG	2.43	0.46
1:BU:85:VAL:HG23	1:BU:86:PRO:HD2	1.95	0.46
1:CU:237:ASP:HB3	1:CU:297:ARG:HG2	1.96	0.46
1:AX:268:SER:CB	1:AX:273:ASP:O	2.63	0.46
1:AX:315:TYR:CE2	1:AX:317:ASP:OD2	2.68	0.46
1:CX:62:ARG:HA	1:CX:200:LEU:HD23	1.95	0.46
1:CX:202:ARG:HH12	1:Cc:46:THR:HB	1.80	0.46
1:BY:205:VAL:HG22	1:BY:206:ARG:N	2.30	0.46
1:BY:214:ASN:HD22	1:BY:215:PRO:HD2	1.79	0.46
1:BZ:142:GLN:HB2	1:CZ:48:PHE:CE1	2.50	0.46
1:CZ:163:THR:OG1	1:CZ:165:THR:HG23	2.14	0.46
1:Ca:101:ARG:CZ	1:Ca:166:LEU:CD1	2.93	0.46
1:Ca:190:ASN:HD22	1:Ca:190:ASN:N	2.14	0.46
1:Cb:101:ARG:CZ	1:Cb:166:LEU:CD1	2.93	0.46
1:Cc:54:ASP:N	1:Cc:54:ASP:OD1	2.46	0.46
1:Cc:112:GLN:NE2	1:Cc:155:SER:OG	2.49	0.46
1:Bd:61:SER:CB	1:Bd:90:PRO:HD2	2.29	0.46
1:BA:168:TRP:CE2	1:AA:176:ARG:HD2	2.50	0.46
1:CB:141:LEU:O	1:CB:142:GLN:C	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:123:TYR:HA	1:CE:188:VAL:HG23	1.97	0.46
1:CF:39:VAL:HA	1:CY:39:VAL:HG21	1.97	0.46
1:CF:138:PHE:C	1:CF:138:PHE:CD1	2.93	0.46
1:AG:298:TRP:NE1	1:AG:312:VAL:CB	2.77	0.46
1:AJ:288:ASN:O	1:AJ:289:ALA:C	2.59	0.46
1:AL:279:TYR:CE2	1:AL:311:GLY:O	2.64	0.46
1:CL:123:TYR:CD1	1:CL:185:LEU:HD21	2.50	0.46
1:BM:232:SER:HB3	1:BM:242:LEU:HD11	1.97	0.46
1:AM:80:VAL:HG13	1:AM:185:LEU:HB3	1.97	0.46
1:AM:124:VAL:HG11	1:AM:138:PHE:CD1	2.50	0.46
1:CM:77:TYR:CD1	1:CM:77:TYR:C	2.90	0.46
1:CM:89:LEU:HD13	1:CM:203:TRP:CG	2.50	0.46
1:CN:77:TYR:CD1	1:CN:77:TYR:C	2.91	0.46
1:BO:142:GLN:HB2	1:CO:48:PHE:CE1	2.49	0.46
1:CO:77:TYR:C	1:CO:77:TYR:CD1	2.93	0.46
1:BP:142:GLN:HB2	1:CP:48:PHE:HE1	1.80	0.46
1:AQ:116:PRO:HG2	1:AQ:119:THR:OG1	2.15	0.46
1:AQ:314:TYR:CD1	1:AQ:314:TYR:C	2.93	0.46
1:CQ:85:VAL:O	1:CQ:86:PRO:C	2.58	0.46
1:BR:123:TYR:HB2	1:BR:185:LEU:CD1	2.45	0.46
1:AR:124:VAL:HG11	1:AR:138:PHE:CD1	2.50	0.46
1:CR:46:THR:HB	1:CT:202:ARG:HH12	1.80	0.46
1:CT:118:ASN:HA	1:Ba:116:PRO:CB	2.45	0.46
1:AU:63:ILE:CD1	1:AU:89:LEU:HD21	2.45	0.46
1:CU:63:ILE:HD12	1:CU:88:LEU:CD1	2.45	0.46
1:CU:91:ARG:HD2	1:Cb:98:ILE:HB	1.97	0.46
1:BV:123:TYR:N	1:BV:188:VAL:HG22	2.30	0.46
1:BW:136:HIS:O	1:BW:186:LEU:HD11	2.15	0.46
1:CW:44:THR:N	1:Cd:112:GLN:HE21	2.12	0.46
1:CY:112:GLN:HE21	1:Ca:44:THR:H	1.63	0.46
1:BZ:165:THR:OG1	1:BZ:166:LEU:N	2.48	0.46
1:BZ:214:ASN:HD22	1:BZ:215:PRO:HD2	1.81	0.46
1:AZ:61:SER:HB2	1:AZ:89:LEU:HD22	1.97	0.46
1:AZ:314:TYR:CD1	1:AZ:314:TYR:C	2.93	0.46
1:Cc:62:ARG:HA	1:Cc:200:LEU:HD23	1.98	0.46
1:Cc:223:MET:HE2	1:Cc:328:GLY:HA2	1.97	0.46
1:BA:225:GLN:HG3	1:BA:244:GLY:O	2.15	0.46
1:AA:91:ARG:NH2	1:BV:98:ILE:HG22	2.31	0.46
1:AA:298:TRP:NE1	1:AA:312:VAL:HA	2.30	0.46
1:CA:80:VAL:HG11	1:CA:185:LEU:HB2	1.97	0.46
1:BB:168:TRP:CE2	1:AB:176:ARG:HD2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:34:ARG:HD3	1:Cb:43:SER:O	2.15	0.46
1:CB:85:VAL:HG13	1:CB:86:PRO:HD2	1.96	0.46
1:BC:123:TYR:HB2	1:BC:185:LEU:HD11	1.97	0.46
1:AC:111:ILE:HG21	1:AC:123:TYR:CZ	2.50	0.46
1:CE:34:ARG:HD3	1:CN:43:SER:O	2.15	0.46
1:CE:80:VAL:HG11	1:CE:185:LEU:HB2	1.97	0.46
1:CE:223:MET:HE2	1:CE:328:GLY:HA2	1.96	0.46
1:AF:63:ILE:CD1	1:AF:89:LEU:HD21	2.46	0.46
1:CF:78:VAL:HG13	1:CF:78:VAL:O	2.15	0.46
1:CF:81:ASP:HA	1:CF:184:ILE:HG22	1.97	0.46
1:CF:99:PHE:CB	1:CF:209:VAL:O	2.63	0.46
1:AH:298:TRP:NE1	1:AH:312:VAL:HA	2.30	0.46
1:AJ:61:SER:HB2	1:AJ:89:LEU:HD22	1.97	0.46
1:AJ:91:ARG:HG2	1:BR:98:ILE:HG23	1.97	0.46
1:BK:163:THR:C	1:BK:165:THR:HG22	2.40	0.46
1:BK:214:ASN:HD22	1:BK:215:PRO:HD2	1.79	0.46
1:AK:234:SER:HB3	1:AK:237:ASP:O	2.15	0.46
1:AL:63:ILE:CD1	1:AL:89:LEU:HD21	2.45	0.46
1:AL:162:TYR:N	1:AL:162:TYR:CD1	2.84	0.46
1:AM:85:VAL:HG22	1:AM:86:PRO:HD2	1.97	0.46
1:BP:150:ALA:HB2	1:BP:156:ARG:HD3	1.98	0.46
1:AP:288:ASN:O	1:AP:289:ALA:C	2.58	0.46
1:CQ:122:GLY:O	1:CQ:188:VAL:CB	2.62	0.46
1:CQ:250:ILE:O	1:CQ:250:ILE:HG22	2.16	0.46
1:CR:237:ASP:HB3	1:CR:297:ARG:HG2	1.96	0.46
1:BS:250:ILE:HG22	1:BS:250:ILE:O	2.15	0.46
1:BT:168:TRP:CE2	1:AT:176:ARG:HD2	2.51	0.46
1:CT:81:ASP:C	1:CT:81:ASP:OD1	2.58	0.46
1:CV:77:TYR:CD1	1:CV:77:TYR:C	2.89	0.46
1:AW:246:THR:N	1:AW:247:PRO:CD	2.79	0.46
1:CW:44:THR:H	1:Cd:112:GLN:HE21	1.64	0.46
1:CW:79:VAL:HG13	1:CW:80:VAL:HG12	1.98	0.46
1:CX:44:THR:H	1:Cc:112:GLN:HE21	1.64	0.46
1:CY:85:VAL:O	1:CY:86:PRO:C	2.59	0.46
1:AZ:80:VAL:HG13	1:AZ:185:LEU:HB3	1.98	0.46
1:Ca:119:THR:O	1:Ca:120:GLY:C	2.58	0.46
1:Bc:123:TYR:HB2	1:Bc:185:LEU:CD1	2.45	0.46
1:Bd:122:GLY:C	1:Bd:188:VAL:CG2	2.84	0.46
1:CB:44:THR:H	1:CF:112:GLN:HE21	1.62	0.46
1:CB:130:ASP:OD2	1:CB:176:ARG:NH2	2.47	0.46
1:AC:302:ASP:C	1:AC:305:ASN:HD21	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:268:SER:CB	1:AD:273:ASP:O	2.64	0.46
1:CD:202:ARG:HH12	1:CI:46:THR:HB	1.80	0.46
1:BE:232:SER:HB3	1:BE:242:LEU:HD11	1.97	0.46
1:CE:81:ASP:HA	1:CE:184:ILE:HG22	1.98	0.46
1:CF:122:GLY:O	1:CF:188:VAL:CB	2.63	0.46
1:AG:127:PHE:O	1:AG:144:THR:OG1	2.28	0.46
1:CH:63:ILE:HD12	1:CH:88:LEU:CD1	2.45	0.46
1:CI:62:ARG:HA	1:CI:200:LEU:HD23	1.97	0.46
1:CI:85:VAL:HG13	1:CI:86:PRO:HD2	1.97	0.46
1:CI:98:ILE:HD11	1:CI:99:PHE:CE2	2.50	0.46
1:CI:113:PRO:HA	1:CI:197:VAL:HA	1.97	0.46
1:BJ:319:GLN:HE21	1:BJ:319:GLN:C	2.23	0.46
1:CJ:98:ILE:HD11	1:CJ:99:PHE:CE2	2.50	0.46
1:BL:98:ILE:CA	1:BL:211:SER:O	2.63	0.46
1:CM:100:GLN:HG2	1:CM:211:SER:HG	1.80	0.46
1:AO:302:ASP:CA	1:AO:305:ASN:ND2	2.78	0.46
1:AS:85:VAL:HG22	1:AS:86:PRO:HD2	1.97	0.46
1:CS:62:ARG:HA	1:CS:200:LEU:HD23	1.98	0.46
1:CS:223:MET:HE2	1:CS:328:GLY:HA2	1.97	0.46
1:AT:62:ARG:CZ	1:Aa:138:PHE:CE2	2.98	0.46
1:CT:223:MET:HE2	1:CT:328:GLY:HA2	1.97	0.46
1:BV:142:GLN:HB2	1:CV:48:PHE:CE1	2.50	0.46
1:CW:98:ILE:HD11	1:CW:99:PHE:CE2	2.51	0.46
1:CX:77:TYR:C	1:CX:77:TYR:CD1	2.91	0.46
1:CX:85:VAL:O	1:CX:86:PRO:C	2.58	0.46
1:BY:150:ALA:HB2	1:BY:156:ARG:HD3	1.97	0.46
1:CY:80:VAL:HG11	1:CY:185:LEU:HB2	1.96	0.46
1:CZ:112:GLN:NE2	1:CZ:155:SER:OG	2.49	0.46
1:CZ:199:VAL:O	1:CZ:199:VAL:CG1	2.64	0.46
1:Ba:232:SER:HB3	1:Ba:242:LEU:HD11	1.97	0.46
1:Bb:98:ILE:CA	1:Bb:211:SER:O	2.64	0.46
1:Bb:163:THR:C	1:Bb:165:THR:HG22	2.41	0.46
1:Cb:89:LEU:HD13	1:Cb:203:TRP:CG	2.51	0.46
1:Bd:234:SER:HB3	1:Bd:237:ASP:OD1	2.16	0.46
1:Cd:288:ASN:OD1	1:Cd:288:ASN:N	2.48	0.46
1:BA:142:GLN:HB2	1:CA:48:PHE:CE1	2.50	0.46
1:AB:298:TRP:NE1	1:AB:312:VAL:HA	2.30	0.46
1:AD:61:SER:HB2	1:AD:89:LEU:HD22	1.96	0.46
1:CE:57:LEU:HD23	1:CE:203:TRP:CH2	2.51	0.46
1:CE:98:ILE:HB	1:CH:91:ARG:HD2	1.96	0.46
1:CE:112:GLN:NE2	1:CE:155:SER:OG	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:123:TYR:N	1:BG:188:VAL:HG22	2.31	0.46
1:AG:91:ARG:CZ	1:Bd:98:ILE:CG2	2.93	0.46
1:CG:101:ARG:CZ	1:CG:166:LEU:CD1	2.94	0.46
1:CG:122:GLY:O	1:CG:188:VAL:CB	2.61	0.46
1:BH:98:ILE:CA	1:BH:211:SER:O	2.64	0.46
1:BH:232:SER:HB3	1:BH:242:LEU:HD11	1.96	0.46
1:CH:80:VAL:HG11	1:CH:185:LEU:HB2	1.96	0.46
1:CH:223:MET:HE2	1:CH:328:GLY:HA2	1.97	0.46
1:AI:69:PRO:C	1:AI:72:THR:HG1	2.24	0.46
1:CI:123:TYR:HA	1:CI:188:VAL:HG23	1.98	0.46
1:AJ:315:TYR:CE2	1:AJ:317:ASP:OD2	2.69	0.46
1:CJ:199:VAL:O	1:CJ:199:VAL:CG1	2.62	0.46
1:AK:110:GLU:HG2	1:AK:112:GLN:HG2	1.97	0.46
1:CM:63:ILE:HD12	1:CM:88:LEU:CD1	2.46	0.46
1:BO:150:ALA:HB2	1:BO:156:ARG:HD3	1.96	0.46
1:CO:34:ARG:CG	1:Bc:156:ARG:HH22	2.29	0.46
1:BQ:98:ILE:HG22	1:AZ:91:ARG:NH2	2.31	0.46
1:AR:85:VAL:HG22	1:AR:86:PRO:HD2	1.98	0.46
1:BS:234:SER:HB3	1:BS:237:ASP:OD1	2.16	0.46
1:CS:99:PHE:HB3	1:CS:209:VAL:O	2.15	0.46
1:BT:136:HIS:O	1:BT:186:LEU:HD11	2.15	0.46
1:BT:234:SER:HB3	1:BT:237:ASP:OD1	2.14	0.46
1:CT:123:TYR:HA	1:CT:188:VAL:HG23	1.98	0.46
1:BU:163:THR:C	1:BU:165:THR:HG22	2.40	0.46
1:BY:319:GLN:HE21	1:BY:319:GLN:C	2.24	0.46
1:CZ:141:LEU:O	1:CZ:142:GLN:C	2.59	0.46
1:Ba:142:GLN:HB2	1:Ca:48:PHE:CE1	2.51	0.46
1:Ca:85:VAL:HG13	1:Ca:86:PRO:HD2	1.97	0.46
1:Bb:205:VAL:HG22	1:Bb:206:ARG:N	2.31	0.46
1:Cd:99:PHE:HB3	1:Cd:209:VAL:O	2.16	0.46
1:Cd:121:GLY:C	1:Cd:152:TRP:CD1	2.93	0.46
1:AA:122:GLY:HA3	1:AI:114:MET:SD	2.55	0.46
1:CB:34:ARG:HG3	1:Bb:156:ARG:NH2	2.31	0.46
1:CD:109:PHE:HB2	1:CD:158:VAL:HG12	1.96	0.46
1:CD:112:GLN:HE21	1:CI:44:THR:H	1.63	0.46
1:AF:298:TRP:NE1	1:AF:312:VAL:HA	2.30	0.46
1:CF:85:VAL:O	1:CF:86:PRO:C	2.59	0.46
1:AG:314:TYR:CD1	1:AG:314:TYR:C	2.93	0.46
1:CG:124:VAL:O	1:CG:124:VAL:HG13	2.16	0.46
1:AH:91:ARG:NE	1:BN:98:ILE:CG2	2.79	0.46
1:AI:268:SER:CB	1:AI:273:ASP:O	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:123:TYR:HB2	1:BK:185:LEU:HD11	1.98	0.46
1:AK:298:TRP:NE1	1:AK:312:VAL:CB	2.78	0.46
1:BN:276:ARG:O	1:AN:276:ARG:NH2	2.48	0.46
1:AN:85:VAL:HG22	1:AN:86:PRO:HD2	1.97	0.46
1:CN:100:GLN:HA	1:CN:213:GLU:OE2	2.15	0.46
1:AO:142:GLN:O	1:AO:142:GLN:NE2	2.49	0.46
1:BQ:142:GLN:HB2	1:CQ:48:PHE:CE1	2.50	0.46
1:AQ:85:VAL:HG22	1:AQ:86:PRO:HD2	1.96	0.46
1:CS:199:VAL:O	1:CS:199:VAL:CG1	2.63	0.46
1:CT:98:ILE:HD11	1:CT:99:PHE:CE2	2.50	0.46
1:AU:314:TYR:CD1	1:AU:314:TYR:C	2.93	0.46
1:BW:98:ILE:CA	1:BW:211:SER:O	2.63	0.46
1:CY:81:ASP:HA	1:CY:184:ILE:HG22	1.96	0.46
1:CY:190:ASN:HD22	1:CY:190:ASN:N	2.13	0.46
1:CZ:122:GLY:O	1:CZ:188:VAL:CB	2.63	0.46
1:Cb:103:ALA:HB2	1:Cb:166:LEU:HB3	1.97	0.46
1:Ac:298:TRP:NE1	1:Ac:312:VAL:HA	2.30	0.46
1:AA:268:SER:CB	1:AA:273:ASP:O	2.64	0.46
1:CB:34:ARG:CD	1:Bb:156:ARG:HH22	2.29	0.46
1:AD:298:TRP:NE1	1:AD:312:VAL:HA	2.31	0.46
1:CD:99:PHE:HB3	1:CD:209:VAL:O	2.15	0.46
1:CE:103:ALA:HB2	1:CE:166:LEU:HB3	1.98	0.46
1:CF:250:ILE:O	1:CF:250:ILE:HG22	2.16	0.46
1:BG:214:ASN:HD22	1:BG:215:PRO:HD2	1.81	0.46
1:BI:98:ILE:CA	1:BI:211:SER:O	2.63	0.46
1:CI:103:ALA:HB2	1:CI:166:LEU:HB3	1.98	0.46
1:BJ:123:TYR:HB2	1:BJ:185:LEU:HD11	1.97	0.46
1:CK:44:THR:N	1:CL:112:GLN:HE21	2.12	0.46
1:CK:98:ILE:HD11	1:CK:99:PHE:CE2	2.51	0.46
1:BL:123:TYR:HB2	1:BL:185:LEU:CD1	2.46	0.46
1:BL:225:GLN:HG3	1:BL:244:GLY:O	2.16	0.46
1:AL:298:TRP:NE1	1:AL:312:VAL:CB	2.76	0.46
1:CM:81:ASP:OD2	1:CM:136:HIS:NE2	2.43	0.46
1:BN:142:GLN:HB2	1:CN:48:PHE:CE1	2.50	0.46
1:BN:205:VAL:HG22	1:BN:206:ARG:N	2.30	0.46
1:BN:232:SER:HB3	1:BN:242:LEU:HD11	1.97	0.46
1:BO:136:HIS:O	1:BO:186:LEU:HD11	2.16	0.46
1:BU:232:SER:HB3	1:BU:242:LEU:HD11	1.98	0.46
1:BU:234:SER:HB3	1:BU:237:ASP:OD1	2.16	0.46
1:CU:72:THR:O	1:CU:191:ASN:OD1	2.34	0.46
1:CU:99:PHE:CB	1:CU:209:VAL:O	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:111:ILE:HG21	1:AV:123:TYR:CZ	2.50	0.46
1:AV:268:SER:CB	1:AV:273:ASP:O	2.64	0.46
1:BW:150:ALA:HB2	1:BW:156:ARG:HD3	1.97	0.46
1:BX:123:TYR:HB2	1:BX:185:LEU:CD1	2.45	0.46
1:BX:214:ASN:HD22	1:BX:215:PRO:HD2	1.79	0.46
1:AX:314:TYR:CD1	1:AX:314:TYR:C	2.93	0.46
1:CX:80:VAL:CG1	1:CX:185:LEU:HB2	2.43	0.46
1:AZ:61:SER:CB	1:AZ:90:PRO:HD2	2.39	0.46
1:AZ:224:THR:HG22	1:AZ:329:THR:N	2.30	0.46
1:Ca:113:PRO:HA	1:Ca:197:VAL:HA	1.98	0.46
1:Ca:250:ILE:O	1:Ca:250:ILE:HG22	2.16	0.46
1:Cb:80:VAL:CG1	1:Cb:185:LEU:HB2	2.45	0.46
1:AD:63:ILE:HG23	1:AD:88:LEU:HD11	1.98	0.46
1:BE:225:GLN:HG3	1:BE:244:GLY:O	2.16	0.46
1:AE:91:ARG:HD2	1:AM:143:ALA:HB1	1.98	0.46
1:AE:268:SER:CB	1:AE:273:ASP:O	2.64	0.46
1:CE:124:VAL:HG13	1:CE:124:VAL:O	2.16	0.46
1:CE:163:THR:OG1	1:CE:165:THR:HG23	2.15	0.46
1:AH:268:SER:CB	1:AH:273:ASP:O	2.63	0.46
1:AJ:298:TRP:NE1	1:AJ:312:VAL:HA	2.31	0.46
1:AK:127:PHE:O	1:AK:144:THR:OG1	2.34	0.46
1:AK:268:SER:HB3	1:AK:273:ASP:O	2.15	0.46
1:AL:64:SER:OG	1:AL:80:VAL:HG21	2.15	0.46
1:CL:100:GLN:N	1:CL:209:VAL:O	2.49	0.46
1:CO:223:MET:HE2	1:CO:328:GLY:HA2	1.98	0.46
1:BP:232:SER:HB3	1:BP:242:LEU:HD11	1.98	0.46
1:CP:81:ASP:HA	1:CP:184:ILE:HG22	1.98	0.46
1:AR:212:LEU:C	1:AR:212:LEU:HD12	2.41	0.46
1:BS:109:PHE:HB2	1:BS:158:VAL:CG1	2.46	0.46
1:CU:62:ARG:HA	1:CU:200:LEU:HD23	1.98	0.46
1:CV:121:GLY:C	1:CV:152:TRP:CD1	2.94	0.46
1:AW:302:ASP:C	1:AW:305:ASN:HD21	2.23	0.46
1:CW:63:ILE:HD12	1:CW:88:LEU:CG	2.43	0.46
1:BY:260:ASP:HA	1:AY:261:ARG:NH2	2.31	0.46
1:AY:80:VAL:HG13	1:AY:185:LEU:HB3	1.96	0.46
1:AY:124:VAL:HG11	1:AY:138:PHE:CD1	2.50	0.46
1:CY:89:LEU:HD13	1:CY:203:TRP:CG	2.51	0.46
1:Ba:109:PHE:HB2	1:Ba:158:VAL:CG1	2.46	0.46
1:Ab:80:VAL:HG13	1:Ab:185:LEU:HB3	1.98	0.46
1:Cc:103:ALA:HB2	1:Cc:166:LEU:HB3	1.97	0.46
1:Ad:298:TRP:NE1	1:Ad:312:VAL:CB	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:142:GLN:HB2	1:CA:48:PHE:HE1	1.80	0.46
1:BA:205:VAL:HG22	1:BA:206:ARG:N	2.31	0.46
1:CA:202:ARG:HH12	1:CG:46:THR:HB	1.81	0.46
1:CA:250:ILE:O	1:CA:250:ILE:HG22	2.15	0.46
1:AB:103:ALA:HB2	1:AB:166:LEU:HA	1.97	0.46
1:AC:61:SER:CB	1:AC:90:PRO:HD2	2.37	0.46
1:CC:188:VAL:HG11	1:BS:114:MET:HE1	1.98	0.46
1:AD:91:ARG:CZ	1:BF:98:ILE:CG2	2.94	0.46
1:BE:74:THR:HA	1:BE:190:ASN:ND2	2.30	0.46
1:CE:63:ILE:HD12	1:CE:88:LEU:CD1	2.46	0.46
1:BF:142:GLN:HB2	1:CF:48:PHE:CE1	2.51	0.46
1:CF:39:VAL:HA	1:CY:39:VAL:CG2	2.45	0.46
1:CF:80:VAL:HG11	1:CF:185:LEU:HB2	1.98	0.46
1:CG:223:MET:HE2	1:CG:328:GLY:HA2	1.98	0.46
1:AH:124:VAL:HG11	1:AH:138:PHE:CD1	2.51	0.46
1:CH:34:ARG:CD	1:BM:156:ARG:HH22	2.28	0.46
1:CH:103:ALA:HB2	1:CH:166:LEU:HB3	1.97	0.46
1:AJ:98:ILE:HG12	1:BR:91:ARG:HG2	1.98	0.46
1:AJ:302:ASP:C	1:AJ:305:ASN:HD21	2.23	0.46
1:CJ:81:ASP:OD2	1:CJ:136:HIS:NE2	2.44	0.46
1:AK:314:TYR:CE1	1:AK:316:SER:HA	2.48	0.46
1:BL:234:SER:HB3	1:BL:237:ASP:OD1	2.15	0.46
1:CL:89:LEU:HD13	1:CL:203:TRP:CG	2.51	0.46
1:BM:163:THR:C	1:BM:165:THR:HG22	2.41	0.46
1:CN:79:VAL:HG13	1:CN:80:VAL:HG12	1.98	0.46
1:BO:98:ILE:CA	1:BO:211:SER:O	2.64	0.46
1:AR:298:TRP:HE1	1:AR:312:VAL:HA	1.81	0.46
1:AS:279:TYR:CE2	1:AS:311:GLY:O	2.64	0.46
1:BT:123:TYR:HB2	1:BT:185:LEU:CD1	2.46	0.46
1:CT:69:PRO:O	1:CT:72:THR:OG1	2.27	0.46
1:CT:101:ARG:CZ	1:CT:166:LEU:CD1	2.94	0.46
1:BV:163:THR:C	1:BV:165:THR:HG22	2.41	0.46
1:AV:246:THR:N	1:AV:247:PRO:CD	2.79	0.46
1:CV:200:LEU:HD13	1:CZ:45:VAL:HG23	1.97	0.46
1:BW:214:ASN:HD22	1:BW:215:PRO:HD2	1.81	0.46
1:AW:85:VAL:HG22	1:AW:86:PRO:HD2	1.97	0.46
1:BX:74:THR:HA	1:BX:190:ASN:ND2	2.31	0.46
1:AX:279:TYR:CE2	1:AX:311:GLY:O	2.65	0.46
1:CY:63:ILE:HD12	1:CY:88:LEU:CD1	2.46	0.46
1:CY:98:ILE:HD11	1:CY:99:PHE:CE2	2.51	0.46
1:BZ:142:GLN:HB2	1:CZ:48:PHE:HE1	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ab:246:THR:N	1:Ab:247:PRO:CD	2.79	0.46
1:BA:232:SER:HB3	1:BA:242:LEU:HD11	1.98	0.46
1:AA:98:ILE:CG2	1:BV:91:ARG:NH1	2.79	0.46
1:CA:79:VAL:HG13	1:CA:80:VAL:HG12	1.97	0.46
1:CA:163:THR:OG1	1:CA:165:THR:HG23	2.15	0.46
1:BD:123:TYR:HB2	1:BD:185:LEU:CD1	2.46	0.46
1:AD:80:VAL:HG13	1:AD:185:LEU:HB3	1.98	0.46
1:CD:81:ASP:OD2	1:CD:136:HIS:NE2	2.45	0.46
1:CD:223:MET:HE2	1:CD:328:GLY:HA2	1.97	0.46
1:CD:250:ILE:HG22	1:CD:250:ILE:O	2.16	0.46
1:CE:44:THR:H	1:CH:112:GLN:HE21	1.62	0.46
1:AG:100:GLN:HA	1:AG:169:THR:OG1	2.16	0.46
1:AG:188:VAL:CG2	1:AP:114:MET:SD	3.05	0.46
1:BH:62:ARG:HB2	1:Cd:138:PHE:HE1	1.81	0.46
1:BH:91:ARG:HG2	1:Ad:98:ILE:HG12	1.98	0.46
1:AH:63:ILE:HG23	1:AH:88:LEU:HD11	1.98	0.46
1:AH:81:ASP:C	1:AH:81:ASP:OD1	2.58	0.46
1:AI:162:TYR:CE2	1:AI:164:ARG:HG2	2.51	0.46
1:AJ:162:TYR:CE2	1:AJ:164:ARG:HG2	2.51	0.46
1:CK:155:SER:O	1:CK:156:ARG:HD3	2.16	0.46
1:CL:103:ALA:HB2	1:CL:166:LEU:HB3	1.97	0.46
1:BN:74:THR:HA	1:BN:190:ASN:HD22	1.81	0.46
1:BN:122:GLY:C	1:BN:188:VAL:CG2	2.85	0.46
1:AN:124:VAL:HG11	1:AN:138:PHE:CD1	2.51	0.46
1:BO:98:ILE:HG22	1:Ab:91:ARG:CZ	2.46	0.46
1:AR:268:SER:CB	1:AR:273:ASP:O	2.64	0.46
1:CR:57:LEU:HD23	1:CR:203:TRP:CH2	2.50	0.46
1:BS:142:GLN:HB2	1:CS:48:PHE:HE1	1.81	0.46
1:AS:288:ASN:O	1:AS:289:ALA:C	2.59	0.46
1:BT:98:ILE:HG22	1:AV:91:ARG:NH2	2.31	0.46
1:BU:184:ILE:HD13	1:BU:184:ILE:N	2.31	0.46
1:BU:250:ILE:O	1:BU:250:ILE:HG22	2.16	0.46
1:AV:105:GLU:C	1:AV:162:TYR:HH	2.18	0.46
1:BW:260:ASP:HA	1:AW:261:ARG:NH2	2.31	0.46
1:AW:268:SER:CB	1:AW:273:ASP:O	2.64	0.46
1:CW:250:ILE:O	1:CW:250:ILE:HG22	2.15	0.46
1:BX:122:GLY:C	1:BX:188:VAL:CG2	2.83	0.46
1:CX:123:TYR:HA	1:CX:188:VAL:HG23	1.98	0.46
1:Bb:124:VAL:HG11	1:Bb:138:PHE:CD2	2.51	0.46
1:Ad:81:ASP:C	1:Ad:81:ASP:OD1	2.59	0.46
1:BA:100:GLN:NE2	1:BA:211:SER:CB	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:116:PRO:HG2	1:AA:119:THR:OG1	2.17	0.45
1:BB:100:GLN:O	1:BB:169:THR:N	2.45	0.45
1:AB:116:PRO:HB3	1:AY:118:ASN:O	2.16	0.45
1:CB:111:ILE:HD11	1:CB:125:ALA:HB3	1.98	0.45
1:BC:276:ARG:O	1:AC:276:ARG:NH2	2.49	0.45
1:BD:122:GLY:C	1:BD:188:VAL:CG2	2.84	0.45
1:CD:121:GLY:C	1:CD:152:TRP:CD1	2.94	0.45
1:CE:151:LYS:NZ	1:BM:153:TRP:O	2.49	0.45
1:AG:122:GLY:C	1:AG:188:VAL:HG22	2.41	0.45
1:CG:57:LEU:HD23	1:CG:203:TRP:CH2	2.51	0.45
1:BH:109:PHE:HB2	1:BH:158:VAL:CG1	2.46	0.45
1:CH:85:VAL:O	1:CH:86:PRO:C	2.58	0.45
1:CI:250:ILE:O	1:CI:250:ILE:HG22	2.16	0.45
1:AJ:124:VAL:HG11	1:AJ:138:PHE:CD1	2.50	0.45
1:CK:237:ASP:HB3	1:CK:297:ARG:HG2	1.97	0.45
1:BN:142:GLN:HB2	1:CN:48:PHE:HE1	1.80	0.45
1:AN:137:THR:HG23	1:AN:140:ALA:CB	2.45	0.45
1:CN:199:VAL:O	1:CN:199:VAL:CG1	2.64	0.45
1:CO:54:ASP:N	1:CO:54:ASP:OD1	2.49	0.45
1:CO:62:ARG:HA	1:CO:200:LEU:HD23	1.97	0.45
1:BQ:98:ILE:CG2	1:AZ:91:ARG:CZ	2.94	0.45
1:BQ:116:PRO:HD3	1:CZ:120:GLY:HA3	1.97	0.45
1:BQ:214:ASN:HD22	1:BQ:215:PRO:HD2	1.81	0.45
1:AQ:138:PHE:CE2	1:AZ:62:ARG:CZ	2.99	0.45
1:AS:61:SER:HB2	1:AS:89:LEU:HD22	1.99	0.45
1:AS:212:LEU:HD12	1:AS:212:LEU:C	2.41	0.45
1:AT:103:ALA:HB2	1:AT:166:LEU:HA	1.97	0.45
1:CT:103:ALA:HB2	1:CT:166:LEU:HB3	1.98	0.45
1:BU:109:PHE:HB2	1:BU:158:VAL:CG1	2.46	0.45
1:AU:298:TRP:NE1	1:AU:312:VAL:CB	2.78	0.45
1:BV:142:GLN:HB2	1:CV:48:PHE:HE1	1.80	0.45
1:AX:61:SER:HB2	1:AX:89:LEU:HD22	1.98	0.45
1:AY:122:GLY:C	1:AY:188:VAL:HG22	2.41	0.45
1:AY:314:TYR:CD1	1:AY:314:TYR:C	2.94	0.45
1:CY:98:ILE:HB	1:Ca:91:ARG:HD2	1.98	0.45
1:BZ:123:TYR:HB2	1:BZ:185:LEU:CD1	2.45	0.45
1:CZ:81:ASP:OD2	1:CZ:136:HIS:NE2	2.43	0.45
1:Aa:85:VAL:HG22	1:Aa:86:PRO:HD2	1.98	0.45
1:Ca:79:VAL:HG13	1:Ca:80:VAL:HG12	1.98	0.45
1:Ab:268:SER:CB	1:Ab:273:ASP:O	2.63	0.45
1:Bd:123:TYR:HB2	1:Bd:185:LEU:HD11	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bd:161:GLN:NE2	1:Cd:210:PRO:HD2	2.30	0.45
1:Ad:69:PRO:C	1:Ad:72:THR:HG1	2.23	0.45
1:Cd:109:PHE:HB2	1:Cd:158:VAL:HG12	1.98	0.45
1:AA:298:TRP:NE1	1:AA:312:VAL:CB	2.77	0.45
1:BB:123:TYR:HB2	1:BB:185:LEU:CD1	2.45	0.45
1:BC:150:ALA:HB2	1:BC:156:ARG:HD3	1.97	0.45
1:AC:88:LEU:HD13	1:AC:88:LEU:C	2.41	0.45
1:AC:91:ARG:HG2	1:BS:98:ILE:HG23	1.97	0.45
1:CC:98:ILE:HD11	1:CC:99:PHE:CE2	2.51	0.45
1:BD:123:TYR:N	1:BD:188:VAL:HG22	2.30	0.45
1:BD:142:GLN:HB2	1:CD:48:PHE:HE1	1.82	0.45
1:BD:232:SER:HB3	1:BD:242:LEU:HD11	1.98	0.45
1:BF:123:TYR:HB2	1:BF:185:LEU:CD1	2.47	0.45
1:BG:130:ASP:HB3	1:BG:133:ASP:HB2	1.98	0.45
1:AG:91:ARG:HD2	1:Ad:143:ALA:HB1	1.98	0.45
1:CG:63:ILE:HD12	1:CG:88:LEU:CD1	2.46	0.45
1:CG:81:ASP:HA	1:CG:184:ILE:HG22	1.98	0.45
1:BH:122:GLY:C	1:BH:188:VAL:CG2	2.86	0.45
1:BH:150:ALA:HB2	1:BH:156:ARG:HD3	1.97	0.45
1:AH:62:ARG:CZ	1:AN:138:PHE:CE2	3.00	0.45
1:AH:288:ASN:O	1:AH:289:ALA:C	2.60	0.45
1:AH:298:TRP:HE1	1:AH:312:VAL:HA	1.82	0.45
1:CH:250:ILE:O	1:CH:250:ILE:HG22	2.17	0.45
1:CI:99:PHE:CB	1:CI:209:VAL:O	2.64	0.45
1:BJ:122:GLY:C	1:BJ:188:VAL:CG2	2.85	0.45
1:CJ:81:ASP:HA	1:CJ:184:ILE:HG22	1.98	0.45
1:CJ:138:PHE:CD1	1:CJ:138:PHE:C	2.94	0.45
1:BK:91:ARG:HG2	1:AS:98:ILE:HG12	1.98	0.45
1:CK:78:VAL:HG13	1:CK:78:VAL:O	2.16	0.45
1:CK:113:PRO:HA	1:CK:197:VAL:HA	1.99	0.45
1:AL:142:GLN:O	1:AL:142:GLN:NE2	2.50	0.45
1:CL:100:GLN:HA	1:CL:213:GLU:OE2	2.16	0.45
1:BM:214:ASN:HD22	1:BM:215:PRO:HD2	1.80	0.45
1:AM:69:PRO:C	1:AM:72:THR:HG1	2.25	0.45
1:CM:57:LEU:HD23	1:CM:203:TRP:CH2	2.51	0.45
1:AP:268:SER:CB	1:AP:273:ASP:O	2.65	0.45
1:CP:89:LEU:HD13	1:CP:203:TRP:CG	2.52	0.45
1:AQ:188:VAL:HG23	1:AZ:114:MET:SD	2.56	0.45
1:BR:184:ILE:HD13	1:BR:184:ILE:N	2.31	0.45
1:BR:205:VAL:HG22	1:BR:206:ARG:N	2.30	0.45
1:AR:314:TYR:CD1	1:AR:314:TYR:C	2.93	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:232:SER:HB3	1:BS:242:LEU:HD11	1.97	0.45
1:AS:124:VAL:HG11	1:AS:138:PHE:CD1	2.50	0.45
1:BU:123:TYR:HB2	1:BU:185:LEU:CD1	2.46	0.45
1:AU:80:VAL:HG13	1:AU:185:LEU:HB3	1.98	0.45
1:CU:85:VAL:O	1:CU:86:PRO:C	2.59	0.45
1:CU:250:ILE:HG22	1:CU:250:ILE:O	2.16	0.45
1:BV:214:ASN:HD22	1:BV:215:PRO:HD2	1.80	0.45
1:CV:89:LEU:HD13	1:CV:203:TRP:CG	2.51	0.45
1:CV:112:GLN:HE21	1:CZ:44:THR:H	1.64	0.45
1:AW:298:TRP:NE1	1:AW:312:VAL:HA	2.31	0.45
1:CW:123:TYR:HB2	1:CW:185:LEU:HD21	1.99	0.45
1:CX:63:ILE:HD12	1:CX:88:LEU:CD1	2.47	0.45
1:CZ:78:VAL:HG13	1:CZ:78:VAL:O	2.15	0.45
1:Ba:124:VAL:HG11	1:Ba:138:PHE:CD2	2.52	0.45
1:Ca:45:VAL:O	1:Ca:45:VAL:HG13	2.17	0.45
1:Bb:123:TYR:HB2	1:Bb:185:LEU:CD1	2.46	0.45
1:Bc:142:GLN:HB2	1:Cc:48:PHE:HE1	1.80	0.45
1:Cc:63:ILE:HD12	1:Cc:88:LEU:CG	2.42	0.45
1:BA:123:TYR:HB2	1:BA:185:LEU:CD1	2.46	0.45
1:BA:166:LEU:CD1	1:BA:166:LEU:C	2.89	0.45
1:CA:54:ASP:N	1:CA:54:ASP:OD1	2.48	0.45
1:CA:130:ASP:OD2	1:CA:176:ARG:NH2	2.49	0.45
1:BB:232:SER:HB3	1:BB:242:LEU:HD11	1.98	0.45
1:BD:210:PRO:HB3	1:AW:91:ARG:NH2	2.31	0.45
1:CD:200:LEU:HD13	1:CI:45:VAL:HG23	1.99	0.45
1:AF:302:ASP:C	1:AF:305:ASN:HD21	2.23	0.45
1:CG:163:THR:OG1	1:CG:165:THR:HG23	2.17	0.45
1:AH:61:SER:HB2	1:AH:89:LEU:HD22	1.97	0.45
1:CH:34:ARG:HG3	1:BM:156:ARG:NH2	2.31	0.45
1:CH:109:PHE:HB2	1:CH:158:VAL:HG12	1.97	0.45
1:CH:141:LEU:O	1:CH:142:GLN:C	2.58	0.45
1:AJ:85:VAL:HG22	1:AJ:86:PRO:HD2	1.97	0.45
1:CJ:85:VAL:HG13	1:CJ:86:PRO:HD2	1.97	0.45
1:CM:99:PHE:CB	1:CM:209:VAL:O	2.64	0.45
1:AN:74:THR:O	1:AN:75:ASP:C	2.60	0.45
1:AO:315:TYR:CE2	1:AO:317:ASP:OD2	2.69	0.45
1:CO:99:PHE:CD2	1:CO:207:LEU:HB3	2.51	0.45
1:BP:250:ILE:O	1:BP:250:ILE:HG22	2.16	0.45
1:CQ:98:ILE:C	1:CQ:211:SER:O	2.56	0.45
1:BT:163:THR:C	1:BT:165:THR:HG22	2.41	0.45
1:AT:85:VAL:HG22	1:AT:86:PRO:HD2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:298:TRP:HE1	1:AV:312:VAL:HA	1.81	0.45
1:AV:302:ASP:C	1:AV:305:ASN:HD21	2.23	0.45
1:CV:99:PHE:HB3	1:CV:209:VAL:O	2.15	0.45
1:CV:250:ILE:O	1:CV:250:ILE:HG22	2.16	0.45
1:CW:63:ILE:HD12	1:CW:88:LEU:CD1	2.45	0.45
1:BX:150:ALA:HB2	1:BX:156:ARG:HD3	1.98	0.45
1:BX:166:LEU:HD13	1:BX:167:LEU:N	2.32	0.45
1:BX:225:GLN:HG3	1:BX:244:GLY:O	2.15	0.45
1:AX:288:ASN:O	1:AX:289:ALA:C	2.60	0.45
1:CX:138:PHE:CD1	1:CX:138:PHE:C	2.95	0.45
1:AY:298:TRP:NE1	1:AY:312:VAL:CB	2.76	0.45
1:BZ:74:THR:HA	1:BZ:190:ASN:HD22	1.82	0.45
1:CZ:54:ASP:N	1:CZ:54:ASP:OD1	2.50	0.45
1:CZ:57:LEU:HD23	1:CZ:203:TRP:CH2	2.52	0.45
1:Aa:103:ALA:HB2	1:Aa:166:LEU:HA	1.99	0.45
1:Cb:119:THR:O	1:Cb:120:GLY:C	2.58	0.45
1:Cb:223:MET:HE2	1:Cb:328:GLY:HA2	1.97	0.45
1:Bc:184:ILE:HD13	1:Bc:184:ILE:N	2.32	0.45
1:Bc:232:SER:HB3	1:Bc:242:LEU:HD11	1.98	0.45
1:Cc:98:ILE:C	1:Cc:211:SER:O	2.58	0.45
1:Cd:92:LEU:HB2	1:Cd:203:TRP:CH2	2.52	0.45
1:CA:81:ASP:HA	1:CA:184:ILE:HG22	1.98	0.45
1:BB:205:VAL:HG22	1:BB:206:ARG:N	2.31	0.45
1:AB:80:VAL:HG13	1:AB:185:LEU:HB3	1.99	0.45
1:AB:314:TYR:CD1	1:AB:314:TYR:C	2.94	0.45
1:AC:281:HIS:ND1	1:AC:301:TRP:HB3	2.31	0.45
1:AC:288:ASN:O	1:AC:289:ALA:C	2.59	0.45
1:CC:155:SER:O	1:CC:156:ARG:HD3	2.17	0.45
1:AD:74:THR:O	1:AD:75:ASP:C	2.59	0.45
1:AF:315:TYR:CE2	1:AF:317:ASP:OD2	2.69	0.45
1:AG:188:VAL:HG23	1:AP:114:MET:SD	2.57	0.45
1:CG:79:VAL:HG13	1:CG:80:VAL:HG12	1.99	0.45
1:CG:103:ALA:HB2	1:CG:166:LEU:HB3	1.97	0.45
1:BH:74:THR:HA	1:BH:190:ASN:HD22	1.81	0.45
1:BI:98:ILE:HG22	1:Aa:91:ARG:HH21	1.82	0.45
1:CI:78:VAL:HG13	1:CI:78:VAL:O	2.16	0.45
1:BJ:142:GLN:HB2	1:CJ:48:PHE:HE1	1.80	0.45
1:BJ:214:ASN:HD22	1:BJ:215:PRO:HD2	1.80	0.45
1:AJ:81:ASP:C	1:AJ:81:ASP:OD1	2.59	0.45
1:AJ:298:TRP:NE1	1:AJ:312:VAL:CB	2.76	0.45
1:AJ:298:TRP:HE1	1:AJ:312:VAL:HA	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:79:VAL:HG13	1:CK:80:VAL:HG12	1.98	0.45
1:BM:123:TYR:HB2	1:BM:185:LEU:HD11	1.98	0.45
1:AN:69:PRO:C	1:AN:72:THR:HG1	2.25	0.45
1:CN:57:LEU:HD23	1:CN:203:TRP:CH2	2.51	0.45
1:CN:81:ASP:OD2	1:CN:136:HIS:NE2	2.44	0.45
1:AO:69:PRO:C	1:AO:72:THR:HG1	2.23	0.45
1:AO:124:VAL:HG11	1:AO:138:PHE:CD1	2.49	0.45
1:CP:138:PHE:CD1	1:CP:138:PHE:C	2.95	0.45
1:CR:98:ILE:HD11	1:CR:99:PHE:CE2	2.52	0.45
1:CR:109:PHE:HB2	1:CR:158:VAL:HG12	1.97	0.45
1:BS:98:ILE:CA	1:BS:211:SER:O	2.64	0.45
1:AS:302:ASP:C	1:AS:305:ASN:HD21	2.23	0.45
1:AT:91:ARG:NH2	1:Ba:210:PRO:HB3	2.32	0.45
1:CU:102:TYR:HD2	1:CU:205:VAL:HG21	1.81	0.45
1:BV:74:THR:HA	1:BV:190:ASN:HD22	1.79	0.45
1:CV:78:VAL:HG13	1:CV:78:VAL:O	2.17	0.45
1:AW:298:TRP:HE1	1:AW:312:VAL:HA	1.82	0.45
1:CW:103:ALA:HB2	1:CW:166:LEU:HB3	1.97	0.45
1:AX:246:THR:N	1:AX:247:PRO:CD	2.79	0.45
1:CX:103:ALA:HB2	1:CX:166:LEU:HB3	1.99	0.45
1:AY:264:SER:OG	1:AY:276:ARG:NH1	2.50	0.45
1:BZ:150:ALA:HB2	1:BZ:156:ARG:HD3	1.98	0.45
1:CZ:77:TYR:CD1	1:CZ:77:TYR:C	2.90	0.45
1:CZ:103:ALA:HB2	1:CZ:166:LEU:HB3	1.97	0.45
1:Aa:224:THR:HG22	1:Aa:329:THR:N	2.32	0.45
1:Bd:214:ASN:HD22	1:Bd:215:PRO:HD2	1.82	0.45
1:Cd:123:TYR:HB2	1:Cd:185:LEU:CD2	2.46	0.45
1:AA:63:ILE:CD1	1:AA:89:LEU:HD21	2.47	0.45
1:BC:161:GLN:NE2	1:CC:210:PRO:HD2	2.32	0.45
1:CC:237:ASP:HB3	1:CC:297:ARG:HG2	1.98	0.45
1:AF:226:GLY:N	1:AF:243:LEU:O	2.47	0.45
1:CG:130:ASP:OD2	1:CG:176:ARG:NH2	2.49	0.45
1:AH:298:TRP:NE1	1:AH:312:VAL:CB	2.76	0.45
1:CH:99:PHE:HB3	1:CH:209:VAL:O	2.17	0.45
1:CH:112:GLN:NE2	1:CH:155:SER:OG	2.49	0.45
1:BI:250:ILE:O	1:BI:250:ILE:HG22	2.16	0.45
1:CJ:112:GLN:NE2	1:CJ:155:SER:OG	2.50	0.45
1:CK:99:PHE:HB3	1:CK:209:VAL:O	2.17	0.45
1:BM:85:VAL:CG2	1:BM:86:PRO:HD2	2.47	0.45
1:AN:226:GLY:N	1:AN:243:LEU:O	2.49	0.45
1:BP:123:TYR:HB2	1:BP:185:LEU:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:99:PHE:HB3	1:CP:209:VAL:O	2.17	0.45
1:CP:109:PHE:HB2	1:CP:158:VAL:HG12	1.98	0.45
1:CQ:63:ILE:HD12	1:CQ:88:LEU:CD1	2.47	0.45
1:CQ:138:PHE:CD1	1:CQ:138:PHE:C	2.94	0.45
1:BR:319:GLN:HE21	1:BR:319:GLN:C	2.24	0.45
1:AS:315:TYR:CE2	1:AS:317:ASP:OD2	2.68	0.45
1:CS:250:ILE:O	1:CS:250:ILE:HG22	2.17	0.45
1:BU:128:LEU:HD12	1:BU:184:ILE:HD11	1.98	0.45
1:CU:58:SER:HB3	1:CU:204:SER:HB2	1.99	0.45
1:AW:288:ASN:O	1:AW:289:ALA:C	2.58	0.45
1:CW:85:VAL:O	1:CW:86:PRO:C	2.60	0.45
1:CX:119:THR:O	1:CX:120:GLY:C	2.59	0.45
1:Aa:100:GLN:HA	1:Aa:169:THR:OG1	2.16	0.45
1:Ab:314:TYR:CD1	1:Ab:314:TYR:C	2.94	0.45
1:Bd:123:TYR:N	1:Bd:188:VAL:HG22	2.32	0.45
1:Cd:72:THR:O	1:Cd:191:ASN:OD1	2.34	0.45
1:BA:123:TYR:N	1:BA:188:VAL:HG22	2.31	0.45
1:AA:288:ASN:O	1:AA:289:ALA:C	2.59	0.45
1:BB:142:GLN:HB2	1:CB:48:PHE:HE1	1.81	0.45
1:CB:109:PHE:HB2	1:CB:158:VAL:HG12	1.97	0.45
1:CC:99:PHE:HB3	1:CC:209:VAL:O	2.17	0.45
1:BF:232:SER:HB3	1:BF:242:LEU:HD11	1.99	0.45
1:AG:85:VAL:HG22	1:AG:86:PRO:HD2	1.98	0.45
1:CG:109:PHE:HB2	1:CG:158:VAL:HG12	1.98	0.45
1:BI:74:THR:HA	1:BI:190:ASN:HD22	1.80	0.45
1:AI:298:TRP:NE1	1:AI:312:VAL:CB	2.78	0.45
1:AI:298:TRP:NE1	1:AI:312:VAL:HA	2.32	0.45
1:CI:130:ASP:OD2	1:CI:176:ARG:NH2	2.50	0.45
1:AK:124:VAL:HG11	1:AK:138:PHE:CD1	2.52	0.45
1:CL:57:LEU:HD23	1:CL:203:TRP:CH2	2.52	0.45
1:CM:101:ARG:CZ	1:CM:166:LEU:CD1	2.94	0.45
1:CM:138:PHE:CD1	1:CM:138:PHE:C	2.93	0.45
1:CO:79:VAL:HG13	1:CO:80:VAL:HG12	1.98	0.45
1:AP:81:ASP:C	1:AP:81:ASP:OD1	2.60	0.45
1:BQ:184:ILE:HD13	1:BQ:184:ILE:N	2.32	0.45
1:BQ:205:VAL:HG22	1:BQ:206:ARG:N	2.32	0.45
1:CQ:89:LEU:HD13	1:CQ:203:TRP:CG	2.52	0.45
1:CQ:123:TYR:HB2	1:CQ:185:LEU:CD2	2.47	0.45
1:CR:112:GLN:HE21	1:CT:44:THR:N	2.14	0.45
1:BT:142:GLN:HB2	1:CT:48:PHE:HE1	1.81	0.45
1:AT:61:SER:HB2	1:AT:89:LEU:HD22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:234:SER:HB3	1:AV:237:ASP:O	2.17	0.45
1:CY:77:TYR:CD1	1:CY:77:TYR:C	2.93	0.45
1:CY:91:ARG:HD2	1:Ca:98:ILE:HB	1.97	0.45
1:BZ:124:VAL:HG11	1:BZ:138:PHE:CD2	2.52	0.45
1:CZ:138:PHE:C	1:CZ:138:PHE:CD1	2.94	0.45
1:Aa:64:SER:OG	1:Aa:80:VAL:HG21	2.17	0.45
1:Aa:127:PHE:O	1:Aa:144:THR:OG1	2.29	0.45
1:Aa:226:GLY:N	1:Aa:243:LEU:O	2.49	0.45
1:Bb:234:SER:HB3	1:Bb:237:ASP:OD1	2.16	0.45
1:Bc:163:THR:C	1:Bc:165:THR:HG22	2.42	0.45
1:Cc:57:LEU:HD23	1:Cc:203:TRP:CH2	2.51	0.45
1:Cd:112:GLN:NE2	1:Cd:155:SER:OG	2.50	0.45
1:AA:91:ARG:NH2	1:BV:210:PRO:HB3	2.32	0.45
1:AA:124:VAL:HG11	1:AA:138:PHE:CD1	2.52	0.45
1:CA:81:ASP:OD2	1:CA:136:HIS:NE2	2.45	0.45
1:BB:128:LEU:HD12	1:BB:184:ILE:HD11	1.98	0.45
1:AB:91:ARG:HD2	1:AY:143:ALA:HB1	1.98	0.45
1:BC:98:ILE:HG22	1:AY:91:ARG:CZ	2.47	0.45
1:BD:254:GLY:CA	1:BD:283:LYS:HE3	2.28	0.45
1:CD:44:THR:H	1:CI:112:GLN:HE21	1.63	0.45
1:CD:118:ASN:HA	1:BF:116:PRO:CB	2.47	0.45
1:BE:122:GLY:C	1:BE:188:VAL:CG2	2.86	0.45
1:AE:298:TRP:NE1	1:AE:312:VAL:HA	2.32	0.45
1:CE:85:VAL:O	1:CE:86:PRO:C	2.60	0.45
1:AF:98:ILE:HG22	1:AF:99:PHE:CD2	2.51	0.45
1:BG:122:GLY:C	1:BG:188:VAL:CG2	2.82	0.45
1:AJ:62:ARG:CZ	1:AR:138:PHE:CE2	3.00	0.45
1:CJ:237:ASP:HB3	1:CJ:297:ARG:HG2	1.97	0.45
1:CL:133:ASP:O	1:CL:182:ARG:NH2	2.49	0.45
1:BM:128:LEU:HD12	1:BM:184:ILE:HD11	1.99	0.45
1:AM:61:SER:CB	1:AM:90:PRO:HD2	2.36	0.45
1:AM:246:THR:N	1:AM:247:PRO:CD	2.79	0.45
1:CM:34:ARG:HG3	1:BW:156:ARG:NH2	2.31	0.45
1:CM:62:ARG:HA	1:CM:200:LEU:HD23	1.98	0.45
1:CO:109:PHE:HB2	1:CO:158:VAL:HG12	1.96	0.45
1:CO:250:ILE:O	1:CO:250:ILE:HG22	2.16	0.45
1:AP:281:HIS:ND1	1:AP:301:TRP:HB3	2.32	0.45
1:CP:130:ASP:OD2	1:CP:176:ARG:NH2	2.50	0.45
1:AQ:268:SER:CB	1:AQ:273:ASP:O	2.64	0.45
1:AQ:298:TRP:NE1	1:AQ:312:VAL:HA	2.32	0.45
1:CQ:119:THR:O	1:CQ:120:GLY:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:99:PHE:HB3	1:CR:209:VAL:O	2.17	0.45
1:AU:118:ASN:O	1:AX:116:PRO:HB3	2.16	0.45
1:CU:63:ILE:HD12	1:CU:88:LEU:CG	2.44	0.45
1:BV:234:SER:HB3	1:BV:237:ASP:OD1	2.16	0.45
1:CV:119:THR:O	1:CV:120:GLY:C	2.59	0.45
1:BW:225:GLN:HG3	1:BW:244:GLY:O	2.17	0.45
1:CW:202:ARG:HH12	1:Cd:46:THR:HB	1.81	0.45
1:CX:250:ILE:HG22	1:CX:250:ILE:O	2.16	0.45
1:CY:46:THR:HB	1:Ca:202:ARG:HH12	1.81	0.45
1:CY:57:LEU:HD23	1:CY:203:TRP:CH2	2.52	0.45
1:CY:81:ASP:OD2	1:CY:136:HIS:NE2	2.46	0.45
1:CY:113:PRO:HA	1:CY:197:VAL:HA	1.99	0.45
1:Ba:122:GLY:C	1:Ba:188:VAL:CG2	2.87	0.45
1:Ba:142:GLN:HB2	1:Ca:48:PHE:HE1	1.82	0.45
1:Ba:234:SER:HB3	1:Ba:237:ASP:OD1	2.17	0.45
1:Ca:63:ILE:HD12	1:Ca:88:LEU:CD1	2.46	0.45
1:Bb:122:GLY:C	1:Bb:188:VAL:CG2	2.86	0.45
1:Cc:81:ASP:HA	1:Cc:184:ILE:HG22	1.98	0.45
1:CA:57:LEU:HD23	1:CA:203:TRP:CH2	2.51	0.45
1:CA:69:PRO:O	1:CA:72:THR:OG1	2.28	0.45
1:CA:199:VAL:O	1:CA:199:VAL:CG1	2.63	0.45
1:AC:109:PHE:HB2	1:AC:158:VAL:CG1	2.47	0.45
1:CC:80:VAL:HG11	1:CC:185:LEU:HB2	1.99	0.45
1:CC:133:ASP:O	1:CC:182:ARG:NH2	2.49	0.45
1:CC:202:ARG:HH12	1:CJ:46:THR:HB	1.80	0.45
1:BD:225:GLN:HG3	1:BD:244:GLY:O	2.17	0.45
1:CD:79:VAL:HG13	1:CD:80:VAL:HG12	1.98	0.45
1:AE:162:TYR:CE2	1:AE:164:ARG:HG2	2.52	0.45
1:AE:288:ASN:O	1:AE:289:ALA:C	2.59	0.45
1:CG:99:PHE:HB3	1:CG:209:VAL:O	2.17	0.45
1:CH:79:VAL:HG13	1:CH:80:VAL:HG12	1.99	0.45
1:AI:188:VAL:HG23	1:Aa:114:MET:SD	2.56	0.45
1:BJ:123:TYR:HB2	1:BJ:185:LEU:CD1	2.47	0.45
1:CJ:57:LEU:HD23	1:CJ:203:TRP:CH2	2.51	0.45
1:AK:279:TYR:CE2	1:AK:311:GLY:O	2.65	0.45
1:AK:314:TYR:CE1	1:AK:316:SER:CA	2.93	0.45
1:CL:54:ASP:OD1	1:CL:54:ASP:N	2.50	0.45
1:CL:74:THR:O	1:CL:75:ASP:C	2.59	0.45
1:CL:123:TYR:HB2	1:CL:185:LEU:CD2	2.47	0.45
1:CL:214:ASN:HA	1:CL:215:PRO:HD3	1.84	0.45
1:CL:237:ASP:HB3	1:CL:297:ARG:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:138:PHE:CE2	1:Bc:62:ARG:NH2	2.85	0.45
1:CN:63:ILE:HD12	1:CN:88:LEU:CG	2.45	0.45
1:CO:155:SER:O	1:CO:156:ARG:HD3	2.17	0.45
1:AQ:288:ASN:O	1:AQ:289:ALA:C	2.60	0.45
1:CQ:199:VAL:O	1:CQ:199:VAL:CG1	2.65	0.45
1:BR:150:ALA:HB2	1:BR:156:ARG:HD3	1.98	0.45
1:AR:288:ASN:O	1:AR:289:ALA:C	2.59	0.45
1:CR:155:SER:O	1:CR:156:ARG:HD3	2.17	0.45
1:CS:57:LEU:HD23	1:CS:203:TRP:CH2	2.51	0.45
1:CT:85:VAL:O	1:CT:86:PRO:C	2.59	0.45
1:CU:46:THR:HB	1:Cb:202:ARG:HH12	1.80	0.45
1:BV:136:HIS:O	1:BV:186:LEU:HD11	2.17	0.45
1:BV:166:LEU:HD13	1:BV:167:LEU:N	2.32	0.45
1:BX:123:TYR:N	1:BX:188:VAL:HG22	2.31	0.45
1:CX:46:THR:HB	1:Cc:202:ARG:HH12	1.82	0.45
1:AY:88:LEU:C	1:AY:88:LEU:HD13	2.42	0.45
1:BZ:205:VAL:HG22	1:BZ:206:ARG:N	2.32	0.45
1:AZ:264:SER:OG	1:AZ:276:ARG:NH1	2.48	0.45
1:Ba:163:THR:C	1:Ba:165:THR:HG22	2.42	0.45
1:Cc:63:ILE:HD12	1:Cc:88:LEU:CD1	2.47	0.45
1:Cc:80:VAL:CG1	1:Cc:185:LEU:HB2	2.45	0.45
1:BA:136:HIS:O	1:BA:186:LEU:HD11	2.17	0.45
1:BA:161:GLN:NE2	1:CA:210:PRO:HD2	2.32	0.45
1:BB:142:GLN:HB2	1:CB:48:PHE:CE1	2.51	0.45
1:AB:246:THR:N	1:AB:247:PRO:CD	2.80	0.45
1:CB:250:ILE:HG22	1:CB:250:ILE:O	2.17	0.45
1:AC:298:TRP:O	1:AC:310:ASP:O	2.35	0.45
1:CC:45:VAL:HG13	1:CC:45:VAL:O	2.17	0.45
1:AE:122:GLY:C	1:AE:188:VAL:HG22	2.41	0.45
1:CI:99:PHE:CD2	1:CI:207:LEU:HB3	2.52	0.45
1:BJ:260:ASP:HA	1:AJ:261:ARG:NH2	2.31	0.45
1:BL:232:SER:HB3	1:BL:242:LEU:HD11	1.99	0.45
1:AL:162:TYR:CE2	1:AL:164:ARG:HG2	2.52	0.45
1:CM:44:THR:H	1:CO:112:GLN:HE21	1.63	0.45
1:CM:79:VAL:HG13	1:CM:80:VAL:HG12	1.97	0.45
1:AO:298:TRP:NE1	1:AO:312:VAL:CB	2.76	0.45
1:CO:199:VAL:O	1:CO:199:VAL:CG1	2.64	0.45
1:CP:223:MET:HE2	1:CP:328:GLY:HA2	1.98	0.45
1:AQ:302:ASP:C	1:AQ:305:ASN:HD21	2.23	0.45
1:CS:130:ASP:OD2	1:CS:176:ARG:NH2	2.49	0.45
1:AT:224:THR:HG22	1:AT:329:THR:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BU:205:VAL:HG22	1:BU:206:ARG:N	2.32	0.45
1:BV:122:GLY:C	1:BV:188:VAL:CG2	2.84	0.45
1:CW:199:VAL:O	1:CW:199:VAL:CG1	2.65	0.45
1:BY:86:PRO:HB3	1:BY:92:LEU:HD22	1.99	0.45
1:CZ:58:SER:HB3	1:CZ:204:SER:HB2	1.98	0.45
1:CZ:80:VAL:HG11	1:CZ:185:LEU:CB	2.45	0.45
1:Aa:63:ILE:CD1	1:Aa:89:LEU:HD21	2.47	0.45
1:Ab:288:ASN:O	1:Ab:289:ALA:C	2.60	0.45
1:Cb:123:TYR:HA	1:Cb:188:VAL:HG23	1.98	0.45
1:Cb:264:SER:HB2	1:Cb:324:LEU:HD22	1.99	0.45
1:Bc:136:HIS:O	1:Bc:186:LEU:HD11	2.16	0.45
1:Cc:77:TYR:C	1:Cc:77:TYR:CD1	2.93	0.45
1:Bd:163:THR:C	1:Bd:165:THR:HG22	2.42	0.45
1:Cd:138:PHE:CD1	1:Cd:138:PHE:C	2.94	0.45
1:BA:109:PHE:HB2	1:BA:158:VAL:CG1	2.47	0.45
1:AA:91:ARG:CZ	1:BV:98:ILE:CG2	2.95	0.45
1:BB:234:SER:HB3	1:BB:237:ASP:OD1	2.17	0.45
1:AB:162:TYR:CE2	1:AB:164:ARG:HG2	2.52	0.45
1:AB:263:LEU:HB3	1:AB:279:TYR:O	2.17	0.45
1:BC:98:ILE:HG22	1:AY:91:ARG:NH2	2.31	0.45
1:BC:109:PHE:HB2	1:BC:158:VAL:CG1	2.47	0.45
1:BC:232:SER:HB3	1:BC:242:LEU:HD11	1.98	0.45
1:CC:113:PRO:HA	1:CC:197:VAL:HA	1.99	0.45
1:BD:260:ASP:HA	1:AD:261:ARG:NH2	2.32	0.45
1:AD:224:THR:HG22	1:AD:329:THR:N	2.32	0.45
1:CD:63:ILE:HD12	1:CD:88:LEU:CD1	2.46	0.45
1:CF:112:GLN:NE2	1:CF:155:SER:OG	2.50	0.45
1:CK:91:ARG:NH1	1:CL:52:THR:O	2.50	0.45
1:CM:62:ARG:H	1:BO:142:GLN:NE2	2.15	0.45
1:CM:119:THR:O	1:CM:120:GLY:C	2.60	0.45
1:BN:163:THR:C	1:BN:165:THR:HG22	2.42	0.45
1:CN:118:ASN:HA	1:BP:116:PRO:CB	2.47	0.45
1:AO:162:TYR:CE2	1:AO:164:ARG:HG2	2.52	0.45
1:AO:298:TRP:NE1	1:AO:312:VAL:HA	2.32	0.45
1:CP:78:VAL:O	1:CP:78:VAL:HG13	2.17	0.45
1:CP:99:PHE:CD2	1:CP:207:LEU:HB3	2.52	0.45
1:BQ:156:ARG:HH22	1:CV:34:ARG:CD	2.30	0.45
1:CQ:78:VAL:HG13	1:CQ:78:VAL:O	2.17	0.45
1:BR:80:VAL:CG1	1:BR:185:LEU:HB3	2.46	0.45
1:BR:168:TRP:CE2	1:AR:176:ARG:HD2	2.52	0.45
1:AR:98:ILE:HG22	1:AR:99:PHE:CD2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:63:ILE:CD1	1:AS:89:LEU:HD21	2.47	0.45
1:AU:127:PHE:O	1:AU:144:THR:OG1	2.32	0.45
1:AW:314:TYR:CE1	1:AW:316:SER:CA	2.91	0.45
1:CW:123:TYR:HB2	1:CW:185:LEU:CD2	2.47	0.45
1:BX:124:VAL:HG11	1:BX:138:PHE:CD2	2.52	0.45
1:BY:165:THR:OG1	1:BY:166:LEU:N	2.49	0.45
1:BZ:163:THR:C	1:BZ:165:THR:HG22	2.42	0.45
1:BZ:234:SER:HB3	1:BZ:237:ASP:OD1	2.17	0.45
1:Cb:109:PHE:HB2	1:Cb:158:VAL:HG12	1.98	0.45
1:Bc:319:GLN:HE21	1:Bc:319:GLN:C	2.25	0.45
1:Bd:260:ASP:HA	1:Ad:261:ARG:NH2	2.33	0.45
1:Cd:89:LEU:HD13	1:Cd:203:TRP:CG	2.52	0.45
1:AA:298:TRP:HE1	1:AA:312:VAL:HA	1.82	0.44
1:CA:138:PHE:C	1:CA:138:PHE:CD1	2.95	0.44
1:BB:163:THR:C	1:BB:165:THR:HG22	2.42	0.44
1:CB:99:PHE:HB3	1:CB:209:VAL:O	2.16	0.44
1:AD:98:ILE:HG22	1:AD:99:PHE:CD2	2.51	0.44
1:CE:121:GLY:C	1:CE:152:TRP:CD1	2.95	0.44
1:AF:61:SER:HB2	1:AF:89:LEU:HD22	1.99	0.44
1:CH:199:VAL:O	1:CH:199:VAL:CG1	2.63	0.44
1:BL:91:ARG:HG2	1:AU:98:ILE:HG12	1.98	0.44
1:BL:319:GLN:HE21	1:BL:319:GLN:C	2.24	0.44
1:AM:238:PHE:CZ	1:AM:296:PHE:HB2	2.52	0.44
1:AM:298:TRP:NE1	1:AM:312:VAL:HA	2.32	0.44
1:CN:223:MET:HE2	1:CN:328:GLY:HA2	1.99	0.44
1:BQ:124:VAL:HG11	1:BQ:138:PHE:CD2	2.52	0.44
1:BR:98:ILE:CA	1:BR:211:SER:O	2.65	0.44
1:AS:98:ILE:HG22	1:AS:99:PHE:CD2	2.52	0.44
1:CS:85:VAL:O	1:CS:86:PRO:C	2.59	0.44
1:BT:142:GLN:HB2	1:CT:48:PHE:CE1	2.51	0.44
1:AT:143:ALA:HB1	1:AV:91:ARG:HD2	1.99	0.44
1:BU:225:GLN:HG3	1:BU:244:GLY:O	2.18	0.44
1:BY:109:PHE:HB2	1:BY:158:VAL:CG1	2.47	0.44
1:BY:142:GLN:HB2	1:CY:48:PHE:CE1	2.52	0.44
1:AY:298:TRP:NE1	1:AY:312:VAL:HA	2.31	0.44
1:Ba:123:TYR:HB2	1:Ba:185:LEU:CD1	2.46	0.44
1:Ca:123:TYR:HA	1:Ca:188:VAL:HG23	1.98	0.44
1:Bb:225:GLN:HG3	1:Bb:244:GLY:O	2.17	0.44
1:Cb:250:ILE:O	1:Cb:250:ILE:HG22	2.17	0.44
1:Ac:288:ASN:O	1:Ac:289:ALA:C	2.58	0.44
1:Bd:205:VAL:HG22	1:Bd:206:ARG:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:124:VAL:O	1:CA:124:VAL:HG13	2.15	0.44
1:BB:150:ALA:HB2	1:BB:156:ARG:HD3	1.98	0.44
1:CC:62:ARG:HA	1:CC:200:LEU:HD23	1.99	0.44
1:CE:133:ASP:O	1:CE:182:ARG:NH2	2.50	0.44
1:CE:190:ASN:HD22	1:CE:190:ASN:N	2.15	0.44
1:BF:260:ASP:HA	1:AF:261:ARG:NH2	2.32	0.44
1:CH:123:TYR:HA	1:CH:188:VAL:HG23	1.99	0.44
1:CI:214:ASN:HA	1:CI:215:PRO:HD3	1.85	0.44
1:BJ:123:TYR:N	1:BJ:188:VAL:HG22	2.32	0.44
1:CJ:99:PHE:CD2	1:CJ:207:LEU:HB3	2.52	0.44
1:CK:123:TYR:CD1	1:CK:185:LEU:HD21	2.52	0.44
1:CK:186:LEU:HD23	1:CK:186:LEU:N	2.32	0.44
1:CK:223:MET:HE2	1:CK:328:GLY:HA2	1.99	0.44
1:BM:74:THR:HA	1:BM:190:ASN:HD22	1.82	0.44
1:AM:64:SER:OG	1:AM:80:VAL:HG21	2.16	0.44
1:CM:199:VAL:O	1:CM:199:VAL:CG1	2.65	0.44
1:BO:122:GLY:C	1:BO:188:VAL:CG2	2.84	0.44
1:BP:136:HIS:O	1:BP:186:LEU:HD11	2.17	0.44
1:CP:112:GLN:NE2	1:CP:155:SER:OG	2.50	0.44
1:CR:130:ASP:OD2	1:CR:176:ARG:NH2	2.51	0.44
1:AT:246:THR:N	1:AT:247:PRO:CD	2.80	0.44
1:AT:298:TRP:HE1	1:AT:312:VAL:HA	1.82	0.44
1:AT:302:ASP:OD2	1:AT:305:ASN:CB	2.60	0.44
1:BU:91:ARG:NH1	1:AX:98:ILE:CG2	2.80	0.44
1:BU:281:HIS:CE1	1:BU:301:TRP:HB3	2.52	0.44
1:CW:57:LEU:HD23	1:CW:203:TRP:CH2	2.52	0.44
1:BX:250:ILE:O	1:BX:250:ILE:HG22	2.16	0.44
1:AX:298:TRP:NE1	1:AX:312:VAL:CB	2.77	0.44
1:AY:64:SER:OG	1:AY:80:VAL:HG21	2.17	0.44
1:AZ:124:VAL:HG11	1:AZ:138:PHE:CD1	2.52	0.44
1:Aa:298:TRP:NE1	1:Aa:312:VAL:HA	2.32	0.44
1:Ab:98:ILE:HG22	1:Ab:99:PHE:CD2	2.52	0.44
1:Cb:78:VAL:HG13	1:Cb:78:VAL:O	2.17	0.44
1:Cb:79:VAL:HG13	1:Cb:80:VAL:HG12	1.98	0.44
1:Cb:85:VAL:O	1:Cb:86:PRO:C	2.58	0.44
1:Ac:298:TRP:HE1	1:Ac:312:VAL:HA	1.82	0.44
1:Ad:288:ASN:O	1:Ad:289:ALA:C	2.59	0.44
1:Cd:81:ASP:HA	1:Cd:184:ILE:HG22	2.00	0.44
1:AB:91:ARG:CZ	1:BY:98:ILE:CG2	2.95	0.44
1:AB:281:HIS:ND1	1:AB:301:TRP:HB3	2.33	0.44
1:CB:163:THR:OG1	1:CB:165:THR:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:45:VAL:HG23	1:CJ:200:LEU:HD13	2.00	0.44
1:BD:115:CYS:C	1:CW:120:GLY:HA2	2.42	0.44
1:BD:124:VAL:HG11	1:BD:138:PHE:CD2	2.52	0.44
1:AD:188:VAL:CG2	1:AW:114:MET:SD	3.05	0.44
1:AD:263:LEU:HB3	1:AD:279:TYR:O	2.17	0.44
1:BE:74:THR:HA	1:BE:190:ASN:HD22	1.83	0.44
1:CE:250:ILE:O	1:CE:250:ILE:HG22	2.18	0.44
1:CF:99:PHE:CD2	1:CF:207:LEU:HB3	2.53	0.44
1:CH:130:ASP:OD2	1:CH:176:ARG:NH2	2.50	0.44
1:BI:91:ARG:HG2	1:Aa:98:ILE:HG12	1.99	0.44
1:BI:136:HIS:O	1:BI:186:LEU:HD11	2.16	0.44
1:AI:80:VAL:HG13	1:AI:185:LEU:HB3	1.97	0.44
1:CJ:250:ILE:HG22	1:CJ:250:ILE:O	2.18	0.44
1:CK:46:THR:HB	1:CL:202:ARG:HH12	1.82	0.44
1:BL:142:GLN:HB2	1:CL:48:PHE:HE1	1.80	0.44
1:BL:166:LEU:HD13	1:BL:167:LEU:N	2.32	0.44
1:CL:99:PHE:HB3	1:CL:209:VAL:O	2.17	0.44
1:BM:136:HIS:O	1:BM:186:LEU:HD11	2.18	0.44
1:AM:263:LEU:HB3	1:AM:279:TYR:O	2.17	0.44
1:BN:111:ILE:HG22	1:BN:155:SER:HA	1.99	0.44
1:CP:80:VAL:HG11	1:CP:185:LEU:HB2	1.99	0.44
1:CP:121:GLY:C	1:CP:152:TRP:CD1	2.96	0.44
1:CP:123:TYR:CD1	1:CP:185:LEU:HD21	2.53	0.44
1:CP:202:ARG:HH12	1:CQ:46:THR:HB	1.83	0.44
1:BQ:98:ILE:CA	1:BQ:211:SER:O	2.65	0.44
1:BQ:163:THR:C	1:BQ:165:THR:HG22	2.42	0.44
1:AQ:63:ILE:HG23	1:AQ:88:LEU:HD11	1.99	0.44
1:AQ:281:HIS:ND1	1:AQ:301:TRP:HB3	2.32	0.44
1:AQ:298:TRP:NE1	1:AQ:312:VAL:CB	2.76	0.44
1:CQ:223:MET:HE2	1:CQ:328:GLY:HA2	1.97	0.44
1:BR:260:ASP:HA	1:AR:261:ARG:NH2	2.31	0.44
1:CR:133:ASP:O	1:CR:182:ARG:NH2	2.50	0.44
1:CR:158:VAL:O	1:CR:158:VAL:HG13	2.18	0.44
1:BU:142:GLN:HB2	1:CU:48:PHE:CE1	2.52	0.44
1:BV:109:PHE:HB2	1:BV:158:VAL:CG1	2.47	0.44
1:BV:260:ASP:HA	1:AV:261:ARG:NH2	2.32	0.44
1:BW:124:VAL:HG11	1:BW:138:PHE:CD2	2.53	0.44
1:BW:165:THR:OG1	1:BW:166:LEU:N	2.49	0.44
1:CX:130:ASP:OD2	1:CX:176:ARG:NH2	2.50	0.44
1:BY:161:GLN:NE2	1:CY:210:PRO:HD2	2.32	0.44
1:AY:162:TYR:CE2	1:AY:164:ARG:HG2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:69:PRO:O	1:CZ:72:THR:OG1	2.26	0.44
1:Ba:100:GLN:O	1:Ba:169:THR:N	2.42	0.44
1:Ba:184:ILE:HD13	1:Ba:184:ILE:N	2.32	0.44
1:Aa:234:SER:HB3	1:Aa:237:ASP:O	2.17	0.44
1:Aa:288:ASN:O	1:Aa:289:ALA:C	2.60	0.44
1:Ac:264:SER:OG	1:Ac:276:ARG:NH1	2.49	0.44
1:Cc:123:TYR:HA	1:Cc:188:VAL:HG23	1.98	0.44
1:Cd:123:TYR:HA	1:Cd:188:VAL:HG23	1.98	0.44
1:CB:43:SER:O	1:CL:34:ARG:HD3	2.17	0.44
1:AC:264:SER:OG	1:AC:276:ARG:NH1	2.47	0.44
1:CC:44:THR:H	1:CJ:112:GLN:HE21	1.65	0.44
1:BD:142:GLN:HB2	1:CD:48:PHE:CE1	2.52	0.44
1:BD:281:HIS:CE1	1:BD:301:TRP:HB3	2.53	0.44
1:AD:63:ILE:CD1	1:AD:89:LEU:HD21	2.48	0.44
1:CD:57:LEU:HD23	1:CD:203:TRP:CH2	2.53	0.44
1:CE:62:ARG:H	1:BH:142:GLN:NE2	2.15	0.44
1:CE:99:PHE:CD2	1:CE:207:LEU:HB3	2.53	0.44
1:AF:91:ARG:CZ	1:Bb:98:ILE:HG22	2.47	0.44
1:AF:263:LEU:HB3	1:AF:279:TYR:O	2.17	0.44
1:CG:190:ASN:HD22	1:CG:190:ASN:N	2.16	0.44
1:AH:314:TYR:CD1	1:AH:314:TYR:C	2.94	0.44
1:CH:54:ASP:OD1	1:CH:54:ASP:N	2.50	0.44
1:CI:80:VAL:HG11	1:CI:185:LEU:CB	2.45	0.44
1:CI:223:MET:HE2	1:CI:328:GLY:HA2	1.98	0.44
1:AJ:74:THR:O	1:AJ:75:ASP:C	2.60	0.44
1:BM:281:HIS:CE1	1:BM:301:TRP:HB3	2.53	0.44
1:AM:61:SER:HB2	1:AM:89:LEU:HD22	1.99	0.44
1:BN:150:ALA:HB2	1:BN:156:ARG:HD3	2.00	0.44
1:CN:54:ASP:OD1	1:CN:54:ASP:N	2.51	0.44
1:CP:57:LEU:HD23	1:CP:203:TRP:CH2	2.51	0.44
1:CP:123:TYR:HB2	1:CP:185:LEU:CD2	2.48	0.44
1:BQ:166:LEU:CD1	1:BQ:166:LEU:C	2.90	0.44
1:BQ:254:GLY:CA	1:BQ:283:LYS:HE3	2.30	0.44
1:BS:142:GLN:HB2	1:CS:48:PHE:CE1	2.52	0.44
1:AU:253:ASP:CG	1:AU:285:PHE:CA	2.78	0.44
1:BW:232:SER:HB3	1:BW:242:LEU:HD11	1.99	0.44
1:CX:123:TYR:HB2	1:CX:185:LEU:CD2	2.47	0.44
1:BY:142:GLN:HB2	1:CY:48:PHE:HE1	1.82	0.44
1:AY:61:SER:HB2	1:AY:89:LEU:HD22	2.00	0.44
1:Ca:62:ARG:HA	1:Ca:200:LEU:HD23	2.00	0.44
1:Bb:130:ASP:HB3	1:Bb:133:ASP:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bc:123:TYR:N	1:Bc:188:VAL:HG22	2.32	0.44
1:Bc:250:ILE:O	1:Bc:250:ILE:HG22	2.16	0.44
1:Cc:317:ASP:HB3	1:Cc:319:GLN:NE2	2.33	0.44
1:AB:124:VAL:HG11	1:AB:138:PHE:CD1	2.52	0.44
1:AB:127:PHE:O	1:AB:144:THR:OG1	2.29	0.44
1:AB:302:ASP:C	1:AB:305:ASN:HD21	2.23	0.44
1:BC:163:THR:O	1:BC:165:THR:HG22	2.17	0.44
1:CC:54:ASP:OD1	1:CC:54:ASP:N	2.51	0.44
1:BD:234:SER:HB3	1:BD:237:ASP:OD1	2.18	0.44
1:CD:74:THR:O	1:CD:75:ASP:C	2.60	0.44
1:CD:98:ILE:C	1:CD:211:SER:O	2.59	0.44
1:AE:298:TRP:NE1	1:AE:312:VAL:CB	2.77	0.44
1:CE:62:ARG:HA	1:CE:200:LEU:HD23	2.00	0.44
1:CE:199:VAL:O	1:CE:199:VAL:CG1	2.66	0.44
1:CF:119:THR:HG22	1:CF:119:THR:O	2.18	0.44
1:CG:123:TYR:HA	1:CG:188:VAL:HG23	1.99	0.44
1:AH:63:ILE:CD1	1:AH:89:LEU:HD21	2.48	0.44
1:AI:264:SER:OG	1:AI:276:ARG:NH1	2.50	0.44
1:CI:138:PHE:CD1	1:CI:138:PHE:C	2.95	0.44
1:BK:61:SER:CB	1:BK:90:PRO:HD2	2.30	0.44
1:AL:224:THR:HG22	1:AL:329:THR:N	2.32	0.44
1:AM:298:TRP:NE1	1:AM:312:VAL:CB	2.77	0.44
1:CM:78:VAL:O	1:CM:78:VAL:HG13	2.18	0.44
1:BN:260:ASP:HA	1:AN:261:ARG:NH2	2.33	0.44
1:BO:91:ARG:NH1	1:Ab:98:ILE:CG2	2.79	0.44
1:BO:123:TYR:N	1:BO:188:VAL:HG22	2.33	0.44
1:AO:61:SER:HB2	1:AO:89:LEU:HD22	2.00	0.44
1:AO:91:ARG:NH2	1:BW:98:ILE:CG2	2.81	0.44
1:BQ:260:ASP:HA	1:AQ:261:ARG:NH2	2.33	0.44
1:CR:62:ARG:HA	1:CR:200:LEU:HD23	1.99	0.44
1:AT:122:GLY:C	1:AT:188:VAL:HG22	2.42	0.44
1:CT:113:PRO:HA	1:CT:197:VAL:HA	2.00	0.44
1:BU:260:ASP:HA	1:AU:261:ARG:NH2	2.33	0.44
1:AV:224:THR:HG22	1:AV:329:THR:N	2.33	0.44
1:CW:112:GLN:HE21	1:Cd:44:THR:H	1.64	0.44
1:Aa:302:ASP:OD2	1:Aa:305:ASN:CB	2.62	0.44
1:Ab:298:TRP:NE1	1:Ab:312:VAL:HA	2.32	0.44
1:Ad:302:ASP:C	1:Ad:305:ASN:HD21	2.23	0.44
1:Cd:123:TYR:CD1	1:Cd:185:LEU:HD21	2.53	0.44
1:AB:61:SER:HB2	1:AB:89:LEU:HD22	1.99	0.44
1:AB:62:ARG:CZ	1:AY:138:PHE:CE2	3.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:288:ASN:O	1:AB:289:ALA:C	2.60	0.44
1:CB:214:ASN:HA	1:CB:215:PRO:HD3	1.85	0.44
1:AC:226:GLY:N	1:AC:243:LEU:O	2.48	0.44
1:CC:89:LEU:HD13	1:CC:203:TRP:CG	2.52	0.44
1:AF:91:ARG:NH2	1:Bb:98:ILE:HG22	2.33	0.44
1:BG:136:HIS:O	1:BG:186:LEU:HD11	2.16	0.44
1:BH:250:ILE:HG22	1:BH:250:ILE:O	2.16	0.44
1:AI:224:THR:HG22	1:AI:329:THR:N	2.33	0.44
1:BJ:142:GLN:HB2	1:CJ:48:PHE:CE1	2.52	0.44
1:CK:80:VAL:HG13	1:CK:185:LEU:N	2.33	0.44
1:BL:98:ILE:HB	1:BL:99:PHE:CD1	2.53	0.44
1:AL:103:ALA:HB2	1:AL:166:LEU:HA	2.00	0.44
1:CN:250:ILE:O	1:CN:250:ILE:HG22	2.17	0.44
1:AO:314:TYR:CD1	1:AO:314:TYR:C	2.95	0.44
1:CO:103:ALA:HB2	1:CO:166:LEU:HB3	2.00	0.44
1:CO:138:PHE:C	1:CO:138:PHE:CD1	2.94	0.44
1:AQ:264:SER:OG	1:AQ:276:ARG:NH1	2.50	0.44
1:CQ:63:ILE:HD12	1:CQ:88:LEU:CG	2.45	0.44
1:BR:163:THR:C	1:BR:165:THR:HG22	2.43	0.44
1:BR:214:ASN:HD22	1:BR:215:PRO:HD2	1.82	0.44
1:AS:256:VAL:HB	1:AS:335:ASP:HB3	1.99	0.44
1:CS:81:ASP:OD2	1:CS:136:HIS:NE2	2.44	0.44
1:AU:122:GLY:C	1:AU:188:VAL:HG22	2.43	0.44
1:AV:288:ASN:O	1:AV:289:ALA:C	2.61	0.44
1:CV:80:VAL:HG11	1:CV:185:LEU:HB2	1.98	0.44
1:CX:74:THR:O	1:CX:75:ASP:C	2.61	0.44
1:CX:80:VAL:HG11	1:CX:185:LEU:HB2	1.99	0.44
1:BY:163:THR:C	1:BY:165:THR:HG22	2.43	0.44
1:AY:298:TRP:HE1	1:AY:312:VAL:HA	1.83	0.44
1:Aa:302:ASP:C	1:Aa:305:ASN:HD21	2.23	0.44
1:Ab:127:PHE:O	1:Ab:144:THR:OG1	2.32	0.44
1:Cb:54:ASP:OD1	1:Cb:54:ASP:N	2.51	0.44
1:Ac:137:THR:HG23	1:Ac:140:ALA:CB	2.47	0.44
1:Ad:100:GLN:HA	1:Ad:169:THR:OG1	2.16	0.44
1:Cd:77:TYR:CD1	1:Cd:78:VAL:N	2.86	0.44
1:AA:61:SER:HB2	1:AA:89:LEU:HD22	1.98	0.44
1:CA:158:VAL:O	1:CA:158:VAL:HG13	2.17	0.44
1:AB:137:THR:HG23	1:AB:140:ALA:CB	2.48	0.44
1:BC:123:TYR:HB2	1:BC:185:LEU:CD1	2.48	0.44
1:BC:136:HIS:O	1:BC:186:LEU:HD11	2.18	0.44
1:BC:214:ASN:HD22	1:BC:215:PRO:HD2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:234:SER:HB3	1:AC:237:ASP:O	2.17	0.44
1:CD:123:TYR:HA	1:CD:188:VAL:HG23	1.98	0.44
1:BE:161:GLN:NE2	1:CE:210:PRO:HD2	2.32	0.44
1:AE:91:ARG:NH2	1:BM:98:ILE:HG22	2.32	0.44
1:CE:89:LEU:HD13	1:CE:203:TRP:CG	2.53	0.44
1:BF:225:GLN:HG3	1:BF:244:GLY:O	2.18	0.44
1:BG:260:ASP:HA	1:AG:261:ARG:NH2	2.32	0.44
1:BI:91:ARG:NH1	1:Aa:98:ILE:CG2	2.80	0.44
1:BI:142:GLN:HB2	1:CI:48:PHE:HE1	1.83	0.44
1:CI:45:VAL:HG13	1:CI:45:VAL:O	2.17	0.44
1:BJ:232:SER:HB3	1:BJ:242:LEU:HD11	2.00	0.44
1:AJ:80:VAL:HG12	1:AJ:185:LEU:HB3	1.99	0.44
1:AK:63:ILE:CD1	1:AK:89:LEU:HD21	2.48	0.44
1:CL:81:ASP:HA	1:CL:184:ILE:HG22	1.98	0.44
1:BM:260:ASP:HA	1:AM:261:ARG:NH2	2.33	0.44
1:CM:109:PHE:HB2	1:CM:158:VAL:HG12	1.98	0.44
1:BN:85:VAL:CG2	1:BN:86:PRO:HD2	2.47	0.44
1:BO:300:ILE:HG23	1:AO:323:ILE:CD1	2.48	0.44
1:CO:123:TYR:HB2	1:CO:185:LEU:HD21	1.99	0.44
1:AP:80:VAL:HG13	1:AP:185:LEU:HB3	1.98	0.44
1:AR:162:TYR:CE2	1:AR:164:ARG:HG2	2.53	0.44
1:CS:77:TYR:CD1	1:CS:77:TYR:C	2.95	0.44
1:AT:100:GLN:HA	1:AT:169:THR:OG1	2.18	0.44
1:AT:238:PHE:CZ	1:AT:296:PHE:HB2	2.53	0.44
1:CV:81:ASP:OD2	1:CV:136:HIS:NE2	2.45	0.44
1:BW:319:GLN:HE21	1:BW:319:GLN:C	2.24	0.44
1:BX:232:SER:HB3	1:BX:242:LEU:HD11	2.00	0.44
1:AY:288:ASN:O	1:AY:289:ALA:C	2.60	0.44
1:Aa:116:PRO:HG2	1:Aa:119:THR:OG1	2.17	0.44
1:Aa:298:TRP:NE1	1:Aa:312:VAL:CB	2.76	0.44
1:Ca:78:VAL:O	1:Ca:78:VAL:HG13	2.18	0.44
1:Cb:63:ILE:HD12	1:Cb:88:LEU:CG	2.47	0.44
1:Cb:123:TYR:HB2	1:Cb:185:LEU:HD21	1.99	0.44
1:Cc:250:ILE:HG22	1:Cc:250:ILE:O	2.17	0.44
1:BA:260:ASP:HA	1:AA:261:ARG:NH2	2.32	0.44
1:CB:158:VAL:HG13	1:CB:158:VAL:O	2.18	0.44
1:CC:62:ARG:H	1:BJ:142:GLN:NE2	2.16	0.44
1:BD:109:PHE:HB2	1:BD:158:VAL:CG1	2.48	0.44
1:BD:156:ARG:HH22	1:Cd:34:ARG:CD	2.31	0.44
1:BF:136:HIS:O	1:BF:186:LEU:HD11	2.18	0.44
1:AF:81:ASP:C	1:AF:81:ASP:OD1	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:100:GLN:HA	1:AF:169:THR:OG1	2.17	0.44
1:AF:212:LEU:C	1:AF:212:LEU:HD12	2.43	0.44
1:AF:298:TRP:HE1	1:AF:312:VAL:HA	1.82	0.44
1:AG:81:ASP:C	1:AG:81:ASP:OD1	2.60	0.44
1:AG:302:ASP:C	1:AG:305:ASN:HD21	2.23	0.44
1:AH:85:VAL:HG22	1:AH:86:PRO:HD2	2.00	0.44
1:AH:98:ILE:HG22	1:AH:99:PHE:CD2	2.53	0.44
1:AH:246:THR:N	1:AH:247:PRO:CD	2.80	0.44
1:CH:99:PHE:CD2	1:CH:207:LEU:HB3	2.53	0.44
1:AI:64:SER:OG	1:AI:80:VAL:HG21	2.17	0.44
1:CI:119:THR:O	1:CI:120:GLY:C	2.61	0.44
1:CJ:74:THR:O	1:CJ:75:ASP:C	2.61	0.44
1:AL:298:TRP:NE1	1:AL:312:VAL:HA	2.33	0.44
1:CM:118:ASN:OD1	1:Bc:118:ASN:ND2	2.51	0.44
1:CM:123:TYR:CD1	1:CM:185:LEU:HD21	2.52	0.44
1:BN:184:ILE:HD13	1:BN:184:ILE:N	2.32	0.44
1:AN:98:ILE:HG22	1:AN:99:PHE:CD2	2.53	0.44
1:CN:99:PHE:CD2	1:CN:207:LEU:HB3	2.53	0.44
1:BR:123:TYR:N	1:BR:188:VAL:HG22	2.33	0.44
1:BR:234:SER:HB3	1:BR:237:ASP:OD1	2.18	0.44
1:AT:80:VAL:HG13	1:AT:185:LEU:HB3	1.99	0.44
1:BU:142:GLN:HB2	1:CU:48:PHE:HE1	1.82	0.44
1:CW:237:ASP:HB3	1:CW:297:ARG:HG2	2.00	0.44
1:AX:63:ILE:HG23	1:AX:88:LEU:HD11	2.00	0.44
1:AX:264:SER:OG	1:AX:276:ARG:NH1	2.50	0.44
1:CX:223:MET:HE2	1:CX:328:GLY:HA2	2.00	0.44
1:AY:127:PHE:O	1:AY:144:THR:OG1	2.32	0.44
1:CY:123:TYR:HB2	1:CY:185:LEU:HD21	2.00	0.44
1:BZ:319:GLN:HE21	1:BZ:319:GLN:C	2.26	0.44
1:Aa:63:ILE:HG23	1:Aa:88:LEU:HD11	2.00	0.44
1:Ca:109:PHE:HB2	1:Ca:158:VAL:HG12	1.99	0.44
1:Bc:205:VAL:HG22	1:Bc:206:ARG:N	2.31	0.44
1:Ac:315:TYR:CE2	1:Ac:317:ASP:OD2	2.71	0.44
1:AA:162:TYR:CE2	1:AA:164:ARG:HG2	2.53	0.44
1:CB:202:ARG:HH12	1:CF:46:THR:HB	1.83	0.44
1:CC:99:PHE:CD2	1:CC:207:LEU:HB3	2.53	0.44
1:CC:123:TYR:HB2	1:CC:185:LEU:HD21	2.00	0.44
1:BD:91:ARG:NH1	1:AW:98:ILE:CG2	2.80	0.44
1:BD:184:ILE:HD13	1:BD:184:ILE:N	2.33	0.44
1:AD:162:TYR:CE2	1:AD:164:ARG:HG2	2.53	0.44
1:CD:45:VAL:HG13	1:CD:45:VAL:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:250:ILE:HG22	1:BE:250:ILE:O	2.17	0.44
1:CF:81:ASP:C	1:CF:81:ASP:OD1	2.60	0.44
1:AG:124:VAL:HG11	1:AG:138:PHE:CD1	2.53	0.44
1:CG:250:ILE:HG22	1:CG:250:ILE:O	2.17	0.44
1:BH:210:PRO:HB3	1:Ad:91:ARG:CZ	2.48	0.44
1:AH:281:HIS:ND1	1:AH:301:TRP:HB3	2.33	0.44
1:CI:123:TYR:HB2	1:CI:185:LEU:HD21	2.00	0.44
1:CJ:122:GLY:O	1:CJ:188:VAL:CB	2.65	0.44
1:AK:103:ALA:HB2	1:AK:166:LEU:HA	1.99	0.44
1:CL:63:ILE:HD12	1:CL:88:LEU:CG	2.47	0.44
1:BM:228:LEU:HD13	1:BM:238:PHE:CD2	2.53	0.44
1:AM:162:TYR:CE2	1:AM:164:ARG:HG2	2.53	0.44
1:CN:130:ASP:OD2	1:CN:176:ARG:NH2	2.51	0.44
1:BO:116:PRO:CB	1:Cb:118:ASN:HA	2.48	0.44
1:CO:78:VAL:O	1:CO:78:VAL:HG13	2.17	0.44
1:BP:281:HIS:CE1	1:BP:301:TRP:HB3	2.53	0.44
1:BQ:210:PRO:HB3	1:AZ:91:ARG:NH2	2.32	0.44
1:AQ:298:TRP:HE1	1:AQ:312:VAL:HA	1.83	0.44
1:AW:64:SER:OG	1:AW:80:VAL:HG21	2.17	0.44
1:AW:137:THR:HG23	1:AW:140:ALA:CB	2.48	0.44
1:CW:123:TYR:HA	1:CW:188:VAL:HG23	2.00	0.44
1:CW:138:PHE:CD1	1:CW:138:PHE:C	2.95	0.44
1:BX:260:ASP:HA	1:AX:261:ARG:NH2	2.33	0.44
1:AX:74:THR:O	1:AX:75:ASP:C	2.61	0.44
1:CX:78:VAL:O	1:CX:78:VAL:HG13	2.17	0.44
1:BY:122:GLY:C	1:BY:188:VAL:CG2	2.83	0.44
1:AY:224:THR:HG22	1:AY:329:THR:N	2.33	0.44
1:CY:121:GLY:C	1:CY:152:TRP:CD1	2.96	0.44
1:AZ:85:VAL:HG22	1:AZ:86:PRO:HD2	2.00	0.44
1:CZ:62:ARG:HA	1:CZ:200:LEU:HD23	1.99	0.44
1:Bb:100:GLN:NE2	1:Bb:211:SER:CB	2.81	0.44
1:Bb:254:GLY:CA	1:Bb:283:LYS:HE3	2.30	0.44
1:Ac:298:TRP:O	1:Ac:310:ASP:O	2.35	0.44
1:Bd:74:THR:HA	1:Bd:190:ASN:HD22	1.82	0.44
1:Bd:99:PHE:HA	1:Bd:209:VAL:O	2.18	0.44
1:Cd:223:MET:HE2	1:Cd:328:GLY:HA2	2.00	0.44
1:BA:75:ASP:C	1:BA:75:ASP:OD1	2.61	0.43
1:AA:256:VAL:HB	1:AA:335:ASP:HB3	2.00	0.43
1:CA:78:VAL:HG13	1:CA:78:VAL:O	2.18	0.43
1:CA:85:VAL:O	1:CA:86:PRO:C	2.60	0.43
1:CA:123:TYR:HA	1:CA:188:VAL:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:63:ILE:CD1	1:AC:89:LEU:HD21	2.48	0.43
1:CC:78:VAL:HG13	1:CC:78:VAL:O	2.18	0.43
1:AD:298:TRP:HE1	1:AD:312:VAL:HA	1.83	0.43
1:BF:205:VAL:HG22	1:BF:206:ARG:N	2.33	0.43
1:CH:63:ILE:HD12	1:CH:88:LEU:CG	2.45	0.43
1:BI:99:PHE:HA	1:BI:209:VAL:O	2.18	0.43
1:BJ:166:LEU:CD1	1:BJ:166:LEU:C	2.90	0.43
1:AJ:63:ILE:CD1	1:AJ:89:LEU:HD21	2.48	0.43
1:AJ:103:ALA:HB2	1:AJ:166:LEU:HA	2.00	0.43
1:BK:123:TYR:N	1:BK:188:VAL:HG22	2.32	0.43
1:AK:288:ASN:O	1:AK:289:ALA:C	2.60	0.43
1:CL:78:VAL:HG13	1:CL:78:VAL:O	2.18	0.43
1:AM:98:ILE:HG22	1:AM:99:PHE:CD2	2.53	0.43
1:AM:288:ASN:O	1:AM:289:ALA:C	2.61	0.43
1:CM:130:ASP:OD2	1:CM:176:ARG:NH2	2.50	0.43
1:BN:250:ILE:O	1:BN:250:ILE:HG22	2.18	0.43
1:AN:80:VAL:HG13	1:AN:185:LEU:HB3	1.99	0.43
1:AO:226:GLY:N	1:AO:243:LEU:O	2.50	0.43
1:AP:137:THR:HG23	1:AP:140:ALA:CB	2.47	0.43
1:CP:85:VAL:O	1:CP:86:PRO:C	2.61	0.43
1:CS:103:ALA:O	1:CS:205:VAL:HG23	2.17	0.43
1:CS:121:GLY:C	1:CS:152:TRP:CD1	2.96	0.43
1:BT:319:GLN:HE21	1:BT:319:GLN:C	2.26	0.43
1:AT:63:ILE:CD1	1:AT:89:LEU:HD21	2.48	0.43
1:CT:62:ARG:HA	1:CT:200:LEU:HD23	1.99	0.43
1:CT:124:VAL:O	1:CT:124:VAL:HG13	2.18	0.43
1:CT:138:PHE:CD1	1:CT:138:PHE:C	2.95	0.43
1:AU:281:HIS:ND1	1:AU:301:TRP:HB3	2.33	0.43
1:CU:99:PHE:HB3	1:CU:209:VAL:O	2.18	0.43
1:AV:314:TYR:HE1	1:AV:316:SER:HG	1.64	0.43
1:CW:69:PRO:O	1:CW:72:THR:OG1	2.25	0.43
1:BZ:260:ASP:HA	1:AZ:261:ARG:NH2	2.33	0.43
1:Ba:99:PHE:HA	1:Ba:209:VAL:O	2.18	0.43
1:Aa:124:VAL:HG11	1:Aa:138:PHE:CD1	2.53	0.43
1:Bb:163:THR:O	1:Bb:165:THR:HG22	2.18	0.43
1:Bb:228:LEU:HD13	1:Bb:238:PHE:CD2	2.53	0.43
1:Ab:298:TRP:O	1:Ab:310:ASP:O	2.36	0.43
1:Bc:85:VAL:CG2	1:Bc:86:PRO:HD2	2.48	0.43
1:Ac:80:VAL:HG12	1:Ac:185:LEU:HB3	2.00	0.43
1:Ad:268:SER:CB	1:Ad:273:ASP:O	2.66	0.43
1:CA:60:MET:CE	1:CA:202:ARG:HB3	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:283:LYS:HG2	1:BB:285:PHE:CE1	2.54	0.43
1:CC:72:THR:O	1:CC:191:ASN:OD1	2.36	0.43
1:CC:81:ASP:HA	1:CC:184:ILE:HG22	2.00	0.43
1:BD:98:ILE:CG2	1:AW:91:ARG:CZ	2.97	0.43
1:AD:81:ASP:C	1:AD:81:ASP:OD1	2.61	0.43
1:CD:138:PHE:CD1	1:CD:138:PHE:C	2.96	0.43
1:BF:250:ILE:O	1:BF:250:ILE:HG22	2.17	0.43
1:CF:79:VAL:HG13	1:CF:80:VAL:HG12	1.99	0.43
1:BG:163:THR:C	1:BG:165:THR:HG22	2.43	0.43
1:AG:64:SER:OG	1:AG:80:VAL:HG21	2.18	0.43
1:CH:121:GLY:C	1:CH:152:TRP:CD1	2.97	0.43
1:CH:122:GLY:O	1:CH:188:VAL:CB	2.65	0.43
1:BK:124:VAL:HG11	1:BK:138:PHE:CD2	2.53	0.43
1:AK:88:LEU:C	1:AK:88:LEU:HD13	2.43	0.43
1:AK:109:PHE:HB2	1:AK:158:VAL:HG12	1.99	0.43
1:AL:268:SER:CB	1:AL:273:ASP:O	2.65	0.43
1:AL:288:ASN:O	1:AL:289:ALA:C	2.60	0.43
1:CL:199:VAL:O	1:CL:199:VAL:CG1	2.65	0.43
1:BM:123:TYR:HB2	1:BM:185:LEU:CD1	2.48	0.43
1:CM:99:PHE:HB3	1:CM:209:VAL:O	2.19	0.43
1:CN:63:ILE:HD12	1:CN:88:LEU:CD1	2.47	0.43
1:BO:234:SER:HB3	1:BO:237:ASP:OD1	2.18	0.43
1:CO:99:PHE:CB	1:CO:209:VAL:O	2.65	0.43
1:CO:278:VAL:HG13	1:CO:278:VAL:O	2.19	0.43
1:BP:205:VAL:HG22	1:BP:206:ARG:N	2.33	0.43
1:AP:302:ASP:OD2	1:AP:305:ASN:CB	2.59	0.43
1:CP:62:ARG:HA	1:CP:200:LEU:HD23	2.00	0.43
1:AQ:69:PRO:C	1:AQ:72:THR:HG1	2.25	0.43
1:AQ:80:VAL:HG12	1:AQ:185:LEU:HB3	2.00	0.43
1:AQ:224:THR:HG22	1:AQ:329:THR:N	2.33	0.43
1:CS:123:TYR:HA	1:CS:188:VAL:HG23	1.99	0.43
1:AT:302:ASP:C	1:AT:305:ASN:HD21	2.22	0.43
1:CT:80:VAL:HG22	1:CT:81:ASP:N	2.32	0.43
1:CT:99:PHE:CD2	1:CT:207:LEU:HB3	2.53	0.43
1:CT:288:ASN:CG	1:CT:291:THR:HB	2.43	0.43
1:BU:163:THR:O	1:BU:165:THR:HG22	2.17	0.43
1:BV:232:SER:HB3	1:BV:242:LEU:HD11	2.00	0.43
1:AV:281:HIS:ND1	1:AV:301:TRP:HB3	2.33	0.43
1:CV:81:ASP:HA	1:CV:184:ILE:HG22	1.99	0.43
1:BW:246:THR:N	1:BW:247:PRO:CD	2.81	0.43
1:CW:81:ASP:HA	1:CW:184:ILE:HG22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:281:HIS:ND1	1:AX:301:TRP:HB3	2.33	0.43
1:CX:112:GLN:NE2	1:CX:155:SER:OG	2.51	0.43
1:BZ:122:GLY:C	1:BZ:188:VAL:CG2	2.85	0.43
1:AZ:111:ILE:O	1:AZ:112:GLN:C	2.61	0.43
1:CZ:250:ILE:O	1:CZ:250:ILE:HG22	2.17	0.43
1:Ba:136:HIS:O	1:Ba:186:LEU:HD11	2.18	0.43
1:Ba:166:LEU:CD1	1:Ba:166:LEU:C	2.91	0.43
1:Ba:281:HIS:CE1	1:Ba:301:TRP:HB3	2.53	0.43
1:Cb:63:ILE:HD12	1:Cb:88:LEU:CD1	2.48	0.43
1:Ac:226:GLY:N	1:Ac:243:LEU:O	2.50	0.43
1:Bd:254:GLY:CA	1:Bd:283:LYS:HE3	2.28	0.43
1:Cd:113:PRO:HA	1:Cd:197:VAL:HA	1.99	0.43
1:CA:102:TYR:HD2	1:CA:205:VAL:HG21	1.83	0.43
1:AB:63:ILE:CD1	1:AB:89:LEU:HD21	2.48	0.43
1:AC:308:PHE:CE2	1:AC:310:ASP:HA	2.53	0.43
1:CC:137:THR:O	1:CC:138:PHE:C	2.61	0.43
1:CD:133:ASP:O	1:CD:182:ARG:NH2	2.52	0.43
1:AE:298:TRP:O	1:AE:310:ASP:O	2.36	0.43
1:CE:317:ASP:HB3	1:CE:319:GLN:NE2	2.34	0.43
1:CF:99:PHE:HB3	1:CF:209:VAL:O	2.17	0.43
1:AG:91:ARG:NH2	1:Bd:210:PRO:HB3	2.33	0.43
1:AG:263:LEU:HB3	1:AG:279:TYR:O	2.19	0.43
1:AG:298:TRP:O	1:AG:310:ASP:O	2.37	0.43
1:BI:232:SER:HB3	1:BI:242:LEU:HD11	1.99	0.43
1:AI:246:THR:N	1:AI:247:PRO:CD	2.81	0.43
1:BK:109:PHE:HB2	1:BK:158:VAL:CG1	2.49	0.43
1:AK:137:THR:HG23	1:AK:140:ALA:CB	2.49	0.43
1:CK:123:TYR:HB2	1:CK:185:LEU:CD2	2.49	0.43
1:BL:246:THR:N	1:BL:247:PRO:CD	2.81	0.43
1:AL:61:SER:CB	1:AL:90:PRO:HD2	2.38	0.43
1:AL:100:GLN:HA	1:AL:169:THR:HG1	1.83	0.43
1:CL:130:ASP:OD2	1:CL:176:ARG:NH2	2.50	0.43
1:BM:166:LEU:CD1	1:BM:166:LEU:C	2.91	0.43
1:CM:121:GLY:C	1:CM:152:TRP:CD1	2.96	0.43
1:CM:223:MET:HE2	1:CM:328:GLY:HA2	2.00	0.43
1:BO:225:GLN:HG3	1:BO:244:GLY:O	2.18	0.43
1:BO:250:ILE:O	1:BO:250:ILE:HG22	2.17	0.43
1:AP:64:SER:OG	1:AP:80:VAL:HG21	2.18	0.43
1:AP:302:ASP:C	1:AP:305:ASN:HD21	2.22	0.43
1:AR:63:ILE:HG23	1:AR:88:LEU:HD11	2.00	0.43
1:AU:302:ASP:OD2	1:AU:305:ASN:CB	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:62:ARG:HA	1:CV:200:LEU:HD23	2.01	0.43
1:CW:62:ARG:HA	1:CW:200:LEU:HD23	1.99	0.43
1:AX:263:LEU:HB3	1:AX:279:TYR:O	2.18	0.43
1:Bb:260:ASP:HA	1:Ab:261:ARG:NH2	2.33	0.43
1:Ab:281:HIS:ND1	1:Ab:301:TRP:HB3	2.33	0.43
1:Bc:122:GLY:C	1:Bc:188:VAL:CG2	2.86	0.43
1:Ac:162:TYR:CE2	1:Ac:164:ARG:HG2	2.53	0.43
1:AA:74:THR:O	1:AA:75:ASP:C	2.59	0.43
1:AA:308:PHE:CE2	1:AA:310:ASP:HA	2.53	0.43
1:BB:142:GLN:NE2	1:CF:62:ARG:H	2.17	0.43
1:AB:91:ARG:NH2	1:BY:210:PRO:HB3	2.34	0.43
1:AB:109:PHE:CE2	1:AB:127:PHE:CD1	3.06	0.43
1:BC:98:ILE:HG22	1:AY:91:ARG:HH21	1.84	0.43
1:BC:122:GLY:C	1:BC:188:VAL:CG2	2.86	0.43
1:BC:234:SER:HB3	1:BC:237:ASP:OD1	2.18	0.43
1:CC:81:ASP:OD2	1:CC:136:HIS:NE2	2.47	0.43
1:CC:119:THR:O	1:CC:120:GLY:C	2.61	0.43
1:CC:214:ASN:HA	1:CC:215:PRO:HD3	1.85	0.43
1:AD:98:ILE:CG2	1:BF:91:ARG:NH1	2.81	0.43
1:CD:103:ALA:HB2	1:CD:166:LEU:HB3	2.00	0.43
1:BE:100:GLN:NE2	1:BE:211:SER:CB	2.81	0.43
1:AG:63:ILE:CD1	1:AG:89:LEU:HD21	2.49	0.43
1:CH:45:VAL:O	1:CH:45:VAL:HG13	2.19	0.43
1:BJ:281:HIS:CE1	1:BJ:301:TRP:HB3	2.53	0.43
1:CJ:80:VAL:HG11	1:CJ:185:LEU:HB2	2.00	0.43
1:CK:72:THR:O	1:CK:191:ASN:OD1	2.36	0.43
1:CK:109:PHE:HB2	1:CK:158:VAL:HG12	2.00	0.43
1:BL:281:HIS:CE1	1:BL:301:TRP:HB3	2.53	0.43
1:AO:100:GLN:HA	1:AO:169:THR:OG1	2.18	0.43
1:CO:81:ASP:OD2	1:CO:136:HIS:NE2	2.44	0.43
1:BP:123:TYR:HB2	1:BP:185:LEU:CD1	2.48	0.43
1:CP:119:THR:O	1:CP:120:GLY:C	2.61	0.43
1:BR:166:LEU:CD1	1:BR:166:LEU:C	2.91	0.43
1:AR:80:VAL:HG13	1:AR:185:LEU:HB3	1.99	0.43
1:CR:121:GLY:C	1:CR:152:TRP:CD1	2.96	0.43
1:AS:137:THR:HG23	1:AS:140:ALA:CB	2.49	0.43
1:AS:298:TRP:NE1	1:AS:312:VAL:HA	2.33	0.43
1:AS:298:TRP:HE1	1:AS:312:VAL:HA	1.84	0.43
1:CT:81:ASP:OD2	1:CT:136:HIS:NE2	2.46	0.43
1:CV:63:ILE:HD12	1:CV:88:LEU:CD1	2.49	0.43
1:CV:264:SER:HB2	1:CV:324:LEU:HD22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:226:GLY:C	1:BW:327:VAL:HG22	2.44	0.43
1:CW:121:GLY:C	1:CW:152:TRP:CD1	2.96	0.43
1:CY:99:PHE:CD2	1:CY:207:LEU:HB3	2.53	0.43
1:BZ:123:TYR:N	1:BZ:188:VAL:HG22	2.34	0.43
1:AZ:74:THR:O	1:AZ:75:ASP:C	2.61	0.43
1:Ba:128:LEU:HD12	1:Ba:184:ILE:HD11	2.00	0.43
1:Ba:130:ASP:HB3	1:Ba:133:ASP:HB2	2.00	0.43
1:Bb:184:ILE:HD13	1:Bb:184:ILE:N	2.34	0.43
1:Cc:81:ASP:OD1	1:Cc:81:ASP:C	2.61	0.43
1:Cc:119:THR:O	1:Cc:120:GLY:C	2.60	0.43
1:Cd:163:THR:OG1	1:Cd:165:THR:HG23	2.19	0.43
1:BA:74:THR:HA	1:BA:190:ASN:HD22	1.82	0.43
1:BB:300:ILE:HG23	1:AB:323:ILE:CD1	2.49	0.43
1:AB:91:ARG:HH21	1:BY:98:ILE:HG22	1.83	0.43
1:CB:81:ASP:HA	1:CB:184:ILE:HG22	2.00	0.43
1:BC:142:GLN:NE2	1:CJ:62:ARG:H	2.17	0.43
1:AC:274:VAL:HG13	1:AC:274:VAL:O	2.18	0.43
1:BD:319:GLN:HE21	1:BD:319:GLN:C	2.25	0.43
1:AD:116:PRO:HG2	1:AD:119:THR:OG1	2.19	0.43
1:CD:78:VAL:O	1:CD:78:VAL:HG13	2.18	0.43
1:AE:238:PHE:CZ	1:AE:296:PHE:HB2	2.54	0.43
1:BF:234:SER:HB3	1:BF:237:ASP:OD1	2.19	0.43
1:CF:89:LEU:HD13	1:CF:203:TRP:CG	2.52	0.43
1:CF:264:SER:HB2	1:CF:324:LEU:HD22	1.99	0.43
1:AG:308:PHE:CE2	1:AG:310:ASP:HA	2.53	0.43
1:BH:142:GLN:HB2	1:CH:48:PHE:HE1	1.83	0.43
1:BH:300:ILE:HG23	1:AH:323:ILE:CD1	2.49	0.43
1:AH:64:SER:OG	1:AH:80:VAL:HG21	2.19	0.43
1:AH:238:PHE:CZ	1:AH:296:PHE:HB2	2.53	0.43
1:CH:89:LEU:HD13	1:CH:203:TRP:CG	2.54	0.43
1:CI:133:ASP:O	1:CI:182:ARG:NH2	2.52	0.43
1:BK:276:ARG:O	1:AK:276:ARG:NH2	2.51	0.43
1:CK:39:VAL:O	1:CL:117:ALA:N	2.30	0.43
1:CL:80:VAL:HG11	1:CL:185:LEU:CB	2.49	0.43
1:CL:163:THR:HG23	1:CL:164:ARG:N	2.33	0.43
1:BM:122:GLY:C	1:BM:188:VAL:CG2	2.81	0.43
1:AM:234:SER:HB3	1:AM:237:ASP:O	2.18	0.43
1:BO:281:HIS:CE1	1:BO:301:TRP:HB3	2.54	0.43
1:AO:281:HIS:ND1	1:AO:301:TRP:HB3	2.33	0.43
1:AP:298:TRP:O	1:AP:310:ASP:O	2.36	0.43
1:BR:163:THR:O	1:BR:165:THR:HG22	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:281:HIS:ND1	1:AS:301:TRP:HB3	2.34	0.43
1:CS:214:ASN:HA	1:CS:215:PRO:HD3	1.85	0.43
1:AT:234:SER:HB3	1:AT:237:ASP:O	2.19	0.43
1:AU:81:ASP:C	1:AU:81:ASP:OD1	2.62	0.43
1:CU:79:VAL:HG13	1:CU:80:VAL:HG12	2.00	0.43
1:CU:133:ASP:O	1:CU:182:ARG:NH2	2.52	0.43
1:CV:63:ILE:HD12	1:CV:88:LEU:CG	2.46	0.43
1:AW:116:PRO:HG2	1:AW:119:THR:OG1	2.19	0.43
1:CW:141:LEU:O	1:CW:144:THR:N	2.48	0.43
1:BX:142:GLN:NE2	1:Cc:62:ARG:H	2.17	0.43
1:AX:298:TRP:NE1	1:AX:312:VAL:HA	2.33	0.43
1:CX:102:TYR:HD2	1:CX:205:VAL:HG21	1.82	0.43
1:CY:119:THR:O	1:CY:119:THR:HG22	2.18	0.43
1:BZ:232:SER:HB3	1:BZ:242:LEU:HD11	2.00	0.43
1:AZ:63:ILE:CD1	1:AZ:89:LEU:HD21	2.47	0.43
1:Ca:119:THR:O	1:Ca:119:THR:HG22	2.18	0.43
1:Ca:121:GLY:C	1:Ca:152:TRP:CD1	2.96	0.43
1:Bb:85:VAL:CG2	1:Bb:86:PRO:HD2	2.49	0.43
1:Bb:142:GLN:HB2	1:Cb:48:PHE:CE1	2.53	0.43
1:Ab:124:VAL:HG11	1:Ab:138:PHE:CD1	2.54	0.43
1:Cb:123:TYR:HB2	1:Cb:185:LEU:CD2	2.49	0.43
1:Ad:310:ASP:HB3	1:Ad:312:VAL:HG22	1.99	0.43
1:AB:298:TRP:HE1	1:AB:312:VAL:HA	1.83	0.43
1:AD:91:ARG:HH21	1:BF:98:ILE:HG22	1.83	0.43
1:BE:163:THR:C	1:BE:165:THR:HG22	2.44	0.43
1:BF:124:VAL:HG11	1:BF:138:PHE:CD2	2.54	0.43
1:CF:60:MET:HE2	1:CF:202:ARG:HB3	2.01	0.43
1:CF:223:MET:HE2	1:CF:328:GLY:HA2	2.00	0.43
1:BG:74:THR:HA	1:BG:190:ASN:ND2	2.34	0.43
1:AH:298:TRP:O	1:AH:310:ASP:O	2.36	0.43
1:AH:314:TYR:HE1	1:AH:316:SER:HG	1.66	0.43
1:CH:80:VAL:HG11	1:CH:185:LEU:CB	2.49	0.43
1:CH:133:ASP:O	1:CH:182:ARG:NH2	2.51	0.43
1:BI:281:HIS:CE1	1:BI:301:TRP:HB3	2.54	0.43
1:AI:63:ILE:HG23	1:AI:88:LEU:HD11	2.01	0.43
1:AI:226:GLY:N	1:AI:243:LEU:O	2.50	0.43
1:AI:308:PHE:CE2	1:AI:310:ASP:HA	2.54	0.43
1:CI:79:VAL:HG13	1:CI:80:VAL:HG12	2.00	0.43
1:BJ:126:GLY:HA3	1:BJ:141:LEU:HD22	2.00	0.43
1:AJ:91:ARG:NH2	1:BR:98:ILE:HG22	2.34	0.43
1:AK:98:ILE:HG22	1:AK:99:PHE:CD2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:54:ASP:OD1	1:CK:54:ASP:N	2.51	0.43
1:AL:143:ALA:HB1	1:AU:91:ARG:HD2	2.01	0.43
1:AL:298:TRP:HE1	1:AL:312:VAL:HA	1.84	0.43
1:BM:150:ALA:HB2	1:BM:156:ARG:HD3	2.00	0.43
1:AM:89:LEU:HD21	1:AM:201:CYS:HB3	2.01	0.43
1:CM:133:ASP:O	1:CM:182:ARG:NH2	2.50	0.43
1:AO:109:PHE:HB2	1:AO:158:VAL:HG12	2.00	0.43
1:AP:212:LEU:HD12	1:AP:212:LEU:C	2.44	0.43
1:CP:54:ASP:N	1:CP:54:ASP:OD1	2.51	0.43
1:AQ:302:ASP:OD2	1:AQ:305:ASN:CB	2.61	0.43
1:CQ:79:VAL:HG13	1:CQ:80:VAL:HG12	2.01	0.43
1:BS:225:GLN:HG3	1:BS:244:GLY:O	2.18	0.43
1:CS:89:LEU:HD13	1:CS:203:TRP:CG	2.54	0.43
1:AT:106:THR:O	1:AT:203:TRP:HA	2.18	0.43
1:AU:298:TRP:NE1	1:AU:312:VAL:HA	2.33	0.43
1:CV:69:PRO:O	1:CV:72:THR:OG1	2.28	0.43
1:BW:281:HIS:CE1	1:BW:301:TRP:HB3	2.53	0.43
1:AW:298:TRP:O	1:AW:310:ASP:O	2.36	0.43
1:CW:89:LEU:HD13	1:CW:203:TRP:CG	2.54	0.43
1:CW:130:ASP:OD2	1:CW:176:ARG:NH2	2.52	0.43
1:CY:130:ASP:OD2	1:CY:176:ARG:NH2	2.50	0.43
1:AZ:63:ILE:HG23	1:AZ:88:LEU:HD11	2.01	0.43
1:Ac:74:THR:O	1:Ac:75:ASP:C	2.61	0.43
1:BB:124:VAL:HG11	1:BB:138:PHE:CD2	2.53	0.43
1:CB:45:VAL:O	1:CB:45:VAL:HG13	2.19	0.43
1:CB:46:THR:HB	1:CF:202:ARG:HH12	1.84	0.43
1:CB:113:PRO:HA	1:CB:197:VAL:HA	2.00	0.43
1:CB:155:SER:O	1:CB:156:ARG:HD3	2.18	0.43
1:BC:111:ILE:HG22	1:BC:155:SER:HA	2.01	0.43
1:AC:238:PHE:CZ	1:AC:296:PHE:HB2	2.54	0.43
1:CD:89:LEU:HD13	1:CD:203:TRP:CG	2.54	0.43
1:CD:122:GLY:O	1:CD:188:VAL:CB	2.65	0.43
1:BE:260:ASP:HA	1:AE:261:ARG:NH2	2.34	0.43
1:AE:91:ARG:CZ	1:BM:98:ILE:HG22	2.48	0.43
1:AG:89:LEU:HD21	1:AG:201:CYS:HB3	2.00	0.43
1:CG:78:VAL:O	1:CG:78:VAL:HG13	2.17	0.43
1:BI:123:TYR:N	1:BI:188:VAL:HG22	2.32	0.43
1:CI:81:ASP:HA	1:CI:184:ILE:HG22	2.00	0.43
1:BJ:225:GLN:HG3	1:BJ:244:GLY:O	2.18	0.43
1:BM:184:ILE:HD13	1:BM:184:ILE:N	2.34	0.43
1:AM:127:PHE:O	1:AM:144:THR:OG1	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:264:SER:OG	1:AM:276:ARG:NH1	2.48	0.43
1:AM:298:TRP:O	1:AM:310:ASP:O	2.37	0.43
1:AM:298:TRP:HE1	1:AM:312:VAL:HA	1.83	0.43
1:AM:314:TYR:HE1	1:AM:316:SER:HG	1.66	0.43
1:AN:162:TYR:CE2	1:AN:164:ARG:HG2	2.53	0.43
1:CN:89:LEU:HD13	1:CN:203:TRP:CG	2.54	0.43
1:CN:111:ILE:HD11	1:CN:125:ALA:HB3	2.01	0.43
1:BO:111:ILE:HG22	1:BO:155:SER:HA	2.00	0.43
1:AO:256:VAL:HB	1:AO:335:ASP:HB3	2.01	0.43
1:BP:260:ASP:HA	1:AP:261:ARG:NH2	2.34	0.43
1:AP:314:TYR:HE1	1:AP:316:SER:HG	1.65	0.43
1:AR:57:LEU:O	1:AR:204:SER:HA	2.18	0.43
1:BT:123:TYR:N	1:BT:188:VAL:HG22	2.33	0.43
1:AT:263:LEU:HB3	1:AT:279:TYR:O	2.19	0.43
1:AT:288:ASN:O	1:AT:289:ALA:C	2.61	0.43
1:CW:74:THR:O	1:CW:75:ASP:C	2.62	0.43
1:AX:69:PRO:C	1:AX:72:THR:HG1	2.25	0.43
1:BY:100:GLN:NE2	1:BY:211:SER:CB	2.81	0.43
1:BY:136:HIS:O	1:BY:186:LEU:HD11	2.19	0.43
1:BY:234:SER:HB3	1:BY:237:ASP:OD1	2.19	0.43
1:AZ:64:SER:OG	1:AZ:80:VAL:HG21	2.19	0.43
1:AZ:234:SER:HB3	1:AZ:237:ASP:O	2.19	0.43
1:AZ:288:ASN:O	1:AZ:289:ALA:C	2.60	0.43
1:Ca:58:SER:HA	1:Ca:203:TRP:CE3	2.54	0.43
1:Ad:63:ILE:HG23	1:Ad:88:LEU:HD11	1.99	0.43
1:Cd:98:ILE:C	1:Cd:211:SER:O	2.60	0.43
1:Cd:158:VAL:HG13	1:Cd:158:VAL:O	2.19	0.43
1:AC:224:THR:HG22	1:AC:329:THR:N	2.34	0.43
1:AC:314:TYR:HE1	1:AC:316:SER:HG	1.66	0.43
1:CC:138:PHE:C	1:CC:138:PHE:CD1	2.96	0.43
1:CD:38:PRO:CB	1:Cd:36:ASP:HB3	2.49	0.43
1:AE:63:ILE:HG23	1:AE:88:LEU:HD11	1.99	0.43
1:BG:226:GLY:C	1:BG:327:VAL:HG22	2.44	0.43
1:BH:100:GLN:NE2	1:BH:211:SER:CB	2.82	0.43
1:AI:124:VAL:HG11	1:AI:138:PHE:CD1	2.54	0.43
1:BJ:161:GLN:NE2	1:CJ:210:PRO:HD2	2.32	0.43
1:CJ:121:GLY:C	1:CJ:152:TRP:CD1	2.97	0.43
1:BK:111:ILE:HG22	1:BK:155:SER:HA	1.99	0.43
1:BK:184:ILE:HD13	1:BK:184:ILE:N	2.33	0.43
1:CK:123:TYR:HB2	1:CK:185:LEU:HD21	2.00	0.43
1:CK:250:ILE:O	1:CK:250:ILE:HG22	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:224:THR:HG22	1:AM:329:THR:N	2.34	0.43
1:AN:103:ALA:HB2	1:AN:166:LEU:HA	2.01	0.43
1:AN:238:PHE:CZ	1:AN:296:PHE:HB2	2.53	0.43
1:BO:124:VAL:HG11	1:BO:138:PHE:CD2	2.54	0.43
1:CO:123:TYR:HA	1:CO:188:VAL:HG23	2.00	0.43
1:CP:46:THR:HB	1:CQ:202:ARG:HH12	1.84	0.43
1:CQ:54:ASP:OD1	1:CQ:54:ASP:N	2.51	0.43
1:BS:226:GLY:C	1:BS:327:VAL:HG22	2.44	0.43
1:BT:99:PHE:HA	1:BT:209:VAL:O	2.19	0.43
1:CT:54:ASP:OD1	1:CT:54:ASP:N	2.51	0.43
1:CU:111:ILE:HD11	1:CU:125:ALA:HB3	1.99	0.43
1:CV:79:VAL:HG13	1:CV:80:VAL:HG12	1.99	0.43
1:BW:163:THR:C	1:BW:165:THR:HG22	2.43	0.43
1:BW:184:ILE:HD13	1:BW:184:ILE:N	2.34	0.43
1:AW:263:LEU:HB3	1:AW:279:TYR:O	2.19	0.43
1:CX:98:ILE:HG13	1:CX:99:PHE:CD2	2.54	0.43
1:AY:88:LEU:HD13	1:AY:88:LEU:O	2.19	0.43
1:CY:78:VAL:HG13	1:CY:78:VAL:O	2.19	0.43
1:CZ:99:PHE:CD2	1:CZ:207:LEU:HB3	2.54	0.43
1:Ba:246:THR:N	1:Ba:247:PRO:CD	2.82	0.43
1:Ca:103:ALA:HB2	1:Ca:166:LEU:HB3	2.01	0.43
1:Ab:298:TRP:NE1	1:Ab:312:VAL:CB	2.80	0.43
1:Bc:214:ASN:HD22	1:Bc:215:PRO:HD2	1.83	0.43
1:Bc:225:GLN:HG3	1:Bc:244:GLY:O	2.18	0.43
1:Cc:102:TYR:HD2	1:Cc:205:VAL:HG21	1.83	0.43
1:Cd:155:SER:O	1:Cd:156:ARG:HD3	2.19	0.43
1:AA:234:SER:HB3	1:AA:237:ASP:O	2.19	0.43
1:CA:133:ASP:O	1:CA:182:ARG:NH2	2.52	0.43
1:CA:141:LEU:O	1:CA:142:GLN:C	2.60	0.43
1:BB:161:GLN:NE2	1:CB:210:PRO:HD2	2.33	0.43
1:AC:162:TYR:CE2	1:AC:164:ARG:HG2	2.53	0.43
1:CC:264:SER:HB2	1:CC:324:LEU:HD22	2.00	0.43
1:BD:99:PHE:HA	1:BD:209:VAL:O	2.18	0.43
1:AD:302:ASP:OD2	1:AD:305:ASN:CB	2.62	0.43
1:CD:45:VAL:HG23	1:CI:200:LEU:HD13	1.99	0.43
1:AE:308:PHE:CE2	1:AE:310:ASP:HA	2.54	0.43
1:AF:288:ASN:O	1:AF:289:ALA:C	2.61	0.43
1:AG:288:ASN:O	1:AG:289:ALA:C	2.61	0.43
1:CG:99:PHE:CD2	1:CG:207:LEU:HB3	2.54	0.43
1:AH:226:GLY:N	1:AH:243:LEU:O	2.49	0.43
1:BI:142:GLN:HB2	1:CI:48:PHE:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:298:TRP:HE1	1:AI:312:VAL:HA	1.84	0.43
1:CI:99:PHE:HB3	1:CI:209:VAL:O	2.17	0.43
1:BK:225:GLN:HG3	1:BK:244:GLY:O	2.18	0.43
1:AM:308:PHE:CE2	1:AM:310:ASP:HA	2.53	0.43
1:BN:166:LEU:CD1	1:BN:166:LEU:C	2.91	0.43
1:BO:184:ILE:HD13	1:BO:184:ILE:N	2.34	0.43
1:AO:288:ASN:O	1:AO:289:ALA:C	2.61	0.43
1:AO:298:TRP:HE1	1:AO:312:VAL:HA	1.83	0.43
1:CO:264:SER:HB2	1:CO:324:LEU:HD22	2.01	0.43
1:AP:302:ASP:CG	1:AP:305:ASN:CG	2.87	0.43
1:CQ:158:VAL:O	1:CQ:158:VAL:HG13	2.18	0.43
1:AR:302:ASP:CG	1:AR:305:ASN:CG	2.87	0.43
1:CR:103:ALA:HB2	1:CR:166:LEU:HB3	2.01	0.43
1:CR:250:ILE:HG22	1:CR:250:ILE:O	2.19	0.43
1:BS:228:LEU:HD13	1:BS:238:PHE:CD2	2.54	0.43
1:BS:281:HIS:CE1	1:BS:301:TRP:HB3	2.54	0.43
1:AS:122:GLY:C	1:AS:188:VAL:HG22	2.43	0.43
1:BT:205:VAL:HG22	1:BT:206:ARG:N	2.33	0.43
1:CT:111:ILE:HD11	1:CT:125:ALA:HB3	2.00	0.43
1:BU:74:THR:HA	1:BU:190:ASN:HD22	1.83	0.43
1:AU:100:GLN:HA	1:AU:169:THR:OG1	2.19	0.43
1:CU:54:ASP:N	1:CU:54:ASP:OD1	2.51	0.43
1:BV:226:GLY:C	1:BV:327:VAL:HG22	2.44	0.43
1:BV:300:ILE:HD13	1:AV:321:ARG:HD2	2.01	0.43
1:AV:100:GLN:HA	1:AV:169:THR:OG1	2.19	0.43
1:CW:46:THR:HB	1:Cd:202:ARG:HH12	1.84	0.43
1:CW:214:ASN:HA	1:CW:215:PRO:HD3	1.82	0.43
1:AX:302:ASP:C	1:AX:305:ASN:HD21	2.24	0.43
1:CZ:45:VAL:HG13	1:CZ:45:VAL:O	2.19	0.43
1:Ca:81:ASP:OD2	1:Ca:136:HIS:NE2	2.49	0.43
1:Bb:166:LEU:CD1	1:Bb:166:LEU:C	2.91	0.43
1:Ab:308:PHE:CE2	1:Ab:310:ASP:HA	2.53	0.43
1:Cc:123:TYR:HB2	1:Cc:185:LEU:HD21	2.01	0.43
1:BA:319:GLN:HE21	1:BA:319:GLN:C	2.27	0.43
1:BB:117:ALA:HB2	1:CK:117:ALA:HB1	2.01	0.43
1:CD:113:PRO:HA	1:CD:197:VAL:HA	2.01	0.43
1:CF:317:ASP:HB3	1:CF:319:GLN:NE2	2.33	0.43
1:AG:298:TRP:NE1	1:AG:312:VAL:HA	2.33	0.43
1:CG:81:ASP:OD2	1:CG:136:HIS:NE2	2.44	0.43
1:BI:260:ASP:HA	1:AI:261:ARG:NH2	2.33	0.43
1:CI:54:ASP:N	1:CI:54:ASP:OD1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:86:PRO:HB3	1:BJ:92:LEU:HD22	2.01	0.43
1:CJ:89:LEU:HD13	1:CJ:203:TRP:CG	2.54	0.43
1:CK:85:VAL:O	1:CK:86:PRO:C	2.61	0.43
1:CK:138:PHE:CD1	1:CK:138:PHE:C	2.97	0.43
1:AL:314:TYR:HE1	1:AL:316:SER:HG	1.65	0.43
1:CL:102:TYR:HD2	1:CL:205:VAL:HG21	1.84	0.43
1:AM:115:CYS:C	1:Ac:120:GLY:HA2	2.44	0.43
1:AN:91:ARG:HD2	1:AP:143:ALA:HB1	1.99	0.43
1:BO:98:ILE:HG22	1:Ab:91:ARG:NH2	2.34	0.43
1:AO:302:ASP:OD2	1:AO:305:ASN:CB	2.63	0.43
1:BP:184:ILE:N	1:BP:184:ILE:HD13	2.34	0.43
1:AQ:298:TRP:O	1:AQ:310:ASP:O	2.36	0.43
1:CQ:141:LEU:O	1:CQ:142:GLN:C	2.62	0.43
1:AR:298:TRP:O	1:AR:310:ASP:O	2.36	0.43
1:CR:98:ILE:C	1:CR:211:SER:O	2.57	0.43
1:AS:80:VAL:HG13	1:AS:185:LEU:HB3	2.00	0.43
1:BU:99:PHE:HA	1:BU:209:VAL:O	2.19	0.43
1:AU:61:SER:HB2	1:AU:89:LEU:HD22	2.00	0.43
1:CU:214:ASN:HA	1:CU:215:PRO:HD3	1.84	0.43
1:AV:98:ILE:HG22	1:AV:99:PHE:CD2	2.53	0.43
1:BX:281:HIS:CE1	1:BX:301:TRP:HB3	2.54	0.43
1:AX:63:ILE:CD1	1:AX:89:LEU:HD21	2.49	0.43
1:CX:155:SER:O	1:CX:156:ARG:HD3	2.18	0.43
1:CY:250:ILE:O	1:CY:250:ILE:HG22	2.18	0.43
1:BZ:226:GLY:C	1:BZ:327:VAL:HG22	2.44	0.43
1:CZ:80:VAL:HG13	1:CZ:185:LEU:N	2.34	0.43
1:Ba:85:VAL:CG2	1:Ba:86:PRO:HD2	2.49	0.43
1:Ba:260:ASP:HA	1:Aa:261:ARG:NH2	2.34	0.43
1:Aa:74:THR:O	1:Aa:75:ASP:C	2.62	0.43
1:Ca:72:THR:O	1:Ca:191:ASN:OD1	2.37	0.43
1:Ca:85:VAL:O	1:Ca:86:PRO:C	2.61	0.43
1:Ca:141:LEU:O	1:Ca:142:GLN:C	2.62	0.43
1:Cb:163:THR:HG23	1:Cb:164:ARG:N	2.33	0.43
1:Cd:69:PRO:O	1:Cd:72:THR:OG1	2.26	0.43
1:BA:111:ILE:CG2	1:BA:112:GLN:N	2.82	0.42
1:BA:226:GLY:C	1:BA:327:VAL:HG22	2.44	0.42
1:AA:226:GLY:N	1:AA:243:LEU:O	2.49	0.42
1:BC:98:ILE:CG2	1:AY:91:ARG:CZ	2.97	0.42
1:AD:188:VAL:HG23	1:AW:114:MET:SD	2.58	0.42
1:AD:298:TRP:O	1:AD:310:ASP:O	2.36	0.42
1:CD:102:TYR:HD2	1:CD:205:VAL:HG21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:155:SER:O	1:CD:156:ARG:HD3	2.19	0.42
1:CD:214:ASN:HA	1:CD:215:PRO:HD3	1.84	0.42
1:BE:234:SER:HB3	1:BE:237:ASP:OD1	2.19	0.42
1:CE:79:VAL:HG13	1:CE:80:VAL:HG12	2.00	0.42
1:CF:103:ALA:HB2	1:CF:166:LEU:HB3	2.01	0.42
1:CG:141:LEU:O	1:CG:142:GLN:C	2.62	0.42
1:CH:123:TYR:HB2	1:CH:185:LEU:HD21	2.00	0.42
1:AI:212:LEU:C	1:AI:212:LEU:HD12	2.44	0.42
1:AJ:63:ILE:HG23	1:AJ:88:LEU:HD11	2.01	0.42
1:AJ:69:PRO:C	1:AJ:72:THR:HG1	2.27	0.42
1:BK:128:LEU:HD12	1:BK:184:ILE:HD11	2.01	0.42
1:AK:81:ASP:OD1	1:AK:81:ASP:C	2.62	0.42
1:AK:116:PRO:HG2	1:AK:119:THR:OG1	2.19	0.42
1:CK:89:LEU:HD13	1:CK:203:TRP:CG	2.54	0.42
1:CK:128:LEU:HA	1:CK:129:PRO:HD3	1.91	0.42
1:BM:321:ARG:HD2	1:CM:300:ILE:HD13	2.02	0.42
1:AM:109:PHE:CE2	1:AM:127:PHE:CD1	3.07	0.42
1:AN:91:ARG:NH2	1:BP:98:ILE:CG2	2.82	0.42
1:CN:119:THR:O	1:CN:120:GLY:C	2.61	0.42
1:AO:264:SER:OG	1:AO:276:ARG:NH1	2.49	0.42
1:AO:302:ASP:C	1:AO:305:ASN:HD21	2.23	0.42
1:AQ:212:LEU:C	1:AQ:212:LEU:HD12	2.44	0.42
1:CQ:57:LEU:HD23	1:CQ:203:TRP:CH2	2.53	0.42
1:CQ:103:ALA:HB2	1:CQ:166:LEU:HB3	2.00	0.42
1:BR:136:HIS:O	1:BR:186:LEU:HD11	2.19	0.42
1:AS:298:TRP:NE1	1:AS:312:VAL:CB	2.79	0.42
1:AS:298:TRP:O	1:AS:310:ASP:O	2.36	0.42
1:AT:264:SER:OG	1:AT:276:ARG:NH1	2.51	0.42
1:BV:130:ASP:HB3	1:BV:133:ASP:HB2	2.01	0.42
1:BV:281:HIS:CE1	1:BV:301:TRP:HB3	2.54	0.42
1:BV:319:GLN:HE21	1:BV:319:GLN:C	2.27	0.42
1:AV:298:TRP:O	1:AV:310:ASP:O	2.37	0.42
1:BY:232:SER:HB3	1:BY:242:LEU:HD11	2.00	0.42
1:Aa:109:PHE:HB2	1:Aa:158:VAL:HG12	2.01	0.42
1:Ca:80:VAL:HG11	1:Ca:185:LEU:CB	2.49	0.42
1:Ab:74:THR:O	1:Ab:75:ASP:C	2.62	0.42
1:Ac:224:THR:HG22	1:Ac:329:THR:N	2.33	0.42
1:Ac:302:ASP:C	1:Ac:305:ASN:HD21	2.23	0.42
1:Ad:88:LEU:C	1:Ad:88:LEU:HD13	2.44	0.42
1:Cd:103:ALA:HB2	1:Cd:166:LEU:HB3	2.00	0.42
1:AA:85:VAL:HG22	1:AA:86:PRO:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:127:PHE:O	1:AA:144:THR:OG1	2.30	0.42
1:CA:288:ASN:CG	1:CA:291:THR:HB	2.44	0.42
1:BB:86:PRO:HB3	1:BB:92:LEU:HD22	2.01	0.42
1:BB:253:ASP:CB	1:BB:286:ALA:HB2	2.49	0.42
1:CB:122:GLY:O	1:CB:188:VAL:CB	2.67	0.42
1:CB:223:MET:HE2	1:CB:328:GLY:HA2	2.01	0.42
1:BE:319:GLN:C	1:BE:319:GLN:HE21	2.27	0.42
1:AE:89:LEU:HD21	1:AE:201:CYS:HB3	1.99	0.42
1:BF:300:ILE:HD13	1:AF:321:ARG:HD2	2.02	0.42
1:AF:116:PRO:HG2	1:AF:119:THR:OG1	2.19	0.42
1:CF:130:ASP:OD2	1:CF:176:ARG:NH2	2.52	0.42
1:AG:264:SER:OG	1:AG:276:ARG:NH1	2.50	0.42
1:AG:298:TRP:HE1	1:AG:312:VAL:HA	1.83	0.42
1:CG:85:VAL:O	1:CG:86:PRO:C	2.61	0.42
1:CG:102:TYR:HD2	1:CG:205:VAL:HG21	1.84	0.42
1:CG:119:THR:O	1:CG:120:GLY:C	2.62	0.42
1:BH:214:ASN:HD22	1:BH:215:PRO:HD2	1.83	0.42
1:AH:302:ASP:CG	1:AH:305:ASN:CG	2.87	0.42
1:CH:111:ILE:HD11	1:CH:125:ALA:HB3	2.01	0.42
1:CI:119:THR:O	1:CI:119:THR:HG22	2.19	0.42
1:BJ:163:THR:O	1:BJ:165:THR:HG22	2.18	0.42
1:CK:58:SER:HA	1:CK:203:TRP:CE3	2.54	0.42
1:CL:250:ILE:O	1:CL:250:ILE:HG22	2.18	0.42
1:AM:226:GLY:N	1:AM:243:LEU:O	2.51	0.42
1:AM:302:ASP:C	1:AM:305:ASN:HD21	2.23	0.42
1:AN:308:PHE:CE2	1:AN:310:ASP:HA	2.54	0.42
1:CN:58:SER:HB3	1:CN:204:SER:HB2	2.01	0.42
1:BO:99:PHE:HA	1:BO:209:VAL:O	2.19	0.42
1:AO:238:PHE:CZ	1:AO:296:PHE:HB2	2.54	0.42
1:BP:126:GLY:HA2	1:BP:158:VAL:HG21	2.01	0.42
1:AP:234:SER:HB3	1:AP:237:ASP:O	2.19	0.42
1:BQ:123:TYR:N	1:BQ:188:VAL:HG22	2.34	0.42
1:CQ:123:TYR:HA	1:CQ:188:VAL:HG23	2.00	0.42
1:CR:45:VAL:HG13	1:CR:45:VAL:O	2.19	0.42
1:CR:54:ASP:OD1	1:CR:54:ASP:N	2.52	0.42
1:CR:119:THR:O	1:CR:119:THR:HG22	2.19	0.42
1:BT:128:LEU:HD12	1:BT:184:ILE:HD11	2.01	0.42
1:AT:63:ILE:HG23	1:AT:88:LEU:HD11	2.01	0.42
1:BV:184:ILE:HD13	1:BV:184:ILE:N	2.33	0.42
1:CV:57:LEU:HD23	1:CV:203:TRP:HH2	1.84	0.42
1:BW:86:PRO:HB3	1:BW:92:LEU:HD22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CW:99:PHE:CD2	1:CW:207:LEU:HB3	2.54	0.42
1:BX:184:ILE:HD13	1:BX:184:ILE:N	2.34	0.42
1:BX:226:GLY:C	1:BX:327:VAL:HG22	2.44	0.42
1:AX:137:THR:HG23	1:AX:140:ALA:CB	2.49	0.42
1:AY:69:PRO:C	1:AY:72:THR:HG1	2.24	0.42
1:Bb:111:ILE:CG2	1:Bb:112:GLN:N	2.82	0.42
1:Bb:136:HIS:O	1:Bb:186:LEU:HD11	2.18	0.42
1:Cb:62:ARG:HA	1:Cb:200:LEU:HD23	2.00	0.42
1:Bd:225:GLN:HG3	1:Bd:244:GLY:O	2.19	0.42
1:Cd:246:THR:N	1:Cd:247:PRO:CD	2.82	0.42
1:BB:116:PRO:HD3	1:CK:120:GLY:HA3	2.00	0.42
1:BB:260:ASP:HA	1:AB:261:ARG:NH2	2.34	0.42
1:BC:123:TYR:N	1:BC:188:VAL:HG22	2.34	0.42
1:BC:184:ILE:HD13	1:BC:184:ILE:N	2.35	0.42
1:AD:64:SER:OG	1:AD:80:VAL:HG21	2.18	0.42
1:CD:63:ILE:HD12	1:CD:88:LEU:CG	2.47	0.42
1:CD:72:THR:O	1:CD:191:ASN:OD1	2.37	0.42
1:CD:123:TYR:HB2	1:CD:185:LEU:HD21	2.01	0.42
1:AE:137:THR:HG23	1:AE:140:ALA:CB	2.49	0.42
1:AF:281:HIS:ND1	1:AF:301:TRP:HB3	2.33	0.42
1:BG:114:MET:HE1	1:CP:188:VAL:HG11	2.01	0.42
1:CH:113:PRO:HA	1:CH:197:VAL:HA	2.00	0.42
1:BI:122:GLY:C	1:BI:188:VAL:CG2	2.85	0.42
1:BI:184:ILE:HD13	1:BI:184:ILE:N	2.35	0.42
1:CI:123:TYR:HB2	1:CI:185:LEU:CD2	2.50	0.42
1:CJ:58:SER:HB3	1:CJ:204:SER:HB2	2.01	0.42
1:BK:123:TYR:HB2	1:BK:185:LEU:CD1	2.49	0.42
1:AL:226:GLY:N	1:AL:243:LEU:O	2.46	0.42
1:AL:298:TRP:CG	1:AL:312:VAL:HG13	2.48	0.42
1:CL:43:SER:O	1:Cb:34:ARG:CD	2.65	0.42
1:BM:300:ILE:HG23	1:AM:323:ILE:CD1	2.50	0.42
1:AM:281:HIS:ND1	1:AM:301:TRP:HB3	2.34	0.42
1:CM:80:VAL:HG22	1:CM:81:ASP:N	2.34	0.42
1:CM:123:TYR:HA	1:CM:188:VAL:HG23	2.01	0.42
1:BN:226:GLY:C	1:BN:327:VAL:HG22	2.44	0.42
1:AN:109:PHE:CE2	1:AN:127:PHE:CD1	3.07	0.42
1:CN:98:ILE:C	1:CN:211:SER:O	2.61	0.42
1:AO:64:SER:OG	1:AO:80:VAL:HG21	2.19	0.42
1:BQ:99:PHE:HA	1:BQ:209:VAL:O	2.19	0.42
1:CR:80:VAL:HG13	1:CR:185:LEU:N	2.34	0.42
1:CR:119:THR:O	1:CR:120:GLY:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:166:LEU:CD1	1:BS:166:LEU:C	2.92	0.42
1:BS:184:ILE:HD13	1:BS:184:ILE:N	2.34	0.42
1:BS:260:ASP:HA	1:AS:261:ARG:NH2	2.34	0.42
1:CU:99:PHE:CD2	1:CU:207:LEU:HB3	2.54	0.42
1:CU:317:ASP:HB3	1:CU:319:GLN:NE2	2.35	0.42
1:BV:99:PHE:HA	1:BV:209:VAL:O	2.20	0.42
1:AW:103:ALA:HB2	1:AW:166:LEU:HA	2.00	0.42
1:AX:234:SER:HB3	1:AX:237:ASP:O	2.19	0.42
1:CY:119:THR:O	1:CY:120:GLY:C	2.62	0.42
1:CZ:113:PRO:HA	1:CZ:197:VAL:HA	2.01	0.42
1:Ca:223:MET:HE2	1:Ca:328:GLY:HA2	2.02	0.42
1:Bb:123:TYR:N	1:Bb:188:VAL:HG22	2.34	0.42
1:Ab:238:PHE:CZ	1:Ab:296:PHE:HB2	2.54	0.42
1:Ac:57:LEU:O	1:Ac:204:SER:HA	2.20	0.42
1:Cc:99:PHE:CD2	1:Cc:207:LEU:HB3	2.54	0.42
1:BB:99:PHE:HA	1:BB:209:VAL:O	2.19	0.42
1:BB:111:ILE:CG2	1:BB:112:GLN:N	2.82	0.42
1:CB:63:ILE:HD12	1:CB:88:LEU:CD1	2.50	0.42
1:BC:166:LEU:CD1	1:BC:166:LEU:C	2.91	0.42
1:CC:122:GLY:O	1:CC:188:VAL:CB	2.68	0.42
1:AG:80:VAL:HG13	1:AG:185:LEU:HB3	2.01	0.42
1:AG:226:GLY:N	1:AG:243:LEU:O	2.51	0.42
1:CG:317:ASP:HB3	1:CG:319:GLN:NE2	2.34	0.42
1:BH:281:HIS:CE1	1:BH:301:TRP:HB3	2.54	0.42
1:CH:119:THR:O	1:CH:119:THR:HG22	2.20	0.42
1:BI:130:ASP:HB3	1:BI:133:ASP:HB2	2.00	0.42
1:AI:127:PHE:O	1:AI:144:THR:OG1	2.35	0.42
1:CI:264:SER:HB2	1:CI:324:LEU:HD22	2.02	0.42
1:AJ:314:TYR:CE1	1:AJ:316:SER:CA	2.88	0.42
1:CJ:34:ARG:HD3	1:CS:43:SER:O	2.19	0.42
1:BL:226:GLY:C	1:BL:327:VAL:HG22	2.44	0.42
1:BM:122:GLY:O	1:BM:188:VAL:HG22	2.19	0.42
1:AN:298:TRP:NE1	1:AN:312:VAL:HA	2.33	0.42
1:BP:99:PHE:HA	1:BP:209:VAL:O	2.19	0.42
1:BS:89:LEU:HA	1:BS:90:PRO:HD3	1.93	0.42
1:BS:163:THR:O	1:BS:165:THR:HG22	2.19	0.42
1:AU:302:ASP:CG	1:AU:305:ASN:CG	2.87	0.42
1:CU:98:ILE:C	1:CU:211:SER:O	2.59	0.42
1:BV:85:VAL:CG2	1:BV:86:PRO:HD2	2.50	0.42
1:AV:124:VAL:HG11	1:AV:138:PHE:CD1	2.54	0.42
1:AV:264:SER:OG	1:AV:276:ARG:NH1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:124:VAL:HG13	1:CV:124:VAL:O	2.19	0.42
1:AW:80:VAL:HG13	1:AW:185:LEU:HB3	2.00	0.42
1:AX:308:PHE:CE2	1:AX:310:ASP:HA	2.54	0.42
1:CX:141:LEU:O	1:CX:142:GLN:C	2.62	0.42
1:CY:317:ASP:HB3	1:CY:319:GLN:NE2	2.35	0.42
1:BZ:166:LEU:CD1	1:BZ:166:LEU:C	2.93	0.42
1:AZ:89:LEU:HD21	1:AZ:201:CYS:HB3	2.01	0.42
1:Cc:89:LEU:HD13	1:Cc:203:TRP:CG	2.54	0.42
1:Ad:57:LEU:O	1:Ad:204:SER:HA	2.20	0.42
1:Cd:54:ASP:OD1	1:Cd:54:ASP:N	2.51	0.42
1:AB:226:GLY:N	1:AB:243:LEU:O	2.51	0.42
1:CB:80:VAL:HG22	1:CB:81:ASP:N	2.35	0.42
1:CB:98:ILE:HB	1:CF:91:ARG:HD2	2.00	0.42
1:CD:186:LEU:HD23	1:CD:186:LEU:N	2.34	0.42
1:BE:111:ILE:HG22	1:BE:155:SER:HA	2.01	0.42
1:AE:281:HIS:ND1	1:AE:301:TRP:HB3	2.34	0.42
1:CE:109:PHE:HB2	1:CE:158:VAL:HG12	2.01	0.42
1:CE:264:SER:HB2	1:CE:324:LEU:HD22	2.01	0.42
1:AF:253:ASP:CG	1:AF:285:PHE:CA	2.80	0.42
1:BG:109:PHE:HB2	1:BG:158:VAL:CG1	2.50	0.42
1:BG:246:THR:N	1:BG:247:PRO:CD	2.82	0.42
1:AI:256:VAL:HB	1:AI:335:ASP:HB3	2.01	0.42
1:BK:136:HIS:O	1:BK:186:LEU:HD11	2.19	0.42
1:BL:122:GLY:C	1:BL:188:VAL:CG2	2.86	0.42
1:CL:128:LEU:HA	1:CL:129:PRO:HD3	1.91	0.42
1:BM:124:VAL:HG11	1:BM:138:PHE:CD2	2.54	0.42
1:BN:136:HIS:O	1:BN:186:LEU:HD11	2.19	0.42
1:AO:60:MET:HE2	1:AO:200:LEU:HB3	2.00	0.42
1:CQ:43:SER:O	1:CV:34:ARG:CD	2.68	0.42
1:BR:232:SER:HB3	1:BR:242:LEU:HD11	2.00	0.42
1:CR:123:TYR:HB2	1:CR:185:LEU:HD21	2.02	0.42
1:CS:141:LEU:O	1:CS:142:GLN:C	2.63	0.42
1:AT:81:ASP:OD1	1:AT:81:ASP:C	2.63	0.42
1:AT:188:VAL:CG2	1:AV:114:MET:SD	3.08	0.42
1:AU:314:TYR:HE1	1:AU:316:SER:HG	1.64	0.42
1:AW:302:ASP:CG	1:AW:305:ASN:CG	2.88	0.42
1:CW:72:THR:O	1:CW:191:ASN:OD1	2.37	0.42
1:BY:166:LEU:CD1	1:BY:166:LEU:C	2.92	0.42
1:BZ:225:GLN:HG3	1:BZ:244:GLY:O	2.19	0.42
1:AZ:98:ILE:HG22	1:AZ:99:PHE:CD2	2.55	0.42
1:AZ:162:TYR:CE2	1:AZ:164:ARG:HG2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bb:281:HIS:CE1	1:Bb:301:TRP:HB3	2.54	0.42
1:Ab:61:SER:HB2	1:Ab:89:LEU:HD22	2.00	0.42
1:Ac:238:PHE:CZ	1:Ac:296:PHE:HB2	2.54	0.42
1:Cd:133:ASP:O	1:Cd:182:ARG:NH2	2.53	0.42
1:AA:111:ILE:O	1:AA:112:GLN:C	2.63	0.42
1:BB:62:ARG:HB2	1:CK:138:PHE:CE1	2.54	0.42
1:BB:115:CYS:C	1:CK:120:GLY:HA2	2.43	0.42
1:AB:64:SER:OG	1:AB:80:VAL:HG21	2.20	0.42
1:BC:260:ASP:HA	1:AC:261:ARG:NH2	2.34	0.42
1:AD:137:THR:HG23	1:AD:140:ALA:CB	2.49	0.42
1:CD:58:SER:HB3	1:CD:204:SER:HB2	2.01	0.42
1:AE:74:THR:O	1:AE:75:ASP:C	2.61	0.42
1:AE:298:TRP:HE1	1:AE:312:VAL:HA	1.84	0.42
1:BF:100:GLN:NE2	1:BF:211:SER:CB	2.82	0.42
1:BF:123:TYR:N	1:BF:188:VAL:HG22	2.34	0.42
1:AF:298:TRP:O	1:AF:310:ASP:O	2.37	0.42
1:BG:75:ASP:C	1:BG:75:ASP:OD1	2.61	0.42
1:BG:321:ARG:HD2	1:CG:300:ILE:HD13	2.02	0.42
1:AG:98:ILE:HG22	1:AG:99:PHE:CD2	2.54	0.42
1:BH:246:THR:N	1:BH:247:PRO:CD	2.83	0.42
1:AJ:127:PHE:O	1:AJ:144:THR:OG1	2.33	0.42
1:AJ:212:LEU:C	1:AJ:212:LEU:HD12	2.45	0.42
1:AJ:314:TYR:HE1	1:AJ:316:SER:HG	1.67	0.42
1:BK:100:GLN:O	1:BK:169:THR:N	2.44	0.42
1:AK:268:SER:CB	1:AK:273:ASP:O	2.67	0.42
1:CM:112:GLN:HE21	1:CO:44:THR:H	1.66	0.42
1:AN:281:HIS:ND1	1:AN:301:TRP:HB3	2.34	0.42
1:BO:74:THR:HA	1:BO:190:ASN:HD22	1.85	0.42
1:CO:39:VAL:HA	1:Cc:39:VAL:CG2	2.48	0.42
1:CO:85:VAL:O	1:CO:86:PRO:C	2.60	0.42
1:AQ:98:ILE:HG22	1:AQ:99:PHE:CD2	2.54	0.42
1:AQ:100:GLN:HA	1:AQ:169:THR:OG1	2.19	0.42
1:BR:281:HIS:CE1	1:BR:301:TRP:HB3	2.54	0.42
1:BS:124:VAL:HG11	1:BS:138:PHE:CD2	2.54	0.42
1:AS:64:SER:OG	1:AS:80:VAL:HG21	2.20	0.42
1:CU:39:VAL:CG2	1:Cc:39:VAL:HA	2.49	0.42
1:BV:225:GLN:HG3	1:BV:244:GLY:O	2.19	0.42
1:AW:98:ILE:HG22	1:AW:99:PHE:CD2	2.54	0.42
1:AW:111:ILE:O	1:AW:112:GLN:C	2.62	0.42
1:CW:122:GLY:O	1:CW:188:VAL:CB	2.66	0.42
1:AX:127:PHE:O	1:AX:144:THR:OG1	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:69:PRO:C	1:AZ:72:THR:HG1	2.28	0.42
1:Aa:308:PHE:CE2	1:Aa:310:ASP:HA	2.55	0.42
1:Ac:281:HIS:ND1	1:Ac:301:TRP:HB3	2.35	0.42
1:Cd:163:THR:HG23	1:Cd:164:ARG:N	2.33	0.42
1:BA:228:LEU:HD13	1:BA:238:PHE:CD2	2.54	0.42
1:CB:54:ASP:N	1:CB:54:ASP:OD1	2.51	0.42
1:AC:246:THR:O	1:AC:250:ILE:HG12	2.19	0.42
1:CC:91:ARG:HD2	1:CJ:98:ILE:HB	2.02	0.42
1:CC:98:ILE:HB	1:CJ:91:ARG:HD2	2.02	0.42
1:CC:317:ASP:HB3	1:CC:319:GLN:NE2	2.34	0.42
1:BD:228:LEU:HD13	1:BD:238:PHE:CD2	2.55	0.42
1:AD:302:ASP:C	1:AD:305:ASN:HD21	2.23	0.42
1:BE:86:PRO:HB3	1:BE:92:LEU:HD22	2.01	0.42
1:AF:98:ILE:CG2	1:Bb:91:ARG:NH1	2.80	0.42
1:AF:103:ALA:HB2	1:AF:166:LEU:HA	2.02	0.42
1:CF:111:ILE:HD11	1:CF:125:ALA:HB3	2.02	0.42
1:BG:228:LEU:HD13	1:BG:238:PHE:CD2	2.55	0.42
1:AG:137:THR:HG23	1:AG:140:ALA:CB	2.49	0.42
1:AG:281:HIS:ND1	1:AG:301:TRP:HB3	2.34	0.42
1:AH:89:LEU:HD21	1:AH:201:CYS:HB3	2.01	0.42
1:CI:85:VAL:O	1:CI:86:PRO:C	2.62	0.42
1:CI:186:LEU:HD23	1:CI:186:LEU:N	2.34	0.42
1:AJ:234:SER:HB3	1:AJ:237:ASP:O	2.20	0.42
1:BK:122:GLY:C	1:BK:188:VAL:CG2	2.84	0.42
1:BK:228:LEU:HD13	1:BK:238:PHE:CD2	2.55	0.42
1:CK:246:THR:N	1:CK:247:PRO:CD	2.83	0.42
1:AL:100:GLN:HA	1:AL:169:THR:OG1	2.19	0.42
1:AL:281:HIS:ND1	1:AL:301:TRP:HB3	2.35	0.42
1:AL:314:TYR:CE1	1:AL:316:SER:CA	2.89	0.42
1:CL:109:PHE:HB2	1:CL:158:VAL:HG12	2.01	0.42
1:BM:253:ASP:CB	1:BM:286:ALA:HB2	2.47	0.42
1:AM:62:ARG:HB2	1:Ac:138:PHE:HE2	1.85	0.42
1:BN:281:HIS:CE1	1:BN:301:TRP:HB3	2.55	0.42
1:AO:234:SER:HB3	1:AO:237:ASP:O	2.20	0.42
1:CO:317:ASP:HB3	1:CO:319:GLN:NE2	2.33	0.42
1:AP:106:THR:O	1:AP:203:TRP:HA	2.19	0.42
1:CP:103:ALA:HB2	1:CP:166:LEU:HB3	2.00	0.42
1:BS:300:ILE:HD13	1:AS:321:ARG:HD2	2.02	0.42
1:AS:302:ASP:OD2	1:AS:305:ASN:CB	2.63	0.42
1:AT:89:LEU:HD21	1:AT:201:CYS:HB3	2.01	0.42
1:AT:98:ILE:HG22	1:AT:99:PHE:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:308:PHE:CE2	1:AT:310:ASP:HA	2.55	0.42
1:CT:80:VAL:HG11	1:CT:185:LEU:CB	2.47	0.42
1:CT:98:ILE:C	1:CT:211:SER:O	2.59	0.42
1:AU:308:PHE:CE2	1:AU:310:ASP:HA	2.55	0.42
1:CU:113:PRO:HA	1:CU:197:VAL:HA	2.01	0.42
1:CU:123:TYR:HB2	1:CU:185:LEU:HD21	2.01	0.42
1:CV:85:VAL:O	1:CV:86:PRO:C	2.63	0.42
1:CV:123:TYR:HA	1:CV:188:VAL:HG23	2.00	0.42
1:AX:122:GLY:C	1:AX:188:VAL:HG22	2.44	0.42
1:AX:302:ASP:CG	1:AX:305:ASN:CG	2.88	0.42
1:CX:264:SER:HB2	1:CX:324:LEU:HD22	2.00	0.42
1:BZ:100:GLN:NE2	1:BZ:211:SER:CB	2.82	0.42
1:BZ:184:ILE:HD13	1:BZ:184:ILE:N	2.34	0.42
1:CZ:72:THR:O	1:CZ:191:ASN:OD1	2.38	0.42
1:CZ:123:TYR:HA	1:CZ:188:VAL:HG23	2.00	0.42
1:Ba:225:GLN:HG3	1:Ba:244:GLY:O	2.19	0.42
1:Ba:226:GLY:C	1:Ba:327:VAL:HG22	2.44	0.42
1:Bc:260:ASP:HA	1:Ac:261:ARG:NH2	2.35	0.42
1:Ac:308:PHE:CE2	1:Ac:310:ASP:HA	2.55	0.42
1:BA:99:PHE:HA	1:BA:209:VAL:O	2.19	0.42
1:CA:123:TYR:CD1	1:CA:185:LEU:HD21	2.54	0.42
1:CA:317:ASP:HB3	1:CA:319:GLN:NE2	2.34	0.42
1:BB:321:ARG:HD2	1:CB:300:ILE:HD13	2.01	0.42
1:CB:118:ASN:HA	1:BY:116:PRO:HB3	2.02	0.42
1:BC:74:THR:HA	1:BC:190:ASN:HD22	1.84	0.42
1:BC:300:ILE:HD13	1:AC:321:ARG:HD2	2.02	0.42
1:BD:100:GLN:O	1:BD:169:THR:N	2.45	0.42
1:BE:99:PHE:HA	1:BE:209:VAL:O	2.19	0.42
1:BE:123:TYR:N	1:BE:188:VAL:HG22	2.34	0.42
1:AE:116:PRO:HG2	1:AE:119:THR:OG1	2.20	0.42
1:AE:224:THR:HG22	1:AE:329:THR:N	2.34	0.42
1:BF:163:THR:C	1:BF:165:THR:HG22	2.45	0.42
1:BF:319:GLN:HE21	1:BF:319:GLN:C	2.28	0.42
1:BG:205:VAL:HG22	1:BG:206:ARG:N	2.35	0.42
1:AG:114:MET:SD	1:Ad:188:VAL:HG23	2.60	0.42
1:AG:256:VAL:HB	1:AG:335:ASP:HB3	2.01	0.42
1:CG:74:THR:O	1:CG:75:ASP:C	2.63	0.42
1:CG:123:TYR:CD1	1:CG:185:LEU:HD21	2.55	0.42
1:AH:308:PHE:CE2	1:AH:310:ASP:HA	2.55	0.42
1:CH:72:THR:O	1:CH:191:ASN:OD1	2.38	0.42
1:CH:214:ASN:HA	1:CH:215:PRO:HD3	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:199:VAL:O	1:CI:199:VAL:CG1	2.66	0.42
1:BJ:234:SER:HB3	1:BJ:237:ASP:OD1	2.20	0.42
1:AJ:302:ASP:CG	1:AJ:305:ASN:CG	2.87	0.42
1:CJ:103:ALA:HB2	1:CJ:166:LEU:HB3	2.00	0.42
1:CJ:317:ASP:HB3	1:CJ:319:GLN:NE2	2.35	0.42
1:BK:163:THR:O	1:BK:165:THR:HG22	2.20	0.42
1:BK:319:GLN:C	1:BK:319:GLN:HE21	2.27	0.42
1:CK:100:GLN:HA	1:CK:213:GLU:OE2	2.19	0.42
1:BL:100:GLN:NE2	1:BL:211:SER:CB	2.82	0.42
1:BM:123:TYR:N	1:BM:188:VAL:HG22	2.31	0.42
1:AM:302:ASP:CG	1:AM:305:ASN:CG	2.87	0.42
1:CM:85:VAL:O	1:CM:86:PRO:C	2.60	0.42
1:AN:288:ASN:O	1:AN:289:ALA:C	2.62	0.42
1:CN:62:ARG:HA	1:CN:200:LEU:HD23	2.02	0.42
1:BO:156:ARG:NH2	1:CU:34:ARG:HG3	2.35	0.42
1:AO:103:ALA:HB2	1:AO:166:LEU:HA	2.01	0.42
1:AO:127:PHE:O	1:AO:144:THR:OG1	2.34	0.42
1:BP:253:ASP:CB	1:BP:286:ALA:HB2	2.49	0.42
1:AP:256:VAL:HB	1:AP:335:ASP:HB3	2.01	0.42
1:CP:102:TYR:HD2	1:CP:205:VAL:HG21	1.85	0.42
1:CP:123:TYR:HA	1:CP:188:VAL:HG23	2.01	0.42
1:BQ:85:VAL:CG2	1:BQ:86:PRO:HD2	2.50	0.42
1:AQ:302:ASP:CG	1:AQ:305:ASN:CG	2.88	0.42
1:BS:136:HIS:O	1:BS:186:LEU:HD11	2.20	0.42
1:AS:63:ILE:HG23	1:AS:88:LEU:HD11	2.02	0.42
1:BT:124:VAL:HG11	1:BT:138:PHE:CD2	2.55	0.42
1:AT:57:LEU:O	1:AT:204:SER:HA	2.20	0.42
1:AV:81:ASP:C	1:AV:81:ASP:OD1	2.62	0.42
1:CV:317:ASP:HB3	1:CV:319:GLN:NE2	2.35	0.42
1:AW:281:HIS:ND1	1:AW:301:TRP:HB3	2.35	0.42
1:BX:142:GLN:HB2	1:CX:48:PHE:CE1	2.55	0.42
1:BX:163:THR:C	1:BX:165:THR:HG22	2.45	0.42
1:CX:72:THR:O	1:CX:191:ASN:OD1	2.37	0.42
1:CY:264:SER:HB2	1:CY:324:LEU:HD22	2.01	0.42
1:BZ:253:ASP:CB	1:BZ:286:ALA:HB2	2.50	0.42
1:AZ:123:TYR:HB2	1:AZ:185:LEU:HD11	2.01	0.42
1:AZ:183:LEU:HG	1:AZ:184:ILE:N	2.33	0.42
1:Ba:319:GLN:HE21	1:Ba:319:GLN:C	2.28	0.42
1:Cb:99:PHE:CD2	1:Cb:207:LEU:HB3	2.54	0.42
1:Bc:86:PRO:HB3	1:Bc:92:LEU:HD22	2.01	0.42
1:Cc:81:ASP:OD2	1:Cc:136:HIS:NE2	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ad:162:TYR:CE2	1:Ad:164:ARG:HG2	2.55	0.42
1:Cd:45:VAL:O	1:Cd:45:VAL:HG13	2.19	0.42
1:Cd:80:VAL:HG11	1:Cd:185:LEU:CB	2.48	0.42
1:AA:80:VAL:HG13	1:AA:185:LEU:HB3	2.02	0.42
1:BB:149:VAL:HG23	1:CB:48:PHE:HE2	1.85	0.42
1:AB:212:LEU:C	1:AB:212:LEU:HD12	2.45	0.42
1:CB:89:LEU:HD13	1:CB:203:TRP:CG	2.55	0.42
1:BC:99:PHE:HA	1:BC:209:VAL:O	2.19	0.42
1:BD:74:THR:HA	1:BD:190:ASN:HD22	1.84	0.42
1:BD:205:VAL:HG22	1:BD:206:ARG:N	2.34	0.42
1:AD:103:ALA:HB2	1:AD:166:LEU:HA	2.02	0.42
1:CD:91:ARG:HD2	1:CI:98:ILE:HB	2.02	0.42
1:CD:119:THR:O	1:CD:119:THR:HG22	2.20	0.42
1:CD:119:THR:O	1:CD:120:GLY:C	2.63	0.42
1:BE:136:HIS:O	1:BE:186:LEU:HD11	2.19	0.42
1:AE:302:ASP:CG	1:AE:305:ASN:CG	2.87	0.42
1:CE:141:LEU:O	1:CE:142:GLN:C	2.62	0.42
1:CF:69:PRO:O	1:CF:72:THR:OG1	2.31	0.42
1:BG:99:PHE:HA	1:BG:209:VAL:O	2.20	0.42
1:AG:101:ARG:NH1	1:AG:166:LEU:HD23	2.35	0.42
1:BH:142:GLN:HB2	1:CH:48:PHE:CE1	2.55	0.42
1:AH:109:PHE:HB2	1:AH:158:VAL:HG12	2.02	0.42
1:AH:137:THR:HG23	1:AH:140:ALA:CB	2.49	0.42
1:BJ:79:VAL:O	1:BJ:79:VAL:CG2	2.67	0.42
1:BJ:300:ILE:HD13	1:AJ:321:ARG:HD2	2.02	0.42
1:BK:98:ILE:CG2	1:AS:91:ARG:HE	2.24	0.42
1:CK:102:TYR:HD2	1:CK:205:VAL:HG21	1.85	0.42
1:BM:86:PRO:HB3	1:BM:92:LEU:HD22	2.02	0.42
1:CM:202:ARG:HH12	1:CO:46:THR:HB	1.84	0.42
1:AN:60:MET:HE2	1:AN:200:LEU:HB3	2.01	0.42
1:AN:264:SER:OG	1:AN:276:ARG:NH1	2.52	0.42
1:AO:102:TYR:O	1:AO:167:LEU:HB2	2.19	0.42
1:BP:74:THR:HA	1:BP:190:ASN:HD22	1.85	0.42
1:BP:163:THR:C	1:BP:165:THR:HG22	2.45	0.42
1:AP:122:GLY:C	1:AP:188:VAL:HG22	2.45	0.42
1:AP:162:TYR:CE2	1:AP:164:ARG:HG2	2.55	0.42
1:AP:263:LEU:HB3	1:AP:279:TYR:O	2.20	0.42
1:BQ:163:THR:O	1:BQ:165:THR:HG22	2.20	0.42
1:BQ:226:GLY:C	1:BQ:327:VAL:HG22	2.45	0.42
1:AQ:308:PHE:CE2	1:AQ:310:ASP:HA	2.55	0.42
1:CR:34:ARG:CD	1:Ca:43:SER:O	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:44:THR:H	1:CT:112:GLN:HE21	1.67	0.42
1:CR:58:SER:HB3	1:CR:204:SER:HB2	2.01	0.42
1:BS:149:VAL:HG23	1:CS:48:PHE:HE2	1.85	0.42
1:AT:226:GLY:N	1:AT:243:LEU:O	2.49	0.42
1:AT:281:HIS:ND1	1:AT:301:TRP:HB3	2.35	0.42
1:AU:63:ILE:HG23	1:AU:88:LEU:HD11	2.00	0.42
1:AV:80:VAL:HG13	1:AV:185:LEU:HB3	2.01	0.42
1:AV:263:LEU:HB3	1:AV:279:TYR:O	2.20	0.42
1:AV:302:ASP:CG	1:AV:305:ASN:CG	2.88	0.42
1:CV:38:PRO:O	1:CZ:117:ALA:HB2	2.19	0.42
1:CW:109:PHE:HB2	1:CW:158:VAL:HG12	2.00	0.42
1:CX:128:LEU:HA	1:CX:129:PRO:HD3	1.93	0.42
1:BY:74:THR:HA	1:BY:190:ASN:HD22	1.85	0.42
1:AY:298:TRP:O	1:AY:310:ASP:O	2.38	0.42
1:CY:45:VAL:HG13	1:CY:45:VAL:O	2.20	0.42
1:Ab:81:ASP:C	1:Ab:81:ASP:OD1	2.62	0.42
1:Bd:149:VAL:HG23	1:Cd:48:PHE:CE2	2.55	0.42
1:CA:93:GLY:O	1:CA:97:ARG:NH1	2.53	0.42
1:AD:100:GLN:HA	1:AD:169:THR:OG1	2.20	0.42
1:CD:58:SER:HA	1:CD:203:TRP:CE3	2.55	0.42
1:BE:191:ASN:HD22	1:BE:191:ASN:H	1.68	0.42
1:CE:130:ASP:OD2	1:CE:176:ARG:NH2	2.52	0.42
1:AF:302:ASP:CG	1:AF:305:ASN:CG	2.87	0.42
1:CF:57:LEU:HD23	1:CF:203:TRP:HH2	1.84	0.42
1:CF:278:VAL:O	1:CF:278:VAL:HG13	2.20	0.42
1:BG:89:LEU:HA	1:BG:90:PRO:HD3	1.95	0.42
1:BH:115:CYS:CA	1:Cd:120:GLY:HA2	2.50	0.42
1:BH:126:GLY:HA3	1:BH:141:LEU:HD22	2.02	0.42
1:AJ:137:THR:HG23	1:AJ:140:ALA:CB	2.50	0.42
1:CJ:109:PHE:HB2	1:CJ:158:VAL:HG12	2.02	0.42
1:CK:99:PHE:CD2	1:CK:207:LEU:HB3	2.55	0.42
1:AL:302:ASP:OD2	1:AL:305:ASN:CB	2.62	0.42
1:BM:300:ILE:HD13	1:AM:321:ARG:HD2	2.02	0.42
1:AM:74:THR:O	1:AM:75:ASP:C	2.62	0.42
1:AM:212:LEU:C	1:AM:212:LEU:HD12	2.45	0.42
1:CM:264:SER:HB2	1:CM:324:LEU:HD22	2.01	0.42
1:BN:225:GLN:HG3	1:BN:244:GLY:O	2.20	0.42
1:CN:58:SER:HA	1:CN:203:TRP:CE3	2.55	0.42
1:BO:226:GLY:C	1:BO:327:VAL:HG22	2.44	0.42
1:BP:225:GLN:HG3	1:BP:244:GLY:O	2.20	0.42
1:CP:317:ASP:HB3	1:CP:319:GLN:NE2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:321:ARG:HD2	1:CR:300:ILE:HD13	2.02	0.42
1:CT:45:VAL:HG13	1:CT:45:VAL:O	2.20	0.42
1:BU:166:LEU:CD1	1:BU:166:LEU:C	2.91	0.42
1:AU:137:THR:HG23	1:AU:140:ALA:CB	2.49	0.42
1:AU:162:TYR:CE2	1:AU:164:ARG:HG2	2.55	0.42
1:CU:264:SER:HB2	1:CU:324:LEU:HD22	2.02	0.42
1:AV:63:ILE:HG23	1:AV:88:LEU:HD11	2.02	0.42
1:CV:62:ARG:H	1:BZ:142:GLN:NE2	2.18	0.42
1:CV:74:THR:O	1:CV:75:ASP:C	2.62	0.42
1:AW:300:ILE:HB	1:AW:309:THR:OG1	2.20	0.42
1:CW:119:THR:O	1:CW:120:GLY:C	2.62	0.42
1:BX:254:GLY:CA	1:BX:283:LYS:HE3	2.31	0.42
1:BZ:128:LEU:HD12	1:BZ:184:ILE:HD11	2.01	0.42
1:CZ:121:GLY:C	1:CZ:152:TRP:CD1	2.98	0.42
1:Ca:284:LYS:HD3	1:Ca:296:PHE:CZ	2.55	0.42
1:Ab:298:TRP:HE1	1:Ab:312:VAL:HA	1.85	0.42
1:Cb:102:TYR:HD2	1:Cb:205:VAL:HG21	1.85	0.42
1:Bc:100:GLN:O	1:Bc:169:THR:N	2.46	0.42
1:Bd:226:GLY:C	1:Bd:327:VAL:HG22	2.45	0.42
1:Cd:99:PHE:CD2	1:Cd:207:LEU:HB3	2.55	0.42
1:Cd:119:THR:O	1:Cd:119:THR:HG22	2.20	0.42
1:BB:61:SER:CB	1:BB:90:PRO:HD2	2.30	0.41
1:BB:281:HIS:CE1	1:BB:301:TRP:HB3	2.55	0.41
1:AB:298:TRP:O	1:AB:310:ASP:O	2.38	0.41
1:CB:99:PHE:CD2	1:CB:207:LEU:HB3	2.55	0.41
1:BC:86:PRO:HB3	1:BC:92:LEU:HD22	2.01	0.41
1:BC:319:GLN:HE21	1:BC:319:GLN:C	2.26	0.41
1:AC:63:ILE:HG23	1:AC:88:LEU:HD11	2.02	0.41
1:AC:98:ILE:HG12	1:BS:91:ARG:HG2	2.01	0.41
1:CC:141:LEU:O	1:CC:142:GLN:C	2.63	0.41
1:AD:302:ASP:CG	1:AD:305:ASN:CG	2.88	0.41
1:BE:85:VAL:CG2	1:BE:86:PRO:HD2	2.50	0.41
1:BE:246:THR:N	1:BE:247:PRO:CD	2.83	0.41
1:AE:91:ARG:NH2	1:BM:210:PRO:HB3	2.34	0.41
1:BG:225:GLN:HG3	1:BG:244:GLY:O	2.20	0.41
1:AG:116:PRO:HG2	1:AG:119:THR:OG1	2.20	0.41
1:CH:78:VAL:HG13	1:CH:78:VAL:O	2.20	0.41
1:CI:121:GLY:C	1:CI:152:TRP:CD1	2.98	0.41
1:AJ:111:ILE:O	1:AJ:112:GLN:C	2.62	0.41
1:BK:150:ALA:HB2	1:BK:156:ARG:HD3	2.01	0.41
1:BK:281:HIS:CE1	1:BK:301:TRP:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:302:ASP:OD2	1:AK:305:ASN:CB	2.61	0.41
1:AK:302:ASP:CG	1:AK:305:ASN:CG	2.88	0.41
1:CK:62:ARG:HA	1:CK:200:LEU:HD23	2.01	0.41
1:CK:103:ALA:HB2	1:CK:166:LEU:HB3	2.01	0.41
1:CK:163:THR:HG23	1:CK:164:ARG:N	2.34	0.41
1:BL:321:ARG:HD2	1:CL:300:ILE:HD13	2.01	0.41
1:AN:89:LEU:HD21	1:AN:201:CYS:HB3	2.02	0.41
1:CN:113:PRO:HA	1:CN:197:VAL:HA	2.02	0.41
1:AO:302:ASP:CG	1:AO:305:ASN:CG	2.88	0.41
1:BP:166:LEU:CD1	1:BP:166:LEU:C	2.91	0.41
1:BP:228:LEU:HD13	1:BP:238:PHE:CD2	2.55	0.41
1:AR:103:ALA:HB2	1:AR:166:LEU:HA	2.01	0.41
1:CR:123:TYR:HA	1:CR:188:VAL:HG23	2.01	0.41
1:CS:80:VAL:HG11	1:CS:185:LEU:CB	2.50	0.41
1:CS:93:GLY:O	1:CS:97:ARG:NH1	2.53	0.41
1:CS:264:SER:HB2	1:CS:324:LEU:HD22	2.01	0.41
1:CT:317:ASP:HB3	1:CT:319:GLN:NE2	2.34	0.41
1:CU:57:LEU:HD23	1:CU:203:TRP:CH2	2.54	0.41
1:CV:130:ASP:OD2	1:CV:176:ARG:NH2	2.53	0.41
1:BW:85:VAL:CG2	1:BW:86:PRO:HD2	2.50	0.41
1:BW:149:VAL:HG23	1:CW:48:PHE:HE2	1.85	0.41
1:AW:302:ASP:OD2	1:AW:305:ASN:CB	2.62	0.41
1:AX:238:PHE:CZ	1:AX:296:PHE:HB2	2.55	0.41
1:CX:122:GLY:O	1:CX:188:VAL:CB	2.68	0.41
1:BY:111:ILE:HG22	1:BY:155:SER:HA	2.01	0.41
1:CY:92:LEU:HB2	1:CY:203:TRP:CH2	2.55	0.41
1:AZ:281:HIS:ND1	1:AZ:301:TRP:HB3	2.35	0.41
1:AZ:298:TRP:O	1:AZ:310:ASP:O	2.37	0.41
1:CZ:119:THR:HG22	1:CZ:119:THR:O	2.19	0.41
1:Cc:78:VAL:O	1:Cc:78:VAL:HG13	2.20	0.41
1:Bd:85:VAL:CG2	1:Bd:86:PRO:HD2	2.50	0.41
1:Ad:89:LEU:HD21	1:Ad:201:CYS:HB3	2.02	0.41
1:Cd:111:ILE:O	1:Cd:112:GLN:C	2.63	0.41
1:AA:81:ASP:C	1:AA:81:ASP:OD1	2.64	0.41
1:AA:100:GLN:HA	1:AA:169:THR:OG1	2.20	0.41
1:AA:265:ILE:HG21	1:AA:313:ALA:O	2.20	0.41
1:CA:45:VAL:HG13	1:CA:45:VAL:O	2.20	0.41
1:BC:281:HIS:CE1	1:BC:301:TRP:HB3	2.56	0.41
1:AC:212:LEU:C	1:AC:212:LEU:HD12	2.44	0.41
1:CC:80:VAL:HG22	1:CC:81:ASP:N	2.35	0.41
1:BD:250:ILE:O	1:BD:250:ILE:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:116:PRO:HB3	1:AF:118:ASN:O	2.20	0.41
1:BE:184:ILE:HD13	1:BE:184:ILE:N	2.34	0.41
1:AE:88:LEU:C	1:AE:88:LEU:HD13	2.45	0.41
1:BF:75:ASP:C	1:BF:75:ASP:OD1	2.64	0.41
1:AF:314:TYR:HE1	1:AF:316:SER:HG	1.65	0.41
1:CF:113:PRO:HA	1:CF:197:VAL:HA	2.02	0.41
1:BG:300:ILE:HG23	1:AG:323:ILE:CD1	2.51	0.41
1:CG:80:VAL:HG11	1:CG:185:LEU:CB	2.48	0.41
1:CG:80:VAL:HG13	1:CG:185:LEU:N	2.35	0.41
1:BH:123:TYR:N	1:BH:188:VAL:HG22	2.35	0.41
1:BH:260:ASP:HA	1:AH:261:ARG:NH2	2.35	0.41
1:CH:317:ASP:HB3	1:CH:319:GLN:NE2	2.34	0.41
1:AI:89:LEU:HD21	1:AI:201:CYS:HB3	2.01	0.41
1:AI:116:PRO:HG2	1:AI:119:THR:OG1	2.20	0.41
1:BJ:111:ILE:HG22	1:BJ:155:SER:HA	2.02	0.41
1:AJ:305:ASN:ND2	1:AJ:307:THR:H	2.18	0.41
1:CJ:123:TYR:HB2	1:CJ:185:LEU:HD21	2.02	0.41
1:BK:130:ASP:HB3	1:BK:133:ASP:HB2	2.00	0.41
1:CL:45:VAL:HG13	1:CL:45:VAL:O	2.20	0.41
1:BM:226:GLY:C	1:BM:327:VAL:HG22	2.44	0.41
1:AM:103:ALA:HB2	1:AM:166:LEU:HA	2.01	0.41
1:CM:111:ILE:HD11	1:CM:125:ALA:HB3	2.02	0.41
1:BN:99:PHE:HA	1:BN:209:VAL:O	2.20	0.41
1:AN:298:TRP:HE1	1:AN:312:VAL:HA	1.85	0.41
1:AN:302:ASP:CG	1:AN:305:ASN:CG	2.87	0.41
1:BO:319:GLN:HE21	1:BO:319:GLN:C	2.27	0.41
1:AO:298:TRP:O	1:AO:310:ASP:O	2.38	0.41
1:CO:99:PHE:HB3	1:CO:209:VAL:O	2.20	0.41
1:CO:214:ASN:HA	1:CO:215:PRO:HD3	1.83	0.41
1:BP:86:PRO:HB3	1:BP:92:LEU:HD22	2.03	0.41
1:CP:214:ASN:HA	1:CP:215:PRO:HD3	1.83	0.41
1:BQ:122:GLY:C	1:BQ:188:VAL:CG2	2.85	0.41
1:BQ:246:THR:N	1:BQ:247:PRO:CD	2.83	0.41
1:AQ:188:VAL:HG21	1:AZ:114:MET:SD	2.60	0.41
1:CQ:123:TYR:CD1	1:CQ:185:LEU:HD21	2.55	0.41
1:AR:89:LEU:HD21	1:AR:201:CYS:HB3	2.02	0.41
1:AR:100:GLN:HA	1:AR:169:THR:OG1	2.21	0.41
1:AS:263:LEU:HB3	1:AS:279:TYR:O	2.21	0.41
1:CS:113:PRO:HA	1:CS:197:VAL:HA	2.02	0.41
1:BT:122:GLY:O	1:BT:188:VAL:HG22	2.20	0.41
1:AT:302:ASP:CG	1:AT:305:ASN:CG	2.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:256:VAL:HB	1:AU:335:ASP:HB3	2.02	0.41
1:CV:113:PRO:HA	1:CV:197:VAL:HA	2.00	0.41
1:BY:176:ARG:HD2	1:CY:168:TRP:CZ2	2.55	0.41
1:AY:81:ASP:OD1	1:AY:81:ASP:C	2.63	0.41
1:AY:302:ASP:OD2	1:AY:305:ASN:CB	2.62	0.41
1:CY:158:VAL:HG13	1:CY:158:VAL:O	2.20	0.41
1:BZ:99:PHE:HA	1:BZ:209:VAL:O	2.21	0.41
1:BZ:300:ILE:HD13	1:AZ:321:ARG:HD2	2.02	0.41
1:AZ:137:THR:HG23	1:AZ:140:ALA:CB	2.50	0.41
1:Aa:281:HIS:ND1	1:Aa:301:TRP:HB3	2.35	0.41
1:Aa:302:ASP:CG	1:Aa:305:ASN:CG	2.87	0.41
1:Bb:109:PHE:HB2	1:Bb:158:VAL:CG1	2.51	0.41
1:Bb:226:GLY:C	1:Bb:327:VAL:HG22	2.45	0.41
1:Ab:256:VAL:HB	1:Ab:335:ASP:HB3	2.01	0.41
1:Cc:121:GLY:C	1:Cc:152:TRP:CD1	2.98	0.41
1:Cc:317:ASP:CB	1:Cc:319:GLN:NE2	2.83	0.41
1:Ad:80:VAL:HG13	1:Ad:185:LEU:HB3	2.02	0.41
1:AA:298:TRP:O	1:AA:310:ASP:O	2.38	0.41
1:CA:219:THR:HG21	1:CA:333:ARG:O	2.19	0.41
1:BB:122:GLY:C	1:BB:188:VAL:CG2	2.86	0.41
1:AB:69:PRO:C	1:AB:72:THR:HG1	2.26	0.41
1:AB:85:VAL:HG22	1:AB:86:PRO:HD2	2.02	0.41
1:AB:308:PHE:CE2	1:AB:310:ASP:HA	2.54	0.41
1:CB:63:ILE:HD12	1:CB:88:LEU:CG	2.47	0.41
1:CB:167:LEU:N	1:CB:167:LEU:HD12	2.35	0.41
1:BD:75:ASP:C	1:BD:75:ASP:OD1	2.62	0.41
1:AD:264:SER:OG	1:AD:276:ARG:NH1	2.53	0.41
1:AE:302:ASP:C	1:AE:305:ASN:HD21	2.23	0.41
1:BG:100:GLN:NE2	1:BG:211:SER:CB	2.83	0.41
1:AG:98:ILE:CG2	1:Bd:91:ARG:NH1	2.80	0.41
1:AG:238:PHE:CZ	1:AG:296:PHE:HB2	2.55	0.41
1:CH:102:TYR:HD2	1:CH:205:VAL:HG21	1.84	0.41
1:CI:123:TYR:CD1	1:CI:185:LEU:HD21	2.55	0.41
1:AJ:298:TRP:O	1:AJ:310:ASP:O	2.37	0.41
1:BK:226:GLY:C	1:BK:327:VAL:HG22	2.45	0.41
1:BK:232:SER:HB3	1:BK:242:LEU:HD11	2.01	0.41
1:AK:61:SER:HB2	1:AK:89:LEU:HD22	2.02	0.41
1:AK:162:TYR:CE2	1:AK:164:ARG:HG2	2.55	0.41
1:BL:163:THR:C	1:BL:165:THR:HG22	2.45	0.41
1:AL:105:GLU:C	1:AL:162:TYR:HH	2.21	0.41
1:CL:98:ILE:C	1:CL:211:SER:O	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:100:GLN:HA	1:AM:169:THR:OG1	2.21	0.41
1:CM:124:VAL:HG13	1:CM:124:VAL:O	2.20	0.41
1:AO:63:ILE:HG23	1:AO:88:LEU:HD11	2.03	0.41
1:AO:263:LEU:HB3	1:AO:279:TYR:O	2.20	0.41
1:AO:308:PHE:CE2	1:AO:310:ASP:HA	2.55	0.41
1:CO:123:TYR:HB2	1:CO:185:LEU:CD2	2.51	0.41
1:BP:109:PHE:HB2	1:BP:158:VAL:CG1	2.51	0.41
1:BQ:149:VAL:HG23	1:CQ:48:PHE:HE2	1.85	0.41
1:AQ:238:PHE:CZ	1:AQ:296:PHE:HB2	2.55	0.41
1:CQ:113:PRO:HA	1:CQ:197:VAL:HA	2.01	0.41
1:AR:300:ILE:HB	1:AR:309:THR:OG1	2.20	0.41
1:CR:202:ARG:HH12	1:CT:46:THR:HB	1.85	0.41
1:CR:214:ASN:HA	1:CR:215:PRO:HD3	1.84	0.41
1:AS:101:ARG:NH1	1:AS:166:LEU:HD23	2.35	0.41
1:BT:85:VAL:CG2	1:BT:86:PRO:HD2	2.50	0.41
1:BT:130:ASP:HB3	1:BT:133:ASP:HB2	2.02	0.41
1:BT:149:VAL:HG23	1:CT:48:PHE:HE2	1.85	0.41
1:BT:281:HIS:CE1	1:BT:301:TRP:HB3	2.55	0.41
1:AT:80:VAL:HG12	1:AT:185:LEU:HB3	2.02	0.41
1:AT:127:PHE:O	1:AT:144:THR:OG1	2.35	0.41
1:CT:123:TYR:CD1	1:CT:185:LEU:HD21	2.55	0.41
1:BU:253:ASP:CB	1:BU:286:ALA:HB2	2.49	0.41
1:BV:100:GLN:NE2	1:BV:211:SER:CB	2.84	0.41
1:BW:166:LEU:CD1	1:BW:166:LEU:C	2.93	0.41
1:AX:80:VAL:HG13	1:AX:185:LEU:HB3	2.01	0.41
1:AX:162:TYR:CE2	1:AX:164:ARG:HG2	2.55	0.41
1:AX:298:TRP:HE1	1:AX:312:VAL:HA	1.85	0.41
1:AX:302:ASP:OD2	1:AX:305:ASN:CB	2.61	0.41
1:BY:126:GLY:HA3	1:BY:141:LEU:HD22	2.02	0.41
1:AY:302:ASP:CG	1:AY:305:ASN:CG	2.87	0.41
1:CY:98:ILE:C	1:CY:211:SER:O	2.61	0.41
1:CY:278:VAL:O	1:CY:278:VAL:HG13	2.20	0.41
1:Aa:162:TYR:CE2	1:Aa:164:ARG:HG2	2.54	0.41
1:Ac:267:TYR:CE2	1:Cc:320:PRO:HD3	2.55	0.41
1:Cc:80:VAL:HG11	1:Cc:185:LEU:HB2	2.01	0.41
1:Bd:149:VAL:HG23	1:Cd:48:PHE:HE2	1.85	0.41
1:Ad:116:PRO:HG2	1:Ad:119:THR:OG1	2.19	0.41
1:Cd:130:ASP:OD2	1:Cd:176:ARG:NH2	2.53	0.41
1:Cd:219:THR:HG21	1:Cd:333:ARG:O	2.20	0.41
1:AA:302:ASP:CG	1:AA:305:ASN:CG	2.88	0.41
1:AB:116:PRO:HG2	1:AB:119:THR:OG1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:183:LEU:HG	1:AD:184:ILE:N	2.32	0.41
1:AE:183:LEU:HG	1:AE:184:ILE:N	2.35	0.41
1:CE:111:ILE:HD11	1:CE:125:ALA:HB3	2.02	0.41
1:BF:128:LEU:HD12	1:BF:184:ILE:HD11	2.02	0.41
1:BF:156:ARG:HH22	1:CI:34:ARG:CD	2.33	0.41
1:BF:214:ASN:HD22	1:BF:215:PRO:HD2	1.85	0.41
1:CF:54:ASP:OD1	1:CF:54:ASP:N	2.53	0.41
1:CF:58:SER:HB3	1:CF:204:SER:HB2	2.02	0.41
1:CF:155:SER:O	1:CF:156:ARG:HD3	2.19	0.41
1:AG:63:ILE:HG23	1:AG:88:LEU:HD11	2.02	0.41
1:AG:103:ALA:HB2	1:AG:166:LEU:HA	2.02	0.41
1:CG:264:SER:HB2	1:CG:324:LEU:HD22	2.01	0.41
1:BH:130:ASP:HB3	1:BH:133:ASP:HB2	2.01	0.41
1:AH:105:GLU:C	1:AH:162:TYR:HH	2.19	0.41
1:AH:116:PRO:HG2	1:AH:119:THR:OG1	2.20	0.41
1:BI:228:LEU:HD13	1:BI:238:PHE:CD2	2.55	0.41
1:AI:98:ILE:HG22	1:AI:99:PHE:CD2	2.55	0.41
1:AI:103:ALA:HB2	1:AI:166:LEU:HA	2.01	0.41
1:AI:281:HIS:ND1	1:AI:301:TRP:HB3	2.34	0.41
1:AI:288:ASN:O	1:AI:289:ALA:C	2.62	0.41
1:AI:314:TYR:HE1	1:AI:316:SER:HG	1.66	0.41
1:AJ:114:MET:SD	1:AR:188:VAL:HG23	2.61	0.41
1:CJ:79:VAL:HG13	1:CJ:80:VAL:HG12	2.01	0.41
1:AK:305:ASN:ND2	1:AK:307:THR:H	2.19	0.41
1:CK:47:GLY:H	1:CL:60:MET:HE1	1.85	0.41
1:BL:111:ILE:HG22	1:BL:155:SER:HA	2.03	0.41
1:AL:256:VAL:HB	1:AL:335:ASP:HB3	2.03	0.41
1:AM:302:ASP:OD2	1:AM:305:ASN:CB	2.61	0.41
1:BN:319:GLN:HE21	1:BN:319:GLN:C	2.28	0.41
1:AN:57:LEU:HD23	1:AN:57:LEU:HA	1.95	0.41
1:AN:263:LEU:HB3	1:AN:279:TYR:O	2.19	0.41
1:CN:278:VAL:O	1:CN:278:VAL:HG13	2.20	0.41
1:BO:228:LEU:HD13	1:BO:238:PHE:CD2	2.54	0.41
1:AO:63:ILE:CD1	1:AO:89:LEU:HD21	2.50	0.41
1:AO:224:THR:HG22	1:AO:329:THR:N	2.35	0.41
1:AP:63:ILE:HG23	1:AP:88:LEU:HD11	2.03	0.41
1:AP:74:THR:O	1:AP:75:ASP:C	2.63	0.41
1:BQ:234:SER:HB3	1:BQ:237:ASP:OD1	2.19	0.41
1:AS:162:TYR:CE2	1:AS:164:ARG:HG2	2.55	0.41
1:CS:79:VAL:CG1	1:CS:80:VAL:N	2.83	0.41
1:CS:317:ASP:HB3	1:CS:319:GLN:NE2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:109:PHE:HB2	1:BT:158:VAL:CG1	2.50	0.41
1:CT:250:ILE:O	1:CT:250:ILE:HG22	2.20	0.41
1:AU:98:ILE:HG22	1:AU:99:PHE:CD2	2.55	0.41
1:AU:111:ILE:O	1:AU:112:GLN:C	2.63	0.41
1:AU:267:TYR:CE2	1:CU:320:PRO:HD3	2.56	0.41
1:AU:302:ASP:C	1:AU:305:ASN:HD21	2.23	0.41
1:CU:63:ILE:HD13	1:CU:63:ILE:HA	1.87	0.41
1:BV:86:PRO:HB3	1:BV:92:LEU:HD22	2.02	0.41
1:BV:111:ILE:HG22	1:BV:155:SER:HA	2.03	0.41
1:BV:253:ASP:CB	1:BV:286:ALA:HB2	2.50	0.41
1:AV:88:LEU:C	1:AV:88:LEU:HD13	2.45	0.41
1:CV:54:ASP:OD1	1:CV:54:ASP:N	2.51	0.41
1:CW:141:LEU:O	1:CW:142:GLN:C	2.62	0.41
1:BX:100:GLN:NE2	1:BX:211:SER:CB	2.83	0.41
1:BX:300:ILE:HD13	1:AX:321:ARG:HD2	2.03	0.41
1:AX:256:VAL:HB	1:AX:335:ASP:HB3	2.02	0.41
1:AZ:116:PRO:HG2	1:AZ:119:THR:OG1	2.20	0.41
1:Aa:298:TRP:HE1	1:Aa:312:VAL:HA	1.85	0.41
1:Bb:99:PHE:HA	1:Bb:209:VAL:O	2.20	0.41
1:Bb:111:ILE:HG22	1:Bb:155:SER:HA	2.02	0.41
1:Cb:45:VAL:HG13	1:Cb:45:VAL:O	2.20	0.41
1:Bc:191:ASN:HD22	1:Bc:191:ASN:H	1.67	0.41
1:Bc:226:GLY:C	1:Bc:327:VAL:HG22	2.45	0.41
1:Bd:100:GLN:NE2	1:Bd:211:SER:CB	2.83	0.41
1:Bd:319:GLN:HE21	1:Bd:319:GLN:C	2.28	0.41
1:Ad:183:LEU:HG	1:Ad:184:ILE:N	2.36	0.41
1:CA:80:VAL:HG11	1:CA:185:LEU:CB	2.49	0.41
1:CA:99:PHE:CD2	1:CA:207:LEU:HB3	2.56	0.41
1:CB:45:VAL:HG23	1:CF:200:LEU:HD13	2.01	0.41
1:CC:163:THR:HG23	1:CC:164:ARG:N	2.35	0.41
1:BD:91:ARG:HG2	1:AW:98:ILE:HG12	2.01	0.41
1:BD:163:THR:O	1:BD:165:THR:HG22	2.21	0.41
1:AD:89:LEU:HD21	1:AD:201:CYS:HB3	2.03	0.41
1:AD:226:GLY:N	1:AD:243:LEU:O	2.52	0.41
1:CD:130:ASP:OD2	1:CD:176:ARG:NH2	2.54	0.41
1:CD:153:TRP:CD1	1:CD:153:TRP:H	2.38	0.41
1:BE:89:LEU:HA	1:BE:90:PRO:HD3	1.94	0.41
1:AE:98:ILE:HG22	1:AE:99:PHE:CD2	2.55	0.41
1:AE:226:GLY:N	1:AE:243:LEU:O	2.52	0.41
1:AF:91:ARG:CZ	1:Bb:98:ILE:CG2	2.98	0.41
1:CF:45:VAL:HG13	1:CF:45:VAL:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:123:TYR:HB2	1:CG:185:LEU:HD21	2.00	0.41
1:BH:163:THR:C	1:BH:165:THR:HG22	2.45	0.41
1:BI:319:GLN:HE21	1:BI:319:GLN:C	2.27	0.41
1:AI:138:PHE:CE2	1:Aa:62:ARG:CZ	3.04	0.41
1:AK:298:TRP:O	1:AK:310:ASP:O	2.37	0.41
1:AM:126:GLY:HA2	1:AM:158:VAL:HG21	2.03	0.41
1:AN:64:SER:OG	1:AN:80:VAL:HG21	2.21	0.41
1:CN:122:GLY:O	1:CN:188:VAL:CB	2.66	0.41
1:CQ:121:GLY:C	1:CQ:152:TRP:CD1	2.98	0.41
1:AR:224:THR:HG22	1:AR:329:THR:N	2.36	0.41
1:BS:115:CYS:HB3	1:BS:195:VAL:HG12	2.03	0.41
1:AS:57:LEU:HD23	1:AS:57:LEU:HA	1.95	0.41
1:BT:199:VAL:HG13	1:BT:199:VAL:O	2.19	0.41
1:BU:226:GLY:C	1:BU:327:VAL:HG22	2.46	0.41
1:AU:288:ASN:O	1:AU:289:ALA:C	2.63	0.41
1:AV:212:LEU:C	1:AV:212:LEU:HD12	2.45	0.41
1:CV:122:GLY:O	1:CV:188:VAL:CB	2.68	0.41
1:CX:317:ASP:HB3	1:CX:319:GLN:NE2	2.35	0.41
1:BY:142:GLN:NE2	1:Ca:62:ARG:H	2.18	0.41
1:CY:102:TYR:HD2	1:CY:205:VAL:HG21	1.85	0.41
1:BZ:136:HIS:O	1:BZ:186:LEU:HD11	2.21	0.41
1:AZ:300:ILE:HB	1:AZ:309:THR:OG1	2.21	0.41
1:AZ:302:ASP:CG	1:AZ:305:ASN:CG	2.88	0.41
1:Aa:81:ASP:C	1:Aa:81:ASP:OD1	2.63	0.41
1:Aa:298:TRP:O	1:Aa:310:ASP:O	2.38	0.41
1:Bb:214:ASN:ND2	1:Bb:215:PRO:HD2	2.35	0.41
1:Ab:162:TYR:CE2	1:Ab:164:ARG:HG2	2.55	0.41
1:Cb:123:TYR:CD1	1:Cb:185:LEU:HD21	2.56	0.41
1:Cb:199:VAL:O	1:Cb:199:VAL:CG1	2.68	0.41
1:Cb:317:ASP:HB3	1:Cb:319:GLN:NE2	2.34	0.41
1:Ac:88:LEU:HD13	1:Ac:88:LEU:C	2.45	0.41
1:Cc:45:VAL:O	1:Cc:45:VAL:HG13	2.20	0.41
1:Bd:130:ASP:HB3	1:Bd:133:ASP:HB2	2.02	0.41
1:Ad:302:ASP:CG	1:Ad:305:ASN:CG	2.88	0.41
1:BA:300:ILE:HD13	1:AA:321:ARG:HD2	2.01	0.41
1:AA:212:LEU:HD12	1:AA:212:LEU:C	2.46	0.41
1:AA:281:HIS:ND1	1:AA:301:TRP:HB3	2.35	0.41
1:AB:109:PHE:HE2	1:AB:127:PHE:CD1	2.38	0.41
1:AB:238:PHE:CZ	1:AB:296:PHE:HB2	2.55	0.41
1:CB:264:SER:HB2	1:CB:324:LEU:HD22	2.02	0.41
1:BC:225:GLN:HG3	1:BC:244:GLY:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:121:GLY:C	1:CC:152:TRP:CD1	2.99	0.41
1:BD:100:GLN:NE2	1:BD:211:SER:CB	2.84	0.41
1:BD:166:LEU:CD1	1:BD:166:LEU:C	2.93	0.41
1:BE:100:GLN:NE2	1:BE:211:SER:OG	2.54	0.41
1:BE:109:PHE:HB2	1:BE:158:VAL:CG1	2.51	0.41
1:AE:64:SER:OG	1:AE:80:VAL:HG21	2.20	0.41
1:AE:298:TRP:CG	1:AE:312:VAL:HG13	2.51	0.41
1:CE:80:VAL:HG22	1:CE:81:ASP:N	2.34	0.41
1:CE:219:THR:HG21	1:CE:333:ARG:O	2.20	0.41
1:BG:281:HIS:CE1	1:BG:301:TRP:HB3	2.55	0.41
1:AG:74:THR:O	1:AG:75:ASP:C	2.64	0.41
1:AG:302:ASP:CG	1:AG:305:ASN:CG	2.88	0.41
1:BH:200:LEU:HD21	1:Cd:138:PHE:HZ	1.86	0.41
1:AH:224:THR:HG22	1:AH:329:THR:N	2.35	0.41
1:CH:264:SER:HB2	1:CH:324:LEU:HD22	2.02	0.41
1:BI:111:ILE:CG2	1:BI:112:GLN:N	2.83	0.41
1:CI:80:VAL:HG13	1:CI:185:LEU:N	2.36	0.41
1:CI:98:ILE:C	1:CI:211:SER:O	2.59	0.41
1:AJ:98:ILE:HG22	1:AJ:99:PHE:CD2	2.55	0.41
1:AJ:114:MET:SD	1:AR:188:VAL:CG2	3.08	0.41
1:CJ:45:VAL:O	1:CJ:45:VAL:HG13	2.21	0.41
1:CJ:113:PRO:HA	1:CJ:197:VAL:HA	2.02	0.41
1:AK:138:PHE:CE2	1:AS:62:ARG:CZ	3.04	0.41
1:CK:77:TYR:CD1	1:CK:78:VAL:N	2.88	0.41
1:CK:81:ASP:HA	1:CK:184:ILE:HG22	2.01	0.41
1:AL:124:VAL:HG11	1:AL:138:PHE:CD1	2.55	0.41
1:BM:225:GLN:HG3	1:BM:244:GLY:O	2.20	0.41
1:CM:317:ASP:HB3	1:CM:319:GLN:NE2	2.36	0.41
1:AP:308:PHE:CE2	1:AP:310:ASP:HA	2.55	0.41
1:AR:63:ILE:CD1	1:AR:89:LEU:HD21	2.51	0.41
1:AR:256:VAL:HB	1:AR:335:ASP:HB3	2.02	0.41
1:CR:85:VAL:O	1:CR:86:PRO:C	2.63	0.41
1:BS:123:TYR:N	1:BS:188:VAL:HG22	2.34	0.41
1:AS:64:SER:O	1:AS:199:VAL:HG12	2.21	0.41
1:AS:81:ASP:OD1	1:AS:81:ASP:C	2.64	0.41
1:CS:98:ILE:HG13	1:CS:99:PHE:CD2	2.55	0.41
1:CS:153:TRP:CD1	1:CS:153:TRP:H	2.36	0.41
1:BT:150:ALA:HB2	1:BT:156:ARG:HD3	2.03	0.41
1:CT:158:VAL:O	1:CT:158:VAL:HG13	2.21	0.41
1:AV:63:ILE:CD1	1:AV:89:LEU:HD21	2.51	0.41
1:AV:137:THR:HG23	1:AV:140:ALA:CB	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:238:PHE:CZ	1:AV:296:PHE:HB2	2.56	0.41
1:CV:60:MET:HE3	1:CV:202:ARG:HB3	2.03	0.41
1:CV:123:TYR:CD1	1:CV:185:LEU:HD21	2.55	0.41
1:CV:163:THR:OG1	1:CV:165:THR:HG23	2.21	0.41
1:AW:162:TYR:CE2	1:AW:164:ARG:HG2	2.56	0.41
1:BX:99:PHE:HA	1:BX:209:VAL:O	2.21	0.41
1:CX:91:ARG:HD2	1:Cc:98:ILE:HB	2.02	0.41
1:CX:113:PRO:HA	1:CX:197:VAL:HA	2.01	0.41
1:BY:254:GLY:CA	1:BY:283:LYS:HE3	2.30	0.41
1:AY:63:ILE:HD11	1:AY:89:LEU:HD21	2.02	0.41
1:AY:109:PHE:HB2	1:AY:158:VAL:HG12	2.03	0.41
1:AZ:302:ASP:C	1:AZ:305:ASN:HD21	2.23	0.41
1:CZ:85:VAL:O	1:CZ:86:PRO:C	2.64	0.41
1:CZ:264:SER:HB2	1:CZ:324:LEU:HD22	2.02	0.41
1:Aa:98:ILE:HG22	1:Aa:99:PHE:CD2	2.55	0.41
1:Bb:321:ARG:HD2	1:Cb:300:ILE:HD13	2.03	0.41
1:Cb:80:VAL:HG11	1:Cb:185:LEU:HB2	2.02	0.41
1:Cb:121:GLY:C	1:Cb:152:TRP:CD1	2.98	0.41
1:Bc:321:ARG:HD2	1:Cc:300:ILE:HD13	2.02	0.41
1:BA:91:ARG:HG2	1:AI:98:ILE:HG12	2.02	0.41
1:BA:246:THR:N	1:BA:247:PRO:CD	2.83	0.41
1:AA:109:PHE:HB2	1:AA:158:VAL:HG12	2.03	0.41
1:CA:188:VAL:HG11	1:BV:114:MET:HE1	2.03	0.41
1:BB:85:VAL:CG2	1:BB:86:PRO:HD2	2.50	0.41
1:AB:74:THR:O	1:AB:75:ASP:C	2.64	0.41
1:CB:119:THR:O	1:CB:120:GLY:C	2.64	0.41
1:CB:317:ASP:HB3	1:CB:319:GLN:NE2	2.35	0.41
1:BC:124:VAL:HG11	1:BC:138:PHE:CD2	2.56	0.41
1:AC:116:PRO:HG2	1:AC:119:THR:OG1	2.21	0.41
1:BD:321:ARG:HD2	1:CD:300:ILE:HD13	2.03	0.41
1:AD:109:PHE:HB2	1:AD:158:VAL:HG12	2.03	0.41
1:CD:123:TYR:HB2	1:CD:185:LEU:CD2	2.51	0.41
1:CD:264:SER:HB2	1:CD:324:LEU:HD22	2.03	0.41
1:BE:166:LEU:CD1	1:BE:166:LEU:C	2.92	0.41
1:CE:60:MET:CE	1:CE:202:ARG:HB3	2.49	0.41
1:CG:98:ILE:C	1:CG:211:SER:O	2.62	0.41
1:CG:113:PRO:HA	1:CG:197:VAL:HA	2.02	0.41
1:BH:86:PRO:HB3	1:BH:92:LEU:HD22	2.01	0.41
1:BH:100:GLN:NE2	1:BH:211:SER:OG	2.54	0.41
1:BH:117:ALA:HB2	1:Cd:117:ALA:HB1	2.03	0.41
1:BI:300:ILE:HD13	1:AI:321:ARG:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:61:SER:CB	1:AI:90:PRO:HD2	2.37	0.41
1:AI:102:TYR:HD2	1:AI:205:VAL:HG21	1.86	0.41
1:AI:109:PHE:CE2	1:AI:127:PHE:CD1	3.08	0.41
1:AI:183:LEU:HG	1:AI:184:ILE:N	2.36	0.41
1:CI:158:VAL:HG13	1:CI:158:VAL:O	2.21	0.41
1:CJ:60:MET:HE2	1:CJ:202:ARG:HB3	2.03	0.41
1:AK:302:ASP:CA	1:AK:305:ASN:CG	2.93	0.41
1:AL:302:ASP:CG	1:AL:305:ASN:CG	2.88	0.41
1:BM:99:PHE:HA	1:BM:209:VAL:O	2.21	0.41
1:CM:200:LEU:HD13	1:CO:45:VAL:HG23	2.03	0.41
1:BN:163:THR:O	1:BN:165:THR:HG22	2.21	0.41
1:AN:234:SER:HB3	1:AN:237:ASP:O	2.19	0.41
1:AO:98:ILE:HG22	1:AO:99:PHE:CD2	2.56	0.41
1:CO:130:ASP:OD2	1:CO:176:ARG:NH2	2.54	0.41
1:CP:45:VAL:O	1:CP:45:VAL:HG13	2.20	0.41
1:CP:113:PRO:HA	1:CP:197:VAL:HA	2.02	0.41
1:AQ:162:TYR:CE2	1:AQ:164:ARG:HG2	2.55	0.41
1:AR:137:THR:HG23	1:AR:140:ALA:CB	2.51	0.41
1:BS:319:GLN:HE21	1:BS:319:GLN:C	2.28	0.41
1:BS:321:ARG:HD2	1:CS:300:ILE:HD13	2.01	0.41
1:AS:308:PHE:CE2	1:AS:310:ASP:HA	2.55	0.41
1:CS:78:VAL:O	1:CS:78:VAL:HG13	2.21	0.41
1:AT:109:PHE:CE2	1:AT:127:PHE:CD1	3.09	0.41
1:AT:298:TRP:O	1:AT:310:ASP:O	2.38	0.41
1:CT:120:GLY:HA3	1:Ba:116:PRO:HD3	2.03	0.41
1:CT:130:ASP:OD2	1:CT:176:ARG:NH2	2.54	0.41
1:BU:228:LEU:HD13	1:BU:238:PHE:CD2	2.56	0.41
1:AV:74:THR:O	1:AV:75:ASP:C	2.63	0.41
1:AX:298:TRP:O	1:AX:310:ASP:O	2.38	0.41
1:CY:79:VAL:CG1	1:CY:80:VAL:N	2.83	0.41
1:CY:163:THR:OG1	1:CY:165:THR:HG23	2.21	0.41
1:CZ:89:LEU:HD13	1:CZ:203:TRP:CG	2.56	0.41
1:CZ:133:ASP:O	1:CZ:182:ARG:NH2	2.54	0.41
1:Ba:321:ARG:HD2	1:Ca:300:ILE:HD13	2.03	0.41
1:Aa:314:TYR:HE1	1:Aa:316:SER:HG	1.64	0.41
1:Ca:186:LEU:HD23	1:Ca:186:LEU:N	2.36	0.41
1:Ab:212:LEU:C	1:Ab:212:LEU:HD12	2.45	0.41
1:Bc:281:HIS:CE1	1:Bc:301:TRP:HB3	2.55	0.41
1:Bd:253:ASP:CB	1:Bd:286:ALA:HB2	2.50	0.41
1:Cd:80:VAL:HG13	1:Cd:185:LEU:N	2.34	0.41
1:AA:103:ALA:HB2	1:AA:166:LEU:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:100:GLN:NE2	1:BB:211:SER:CB	2.84	0.41
1:BB:263:LEU:CD2	1:BB:298:TRP:HB3	2.51	0.41
1:AB:314:TYR:HE1	1:AB:316:SER:HG	1.66	0.41
1:CB:78:VAL:O	1:CB:78:VAL:HG13	2.21	0.41
1:BC:191:ASN:H	1:BC:191:ASN:HD22	1.69	0.41
1:AC:302:ASP:CG	1:AC:305:ASN:CG	2.89	0.41
1:CC:85:VAL:O	1:CC:86:PRO:C	2.63	0.41
1:AD:281:HIS:ND1	1:AD:301:TRP:HB3	2.36	0.41
1:BE:226:GLY:C	1:BE:327:VAL:HG22	2.46	0.41
1:BE:281:HIS:CE1	1:BE:301:TRP:HB3	2.56	0.41
1:AF:91:ARG:HG2	1:Bb:98:ILE:HG23	2.02	0.41
1:AF:183:LEU:HG	1:AF:184:ILE:N	2.35	0.41
1:AF:308:PHE:CE2	1:AF:310:ASP:HA	2.55	0.41
1:BG:86:PRO:HB3	1:BG:92:LEU:HD22	2.03	0.41
1:BG:184:ILE:HD13	1:BG:184:ILE:N	2.35	0.41
1:CG:278:VAL:HG13	1:CG:278:VAL:O	2.20	0.41
1:BH:228:LEU:HD13	1:BH:238:PHE:CD2	2.56	0.41
1:BH:254:GLY:CA	1:BH:283:LYS:HE3	2.28	0.41
1:BH:300:ILE:HD13	1:AH:321:ARG:HD2	2.02	0.41
1:AH:264:SER:OG	1:AH:276:ARG:NH1	2.51	0.41
1:BI:163:THR:C	1:BI:165:THR:HG22	2.46	0.41
1:AI:234:SER:HB3	1:AI:237:ASP:O	2.20	0.41
1:AI:302:ASP:CG	1:AI:305:ASN:CG	2.87	0.41
1:AJ:91:ARG:NH2	1:BR:210:PRO:HB3	2.36	0.41
1:AJ:100:GLN:HA	1:AJ:169:THR:OG1	2.21	0.41
1:AJ:281:HIS:ND1	1:AJ:301:TRP:HB3	2.36	0.41
1:CK:103:ALA:O	1:CK:205:VAL:HG23	2.21	0.41
1:BL:128:LEU:HD12	1:BL:184:ILE:HD11	2.02	0.41
1:CL:119:THR:O	1:CL:119:THR:HG22	2.20	0.41
1:BM:130:ASP:HB3	1:BM:133:ASP:HB2	2.02	0.41
1:CM:54:ASP:N	1:CM:54:ASP:OD1	2.54	0.41
1:CM:128:LEU:HA	1:CM:129:PRO:HD3	1.97	0.41
1:CM:278:VAL:HG13	1:CM:278:VAL:O	2.21	0.41
1:CN:155:SER:O	1:CN:156:ARG:HD3	2.21	0.41
1:BO:98:ILE:CG2	1:Ab:91:ARG:CZ	2.98	0.41
1:BO:321:ARG:HD2	1:CO:300:ILE:HD13	2.02	0.41
1:AO:116:PRO:HG2	1:AO:119:THR:OG1	2.21	0.41
1:CO:128:LEU:HA	1:CO:129:PRO:HD3	1.94	0.41
1:CP:119:THR:O	1:CP:119:THR:HG22	2.19	0.41
1:BQ:321:ARG:HD2	1:CQ:300:ILE:HD13	2.03	0.41
1:CQ:278:VAL:O	1:CQ:278:VAL:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:317:ASP:HB3	1:CQ:319:GLN:NE2	2.35	0.41
1:BS:111:ILE:CG2	1:BS:112:GLN:N	2.82	0.41
1:BT:232:SER:HB3	1:BT:242:LEU:HD11	2.02	0.41
1:AU:64:SER:OG	1:AU:80:VAL:HG21	2.19	0.41
1:AU:298:TRP:O	1:AU:310:ASP:O	2.39	0.41
1:AU:298:TRP:HE1	1:AU:312:VAL:HA	1.85	0.41
1:BW:130:ASP:HB3	1:BW:133:ASP:HB2	2.02	0.41
1:BX:228:LEU:HD13	1:BX:238:PHE:CD2	2.55	0.41
1:CX:63:ILE:HG23	1:CX:88:LEU:HD21	2.03	0.41
1:AY:89:LEU:HD21	1:AY:201:CYS:HB3	2.02	0.41
1:AY:98:ILE:HG22	1:AY:99:PHE:CD2	2.56	0.41
1:AY:101:ARG:NH1	1:AY:166:LEU:HD23	2.36	0.41
1:CY:122:GLY:O	1:CY:188:VAL:CB	2.68	0.41
1:AZ:81:ASP:C	1:AZ:81:ASP:OD1	2.63	0.41
1:AZ:100:GLN:HA	1:AZ:169:THR:OG1	2.20	0.41
1:Aa:80:VAL:HG12	1:Aa:185:LEU:HB3	2.03	0.41
1:Ab:100:GLN:HA	1:Ab:169:THR:OG1	2.20	0.41
1:Ab:183:LEU:HG	1:Ab:184:ILE:N	2.35	0.41
1:Ab:302:ASP:CG	1:Ab:305:ASN:CG	2.88	0.41
1:Ad:226:GLY:N	1:Ad:243:LEU:O	2.49	0.41
1:Cd:57:LEU:HD23	1:Cd:203:TRP:CH2	2.56	0.41
1:BA:111:ILE:HG22	1:BA:155:SER:HA	2.02	0.41
1:BA:196:ASN:HD22	1:BA:196:ASN:C	2.29	0.41
1:AA:126:GLY:HA2	1:AA:158:VAL:HG21	2.03	0.41
1:AA:224:THR:HG22	1:AA:329:THR:N	2.36	0.41
1:BB:210:PRO:HB3	1:AK:91:ARG:CZ	2.50	0.41
1:BB:228:LEU:HD13	1:BB:238:PHE:CD2	2.56	0.41
1:AB:126:GLY:HA2	1:AB:158:VAL:HG21	2.03	0.41
1:CB:34:ARG:CG	1:Bb:156:ARG:HH22	2.34	0.41
1:CB:74:THR:O	1:CB:75:ASP:C	2.62	0.41
1:CB:119:THR:O	1:CB:119:THR:HG22	2.21	0.41
1:CB:121:GLY:HA3	1:CB:152:TRP:HD1	1.85	0.41
1:CB:138:PHE:CD2	1:BY:62:ARG:NH2	2.89	0.41
1:AC:263:LEU:HB3	1:AC:279:TYR:O	2.21	0.41
1:CC:123:TYR:HB2	1:CC:185:LEU:CD2	2.51	0.41
1:BD:62:ARG:NH2	1:CW:138:PHE:CD2	2.89	0.41
1:AE:123:TYR:HB2	1:AE:185:LEU:HD11	2.02	0.41
1:AE:212:LEU:HD12	1:AE:212:LEU:C	2.46	0.41
1:AE:264:SER:OG	1:AE:276:ARG:NH1	2.52	0.41
1:AE:300:ILE:HB	1:AE:309:THR:OG1	2.21	0.41
1:CE:98:ILE:O	1:CH:91:ARG:NH2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:317:ASP:CB	1:CE:319:GLN:NE2	2.84	0.41
1:BF:74:THR:HA	1:BF:190:ASN:HD22	1.85	0.41
1:BF:99:PHE:HA	1:BF:209:VAL:O	2.20	0.41
1:BF:166:LEU:CD1	1:BF:166:LEU:C	2.94	0.41
1:BF:281:HIS:CE1	1:BF:301:TRP:HB3	2.55	0.41
1:AF:137:THR:HG23	1:AF:140:ALA:CB	2.51	0.41
1:BG:84:ILE:HG13	1:BG:127:PHE:HE2	1.86	0.41
1:BG:319:GLN:HE21	1:BG:319:GLN:C	2.28	0.41
1:AG:109:PHE:CE2	1:AG:127:PHE:CD1	3.09	0.41
1:CG:69:PRO:O	1:CG:72:THR:OG1	2.26	0.41
1:CG:111:ILE:HD11	1:CG:125:ALA:HB3	2.01	0.41
1:CG:123:TYR:HB2	1:CG:185:LEU:CD2	2.51	0.41
1:BH:253:ASP:CB	1:BH:286:ALA:HB2	2.50	0.41
1:AH:302:ASP:OD2	1:AH:305:ASN:CB	2.62	0.41
1:CH:284:LYS:HD3	1:CH:296:PHE:CZ	2.55	0.41
1:BI:75:ASP:C	1:BI:75:ASP:OD1	2.63	0.41
1:BI:283:LYS:HG2	1:BI:285:PHE:CE1	2.56	0.41
1:CI:317:ASP:HB3	1:CI:319:GLN:NE2	2.35	0.41
1:BJ:74:THR:HA	1:BJ:190:ASN:HD22	1.86	0.41
1:BJ:99:PHE:HA	1:BJ:209:VAL:O	2.21	0.41
1:BJ:246:THR:N	1:BJ:247:PRO:CD	2.84	0.41
1:AJ:264:SER:OG	1:AJ:276:ARG:NH1	2.53	0.41
1:BK:166:LEU:CD1	1:BK:166:LEU:C	2.93	0.41
1:AK:183:LEU:HG	1:AK:184:ILE:N	2.36	0.41
1:AK:246:THR:N	1:AK:247:PRO:HD2	2.36	0.41
1:CK:57:LEU:HD23	1:CK:203:TRP:CH2	2.56	0.41
1:CK:306:LYS:HE3	1:CK:336:SER:HB2	2.03	0.41
1:BL:116:PRO:O	1:BL:119:THR:OG1	2.36	0.41
1:AL:127:PHE:O	1:AL:144:THR:OG1	2.34	0.41
1:AL:298:TRP:O	1:AL:310:ASP:O	2.39	0.41
1:AL:300:ILE:HB	1:AL:309:THR:OG1	2.21	0.41
1:CL:264:SER:HB2	1:CL:324:LEU:HD22	2.03	0.41
1:BM:111:ILE:CG2	1:BM:112:GLN:N	2.84	0.41
1:BM:149:VAL:HG23	1:CM:48:PHE:HE2	1.86	0.41
1:CM:122:GLY:O	1:CM:188:VAL:CB	2.66	0.41
1:CM:155:SER:O	1:CM:156:ARG:HD3	2.21	0.41
1:CN:317:ASP:HB3	1:CN:319:GLN:NE2	2.35	0.41
1:BO:128:LEU:HD12	1:BO:184:ILE:HD11	2.02	0.41
1:AO:91:ARG:HD2	1:AW:143:ALA:HB1	2.02	0.41
1:CO:119:THR:O	1:CO:119:THR:HG22	2.21	0.41
1:CO:317:ASP:CB	1:CO:319:GLN:NE2	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:122:GLY:C	1:BP:188:VAL:CG2	2.85	0.41
1:BP:226:GLY:C	1:BP:327:VAL:HG22	2.45	0.41
1:CP:58:SER:HA	1:CP:203:TRP:CE3	2.56	0.41
1:CP:141:LEU:O	1:CP:142:GLN:C	2.62	0.41
1:BQ:250:ILE:O	1:BQ:250:ILE:HG22	2.20	0.41
1:CQ:45:VAL:HG13	1:CQ:45:VAL:O	2.20	0.41
1:CQ:80:VAL:HG11	1:CQ:185:LEU:CB	2.47	0.41
1:CQ:99:PHE:CD2	1:CQ:207:LEU:HB3	2.56	0.41
1:BR:149:VAL:HG23	1:CR:48:PHE:HE2	1.86	0.41
1:AR:88:LEU:C	1:AR:88:LEU:HD13	2.45	0.41
1:CR:89:LEU:HD13	1:CR:203:TRP:CG	2.56	0.41
1:AS:74:THR:O	1:AS:75:ASP:C	2.60	0.41
1:AS:101:ARG:CZ	1:AS:166:LEU:CD2	2.99	0.41
1:AS:224:THR:HG22	1:AS:329:THR:N	2.36	0.41
1:AS:234:SER:HB3	1:AS:237:ASP:O	2.20	0.41
1:CS:123:TYR:HB2	1:CS:185:LEU:HD21	2.03	0.41
1:CS:158:VAL:HG13	1:CS:158:VAL:O	2.20	0.41
1:BT:100:GLN:NE2	1:BT:211:SER:CB	2.84	0.41
1:BT:114:MET:HE1	1:CV:188:VAL:HG11	2.03	0.41
1:BT:226:GLY:C	1:BT:327:VAL:HG22	2.44	0.41
1:AT:162:TYR:CE2	1:AT:164:ARG:HG2	2.56	0.41
1:CT:264:SER:HB2	1:CT:324:LEU:HD22	2.02	0.41
1:BU:100:GLN:NE2	1:BU:211:SER:CB	2.84	0.41
1:AU:234:SER:HB3	1:AU:237:ASP:O	2.21	0.41
1:CU:80:VAL:HG22	1:CU:81:ASP:N	2.35	0.41
1:BV:124:VAL:HG11	1:BV:138:PHE:CD2	2.56	0.41
1:AV:111:ILE:O	1:AV:112:GLN:C	2.63	0.41
1:CV:98:ILE:HG13	1:CV:99:PHE:CD2	2.56	0.41
1:CW:80:VAL:HG22	1:CW:81:ASP:N	2.36	0.41
1:CW:137:THR:O	1:CW:138:PHE:C	2.64	0.41
1:BX:85:VAL:CG2	1:BX:86:PRO:HD2	2.51	0.41
1:BX:142:GLN:HB2	1:CX:48:PHE:HE1	1.86	0.41
1:AX:224:THR:HG22	1:AX:329:THR:N	2.36	0.41
1:CX:121:GLY:C	1:CX:152:TRP:CD1	2.99	0.41
1:CX:158:VAL:HG13	1:CX:158:VAL:O	2.21	0.41
1:CX:214:ASN:HA	1:CX:215:PRO:HD3	1.83	0.41
1:BY:281:HIS:CE1	1:BY:301:TRP:HB3	2.55	0.41
1:AY:302:ASP:C	1:AY:305:ASN:HD21	2.22	0.41
1:CY:54:ASP:OD1	1:CY:54:ASP:N	2.52	0.41
1:BZ:321:ARG:HD2	1:CZ:300:ILE:HD13	2.03	0.41
1:CZ:123:TYR:CD1	1:CZ:185:LEU:HD21	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:137:THR:O	1:CZ:138:PHE:C	2.62	0.41
1:CZ:317:ASP:HB3	1:CZ:319:GLN:NE2	2.35	0.41
1:Cb:98:ILE:HG13	1:Cb:99:PHE:CD2	2.56	0.41
1:Cb:278:VAL:HG13	1:Cb:278:VAL:O	2.20	0.41
1:Bc:166:LEU:CD1	1:Bc:166:LEU:C	2.93	0.41
1:Ac:100:GLN:HA	1:Ac:169:THR:OG1	2.21	0.41
1:Ac:302:ASP:CG	1:Ac:305:ASN:CG	2.88	0.41
1:Cd:81:ASP:OD2	1:Cd:136:HIS:NE2	2.48	0.41
1:Cd:214:ASN:HA	1:Cd:215:PRO:HD3	1.83	0.41
1:Cd:250:ILE:O	1:Cd:250:ILE:HG22	2.19	0.41
1:BA:103:ALA:HB2	1:BA:166:LEU:HD22	2.03	0.41
1:CA:74:THR:O	1:CA:75:ASP:C	2.63	0.41
1:CA:137:THR:O	1:CA:138:PHE:C	2.65	0.41
1:CA:246:THR:N	1:CA:247:PRO:CD	2.84	0.41
1:CA:317:ASP:CB	1:CA:319:GLN:NE2	2.84	0.41
1:BB:91:ARG:NH1	1:AK:98:ILE:O	2.54	0.41
1:BB:123:TYR:N	1:BB:188:VAL:HG22	2.36	0.41
1:AB:91:ARG:HE	1:BY:98:ILE:CG2	2.28	0.41
1:CB:58:SER:HA	1:CB:203:TRP:CE3	2.56	0.41
1:BC:226:GLY:C	1:BC:327:VAL:HG22	2.46	0.41
1:CC:74:THR:O	1:CC:75:ASP:C	2.64	0.41
1:BF:246:THR:N	1:BF:247:PRO:CD	2.84	0.41
1:AF:74:THR:O	1:AF:75:ASP:C	2.63	0.41
1:CF:317:ASP:CB	1:CF:319:GLN:NE2	2.83	0.41
1:BG:111:ILE:HG22	1:BG:155:SER:HA	2.02	0.41
1:AG:114:MET:SD	1:Ad:188:VAL:CG2	3.09	0.41
1:CG:58:SER:HB3	1:CG:204:SER:HB2	2.03	0.41
1:BH:136:HIS:O	1:BH:186:LEU:HD11	2.20	0.41
1:AH:103:ALA:HB2	1:AH:166:LEU:HA	2.03	0.41
1:AH:162:TYR:CE2	1:AH:164:ARG:HG2	2.55	0.41
1:BI:226:GLY:C	1:BI:327:VAL:HG22	2.46	0.41
1:AI:188:VAL:CG2	1:Aa:114:MET:SD	3.08	0.41
1:CI:219:THR:HG21	1:CI:333:ARG:O	2.21	0.41
1:AK:68:LEU:HB2	1:AK:195:VAL:HG23	2.03	0.41
1:CK:123:TYR:HA	1:CK:188:VAL:HG23	2.03	0.41
1:CK:219:THR:HG21	1:CK:333:ARG:O	2.21	0.41
1:CL:158:VAL:O	1:CL:158:VAL:HG13	2.20	0.41
1:BM:109:PHE:HB2	1:BM:158:VAL:CG1	2.50	0.41
1:BM:115:CYS:HB3	1:BM:195:VAL:HG12	2.03	0.41
1:AO:57:LEU:O	1:AO:204:SER:HA	2.20	0.41
1:AO:212:LEU:HD12	1:AO:212:LEU:C	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:267:TYR:CE2	1:CO:320:PRO:HD3	2.55	0.41
1:BP:300:ILE:HD13	1:AP:321:ARG:HD2	2.03	0.41
1:AP:246:THR:N	1:AP:247:PRO:HD2	2.36	0.41
1:BQ:100:GLN:NE2	1:BQ:211:SER:CB	2.84	0.41
1:CQ:284:LYS:HD3	1:CQ:296:PHE:CZ	2.56	0.41
1:BR:85:VAL:CG2	1:BR:86:PRO:HD2	2.51	0.41
1:CR:317:ASP:HB3	1:CR:319:GLN:NE2	2.36	0.41
1:BT:98:ILE:CG2	1:AV:91:ARG:CZ	2.99	0.41
1:CT:119:THR:O	1:CT:120:GLY:C	2.63	0.41
1:CT:317:ASP:CB	1:CT:319:GLN:NE2	2.84	0.41
1:AU:238:PHE:CZ	1:AU:296:PHE:HB2	2.55	0.41
1:CU:153:TRP:CD1	1:CU:153:TRP:H	2.39	0.41
1:BV:116:PRO:O	1:BV:119:THR:OG1	2.38	0.41
1:AW:100:GLN:HA	1:AW:169:THR:OG1	2.20	0.41
1:BY:99:PHE:HA	1:BY:209:VAL:O	2.20	0.41
1:CY:58:SER:HA	1:CY:203:TRP:CE3	2.56	0.41
1:CY:133:ASP:O	1:CY:182:ARG:NH2	2.54	0.41
1:CY:200:LEU:HD13	1:Ca:45:VAL:HG23	2.02	0.41
1:BZ:250:ILE:O	1:BZ:250:ILE:HG22	2.20	0.41
1:Ba:191:ASN:H	1:Ba:191:ASN:HD22	1.68	0.41
1:Cb:219:THR:HG21	1:Cb:333:ARG:O	2.21	0.41
1:Bc:163:THR:O	1:Bc:165:THR:HG22	2.21	0.41
1:BA:85:VAL:CG2	1:BA:86:PRO:HD2	2.51	0.40
1:CA:62:ARG:HA	1:CA:200:LEU:HD23	2.02	0.40
1:CA:264:SER:HB2	1:CA:324:LEU:HD22	2.01	0.40
1:BB:149:VAL:HG23	1:CB:48:PHE:CE2	2.56	0.40
1:BB:222:ILE:HG21	1:BB:248:LEU:HG	2.03	0.40
1:CB:72:THR:O	1:CB:191:ASN:OD1	2.39	0.40
1:AC:91:ARG:CZ	1:BS:98:ILE:HG22	2.51	0.40
1:AC:111:ILE:O	1:AC:112:GLN:C	2.64	0.40
1:CC:111:ILE:O	1:CC:112:GLN:C	2.64	0.40
1:BD:246:THR:N	1:BD:247:PRO:CD	2.84	0.40
1:CF:118:ASN:HA	1:Bb:116:PRO:CB	2.51	0.40
1:BH:99:PHE:HA	1:BH:209:VAL:O	2.21	0.40
1:AH:74:THR:O	1:AH:75:ASP:C	2.63	0.40
1:AI:60:MET:HA	1:AI:201:CYS:O	2.21	0.40
1:AI:298:TRP:O	1:AI:310:ASP:O	2.38	0.40
1:BJ:199:VAL:O	1:BJ:199:VAL:HG13	2.21	0.40
1:AJ:224:THR:HG22	1:AJ:329:THR:N	2.37	0.40
1:BL:280:TRP:CD2	1:AL:326:PRO:HG3	2.56	0.40
1:CL:190:ASN:N	1:CL:190:ASN:ND2	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CN:85:VAL:O	1:CN:86:PRO:C	2.61	0.40
1:BO:141:LEU:HD21	1:BO:184:ILE:HG12	2.03	0.40
1:BP:214:ASN:HD22	1:BP:215:PRO:HD2	1.86	0.40
1:BP:319:GLN:HE21	1:BP:319:GLN:C	2.30	0.40
1:CP:80:VAL:HG22	1:CP:81:ASP:N	2.35	0.40
1:CP:91:ARG:HD2	1:CQ:98:ILE:HB	2.03	0.40
1:AQ:267:TYR:CE2	1:CQ:320:PRO:HD3	2.56	0.40
1:AR:81:ASP:OD1	1:AR:81:ASP:C	2.64	0.40
1:BS:130:ASP:HB3	1:BS:133:ASP:HB2	2.03	0.40
1:BS:149:VAL:HG23	1:CS:48:PHE:CE2	2.55	0.40
1:CS:103:ALA:HB2	1:CS:166:LEU:HB3	2.03	0.40
1:BT:98:ILE:HG23	1:AV:91:ARG:HG2	2.03	0.40
1:CT:284:LYS:HD3	1:CT:296:PHE:CZ	2.56	0.40
1:AU:123:TYR:HB2	1:AU:185:LEU:HD11	2.03	0.40
1:AU:224:THR:HG22	1:AU:329:THR:N	2.36	0.40
1:CU:284:LYS:HD3	1:CU:296:PHE:CZ	2.56	0.40
1:AV:302:ASP:OD2	1:AV:305:ASN:CB	2.62	0.40
1:AW:63:ILE:CD1	1:AW:89:LEU:HD21	2.51	0.40
1:AW:80:VAL:HG12	1:AW:185:LEU:HB3	2.03	0.40
1:CW:112:GLN:HE21	1:Cd:44:THR:N	2.19	0.40
1:AX:116:PRO:HG2	1:AX:119:THR:OG1	2.21	0.40
1:AZ:127:PHE:O	1:AZ:144:THR:OG1	2.32	0.40
1:CZ:130:ASP:OD2	1:CZ:176:ARG:NH2	2.54	0.40
1:Ca:317:ASP:HB3	1:Ca:319:GLN:NE2	2.36	0.40
1:Bb:142:GLN:HB2	1:Cb:48:PHE:HE1	1.86	0.40
1:Cb:74:THR:O	1:Cb:75:ASP:C	2.64	0.40
1:Bd:232:SER:HB3	1:Bd:242:LEU:HD11	2.03	0.40
1:Ad:98:ILE:HG22	1:Ad:99:PHE:CD2	2.56	0.40
1:Ad:302:ASP:OD2	1:Ad:305:ASN:CB	2.61	0.40
1:Cd:93:GLY:O	1:Cd:97:ARG:NH1	2.52	0.40
1:BA:96:ALA:C	1:BA:98:ILE:H	2.30	0.40
1:BA:250:ILE:O	1:BA:250:ILE:HG22	2.21	0.40
1:BA:281:HIS:CE1	1:BA:301:TRP:HB3	2.56	0.40
1:AB:302:ASP:OD2	1:AB:305:ASN:CB	2.64	0.40
1:CB:57:LEU:HD23	1:CB:203:TRP:HH2	1.85	0.40
1:CB:91:ARG:HD2	1:CF:98:ILE:HB	2.03	0.40
1:CB:219:THR:HG21	1:CB:333:ARG:O	2.21	0.40
1:AC:100:GLN:HA	1:AC:169:THR:OG1	2.21	0.40
1:AC:127:PHE:O	1:AC:144:THR:OG1	2.33	0.40
1:BE:130:ASP:HB3	1:BE:133:ASP:HB2	2.03	0.40
1:AE:80:VAL:HG13	1:AE:185:LEU:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:101:ARG:CZ	1:AE:166:LEU:CD2	2.99	0.40
1:AE:124:VAL:HG11	1:AE:138:PHE:CD1	2.56	0.40
1:CE:123:TYR:HB2	1:CE:185:LEU:HD21	2.02	0.40
1:AF:224:THR:HG22	1:AF:329:THR:N	2.36	0.40
1:CF:34:ARG:CG	1:BY:156:ARG:HH22	2.34	0.40
1:AG:162:TYR:CE2	1:AG:164:ARG:HG2	2.55	0.40
1:CH:317:ASP:CB	1:CH:319:GLN:NE2	2.84	0.40
1:BJ:163:THR:C	1:BJ:165:THR:HG22	2.47	0.40
1:AK:226:GLY:N	1:AK:243:LEU:O	2.50	0.40
1:CK:119:THR:O	1:CK:120:GLY:C	2.63	0.40
1:BL:124:VAL:HG11	1:BL:138:PHE:CD2	2.56	0.40
1:AN:63:ILE:HG23	1:AN:88:LEU:HD11	2.04	0.40
1:AN:81:ASP:C	1:AN:81:ASP:OD1	2.64	0.40
1:AN:114:MET:SD	1:AP:122:GLY:HA3	2.61	0.40
1:CN:284:LYS:HD3	1:CN:296:PHE:CZ	2.57	0.40
1:CP:317:ASP:CB	1:CP:319:GLN:NE2	2.84	0.40
1:AQ:109:PHE:HB2	1:AQ:158:VAL:HG12	2.03	0.40
1:AQ:226:GLY:N	1:AQ:243:LEU:O	2.53	0.40
1:BT:246:THR:N	1:BT:247:PRO:CD	2.83	0.40
1:BT:250:ILE:O	1:BT:250:ILE:HG22	2.21	0.40
1:BU:300:ILE:HD13	1:AU:321:ARG:HD2	2.03	0.40
1:BV:166:LEU:CD1	1:BV:166:LEU:C	2.94	0.40
1:AV:100:GLN:NE2	1:CV:129:PRO:HB2	2.36	0.40
1:CX:284:LYS:HD3	1:CX:296:PHE:CZ	2.57	0.40
1:BY:300:ILE:HD13	1:AY:321:ARG:HD2	2.03	0.40
1:BZ:100:GLN:O	1:BZ:169:THR:N	2.43	0.40
1:Ba:75:ASP:C	1:Ba:75:ASP:OD1	2.64	0.40
1:Ab:226:GLY:N	1:Ab:243:LEU:O	2.51	0.40
1:Ab:300:ILE:HB	1:Ab:309:THR:OG1	2.21	0.40
1:Bc:74:THR:HA	1:Bc:190:ASN:HD22	1.86	0.40
1:Bc:300:ILE:HD13	1:Ac:321:ARG:HD2	2.03	0.40
1:Ac:89:LEU:HD21	1:Ac:201:CYS:HB3	2.04	0.40
1:Ac:234:SER:HB3	1:Ac:237:ASP:O	2.20	0.40
1:Cc:264:SER:HB2	1:Cc:324:LEU:HD22	2.02	0.40
1:Ad:263:LEU:HB3	1:Ad:279:TYR:O	2.21	0.40
1:Ad:302:ASP:CA	1:Ad:305:ASN:CG	2.94	0.40
1:BC:96:ALA:C	1:BC:98:ILE:H	2.29	0.40
1:AC:80:VAL:HG13	1:AC:185:LEU:HB3	2.02	0.40
1:CC:102:TYR:HD2	1:CC:205:VAL:HG21	1.85	0.40
1:BE:142:GLN:HB2	1:CE:48:PHE:CE1	2.57	0.40
1:AE:63:ILE:CD1	1:AE:89:LEU:HD21	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:54:ASP:OD1	1:CE:54:ASP:N	2.53	0.40
1:CE:102:TYR:HD2	1:CE:205:VAL:HG21	1.86	0.40
1:AF:116:PRO:HB3	1:Ab:118:ASN:O	2.21	0.40
1:CF:72:THR:O	1:CF:191:ASN:OD1	2.39	0.40
1:AG:100:GLN:NE2	1:CG:129:PRO:HB2	2.37	0.40
1:AG:300:ILE:HB	1:AG:309:THR:OG1	2.21	0.40
1:AI:143:ALA:HB1	1:Aa:91:ARG:HD2	2.01	0.40
1:BJ:85:VAL:CG2	1:BJ:86:PRO:HD2	2.50	0.40
1:AJ:109:PHE:HB2	1:AJ:158:VAL:HG12	2.03	0.40
1:CJ:58:SER:HA	1:CJ:203:TRP:CE3	2.56	0.40
1:CJ:119:THR:O	1:CJ:119:THR:HG22	2.21	0.40
1:BK:300:ILE:HG23	1:AK:323:ILE:CD1	2.51	0.40
1:BL:109:PHE:HB2	1:BL:158:VAL:CG1	2.51	0.40
1:AM:256:VAL:HB	1:AM:335:ASP:HB3	2.02	0.40
1:BN:300:ILE:HD13	1:AN:321:ARG:HD2	2.03	0.40
1:CN:264:SER:HB2	1:CN:324:LEU:HD22	2.03	0.40
1:BO:166:LEU:CD1	1:BO:166:LEU:C	2.94	0.40
1:CP:62:ARG:H	1:BQ:142:GLN:NE2	2.19	0.40
1:BQ:109:PHE:HB2	1:BQ:158:VAL:CG1	2.52	0.40
1:AQ:234:SER:HB3	1:AQ:237:ASP:O	2.21	0.40
1:CQ:264:SER:HB2	1:CQ:324:LEU:HD22	2.02	0.40
1:CR:74:THR:O	1:CR:75:ASP:C	2.63	0.40
1:CR:111:ILE:HG21	1:CR:123:TYR:CE1	2.56	0.40
1:CR:199:VAL:O	1:CR:199:VAL:CG1	2.68	0.40
1:BS:196:ASN:HD22	1:BS:196:ASN:C	2.29	0.40
1:CS:45:VAL:O	1:CS:45:VAL:HG13	2.21	0.40
1:AU:103:ALA:HB2	1:AU:166:LEU:HA	2.03	0.40
1:AU:212:LEU:C	1:AU:212:LEU:HD12	2.45	0.40
1:AU:264:SER:OG	1:AU:276:ARG:NH1	2.51	0.40
1:CV:89:LEU:HD22	1:CV:203:TRP:CD1	2.56	0.40
1:CY:214:ASN:HA	1:CY:215:PRO:HD3	1.86	0.40
1:AZ:102:TYR:O	1:AZ:167:LEU:HB2	2.20	0.40
1:Ca:214:ASN:HA	1:Ca:215:PRO:HD3	1.81	0.40
1:Ab:89:LEU:HD21	1:Ab:201:CYS:HB3	2.02	0.40
1:Cb:284:LYS:HD3	1:Cb:296:PHE:CZ	2.56	0.40
1:Bc:111:ILE:CG2	1:Bc:112:GLN:N	2.83	0.40
1:Ac:116:PRO:HG2	1:Ac:119:THR:OG1	2.21	0.40
1:Cc:98:ILE:HG13	1:Cc:99:PHE:CD2	2.57	0.40
1:Ad:298:TRP:NE1	1:Ad:312:VAL:HA	2.35	0.40
1:Cd:141:LEU:O	1:Cd:144:THR:N	2.51	0.40
1:CA:114:MET:O	1:CA:115:CYS:HB3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:284:LYS:HD3	1:CA:296:PHE:CZ	2.57	0.40
1:BB:226:GLY:C	1:BB:327:VAL:HG22	2.46	0.40
1:BB:246:THR:N	1:BB:247:PRO:CD	2.85	0.40
1:CB:98:ILE:HG13	1:CB:99:PHE:CD2	2.56	0.40
1:CC:219:THR:HG21	1:CC:333:ARG:O	2.20	0.40
1:CC:317:ASP:CB	1:CC:319:GLN:NE2	2.84	0.40
1:BD:130:ASP:HB3	1:BD:133:ASP:HB2	2.04	0.40
1:BD:226:GLY:C	1:BD:327:VAL:HG22	2.47	0.40
1:AD:102:TYR:HD2	1:AD:205:VAL:HG21	1.85	0.40
1:CD:137:THR:O	1:CD:138:PHE:C	2.65	0.40
1:BE:142:GLN:HB2	1:CE:48:PHE:HE1	1.86	0.40
1:CE:113:PRO:HA	1:CE:197:VAL:HA	2.04	0.40
1:BF:130:ASP:HB3	1:BF:133:ASP:HB2	2.03	0.40
1:CF:306:LYS:HE3	1:CF:336:SER:HB2	2.03	0.40
1:CH:123:TYR:HB2	1:CH:185:LEU:CD2	2.52	0.40
1:BI:139:ASP:O	1:BI:142:GLN:HG3	2.21	0.40
1:CI:93:GLY:O	1:CI:97:ARG:NH1	2.53	0.40
1:BJ:109:PHE:HB2	1:BJ:158:VAL:CG1	2.52	0.40
1:CJ:102:TYR:HD2	1:CJ:205:VAL:HG21	1.87	0.40
1:CJ:103:ALA:O	1:CJ:205:VAL:HG23	2.21	0.40
1:BK:191:ASN:H	1:BK:191:ASN:HD22	1.69	0.40
1:BK:246:THR:N	1:BK:247:PRO:CD	2.84	0.40
1:AK:302:ASP:C	1:AK:305:ASN:HD21	2.22	0.40
1:BL:300:ILE:HG23	1:AL:323:ILE:CD1	2.52	0.40
1:CL:219:THR:HG21	1:CL:333:ARG:O	2.22	0.40
1:BM:141:LEU:HD21	1:BM:184:ILE:HG12	2.03	0.40
1:CM:45:VAL:O	1:CM:45:VAL:HG13	2.21	0.40
1:AN:63:ILE:CD1	1:AN:89:LEU:HD21	2.52	0.40
1:CN:123:TYR:HA	1:CN:188:VAL:HG23	2.04	0.40
1:BO:85:VAL:CG2	1:BO:86:PRO:HD2	2.51	0.40
1:BO:100:GLN:NE2	1:BO:211:SER:CB	2.84	0.40
1:BO:214:ASN:ND2	1:BO:215:PRO:HD2	2.37	0.40
1:BP:300:ILE:HG23	1:AP:323:ILE:CD1	2.51	0.40
1:CP:284:LYS:HD3	1:CP:296:PHE:CZ	2.57	0.40
1:CQ:58:SER:HA	1:CQ:203:TRP:CE3	2.57	0.40
1:CQ:306:LYS:HE3	1:CQ:336:SER:HB2	2.03	0.40
1:AR:234:SER:HB3	1:AR:237:ASP:O	2.21	0.40
1:AR:302:ASP:CA	1:AR:305:ASN:CG	2.94	0.40
1:CR:44:THR:OG1	1:CT:110:GLU:OE1	2.32	0.40
1:CR:81:ASP:HA	1:CR:184:ILE:HG22	2.04	0.40
1:CR:113:PRO:HA	1:CR:197:VAL:HA	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:123:TYR:HB2	1:CR:185:LEU:CD2	2.51	0.40
1:BS:141:LEU:HD21	1:BS:184:ILE:HG12	2.04	0.40
1:AS:302:ASP:CG	1:AS:305:ASN:CG	2.88	0.40
1:CS:155:SER:O	1:CS:156:ARG:HD3	2.21	0.40
1:BT:184:ILE:HD13	1:BT:184:ILE:N	2.36	0.40
1:AT:188:VAL:HG23	1:AV:114:MET:SD	2.62	0.40
1:AT:302:ASP:CA	1:AT:305:ASN:CG	2.94	0.40
1:CT:117:ALA:HB1	1:Ba:117:ALA:HB2	2.03	0.40
1:CT:122:GLY:O	1:CT:188:VAL:CB	2.67	0.40
1:BU:319:GLN:C	1:BU:319:GLN:HE21	2.29	0.40
1:CU:81:ASP:OD2	1:CU:136:HIS:NE2	2.46	0.40
1:CU:137:THR:O	1:CU:138:PHE:C	2.64	0.40
1:AV:162:TYR:CE2	1:AV:164:ARG:HG2	2.56	0.40
1:BW:163:THR:O	1:BW:165:THR:HG22	2.21	0.40
1:BW:321:ARG:HD2	1:CW:300:ILE:HD13	2.04	0.40
1:AW:81:ASP:OD1	1:AW:81:ASP:C	2.64	0.40
1:AW:113:PRO:HA	1:AW:197:VAL:HA	2.03	0.40
1:BY:226:GLY:C	1:BY:327:VAL:HG22	2.47	0.40
1:CY:100:GLN:HG2	1:CY:211:SER:HG	1.86	0.40
1:CZ:80:VAL:HG22	1:CZ:81:ASP:N	2.37	0.40
1:Ba:300:ILE:HD13	1:Aa:321:ARG:HD2	2.04	0.40
1:Ab:64:SER:OG	1:Ab:80:VAL:HG21	2.21	0.40
1:Cb:133:ASP:O	1:Cb:182:ARG:NH2	2.55	0.40
1:Bd:166:LEU:CD1	1:Bd:166:LEU:C	2.94	0.40
1:AA:302:ASP:CA	1:AA:305:ASN:CG	2.94	0.40
1:AB:302:ASP:CG	1:AB:305:ASN:CG	2.88	0.40
1:CB:34:ARG:CG	1:Bb:156:ARG:NH2	2.84	0.40
1:BC:85:VAL:CG2	1:BC:86:PRO:HD2	2.52	0.40
1:CC:103:ALA:HB2	1:CC:166:LEU:HB3	2.02	0.40
1:AD:69:PRO:C	1:AD:72:THR:HG1	2.30	0.40
1:BE:228:LEU:HD13	1:BE:238:PHE:CD2	2.56	0.40
1:AE:263:LEU:HB3	1:AE:279:TYR:O	2.21	0.40
1:AF:80:VAL:HG13	1:AF:185:LEU:HB3	2.01	0.40
1:AF:91:ARG:HD2	1:Ab:143:ALA:HB1	2.04	0.40
1:AF:106:THR:O	1:AF:203:TRP:HA	2.21	0.40
1:CF:58:SER:HA	1:CF:203:TRP:CE3	2.57	0.40
1:BG:126:GLY:HA3	1:BG:141:LEU:HD22	2.02	0.40
1:CG:72:THR:O	1:CG:191:ASN:OD1	2.39	0.40
1:CG:141:LEU:O	1:CG:144:THR:N	2.48	0.40
1:BH:226:GLY:C	1:BH:327:VAL:HG22	2.47	0.40
1:AH:100:GLN:HA	1:AH:169:THR:OG1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:100:GLN:NE2	1:BI:211:SER:CB	2.85	0.40
1:AI:137:THR:HG23	1:AI:140:ALA:CB	2.52	0.40
1:AI:238:PHE:CZ	1:AI:296:PHE:HB2	2.56	0.40
1:BJ:321:ARG:HD2	1:CJ:300:ILE:HD13	2.03	0.40
1:BK:99:PHE:HA	1:BK:209:VAL:O	2.22	0.40
1:CK:137:THR:O	1:CK:138:PHE:C	2.63	0.40
1:AL:61:SER:HB2	1:AL:89:LEU:HD22	2.04	0.40
1:CL:123:TYR:HA	1:CL:188:VAL:HG23	2.04	0.40
1:BM:163:THR:O	1:BM:165:THR:HG22	2.21	0.40
1:CM:163:THR:HG23	1:CM:164:ARG:N	2.37	0.40
1:BN:253:ASP:CB	1:BN:286:ALA:HB2	2.49	0.40
1:BN:321:ARG:HD2	1:CN:300:ILE:HD13	2.02	0.40
1:AN:100:GLN:HA	1:AN:169:THR:OG1	2.21	0.40
1:AN:137:THR:HG23	1:AN:140:ALA:HB3	2.04	0.40
1:AN:256:VAL:HB	1:AN:335:ASP:HB3	2.03	0.40
1:BO:163:THR:C	1:BO:165:THR:HG22	2.46	0.40
1:AO:101:ARG:NH1	1:AO:166:LEU:HD23	2.37	0.40
1:CO:121:GLY:HA3	1:CO:152:TRP:HD1	1.87	0.40
1:BQ:136:HIS:O	1:BQ:186:LEU:HD11	2.21	0.40
1:BQ:300:ILE:HG23	1:AQ:323:ILE:CD1	2.51	0.40
1:AQ:101:ARG:NH1	1:AQ:166:LEU:HD23	2.37	0.40
1:AQ:103:ALA:HB2	1:AQ:166:LEU:HA	2.03	0.40
1:CQ:155:SER:O	1:CQ:156:ARG:HD3	2.22	0.40
1:BR:226:GLY:C	1:BR:327:VAL:HG22	2.46	0.40
1:AR:302:ASP:C	1:AR:305:ASN:HD21	2.22	0.40
1:AR:305:ASN:ND2	1:AR:307:THR:H	2.19	0.40
1:AR:308:PHE:CE2	1:AR:310:ASP:HA	2.56	0.40
1:BS:300:ILE:HG23	1:AS:323:ILE:CD1	2.52	0.40
1:AS:238:PHE:CZ	1:AS:296:PHE:HB2	2.56	0.40
1:CS:197:VAL:HG22	1:CS:198:SER:N	2.36	0.40
1:BT:122:GLY:C	1:BT:188:VAL:CG2	2.84	0.40
1:AT:101:ARG:CZ	1:AT:166:LEU:CD2	3.00	0.40
1:BU:246:THR:N	1:BU:247:PRO:CD	2.85	0.40
1:CV:100:GLN:HG2	1:CV:211:SER:HG	1.85	0.40
1:CV:214:ASN:HA	1:CV:215:PRO:HD3	1.82	0.40
1:BW:100:GLN:NE2	1:BW:211:SER:CB	2.84	0.40
1:BX:111:ILE:HG22	1:BX:155:SER:HA	2.04	0.40
1:BX:321:ARG:HD2	1:CX:300:ILE:HD13	2.04	0.40
1:AX:98:ILE:HG22	1:AX:99:PHE:CD2	2.57	0.40
1:BY:123:TYR:N	1:BY:188:VAL:HG22	2.33	0.40
1:CY:44:THR:H	1:Ca:112:GLN:HE21	1.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:300:ILE:HG23	1:AZ:323:ILE:CD1	2.52	0.40
1:AZ:238:PHE:CZ	1:AZ:296:PHE:HB2	2.57	0.40
1:Aa:238:PHE:CZ	1:Aa:296:PHE:HB2	2.56	0.40
1:Aa:302:ASP:CA	1:Aa:305:ASN:CG	2.95	0.40
1:Ab:63:ILE:HG23	1:Ab:88:LEU:HD11	2.03	0.40
1:Bc:99:PHE:HA	1:Bc:209:VAL:O	2.21	0.40
1:Ac:64:SER:OG	1:Ac:80:VAL:HG21	2.22	0.40
1:Bd:128:LEU:HD12	1:Bd:184:ILE:HD11	2.04	0.40
1:Ad:74:THR:O	1:Ad:75:ASP:C	2.65	0.40
1:Ad:106:THR:O	1:Ad:203:TRP:HA	2.21	0.40
1:Ad:109:PHE:CE2	1:Ad:127:PHE:CD1	3.10	0.40
1:Ad:137:THR:HG23	1:Ad:140:ALA:CB	2.52	0.40
1:Ad:298:TRP:HE1	1:Ad:312:VAL:HA	1.87	0.40

All (71) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:297:ARG:CZ	1:Cd:271:THR:OG1[4_546]	0.58	1.62
1:AC:318:GLU:CD	1:CZ:235:THR:CA[4_545]	0.93	1.27
1:BI:318:GLU:OE1	1:BI:318:GLU:OE2[2_656]	1.02	1.18
1:CQ:271:THR:O	1:Ba:290:GLY:O[4_555]	1.05	1.15
1:AC:318:GLU:CG	1:CZ:235:THR:CA[4_545]	1.06	1.14
1:CQ:271:THR:CA	1:Ba:290:GLY:CA[4_555]	1.07	1.13
1:CK:271:THR:OG1	1:BW:297:ARG:CZ[4_546]	1.16	1.04
1:BI:318:GLU:CD	1:BI:318:GLU:OE1[2_656]	1.20	1.00
1:AC:318:GLU:CG	1:CZ:235:THR:C[4_545]	1.37	0.83
1:BL:297:ARG:NE	1:Cd:271:THR:OG1[4_546]	1.37	0.83
1:BL:297:ARG:NH1	1:Cd:271:THR:OG1[4_546]	1.40	0.80
1:BC:271:THR:OG1	1:CZ:295:TRP:CE2[4_545]	1.41	0.79
1:AC:318:GLU:CG	1:CZ:235:THR:N[4_545]	1.41	0.79
1:BI:318:GLU:CD	1:BI:318:GLU:OE2[2_656]	1.41	0.79
1:AC:318:GLU:CD	1:CZ:235:THR:N[4_545]	1.44	0.76
1:AC:318:GLU:CB	1:CZ:235:THR:N[4_545]	1.48	0.72
1:BI:318:GLU:CG	1:BI:318:GLU:CD[2_656]	1.55	0.65
1:AC:318:GLU:OE1	1:CZ:235:THR:N[4_545]	1.56	0.64
1:CQ:270:GLY:O	1:Ba:290:GLY:N[4_555]	1.56	0.64
1:BI:318:GLU:CG	1:BI:318:GLU:CG[2_656]	1.57	0.63
1:BL:297:ARG:NH2	1:Cd:271:THR:OG1[4_546]	1.59	0.61
1:CQ:271:THR:C	1:Ba:290:GLY:O[4_555]	1.60	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:271:THR:OG1	1:CZ:295:TRP:CZ2[4_545]	1.62	0.58
1:CK:271:THR:OG1	1:BW:297:ARG:NH2[4_546]	1.64	0.56
1:AC:318:GLU:CG	1:CZ:236:ASN:N[4_545]	1.71	0.49
1:BC:271:THR:OG1	1:CZ:295:TRP:CD2[4_545]	1.72	0.48
1:CK:271:THR:OG1	1:BW:297:ARG:NE[4_546]	1.75	0.45
1:BC:315:TYR:OH	1:CZ:290:GLY:CA[4_545]	1.78	0.42
1:CQ:271:THR:CA	1:Ba:290:GLY:C[4_555]	1.79	0.41
1:BI:318:GLU:OE1	1:BI:318:GLU:OE1[2_656]	1.80	0.40
1:CQ:271:THR:C	1:Ba:290:GLY:C[4_555]	1.80	0.40
1:AC:318:GLU:OE1	1:CZ:235:THR:CA[4_545]	1.81	0.39
1:AC:318:GLU:OE2	1:CZ:235:THR:CA[4_545]	1.84	0.36
1:CQ:271:THR:N	1:Ba:290:GLY:CA[4_555]	1.84	0.36
1:BC:269:LEU:O	1:CZ:295:TRP:NE1[4_545]	1.86	0.34
1:CK:271:THR:OG1	1:BW:297:ARG:NH1[4_546]	1.86	0.34
1:CK:270:GLY:O	1:BW:237:ASP:OD2[4_546]	1.88	0.32
1:AP:297:ARG:NH2	1:BR:315:TYR:OH[4_555]	1.88	0.32
1:BI:318:GLU:CG	1:BI:318:GLU:OE2[2_656]	1.92	0.28
1:Bc:236:ASN:ND2	1:Bc:270:GLY:O[2_556]	1.94	0.26
1:BC:271:THR:OG1	1:CZ:295:TRP:CH2[4_545]	1.96	0.24
1:BC:315:TYR:OH	1:CZ:290:GLY:N[4_545]	1.96	0.24
1:BC:315:TYR:OH	1:CZ:291:THR:N[4_545]	1.96	0.24
1:CQ:271:THR:O	1:Ba:290:GLY:C[4_555]	1.96	0.24
1:CP:271:THR:OG1	1:CT:288:ASN:ND2[4_555]	1.98	0.22
1:CQ:271:THR:C	1:Ba:290:GLY:CA[4_555]	1.98	0.22
1:CK:270:GLY:O	1:BW:237:ASP:CG[4_546]	1.99	0.21
1:BL:237:ASP:CB	1:Cd:270:GLY:O[4_546]	1.99	0.21
1:BL:297:ARG:CZ	1:Cd:271:THR:CB[4_546]	2.00	0.20
1:BJ:153:TRP:O	1:CL:151:LYS:NZ[2_555]	2.02	0.18
1:AC:318:GLU:CD	1:CZ:235:THR:C[4_545]	2.04	0.16
1:CP:270:GLY:O	1:CT:288:ASN:CB[4_555]	2.04	0.16
1:BC:269:LEU:O	1:CZ:295:TRP:CD1[4_545]	2.05	0.15
1:BC:269:LEU:C	1:CZ:295:TRP:NE1[4_545]	2.05	0.15
1:BL:237:ASP:CG	1:Cd:270:GLY:O[4_546]	2.05	0.15
1:CA:288:ASN:ND2	1:AJ:273:ASP:OD1[4_555]	2.06	0.14
1:BC:271:THR:OG1	1:CZ:295:TRP:CE3[4_545]	2.08	0.12
1:BC:315:TYR:OH	1:CZ:290:GLY:C[4_545]	2.08	0.12
1:CQ:271:THR:CA	1:Ba:290:GLY:O[4_555]	2.08	0.12
1:CR:151:LYS:NZ	1:BX:153:TRP:O[2_555]	2.08	0.12
1:BI:318:GLU:CB	1:BI:318:GLU:CG[2_656]	2.09	0.11
1:AC:318:GLU:CD	1:CZ:234:SER:C[4_545]	2.10	0.10
1:AC:318:GLU:OE2	1:CZ:314:TYR:CB[4_545]	2.12	0.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:271:THR:CG2	1:Ba:290:GLY:O[4_555]	2.13	0.07
1:AC:318:GLU:N	1:CZ:235:THR:CB[4_545]	2.14	0.06
1:BC:271:THR:OG1	1:CZ:295:TRP:CZ3[4_545]	2.16	0.04
1:AC:318:GLU:CG	1:CZ:235:THR:CB[4_545]	2.16	0.04
1:AC:318:GLU:OE2	1:CZ:235:THR:C[4_545]	2.16	0.04
1:AC:318:GLU:CG	1:CZ:234:SER:C[4_545]	2.17	0.03
1:AC:318:GLU:OE2	1:CZ:235:THR:O[4_545]	2.17	0.03
1:AC:318:GLU:CA	1:CZ:235:THR:OG1[4_545]	2.18	0.02

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AB	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AC	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AD	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AE	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AF	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AG	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AH	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AI	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AJ	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AK	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AL	285/338 (84%)	275 (96%)	10 (4%)	0	100	100
1	AM	285/338 (84%)	279 (98%)	6 (2%)	0	100	100
1	AN	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AO	285/338 (84%)	277 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AP	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AQ	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AR	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AS	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AT	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AU	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AV	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AW	285/338 (84%)	275 (96%)	10 (4%)	0	100	100
1	AX	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AY	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AZ	285/338 (84%)	279 (98%)	6 (2%)	0	100	100
1	Aa	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	Ab	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	Ac	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	Ad	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	BA	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BB	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BC	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BD	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BE	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BF	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BG	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BH	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BI	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BJ	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BK	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BL	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BM	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BN	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BO	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BP	284/338 (84%)	279 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BQ	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BR	284/338 (84%)	278 (98%)	6 (2%)	0	100	100
1	BS	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BT	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BU	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BV	284/338 (84%)	283 (100%)	1 (0%)	0	100	100
1	BW	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BX	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BY	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BZ	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	Ba	284/338 (84%)	279 (98%)	5 (2%)	0	100	100
1	Bb	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	Bc	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	Bd	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	CA	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CB	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CC	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CD	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CE	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CF	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CG	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CH	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CI	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CJ	302/338 (89%)	289 (96%)	13 (4%)	0	100	100
1	CK	302/338 (89%)	286 (95%)	16 (5%)	0	100	100
1	CL	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CM	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CN	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CO	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CP	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CQ	302/338 (89%)	287 (95%)	15 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CR	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CS	302/338 (89%)	290 (96%)	12 (4%)	0	100	100
1	CT	302/338 (89%)	285 (94%)	17 (6%)	0	100	100
1	CU	302/338 (89%)	285 (94%)	17 (6%)	0	100	100
1	CV	302/338 (89%)	286 (95%)	16 (5%)	0	100	100
1	CW	302/338 (89%)	286 (95%)	16 (5%)	0	100	100
1	CX	302/338 (89%)	289 (96%)	13 (4%)	0	100	100
1	CY	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CZ	302/338 (89%)	286 (95%)	16 (5%)	0	100	100
1	Ca	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	Cb	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	Cc	302/338 (89%)	290 (96%)	12 (4%)	0	100	100
1	Cd	302/338 (89%)	289 (96%)	13 (4%)	0	100	100
All	All	26130/30420 (86%)	25356 (97%)	774 (3%)	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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	242/283 (86%)	206 (85%)	36 (15%)	3	17
1	AB	242/283 (86%)	202 (84%)	40 (16%)	2	14
1	AC	242/283 (86%)	206 (85%)	36 (15%)	3	17
1	AD	242/283 (86%)	205 (85%)	37 (15%)	3	16
1	AE	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AF	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AG	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AH	242/283 (86%)	207 (86%)	35 (14%)	3	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AI	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AJ	242/283 (86%)	205 (85%)	37 (15%)	3	16
1	AK	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AL	242/283 (86%)	206 (85%)	36 (15%)	3	17
1	AM	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AN	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AO	242/283 (86%)	204 (84%)	38 (16%)	2	15
1	AP	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AQ	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AR	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AS	242/283 (86%)	201 (83%)	41 (17%)	2	13
1	AT	242/283 (86%)	204 (84%)	38 (16%)	2	15
1	AU	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AV	242/283 (86%)	205 (85%)	37 (15%)	3	16
1	AW	242/283 (86%)	204 (84%)	38 (16%)	2	15
1	AX	242/283 (86%)	206 (85%)	36 (15%)	3	17
1	AY	242/283 (86%)	203 (84%)	39 (16%)	2	15
1	AZ	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	Aa	242/283 (86%)	200 (83%)	42 (17%)	2	12
1	Ab	242/283 (86%)	199 (82%)	43 (18%)	2	11
1	Ac	242/283 (86%)	202 (84%)	40 (16%)	2	14
1	Ad	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BA	242/283 (86%)	206 (85%)	36 (15%)	3	17
1	BB	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BC	242/283 (86%)	206 (85%)	36 (15%)	3	17
1	BD	242/283 (86%)	208 (86%)	34 (14%)	3	19
1	BE	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BF	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BG	242/283 (86%)	209 (86%)	33 (14%)	3	20
1	BH	242/283 (86%)	206 (85%)	36 (15%)	3	17
1	BI	242/283 (86%)	208 (86%)	34 (14%)	3	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BJ	242/283 (86%)	209 (86%)	33 (14%)	3	20
1	BK	242/283 (86%)	209 (86%)	33 (14%)	3	20
1	BL	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BM	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BN	242/283 (86%)	210 (87%)	32 (13%)	4	21
1	BO	242/283 (86%)	208 (86%)	34 (14%)	3	19
1	BP	242/283 (86%)	208 (86%)	34 (14%)	3	19
1	BQ	242/283 (86%)	209 (86%)	33 (14%)	3	20
1	BR	242/283 (86%)	208 (86%)	34 (14%)	3	19
1	BS	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BT	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BU	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BV	242/283 (86%)	210 (87%)	32 (13%)	4	21
1	BW	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BX	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	BY	242/283 (86%)	209 (86%)	33 (14%)	3	20
1	BZ	242/283 (86%)	210 (87%)	32 (13%)	4	21
1	Ba	242/283 (86%)	208 (86%)	34 (14%)	3	19
1	Bb	242/283 (86%)	208 (86%)	34 (14%)	3	19
1	Bc	242/283 (86%)	207 (86%)	35 (14%)	3	18
1	Bd	242/283 (86%)	208 (86%)	34 (14%)	3	19
1	CA	255/283 (90%)	225 (88%)	30 (12%)	5	24
1	CB	255/283 (90%)	226 (89%)	29 (11%)	5	26
1	CC	255/283 (90%)	225 (88%)	30 (12%)	5	24
1	CD	255/283 (90%)	227 (89%)	28 (11%)	6	27
1	CE	255/283 (90%)	226 (89%)	29 (11%)	5	26
1	CF	255/283 (90%)	225 (88%)	30 (12%)	5	24
1	CG	255/283 (90%)	227 (89%)	28 (11%)	6	27
1	CH	255/283 (90%)	225 (88%)	30 (12%)	5	24
1	CI	255/283 (90%)	228 (89%)	27 (11%)	6	28
1	CJ	255/283 (90%)	225 (88%)	30 (12%)	5	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CK	255/283 (90%)	224 (88%)	31 (12%)	5	23
1	CL	255/283 (90%)	226 (89%)	29 (11%)	5	26
1	CM	255/283 (90%)	227 (89%)	28 (11%)	6	27
1	CN	255/283 (90%)	226 (89%)	29 (11%)	5	26
1	CO	255/283 (90%)	227 (89%)	28 (11%)	6	27
1	CP	255/283 (90%)	223 (88%)	32 (12%)	4	22
1	CQ	255/283 (90%)	225 (88%)	30 (12%)	5	24
1	CR	255/283 (90%)	227 (89%)	28 (11%)	6	27
1	CS	255/283 (90%)	225 (88%)	30 (12%)	5	24
1	CT	255/283 (90%)	225 (88%)	30 (12%)	5	24
1	CU	255/283 (90%)	225 (88%)	30 (12%)	5	24
1	CV	255/283 (90%)	226 (89%)	29 (11%)	5	26
1	CW	255/283 (90%)	227 (89%)	28 (11%)	6	27
1	CX	255/283 (90%)	226 (89%)	29 (11%)	5	26
1	CY	255/283 (90%)	227 (89%)	28 (11%)	6	27
1	CZ	255/283 (90%)	227 (89%)	28 (11%)	6	27
1	Ca	255/283 (90%)	228 (89%)	27 (11%)	6	28
1	Cb	255/283 (90%)	226 (89%)	29 (11%)	5	26
1	Cc	255/283 (90%)	226 (89%)	29 (11%)	5	26
1	Cd	255/283 (90%)	226 (89%)	29 (11%)	5	26
All	All	22170/25470 (87%)	19124 (86%)	3046 (14%)	3	20

All (3046) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BA	57	LEU
1	BA	58	SER
1	BA	63	ILE
1	BA	67	VAL
1	BA	68	LEU
1	BA	78	VAL
1	BA	79	VAL
1	BA	80	VAL
1	BA	85	VAL
1	BA	86	PRO

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Mol	Chain	Res	Type
1	BA	88	LEU
1	BA	92	LEU
1	BA	100	GLN
1	BA	101	ARG
1	BA	104	VAL
1	BA	105	GLU
1	BA	111	ILE
1	BA	128	LEU
1	BA	134	ASN
1	BA	145	ARG
1	BA	156	ARG
1	BA	165	THR
1	BA	167	LEU
1	BA	173	LYS
1	BA	176	ARG
1	BA	183	LEU
1	BA	184	ILE
1	BA	185	LEU
1	BA	191	ASN
1	BA	196	ASN
1	BA	198	SER
1	BA	202	ARG
1	BA	207	LEU
1	BA	212	LEU
1	BA	271	THR
1	BA	319	GLN
1	AA	55	VAL
1	AA	58	SER
1	AA	62	ARG
1	AA	67	VAL
1	AA	72	THR
1	AA	74	THR
1	AA	75	ASP
1	AA	87	ASP
1	AA	111	ILE
1	AA	118	ASN
1	AA	124	VAL
1	AA	128	LEU
1	AA	137	THR
1	AA	141	LEU
1	AA	142	GLN
1	AA	149	VAL

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Mol	Chain	Res	Type
1	AA	159	ARG
1	AA	162	TYR
1	AA	163	THR
1	AA	165	THR
1	AA	167	LEU
1	AA	170	SER
1	AA	176	ARG
1	AA	183	LEU
1	AA	186	LEU
1	AA	196	ASN
1	AA	208	SER
1	AA	211	SER
1	AA	225	GLN
1	AA	236	ASN
1	AA	253	ASP
1	AA	264	SER
1	AA	271	THR
1	AA	312	VAL
1	AA	315	TYR
1	AA	317	ASP
1	CA	35	THR
1	CA	43	SER
1	CA	54	ASP
1	CA	63	ILE
1	CA	72	THR
1	CA	74	THR
1	CA	75	ASP
1	CA	87	ASP
1	CA	101	ARG
1	CA	106	THR
1	CA	112	GLN
1	CA	114	MET
1	CA	137	THR
1	CA	141	LEU
1	CA	151	LYS
1	CA	173	LYS
1	CA	175	GLN
1	CA	176	ARG
1	CA	177	LEU
1	CA	185	LEU
1	CA	186	LEU
1	CA	190	ASN

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Mol	Chain	Res	Type
1	CA	198	SER
1	CA	204	SER
1	CA	208	SER
1	CA	217	GLU
1	CA	246	THR
1	CA	288	ASN
1	CA	316	SER
1	CA	337	GLU
1	BB	57	LEU
1	BB	58	SER
1	BB	63	ILE
1	BB	67	VAL
1	BB	68	LEU
1	BB	78	VAL
1	BB	79	VAL
1	BB	80	VAL
1	BB	85	VAL
1	BB	88	LEU
1	BB	92	LEU
1	BB	100	GLN
1	BB	101	ARG
1	BB	104	VAL
1	BB	105	GLU
1	BB	111	ILE
1	BB	128	LEU
1	BB	134	ASN
1	BB	145	ARG
1	BB	156	ARG
1	BB	165	THR
1	BB	167	LEU
1	BB	173	LYS
1	BB	176	ARG
1	BB	183	LEU
1	BB	184	ILE
1	BB	185	LEU
1	BB	191	ASN
1	BB	196	ASN
1	BB	198	SER
1	BB	202	ARG
1	BB	207	LEU
1	BB	212	LEU
1	BB	271	THR

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Mol	Chain	Res	Type
1	BB	319	GLN
1	AB	55	VAL
1	AB	58	SER
1	AB	62	ARG
1	AB	67	VAL
1	AB	72	THR
1	AB	74	THR
1	AB	75	ASP
1	AB	83	THR
1	AB	87	ASP
1	AB	111	ILE
1	AB	118	ASN
1	AB	124	VAL
1	AB	128	LEU
1	AB	137	THR
1	AB	141	LEU
1	AB	142	GLN
1	AB	144	THR
1	AB	149	VAL
1	AB	157	THR
1	AB	159	ARG
1	AB	162	TYR
1	AB	163	THR
1	AB	165	THR
1	AB	167	LEU
1	AB	170	SER
1	AB	176	ARG
1	AB	183	LEU
1	AB	186	LEU
1	AB	192	THR
1	AB	196	ASN
1	AB	208	SER
1	AB	211	SER
1	AB	212	LEU
1	AB	225	GLN
1	AB	236	ASN
1	AB	264	SER
1	AB	271	THR
1	AB	312	VAL
1	AB	315	TYR
1	AB	317	ASP
1	CB	35	THR

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Mol	Chain	Res	Type
1	CB	43	SER
1	CB	54	ASP
1	CB	63	ILE
1	CB	72	THR
1	CB	74	THR
1	CB	75	ASP
1	CB	87	ASP
1	CB	101	ARG
1	CB	106	THR
1	CB	112	GLN
1	CB	114	MET
1	CB	137	THR
1	CB	141	LEU
1	CB	151	LYS
1	CB	173	LYS
1	CB	175	GLN
1	CB	176	ARG
1	CB	177	LEU
1	CB	185	LEU
1	CB	186	LEU
1	CB	198	SER
1	CB	204	SER
1	CB	208	SER
1	CB	217	GLU
1	CB	246	THR
1	CB	288	ASN
1	CB	316	SER
1	CB	337	GLU
1	BC	57	LEU
1	BC	58	SER
1	BC	63	ILE
1	BC	67	VAL
1	BC	68	LEU
1	BC	78	VAL
1	BC	79	VAL
1	BC	80	VAL
1	BC	85	VAL
1	BC	88	LEU
1	BC	91	ARG
1	BC	92	LEU
1	BC	100	GLN
1	BC	101	ARG

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Mol	Chain	Res	Type
1	BC	104	VAL
1	BC	105	GLU
1	BC	111	ILE
1	BC	128	LEU
1	BC	134	ASN
1	BC	145	ARG
1	BC	156	ARG
1	BC	165	THR
1	BC	167	LEU
1	BC	173	LYS
1	BC	176	ARG
1	BC	183	LEU
1	BC	184	ILE
1	BC	185	LEU
1	BC	191	ASN
1	BC	196	ASN
1	BC	198	SER
1	BC	202	ARG
1	BC	207	LEU
1	BC	212	LEU
1	BC	271	THR
1	BC	319	GLN
1	AC	55	VAL
1	AC	58	SER
1	AC	62	ARG
1	AC	67	VAL
1	AC	72	THR
1	AC	74	THR
1	AC	75	ASP
1	AC	87	ASP
1	AC	111	ILE
1	AC	118	ASN
1	AC	124	VAL
1	AC	128	LEU
1	AC	137	THR
1	AC	141	LEU
1	AC	142	GLN
1	AC	149	VAL
1	AC	156	ARG
1	AC	157	THR
1	AC	159	ARG
1	AC	162	TYR

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Mol	Chain	Res	Type
1	AC	163	THR
1	AC	165	THR
1	AC	167	LEU
1	AC	170	SER
1	AC	176	ARG
1	AC	183	LEU
1	AC	186	LEU
1	AC	196	ASN
1	AC	208	SER
1	AC	211	SER
1	AC	225	GLN
1	AC	236	ASN
1	AC	264	SER
1	AC	271	THR
1	AC	312	VAL
1	AC	317	ASP
1	CC	35	THR
1	CC	43	SER
1	CC	54	ASP
1	CC	63	ILE
1	CC	72	THR
1	CC	74	THR
1	CC	75	ASP
1	CC	87	ASP
1	CC	101	ARG
1	CC	106	THR
1	CC	112	GLN
1	CC	114	MET
1	CC	137	THR
1	CC	141	LEU
1	CC	151	LYS
1	CC	173	LYS
1	CC	175	GLN
1	CC	176	ARG
1	CC	177	LEU
1	CC	185	LEU
1	CC	186	LEU
1	CC	198	SER
1	CC	204	SER
1	CC	208	SER
1	CC	211	SER
1	CC	217	GLU

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Mol	Chain	Res	Type
1	CC	288	ASN
1	CC	316	SER
1	CC	331	CYS
1	CC	337	GLU
1	BD	57	LEU
1	BD	58	SER
1	BD	63	ILE
1	BD	67	VAL
1	BD	68	LEU
1	BD	78	VAL
1	BD	79	VAL
1	BD	80	VAL
1	BD	85	VAL
1	BD	88	LEU
1	BD	92	LEU
1	BD	100	GLN
1	BD	101	ARG
1	BD	104	VAL
1	BD	105	GLU
1	BD	111	ILE
1	BD	128	LEU
1	BD	134	ASN
1	BD	145	ARG
1	BD	156	ARG
1	BD	165	THR
1	BD	167	LEU
1	BD	173	LYS
1	BD	183	LEU
1	BD	184	ILE
1	BD	185	LEU
1	BD	191	ASN
1	BD	196	ASN
1	BD	198	SER
1	BD	202	ARG
1	BD	207	LEU
1	BD	212	LEU
1	BD	271	THR
1	BD	319	GLN
1	AD	55	VAL
1	AD	58	SER
1	AD	62	ARG
1	AD	67	VAL

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Mol	Chain	Res	Type
1	AD	72	THR
1	AD	74	THR
1	AD	75	ASP
1	AD	87	ASP
1	AD	111	ILE
1	AD	124	VAL
1	AD	128	LEU
1	AD	137	THR
1	AD	141	LEU
1	AD	142	GLN
1	AD	144	THR
1	AD	149	VAL
1	AD	156	ARG
1	AD	157	THR
1	AD	159	ARG
1	AD	162	TYR
1	AD	163	THR
1	AD	165	THR
1	AD	167	LEU
1	AD	170	SER
1	AD	176	ARG
1	AD	183	LEU
1	AD	186	LEU
1	AD	196	ASN
1	AD	208	SER
1	AD	211	SER
1	AD	225	GLN
1	AD	236	ASN
1	AD	264	SER
1	AD	271	THR
1	AD	312	VAL
1	AD	315	TYR
1	AD	317	ASP
1	CD	35	THR
1	CD	43	SER
1	CD	54	ASP
1	CD	63	ILE
1	CD	72	THR
1	CD	74	THR
1	CD	75	ASP
1	CD	87	ASP
1	CD	101	ARG

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Mol	Chain	Res	Type
1	CD	112	GLN
1	CD	114	MET
1	CD	137	THR
1	CD	141	LEU
1	CD	151	LYS
1	CD	173	LYS
1	CD	175	GLN
1	CD	176	ARG
1	CD	177	LEU
1	CD	185	LEU
1	CD	186	LEU
1	CD	198	SER
1	CD	204	SER
1	CD	208	SER
1	CD	217	GLU
1	CD	246	THR
1	CD	288	ASN
1	CD	316	SER
1	CD	337	GLU
1	BE	57	LEU
1	BE	58	SER
1	BE	63	ILE
1	BE	67	VAL
1	BE	68	LEU
1	BE	78	VAL
1	BE	79	VAL
1	BE	80	VAL
1	BE	85	VAL
1	BE	88	LEU
1	BE	92	LEU
1	BE	100	GLN
1	BE	101	ARG
1	BE	104	VAL
1	BE	105	GLU
1	BE	111	ILE
1	BE	128	LEU
1	BE	134	ASN
1	BE	145	ARG
1	BE	156	ARG
1	BE	165	THR
1	BE	167	LEU
1	BE	173	LYS

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Mol	Chain	Res	Type
1	BE	176	ARG
1	BE	183	LEU
1	BE	184	ILE
1	BE	185	LEU
1	BE	191	ASN
1	BE	196	ASN
1	BE	198	SER
1	BE	202	ARG
1	BE	207	LEU
1	BE	212	LEU
1	BE	271	THR
1	BE	319	GLN
1	AE	55	VAL
1	AE	58	SER
1	AE	62	ARG
1	AE	67	VAL
1	AE	72	THR
1	AE	74	THR
1	AE	75	ASP
1	AE	87	ASP
1	AE	111	ILE
1	AE	118	ASN
1	AE	124	VAL
1	AE	128	LEU
1	AE	137	THR
1	AE	141	LEU
1	AE	142	GLN
1	AE	144	THR
1	AE	149	VAL
1	AE	156	ARG
1	AE	157	THR
1	AE	159	ARG
1	AE	162	TYR
1	AE	163	THR
1	AE	165	THR
1	AE	167	LEU
1	AE	170	SER
1	AE	176	ARG
1	AE	183	LEU
1	AE	186	LEU
1	AE	196	ASN
1	AE	208	SER

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Mol	Chain	Res	Type
1	AE	211	SER
1	AE	225	GLN
1	AE	236	ASN
1	AE	253	ASP
1	AE	264	SER
1	AE	271	THR
1	AE	312	VAL
1	AE	315	TYR
1	AE	317	ASP
1	CE	35	THR
1	CE	43	SER
1	CE	54	ASP
1	CE	63	ILE
1	CE	72	THR
1	CE	74	THR
1	CE	75	ASP
1	CE	87	ASP
1	CE	101	ARG
1	CE	106	THR
1	CE	112	GLN
1	CE	114	MET
1	CE	137	THR
1	CE	141	LEU
1	CE	151	LYS
1	CE	173	LYS
1	CE	175	GLN
1	CE	176	ARG
1	CE	177	LEU
1	CE	185	LEU
1	CE	186	LEU
1	CE	190	ASN
1	CE	198	SER
1	CE	204	SER
1	CE	208	SER
1	CE	217	GLU
1	CE	288	ASN
1	CE	316	SER
1	CE	337	GLU
1	BF	57	LEU
1	BF	58	SER
1	BF	63	ILE
1	BF	67	VAL

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Mol	Chain	Res	Type
1	BF	68	LEU
1	BF	78	VAL
1	BF	79	VAL
1	BF	80	VAL
1	BF	85	VAL
1	BF	86	PRO
1	BF	88	LEU
1	BF	92	LEU
1	BF	100	GLN
1	BF	101	ARG
1	BF	104	VAL
1	BF	105	GLU
1	BF	111	ILE
1	BF	128	LEU
1	BF	134	ASN
1	BF	145	ARG
1	BF	156	ARG
1	BF	165	THR
1	BF	167	LEU
1	BF	173	LYS
1	BF	183	LEU
1	BF	184	ILE
1	BF	185	LEU
1	BF	191	ASN
1	BF	196	ASN
1	BF	198	SER
1	BF	202	ARG
1	BF	207	LEU
1	BF	212	LEU
1	BF	271	THR
1	BF	319	GLN
1	AF	55	VAL
1	AF	58	SER
1	AF	62	ARG
1	AF	67	VAL
1	AF	72	THR
1	AF	74	THR
1	AF	75	ASP
1	AF	87	ASP
1	AF	111	ILE
1	AF	118	ASN
1	AF	119	THR

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Mol	Chain	Res	Type
1	AF	124	VAL
1	AF	128	LEU
1	AF	137	THR
1	AF	141	LEU
1	AF	142	GLN
1	AF	149	VAL
1	AF	156	ARG
1	AF	157	THR
1	AF	159	ARG
1	AF	162	TYR
1	AF	163	THR
1	AF	165	THR
1	AF	167	LEU
1	AF	170	SER
1	AF	176	ARG
1	AF	183	LEU
1	AF	186	LEU
1	AF	192	THR
1	AF	196	ASN
1	AF	208	SER
1	AF	211	SER
1	AF	225	GLN
1	AF	236	ASN
1	AF	264	SER
1	AF	271	THR
1	AF	312	VAL
1	AF	315	TYR
1	AF	317	ASP
1	CF	35	THR
1	CF	43	SER
1	CF	54	ASP
1	CF	63	ILE
1	CF	72	THR
1	CF	74	THR
1	CF	75	ASP
1	CF	87	ASP
1	CF	101	ARG
1	CF	106	THR
1	CF	112	GLN
1	CF	114	MET
1	CF	137	THR
1	CF	141	LEU

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Mol	Chain	Res	Type
1	CF	151	LYS
1	CF	173	LYS
1	CF	175	GLN
1	CF	176	ARG
1	CF	177	LEU
1	CF	185	LEU
1	CF	186	LEU
1	CF	190	ASN
1	CF	198	SER
1	CF	204	SER
1	CF	208	SER
1	CF	217	GLU
1	CF	246	THR
1	CF	288	ASN
1	CF	316	SER
1	CF	337	GLU
1	BG	57	LEU
1	BG	58	SER
1	BG	63	ILE
1	BG	67	VAL
1	BG	68	LEU
1	BG	78	VAL
1	BG	79	VAL
1	BG	80	VAL
1	BG	85	VAL
1	BG	88	LEU
1	BG	92	LEU
1	BG	100	GLN
1	BG	101	ARG
1	BG	104	VAL
1	BG	105	GLU
1	BG	111	ILE
1	BG	128	LEU
1	BG	134	ASN
1	BG	145	ARG
1	BG	156	ARG
1	BG	165	THR
1	BG	167	LEU
1	BG	173	LYS
1	BG	183	LEU
1	BG	184	ILE
1	BG	185	LEU

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Mol	Chain	Res	Type
1	BG	196	ASN
1	BG	198	SER
1	BG	202	ARG
1	BG	207	LEU
1	BG	212	LEU
1	BG	271	THR
1	BG	319	GLN
1	AG	55	VAL
1	AG	58	SER
1	AG	62	ARG
1	AG	67	VAL
1	AG	72	THR
1	AG	74	THR
1	AG	75	ASP
1	AG	83	THR
1	AG	87	ASP
1	AG	111	ILE
1	AG	118	ASN
1	AG	124	VAL
1	AG	128	LEU
1	AG	137	THR
1	AG	141	LEU
1	AG	142	GLN
1	AG	149	VAL
1	AG	156	ARG
1	AG	157	THR
1	AG	159	ARG
1	AG	162	TYR
1	AG	163	THR
1	AG	165	THR
1	AG	167	LEU
1	AG	170	SER
1	AG	176	ARG
1	AG	183	LEU
1	AG	186	LEU
1	AG	196	ASN
1	AG	208	SER
1	AG	211	SER
1	AG	212	LEU
1	AG	225	GLN
1	AG	236	ASN
1	AG	253	ASP

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Mol	Chain	Res	Type
1	AG	264	SER
1	AG	271	THR
1	AG	312	VAL
1	AG	317	ASP
1	CG	35	THR
1	CG	43	SER
1	CG	54	ASP
1	CG	63	ILE
1	CG	72	THR
1	CG	74	THR
1	CG	75	ASP
1	CG	87	ASP
1	CG	101	ARG
1	CG	106	THR
1	CG	112	GLN
1	CG	114	MET
1	CG	137	THR
1	CG	141	LEU
1	CG	151	LYS
1	CG	173	LYS
1	CG	175	GLN
1	CG	176	ARG
1	CG	177	LEU
1	CG	185	LEU
1	CG	186	LEU
1	CG	198	SER
1	CG	204	SER
1	CG	208	SER
1	CG	217	GLU
1	CG	288	ASN
1	CG	316	SER
1	CG	337	GLU
1	BH	57	LEU
1	BH	58	SER
1	BH	63	ILE
1	BH	67	VAL
1	BH	68	LEU
1	BH	78	VAL
1	BH	79	VAL
1	BH	80	VAL
1	BH	85	VAL
1	BH	86	PRO

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Mol	Chain	Res	Type
1	BH	88	LEU
1	BH	92	LEU
1	BH	100	GLN
1	BH	101	ARG
1	BH	104	VAL
1	BH	105	GLU
1	BH	111	ILE
1	BH	128	LEU
1	BH	134	ASN
1	BH	145	ARG
1	BH	156	ARG
1	BH	165	THR
1	BH	167	LEU
1	BH	173	LYS
1	BH	176	ARG
1	BH	183	LEU
1	BH	184	ILE
1	BH	185	LEU
1	BH	191	ASN
1	BH	196	ASN
1	BH	198	SER
1	BH	202	ARG
1	BH	207	LEU
1	BH	212	LEU
1	BH	271	THR
1	BH	319	GLN
1	AH	55	VAL
1	AH	58	SER
1	AH	62	ARG
1	AH	67	VAL
1	AH	72	THR
1	AH	74	THR
1	AH	75	ASP
1	AH	87	ASP
1	AH	111	ILE
1	AH	124	VAL
1	AH	128	LEU
1	AH	137	THR
1	AH	141	LEU
1	AH	142	GLN
1	AH	144	THR
1	AH	149	VAL

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Mol	Chain	Res	Type
1	AH	156	ARG
1	AH	159	ARG
1	AH	162	TYR
1	AH	163	THR
1	AH	165	THR
1	AH	167	LEU
1	AH	170	SER
1	AH	176	ARG
1	AH	183	LEU
1	AH	186	LEU
1	AH	196	ASN
1	AH	208	SER
1	AH	211	SER
1	AH	225	GLN
1	AH	236	ASN
1	AH	264	SER
1	AH	271	THR
1	AH	312	VAL
1	AH	317	ASP
1	CH	35	THR
1	CH	43	SER
1	CH	54	ASP
1	CH	63	ILE
1	CH	72	THR
1	CH	74	THR
1	CH	75	ASP
1	CH	87	ASP
1	CH	101	ARG
1	CH	106	THR
1	CH	112	GLN
1	CH	114	MET
1	CH	137	THR
1	CH	141	LEU
1	CH	151	LYS
1	CH	173	LYS
1	CH	175	GLN
1	CH	176	ARG
1	CH	177	LEU
1	CH	185	LEU
1	CH	186	LEU
1	CH	190	ASN
1	CH	198	SER

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Mol	Chain	Res	Type
1	CH	204	SER
1	CH	208	SER
1	CH	217	GLU
1	CH	246	THR
1	CH	288	ASN
1	CH	316	SER
1	CH	337	GLU
1	BI	57	LEU
1	BI	58	SER
1	BI	63	ILE
1	BI	67	VAL
1	BI	68	LEU
1	BI	78	VAL
1	BI	79	VAL
1	BI	80	VAL
1	BI	85	VAL
1	BI	88	LEU
1	BI	92	LEU
1	BI	100	GLN
1	BI	101	ARG
1	BI	104	VAL
1	BI	105	GLU
1	BI	111	ILE
1	BI	134	ASN
1	BI	145	ARG
1	BI	156	ARG
1	BI	165	THR
1	BI	167	LEU
1	BI	173	LYS
1	BI	176	ARG
1	BI	183	LEU
1	BI	184	ILE
1	BI	185	LEU
1	BI	191	ASN
1	BI	196	ASN
1	BI	198	SER
1	BI	202	ARG
1	BI	207	LEU
1	BI	212	LEU
1	BI	271	THR
1	BI	319	GLN
1	AI	55	VAL

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Mol	Chain	Res	Type
1	AI	58	SER
1	AI	62	ARG
1	AI	67	VAL
1	AI	72	THR
1	AI	74	THR
1	AI	75	ASP
1	AI	87	ASP
1	AI	111	ILE
1	AI	118	ASN
1	AI	124	VAL
1	AI	128	LEU
1	AI	137	THR
1	AI	141	LEU
1	AI	142	GLN
1	AI	144	THR
1	AI	149	VAL
1	AI	156	ARG
1	AI	157	THR
1	AI	159	ARG
1	AI	162	TYR
1	AI	163	THR
1	AI	165	THR
1	AI	167	LEU
1	AI	170	SER
1	AI	176	ARG
1	AI	183	LEU
1	AI	186	LEU
1	AI	192	THR
1	AI	196	ASN
1	AI	208	SER
1	AI	211	SER
1	AI	212	LEU
1	AI	225	GLN
1	AI	236	ASN
1	AI	253	ASP
1	AI	271	THR
1	AI	312	VAL
1	AI	317	ASP
1	CI	35	THR
1	CI	43	SER
1	CI	54	ASP
1	CI	72	THR

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Mol	Chain	Res	Type
1	CI	74	THR
1	CI	75	ASP
1	CI	87	ASP
1	CI	101	ARG
1	CI	106	THR
1	CI	112	GLN
1	CI	114	MET
1	CI	137	THR
1	CI	141	LEU
1	CI	151	LYS
1	CI	173	LYS
1	CI	175	GLN
1	CI	176	ARG
1	CI	177	LEU
1	CI	185	LEU
1	CI	186	LEU
1	CI	198	SER
1	CI	204	SER
1	CI	208	SER
1	CI	217	GLU
1	CI	288	ASN
1	CI	316	SER
1	CI	337	GLU
1	BJ	57	LEU
1	BJ	58	SER
1	BJ	63	ILE
1	BJ	67	VAL
1	BJ	68	LEU
1	BJ	78	VAL
1	BJ	79	VAL
1	BJ	80	VAL
1	BJ	85	VAL
1	BJ	86	PRO
1	BJ	88	LEU
1	BJ	92	LEU
1	BJ	100	GLN
1	BJ	101	ARG
1	BJ	104	VAL
1	BJ	105	GLU
1	BJ	111	ILE
1	BJ	134	ASN
1	BJ	145	ARG

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Mol	Chain	Res	Type
1	BJ	156	ARG
1	BJ	165	THR
1	BJ	167	LEU
1	BJ	173	LYS
1	BJ	183	LEU
1	BJ	184	ILE
1	BJ	185	LEU
1	BJ	196	ASN
1	BJ	198	SER
1	BJ	202	ARG
1	BJ	207	LEU
1	BJ	212	LEU
1	BJ	271	THR
1	BJ	319	GLN
1	AJ	55	VAL
1	AJ	58	SER
1	AJ	62	ARG
1	AJ	67	VAL
1	AJ	72	THR
1	AJ	74	THR
1	AJ	75	ASP
1	AJ	87	ASP
1	AJ	111	ILE
1	AJ	124	VAL
1	AJ	128	LEU
1	AJ	137	THR
1	AJ	141	LEU
1	AJ	142	GLN
1	AJ	144	THR
1	AJ	149	VAL
1	AJ	156	ARG
1	AJ	159	ARG
1	AJ	162	TYR
1	AJ	163	THR
1	AJ	165	THR
1	AJ	167	LEU
1	AJ	170	SER
1	AJ	176	ARG
1	AJ	183	LEU
1	AJ	186	LEU
1	AJ	192	THR
1	AJ	196	ASN

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Mol	Chain	Res	Type
1	AJ	208	SER
1	AJ	211	SER
1	AJ	225	GLN
1	AJ	236	ASN
1	AJ	253	ASP
1	AJ	264	SER
1	AJ	271	THR
1	AJ	312	VAL
1	AJ	317	ASP
1	CJ	35	THR
1	CJ	43	SER
1	CJ	54	ASP
1	CJ	63	ILE
1	CJ	72	THR
1	CJ	74	THR
1	CJ	75	ASP
1	CJ	87	ASP
1	CJ	101	ARG
1	CJ	106	THR
1	CJ	112	GLN
1	CJ	114	MET
1	CJ	137	THR
1	CJ	141	LEU
1	CJ	151	LYS
1	CJ	173	LYS
1	CJ	175	GLN
1	CJ	176	ARG
1	CJ	177	LEU
1	CJ	185	LEU
1	CJ	186	LEU
1	CJ	190	ASN
1	CJ	198	SER
1	CJ	204	SER
1	CJ	208	SER
1	CJ	211	SER
1	CJ	217	GLU
1	CJ	288	ASN
1	CJ	316	SER
1	CJ	337	GLU
1	BK	57	LEU
1	BK	58	SER
1	BK	63	ILE

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Mol	Chain	Res	Type
1	BK	67	VAL
1	BK	68	LEU
1	BK	78	VAL
1	BK	79	VAL
1	BK	80	VAL
1	BK	85	VAL
1	BK	88	LEU
1	BK	92	LEU
1	BK	100	GLN
1	BK	101	ARG
1	BK	104	VAL
1	BK	105	GLU
1	BK	111	ILE
1	BK	134	ASN
1	BK	145	ARG
1	BK	156	ARG
1	BK	165	THR
1	BK	167	LEU
1	BK	173	LYS
1	BK	183	LEU
1	BK	184	ILE
1	BK	185	LEU
1	BK	191	ASN
1	BK	196	ASN
1	BK	198	SER
1	BK	202	ARG
1	BK	207	LEU
1	BK	212	LEU
1	BK	271	THR
1	BK	319	GLN
1	AK	55	VAL
1	AK	58	SER
1	AK	62	ARG
1	AK	67	VAL
1	AK	72	THR
1	AK	74	THR
1	AK	75	ASP
1	AK	83	THR
1	AK	87	ASP
1	AK	111	ILE
1	AK	118	ASN
1	AK	124	VAL

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Mol	Chain	Res	Type
1	AK	128	LEU
1	AK	137	THR
1	AK	141	LEU
1	AK	142	GLN
1	AK	144	THR
1	AK	149	VAL
1	AK	156	ARG
1	AK	159	ARG
1	AK	162	TYR
1	AK	163	THR
1	AK	165	THR
1	AK	167	LEU
1	AK	170	SER
1	AK	176	ARG
1	AK	183	LEU
1	AK	186	LEU
1	AK	192	THR
1	AK	196	ASN
1	AK	208	SER
1	AK	211	SER
1	AK	225	GLN
1	AK	236	ASN
1	AK	253	ASP
1	AK	264	SER
1	AK	271	THR
1	AK	312	VAL
1	AK	317	ASP
1	CK	35	THR
1	CK	43	SER
1	CK	54	ASP
1	CK	63	ILE
1	CK	72	THR
1	CK	74	THR
1	CK	75	ASP
1	CK	81	ASP
1	CK	87	ASP
1	CK	101	ARG
1	CK	106	THR
1	CK	112	GLN
1	CK	114	MET
1	CK	137	THR
1	CK	141	LEU

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Mol	Chain	Res	Type
1	CK	151	LYS
1	CK	173	LYS
1	CK	175	GLN
1	CK	176	ARG
1	CK	177	LEU
1	CK	185	LEU
1	CK	186	LEU
1	CK	198	SER
1	CK	204	SER
1	CK	208	SER
1	CK	217	GLU
1	CK	246	THR
1	CK	288	ASN
1	CK	316	SER
1	CK	331	CYS
1	CK	337	GLU
1	BL	57	LEU
1	BL	58	SER
1	BL	63	ILE
1	BL	67	VAL
1	BL	68	LEU
1	BL	78	VAL
1	BL	79	VAL
1	BL	80	VAL
1	BL	85	VAL
1	BL	88	LEU
1	BL	92	LEU
1	BL	100	GLN
1	BL	101	ARG
1	BL	104	VAL
1	BL	105	GLU
1	BL	111	ILE
1	BL	128	LEU
1	BL	134	ASN
1	BL	145	ARG
1	BL	156	ARG
1	BL	165	THR
1	BL	167	LEU
1	BL	173	LYS
1	BL	176	ARG
1	BL	183	LEU
1	BL	184	ILE

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Mol	Chain	Res	Type
1	BL	185	LEU
1	BL	191	ASN
1	BL	196	ASN
1	BL	198	SER
1	BL	202	ARG
1	BL	207	LEU
1	BL	212	LEU
1	BL	271	THR
1	BL	319	GLN
1	AL	55	VAL
1	AL	58	SER
1	AL	62	ARG
1	AL	67	VAL
1	AL	72	THR
1	AL	74	THR
1	AL	75	ASP
1	AL	87	ASP
1	AL	114	MET
1	AL	118	ASN
1	AL	124	VAL
1	AL	128	LEU
1	AL	137	THR
1	AL	141	LEU
1	AL	142	GLN
1	AL	144	THR
1	AL	149	VAL
1	AL	156	ARG
1	AL	157	THR
1	AL	159	ARG
1	AL	163	THR
1	AL	165	THR
1	AL	167	LEU
1	AL	170	SER
1	AL	176	ARG
1	AL	183	LEU
1	AL	186	LEU
1	AL	196	ASN
1	AL	208	SER
1	AL	211	SER
1	AL	225	GLN
1	AL	236	ASN
1	AL	264	SER

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Mol	Chain	Res	Type
1	AL	271	THR
1	AL	312	VAL
1	AL	317	ASP
1	CL	35	THR
1	CL	43	SER
1	CL	54	ASP
1	CL	63	ILE
1	CL	72	THR
1	CL	74	THR
1	CL	75	ASP
1	CL	87	ASP
1	CL	101	ARG
1	CL	106	THR
1	CL	112	GLN
1	CL	114	MET
1	CL	137	THR
1	CL	141	LEU
1	CL	151	LYS
1	CL	173	LYS
1	CL	175	GLN
1	CL	176	ARG
1	CL	177	LEU
1	CL	185	LEU
1	CL	186	LEU
1	CL	198	SER
1	CL	204	SER
1	CL	208	SER
1	CL	217	GLU
1	CL	288	ASN
1	CL	316	SER
1	CL	331	CYS
1	CL	337	GLU
1	BM	57	LEU
1	BM	58	SER
1	BM	63	ILE
1	BM	67	VAL
1	BM	68	LEU
1	BM	78	VAL
1	BM	79	VAL
1	BM	80	VAL
1	BM	85	VAL
1	BM	86	PRO

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Mol	Chain	Res	Type
1	BM	88	LEU
1	BM	92	LEU
1	BM	100	GLN
1	BM	101	ARG
1	BM	104	VAL
1	BM	105	GLU
1	BM	111	ILE
1	BM	128	LEU
1	BM	134	ASN
1	BM	145	ARG
1	BM	156	ARG
1	BM	165	THR
1	BM	167	LEU
1	BM	173	LYS
1	BM	176	ARG
1	BM	183	LEU
1	BM	184	ILE
1	BM	185	LEU
1	BM	196	ASN
1	BM	198	SER
1	BM	202	ARG
1	BM	207	LEU
1	BM	212	LEU
1	BM	271	THR
1	BM	319	GLN
1	AM	55	VAL
1	AM	58	SER
1	AM	62	ARG
1	AM	67	VAL
1	AM	72	THR
1	AM	74	THR
1	AM	75	ASP
1	AM	87	ASP
1	AM	111	ILE
1	AM	118	ASN
1	AM	119	THR
1	AM	124	VAL
1	AM	128	LEU
1	AM	137	THR
1	AM	141	LEU
1	AM	142	GLN
1	AM	149	VAL

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Mol	Chain	Res	Type
1	AM	156	ARG
1	AM	157	THR
1	AM	159	ARG
1	AM	162	TYR
1	AM	163	THR
1	AM	165	THR
1	AM	167	LEU
1	AM	170	SER
1	AM	176	ARG
1	AM	183	LEU
1	AM	186	LEU
1	AM	192	THR
1	AM	196	ASN
1	AM	208	SER
1	AM	211	SER
1	AM	225	GLN
1	AM	236	ASN
1	AM	264	SER
1	AM	271	THR
1	AM	312	VAL
1	AM	315	TYR
1	AM	317	ASP
1	CM	35	THR
1	CM	43	SER
1	CM	54	ASP
1	CM	72	THR
1	CM	74	THR
1	CM	75	ASP
1	CM	87	ASP
1	CM	101	ARG
1	CM	106	THR
1	CM	112	GLN
1	CM	114	MET
1	CM	137	THR
1	CM	141	LEU
1	CM	151	LYS
1	CM	173	LYS
1	CM	175	GLN
1	CM	176	ARG
1	CM	177	LEU
1	CM	185	LEU
1	CM	186	LEU

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Mol	Chain	Res	Type
1	CM	198	SER
1	CM	204	SER
1	CM	208	SER
1	CM	217	GLU
1	CM	246	THR
1	CM	288	ASN
1	CM	316	SER
1	CM	337	GLU
1	BN	57	LEU
1	BN	58	SER
1	BN	63	ILE
1	BN	67	VAL
1	BN	68	LEU
1	BN	78	VAL
1	BN	79	VAL
1	BN	80	VAL
1	BN	85	VAL
1	BN	88	LEU
1	BN	92	LEU
1	BN	100	GLN
1	BN	101	ARG
1	BN	104	VAL
1	BN	105	GLU
1	BN	111	ILE
1	BN	134	ASN
1	BN	145	ARG
1	BN	156	ARG
1	BN	165	THR
1	BN	167	LEU
1	BN	173	LYS
1	BN	183	LEU
1	BN	184	ILE
1	BN	185	LEU
1	BN	196	ASN
1	BN	198	SER
1	BN	202	ARG
1	BN	207	LEU
1	BN	212	LEU
1	BN	271	THR
1	BN	319	GLN
1	AN	55	VAL
1	AN	62	ARG

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Mol	Chain	Res	Type
1	AN	67	VAL
1	AN	72	THR
1	AN	74	THR
1	AN	75	ASP
1	AN	87	ASP
1	AN	111	ILE
1	AN	118	ASN
1	AN	119	THR
1	AN	124	VAL
1	AN	128	LEU
1	AN	137	THR
1	AN	141	LEU
1	AN	142	GLN
1	AN	144	THR
1	AN	149	VAL
1	AN	156	ARG
1	AN	157	THR
1	AN	159	ARG
1	AN	162	TYR
1	AN	163	THR
1	AN	165	THR
1	AN	167	LEU
1	AN	170	SER
1	AN	176	ARG
1	AN	183	LEU
1	AN	186	LEU
1	AN	196	ASN
1	AN	208	SER
1	AN	211	SER
1	AN	225	GLN
1	AN	236	ASN
1	AN	253	ASP
1	AN	264	SER
1	AN	271	THR
1	AN	312	VAL
1	AN	315	TYR
1	AN	317	ASP
1	CN	35	THR
1	CN	43	SER
1	CN	46	THR
1	CN	54	ASP
1	CN	72	THR

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Mol	Chain	Res	Type
1	CN	74	THR
1	CN	75	ASP
1	CN	87	ASP
1	CN	101	ARG
1	CN	112	GLN
1	CN	114	MET
1	CN	137	THR
1	CN	141	LEU
1	CN	151	LYS
1	CN	173	LYS
1	CN	175	GLN
1	CN	176	ARG
1	CN	177	LEU
1	CN	185	LEU
1	CN	186	LEU
1	CN	190	ASN
1	CN	198	SER
1	CN	204	SER
1	CN	208	SER
1	CN	217	GLU
1	CN	246	THR
1	CN	288	ASN
1	CN	316	SER
1	CN	337	GLU
1	BO	57	LEU
1	BO	58	SER
1	BO	63	ILE
1	BO	67	VAL
1	BO	68	LEU
1	BO	78	VAL
1	BO	79	VAL
1	BO	80	VAL
1	BO	85	VAL
1	BO	88	LEU
1	BO	92	LEU
1	BO	100	GLN
1	BO	101	ARG
1	BO	104	VAL
1	BO	105	GLU
1	BO	111	ILE
1	BO	128	LEU
1	BO	134	ASN

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Mol	Chain	Res	Type
1	BO	145	ARG
1	BO	156	ARG
1	BO	165	THR
1	BO	167	LEU
1	BO	173	LYS
1	BO	183	LEU
1	BO	184	ILE
1	BO	185	LEU
1	BO	191	ASN
1	BO	196	ASN
1	BO	198	SER
1	BO	202	ARG
1	BO	207	LEU
1	BO	212	LEU
1	BO	271	THR
1	BO	319	GLN
1	AO	55	VAL
1	AO	58	SER
1	AO	62	ARG
1	AO	67	VAL
1	AO	72	THR
1	AO	74	THR
1	AO	75	ASP
1	AO	87	ASP
1	AO	111	ILE
1	AO	118	ASN
1	AO	119	THR
1	AO	124	VAL
1	AO	128	LEU
1	AO	137	THR
1	AO	141	LEU
1	AO	142	GLN
1	AO	149	VAL
1	AO	156	ARG
1	AO	157	THR
1	AO	159	ARG
1	AO	163	THR
1	AO	165	THR
1	AO	167	LEU
1	AO	170	SER
1	AO	176	ARG
1	AO	183	LEU

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Mol	Chain	Res	Type
1	AO	186	LEU
1	AO	192	THR
1	AO	196	ASN
1	AO	208	SER
1	AO	211	SER
1	AO	225	GLN
1	AO	236	ASN
1	AO	253	ASP
1	AO	271	THR
1	AO	312	VAL
1	AO	315	TYR
1	AO	317	ASP
1	CO	35	THR
1	CO	43	SER
1	CO	54	ASP
1	CO	63	ILE
1	CO	72	THR
1	CO	74	THR
1	CO	75	ASP
1	CO	87	ASP
1	CO	101	ARG
1	CO	106	THR
1	CO	112	GLN
1	CO	114	MET
1	CO	141	LEU
1	CO	151	LYS
1	CO	173	LYS
1	CO	175	GLN
1	CO	176	ARG
1	CO	177	LEU
1	CO	185	LEU
1	CO	186	LEU
1	CO	190	ASN
1	CO	198	SER
1	CO	204	SER
1	CO	208	SER
1	CO	217	GLU
1	CO	288	ASN
1	CO	316	SER
1	CO	337	GLU
1	BP	57	LEU
1	BP	58	SER

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Mol	Chain	Res	Type
1	BP	63	ILE
1	BP	67	VAL
1	BP	68	LEU
1	BP	78	VAL
1	BP	79	VAL
1	BP	80	VAL
1	BP	85	VAL
1	BP	88	LEU
1	BP	92	LEU
1	BP	100	GLN
1	BP	101	ARG
1	BP	104	VAL
1	BP	105	GLU
1	BP	111	ILE
1	BP	128	LEU
1	BP	134	ASN
1	BP	145	ARG
1	BP	156	ARG
1	BP	165	THR
1	BP	167	LEU
1	BP	173	LYS
1	BP	176	ARG
1	BP	183	LEU
1	BP	184	ILE
1	BP	185	LEU
1	BP	196	ASN
1	BP	198	SER
1	BP	202	ARG
1	BP	207	LEU
1	BP	212	LEU
1	BP	271	THR
1	BP	319	GLN
1	AP	55	VAL
1	AP	58	SER
1	AP	62	ARG
1	AP	67	VAL
1	AP	72	THR
1	AP	74	THR
1	AP	75	ASP
1	AP	87	ASP
1	AP	111	ILE
1	AP	118	ASN

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Mol	Chain	Res	Type
1	AP	119	THR
1	AP	124	VAL
1	AP	128	LEU
1	AP	137	THR
1	AP	141	LEU
1	AP	142	GLN
1	AP	144	THR
1	AP	149	VAL
1	AP	156	ARG
1	AP	159	ARG
1	AP	162	TYR
1	AP	163	THR
1	AP	165	THR
1	AP	167	LEU
1	AP	170	SER
1	AP	176	ARG
1	AP	183	LEU
1	AP	186	LEU
1	AP	196	ASN
1	AP	208	SER
1	AP	211	SER
1	AP	225	GLN
1	AP	236	ASN
1	AP	253	ASP
1	AP	264	SER
1	AP	271	THR
1	AP	312	VAL
1	AP	315	TYR
1	AP	317	ASP
1	CP	35	THR
1	CP	43	SER
1	CP	54	ASP
1	CP	63	ILE
1	CP	72	THR
1	CP	74	THR
1	CP	75	ASP
1	CP	87	ASP
1	CP	101	ARG
1	CP	106	THR
1	CP	112	GLN
1	CP	114	MET
1	CP	137	THR

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Mol	Chain	Res	Type
1	CP	141	LEU
1	CP	151	LYS
1	CP	173	LYS
1	CP	175	GLN
1	CP	176	ARG
1	CP	177	LEU
1	CP	185	LEU
1	CP	186	LEU
1	CP	190	ASN
1	CP	198	SER
1	CP	204	SER
1	CP	208	SER
1	CP	211	SER
1	CP	217	GLU
1	CP	246	THR
1	CP	288	ASN
1	CP	316	SER
1	CP	331	CYS
1	CP	337	GLU
1	BQ	57	LEU
1	BQ	58	SER
1	BQ	63	ILE
1	BQ	67	VAL
1	BQ	68	LEU
1	BQ	78	VAL
1	BQ	79	VAL
1	BQ	80	VAL
1	BQ	86	PRO
1	BQ	88	LEU
1	BQ	92	LEU
1	BQ	100	GLN
1	BQ	101	ARG
1	BQ	104	VAL
1	BQ	105	GLU
1	BQ	111	ILE
1	BQ	128	LEU
1	BQ	134	ASN
1	BQ	145	ARG
1	BQ	156	ARG
1	BQ	165	THR
1	BQ	167	LEU
1	BQ	173	LYS

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Mol	Chain	Res	Type
1	BQ	183	LEU
1	BQ	184	ILE
1	BQ	185	LEU
1	BQ	196	ASN
1	BQ	198	SER
1	BQ	202	ARG
1	BQ	207	LEU
1	BQ	212	LEU
1	BQ	271	THR
1	BQ	319	GLN
1	AQ	55	VAL
1	AQ	58	SER
1	AQ	62	ARG
1	AQ	67	VAL
1	AQ	72	THR
1	AQ	74	THR
1	AQ	75	ASP
1	AQ	87	ASP
1	AQ	111	ILE
1	AQ	114	MET
1	AQ	118	ASN
1	AQ	124	VAL
1	AQ	128	LEU
1	AQ	137	THR
1	AQ	141	LEU
1	AQ	142	GLN
1	AQ	144	THR
1	AQ	149	VAL
1	AQ	156	ARG
1	AQ	157	THR
1	AQ	159	ARG
1	AQ	162	TYR
1	AQ	163	THR
1	AQ	165	THR
1	AQ	167	LEU
1	AQ	170	SER
1	AQ	176	ARG
1	AQ	183	LEU
1	AQ	186	LEU
1	AQ	196	ASN
1	AQ	208	SER
1	AQ	211	SER

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Mol	Chain	Res	Type
1	AQ	225	GLN
1	AQ	236	ASN
1	AQ	264	SER
1	AQ	271	THR
1	AQ	312	VAL
1	AQ	315	TYR
1	AQ	317	ASP
1	CQ	35	THR
1	CQ	43	SER
1	CQ	54	ASP
1	CQ	63	ILE
1	CQ	72	THR
1	CQ	74	THR
1	CQ	75	ASP
1	CQ	87	ASP
1	CQ	101	ARG
1	CQ	106	THR
1	CQ	112	GLN
1	CQ	114	MET
1	CQ	137	THR
1	CQ	141	LEU
1	CQ	151	LYS
1	CQ	157	THR
1	CQ	173	LYS
1	CQ	175	GLN
1	CQ	176	ARG
1	CQ	177	LEU
1	CQ	185	LEU
1	CQ	186	LEU
1	CQ	190	ASN
1	CQ	198	SER
1	CQ	204	SER
1	CQ	208	SER
1	CQ	217	GLU
1	CQ	288	ASN
1	CQ	316	SER
1	CQ	337	GLU
1	BR	57	LEU
1	BR	58	SER
1	BR	63	ILE
1	BR	67	VAL
1	BR	68	LEU

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Mol	Chain	Res	Type
1	BR	78	VAL
1	BR	79	VAL
1	BR	80	VAL
1	BR	85	VAL
1	BR	86	PRO
1	BR	88	LEU
1	BR	92	LEU
1	BR	100	GLN
1	BR	101	ARG
1	BR	104	VAL
1	BR	105	GLU
1	BR	111	ILE
1	BR	134	ASN
1	BR	145	ARG
1	BR	156	ARG
1	BR	165	THR
1	BR	167	LEU
1	BR	173	LYS
1	BR	176	ARG
1	BR	183	LEU
1	BR	184	ILE
1	BR	185	LEU
1	BR	196	ASN
1	BR	198	SER
1	BR	202	ARG
1	BR	207	LEU
1	BR	212	LEU
1	BR	271	THR
1	BR	319	GLN
1	AR	55	VAL
1	AR	62	ARG
1	AR	67	VAL
1	AR	72	THR
1	AR	74	THR
1	AR	75	ASP
1	AR	87	ASP
1	AR	111	ILE
1	AR	118	ASN
1	AR	119	THR
1	AR	124	VAL
1	AR	128	LEU
1	AR	137	THR

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Mol	Chain	Res	Type
1	AR	141	LEU
1	AR	142	GLN
1	AR	144	THR
1	AR	149	VAL
1	AR	157	THR
1	AR	159	ARG
1	AR	162	TYR
1	AR	163	THR
1	AR	165	THR
1	AR	167	LEU
1	AR	170	SER
1	AR	176	ARG
1	AR	183	LEU
1	AR	186	LEU
1	AR	192	THR
1	AR	196	ASN
1	AR	208	SER
1	AR	211	SER
1	AR	212	LEU
1	AR	225	GLN
1	AR	236	ASN
1	AR	253	ASP
1	AR	264	SER
1	AR	271	THR
1	AR	312	VAL
1	AR	317	ASP
1	CR	35	THR
1	CR	43	SER
1	CR	54	ASP
1	CR	63	ILE
1	CR	72	THR
1	CR	74	THR
1	CR	75	ASP
1	CR	87	ASP
1	CR	101	ARG
1	CR	106	THR
1	CR	112	GLN
1	CR	114	MET
1	CR	137	THR
1	CR	141	LEU
1	CR	151	LYS
1	CR	173	LYS

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Mol	Chain	Res	Type
1	CR	175	GLN
1	CR	176	ARG
1	CR	177	LEU
1	CR	185	LEU
1	CR	186	LEU
1	CR	198	SER
1	CR	204	SER
1	CR	208	SER
1	CR	217	GLU
1	CR	288	ASN
1	CR	316	SER
1	CR	337	GLU
1	BS	57	LEU
1	BS	58	SER
1	BS	63	ILE
1	BS	67	VAL
1	BS	68	LEU
1	BS	78	VAL
1	BS	79	VAL
1	BS	80	VAL
1	BS	85	VAL
1	BS	88	LEU
1	BS	92	LEU
1	BS	100	GLN
1	BS	101	ARG
1	BS	104	VAL
1	BS	105	GLU
1	BS	111	ILE
1	BS	128	LEU
1	BS	134	ASN
1	BS	145	ARG
1	BS	156	ARG
1	BS	165	THR
1	BS	167	LEU
1	BS	173	LYS
1	BS	176	ARG
1	BS	183	LEU
1	BS	184	ILE
1	BS	185	LEU
1	BS	191	ASN
1	BS	196	ASN
1	BS	198	SER

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Mol	Chain	Res	Type
1	BS	202	ARG
1	BS	207	LEU
1	BS	212	LEU
1	BS	271	THR
1	BS	319	GLN
1	AS	55	VAL
1	AS	58	SER
1	AS	62	ARG
1	AS	67	VAL
1	AS	72	THR
1	AS	74	THR
1	AS	75	ASP
1	AS	87	ASP
1	AS	111	ILE
1	AS	118	ASN
1	AS	124	VAL
1	AS	128	LEU
1	AS	137	THR
1	AS	141	LEU
1	AS	142	GLN
1	AS	144	THR
1	AS	149	VAL
1	AS	156	ARG
1	AS	157	THR
1	AS	159	ARG
1	AS	162	TYR
1	AS	163	THR
1	AS	165	THR
1	AS	167	LEU
1	AS	170	SER
1	AS	176	ARG
1	AS	183	LEU
1	AS	186	LEU
1	AS	192	THR
1	AS	196	ASN
1	AS	208	SER
1	AS	211	SER
1	AS	212	LEU
1	AS	225	GLN
1	AS	236	ASN
1	AS	253	ASP
1	AS	264	SER

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Mol	Chain	Res	Type
1	AS	271	THR
1	AS	312	VAL
1	AS	315	TYR
1	AS	317	ASP
1	CS	35	THR
1	CS	43	SER
1	CS	54	ASP
1	CS	63	ILE
1	CS	72	THR
1	CS	74	THR
1	CS	75	ASP
1	CS	87	ASP
1	CS	101	ARG
1	CS	106	THR
1	CS	112	GLN
1	CS	114	MET
1	CS	137	THR
1	CS	141	LEU
1	CS	151	LYS
1	CS	173	LYS
1	CS	175	GLN
1	CS	176	ARG
1	CS	177	LEU
1	CS	185	LEU
1	CS	186	LEU
1	CS	190	ASN
1	CS	198	SER
1	CS	204	SER
1	CS	208	SER
1	CS	217	GLU
1	CS	246	THR
1	CS	288	ASN
1	CS	316	SER
1	CS	337	GLU
1	BT	57	LEU
1	BT	58	SER
1	BT	63	ILE
1	BT	67	VAL
1	BT	68	LEU
1	BT	78	VAL
1	BT	79	VAL
1	BT	80	VAL

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Mol	Chain	Res	Type
1	BT	85	VAL
1	BT	88	LEU
1	BT	92	LEU
1	BT	100	GLN
1	BT	101	ARG
1	BT	104	VAL
1	BT	105	GLU
1	BT	111	ILE
1	BT	128	LEU
1	BT	134	ASN
1	BT	145	ARG
1	BT	156	ARG
1	BT	165	THR
1	BT	167	LEU
1	BT	173	LYS
1	BT	176	ARG
1	BT	183	LEU
1	BT	184	ILE
1	BT	185	LEU
1	BT	191	ASN
1	BT	196	ASN
1	BT	198	SER
1	BT	202	ARG
1	BT	207	LEU
1	BT	212	LEU
1	BT	271	THR
1	BT	319	GLN
1	AT	55	VAL
1	AT	58	SER
1	AT	62	ARG
1	AT	67	VAL
1	AT	72	THR
1	AT	74	THR
1	AT	75	ASP
1	AT	83	THR
1	AT	87	ASP
1	AT	118	ASN
1	AT	124	VAL
1	AT	128	LEU
1	AT	137	THR
1	AT	141	LEU
1	AT	142	GLN

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Mol	Chain	Res	Type
1	AT	144	THR
1	AT	149	VAL
1	AT	156	ARG
1	AT	157	THR
1	AT	159	ARG
1	AT	162	TYR
1	AT	163	THR
1	AT	165	THR
1	AT	167	LEU
1	AT	170	SER
1	AT	176	ARG
1	AT	183	LEU
1	AT	186	LEU
1	AT	196	ASN
1	AT	208	SER
1	AT	211	SER
1	AT	225	GLN
1	AT	236	ASN
1	AT	253	ASP
1	AT	264	SER
1	AT	271	THR
1	AT	312	VAL
1	AT	317	ASP
1	CT	35	THR
1	CT	43	SER
1	CT	54	ASP
1	CT	63	ILE
1	CT	72	THR
1	CT	74	THR
1	CT	75	ASP
1	CT	87	ASP
1	CT	101	ARG
1	CT	106	THR
1	CT	112	GLN
1	CT	114	MET
1	CT	137	THR
1	CT	141	LEU
1	CT	151	LYS
1	CT	173	LYS
1	CT	175	GLN
1	CT	176	ARG
1	CT	177	LEU

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Mol	Chain	Res	Type
1	CT	185	LEU
1	CT	186	LEU
1	CT	190	ASN
1	CT	198	SER
1	CT	204	SER
1	CT	208	SER
1	CT	217	GLU
1	CT	288	ASN
1	CT	316	SER
1	CT	331	CYS
1	CT	337	GLU
1	BU	57	LEU
1	BU	58	SER
1	BU	63	ILE
1	BU	67	VAL
1	BU	68	LEU
1	BU	78	VAL
1	BU	79	VAL
1	BU	80	VAL
1	BU	85	VAL
1	BU	88	LEU
1	BU	92	LEU
1	BU	100	GLN
1	BU	101	ARG
1	BU	104	VAL
1	BU	105	GLU
1	BU	111	ILE
1	BU	128	LEU
1	BU	134	ASN
1	BU	145	ARG
1	BU	156	ARG
1	BU	165	THR
1	BU	167	LEU
1	BU	173	LYS
1	BU	176	ARG
1	BU	183	LEU
1	BU	184	ILE
1	BU	185	LEU
1	BU	191	ASN
1	BU	196	ASN
1	BU	198	SER
1	BU	202	ARG

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Mol	Chain	Res	Type
1	BU	207	LEU
1	BU	212	LEU
1	BU	271	THR
1	BU	319	GLN
1	AU	55	VAL
1	AU	58	SER
1	AU	62	ARG
1	AU	67	VAL
1	AU	72	THR
1	AU	74	THR
1	AU	75	ASP
1	AU	87	ASP
1	AU	111	ILE
1	AU	118	ASN
1	AU	119	THR
1	AU	124	VAL
1	AU	128	LEU
1	AU	137	THR
1	AU	141	LEU
1	AU	142	GLN
1	AU	149	VAL
1	AU	156	ARG
1	AU	157	THR
1	AU	159	ARG
1	AU	163	THR
1	AU	165	THR
1	AU	167	LEU
1	AU	170	SER
1	AU	176	ARG
1	AU	183	LEU
1	AU	186	LEU
1	AU	192	THR
1	AU	196	ASN
1	AU	208	SER
1	AU	211	SER
1	AU	225	GLN
1	AU	236	ASN
1	AU	253	ASP
1	AU	264	SER
1	AU	271	THR
1	AU	312	VAL
1	AU	315	TYR

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Mol	Chain	Res	Type
1	AU	317	ASP
1	CU	35	THR
1	CU	43	SER
1	CU	54	ASP
1	CU	63	ILE
1	CU	72	THR
1	CU	74	THR
1	CU	75	ASP
1	CU	87	ASP
1	CU	101	ARG
1	CU	106	THR
1	CU	112	GLN
1	CU	114	MET
1	CU	137	THR
1	CU	141	LEU
1	CU	151	LYS
1	CU	173	LYS
1	CU	175	GLN
1	CU	176	ARG
1	CU	177	LEU
1	CU	185	LEU
1	CU	186	LEU
1	CU	190	ASN
1	CU	198	SER
1	CU	204	SER
1	CU	208	SER
1	CU	217	GLU
1	CU	246	THR
1	CU	288	ASN
1	CU	316	SER
1	CU	337	GLU
1	BV	57	LEU
1	BV	58	SER
1	BV	63	ILE
1	BV	67	VAL
1	BV	68	LEU
1	BV	78	VAL
1	BV	79	VAL
1	BV	80	VAL
1	BV	85	VAL
1	BV	88	LEU
1	BV	92	LEU

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Mol	Chain	Res	Type
1	BV	100	GLN
1	BV	101	ARG
1	BV	104	VAL
1	BV	105	GLU
1	BV	111	ILE
1	BV	134	ASN
1	BV	145	ARG
1	BV	156	ARG
1	BV	165	THR
1	BV	167	LEU
1	BV	173	LYS
1	BV	183	LEU
1	BV	184	ILE
1	BV	185	LEU
1	BV	196	ASN
1	BV	198	SER
1	BV	202	ARG
1	BV	207	LEU
1	BV	212	LEU
1	BV	271	THR
1	BV	319	GLN
1	AV	55	VAL
1	AV	58	SER
1	AV	62	ARG
1	AV	67	VAL
1	AV	72	THR
1	AV	74	THR
1	AV	75	ASP
1	AV	87	ASP
1	AV	111	ILE
1	AV	118	ASN
1	AV	124	VAL
1	AV	128	LEU
1	AV	137	THR
1	AV	141	LEU
1	AV	142	GLN
1	AV	144	THR
1	AV	149	VAL
1	AV	156	ARG
1	AV	157	THR
1	AV	159	ARG
1	AV	162	TYR

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Mol	Chain	Res	Type
1	AV	163	THR
1	AV	165	THR
1	AV	167	LEU
1	AV	170	SER
1	AV	176	ARG
1	AV	183	LEU
1	AV	186	LEU
1	AV	196	ASN
1	AV	208	SER
1	AV	211	SER
1	AV	225	GLN
1	AV	236	ASN
1	AV	264	SER
1	AV	271	THR
1	AV	312	VAL
1	AV	317	ASP
1	CV	35	THR
1	CV	43	SER
1	CV	54	ASP
1	CV	72	THR
1	CV	74	THR
1	CV	75	ASP
1	CV	87	ASP
1	CV	101	ARG
1	CV	106	THR
1	CV	112	GLN
1	CV	114	MET
1	CV	137	THR
1	CV	141	LEU
1	CV	151	LYS
1	CV	173	LYS
1	CV	175	GLN
1	CV	176	ARG
1	CV	177	LEU
1	CV	185	LEU
1	CV	186	LEU
1	CV	190	ASN
1	CV	198	SER
1	CV	204	SER
1	CV	208	SER
1	CV	217	GLU
1	CV	288	ASN

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Mol	Chain	Res	Type
1	CV	316	SER
1	CV	331	CYS
1	CV	337	GLU
1	BW	57	LEU
1	BW	58	SER
1	BW	63	ILE
1	BW	67	VAL
1	BW	68	LEU
1	BW	78	VAL
1	BW	79	VAL
1	BW	80	VAL
1	BW	85	VAL
1	BW	86	PRO
1	BW	88	LEU
1	BW	92	LEU
1	BW	100	GLN
1	BW	101	ARG
1	BW	104	VAL
1	BW	105	GLU
1	BW	111	ILE
1	BW	128	LEU
1	BW	134	ASN
1	BW	145	ARG
1	BW	156	ARG
1	BW	165	THR
1	BW	167	LEU
1	BW	173	LYS
1	BW	183	LEU
1	BW	184	ILE
1	BW	191	ASN
1	BW	196	ASN
1	BW	198	SER
1	BW	202	ARG
1	BW	207	LEU
1	BW	212	LEU
1	BW	271	THR
1	BW	319	GLN
1	BW	332	THR
1	AW	55	VAL
1	AW	58	SER
1	AW	62	ARG
1	AW	67	VAL

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Mol	Chain	Res	Type
1	AW	72	THR
1	AW	74	THR
1	AW	75	ASP
1	AW	87	ASP
1	AW	111	ILE
1	AW	118	ASN
1	AW	119	THR
1	AW	124	VAL
1	AW	128	LEU
1	AW	137	THR
1	AW	141	LEU
1	AW	142	GLN
1	AW	149	VAL
1	AW	156	ARG
1	AW	157	THR
1	AW	159	ARG
1	AW	162	TYR
1	AW	163	THR
1	AW	165	THR
1	AW	167	LEU
1	AW	170	SER
1	AW	176	ARG
1	AW	183	LEU
1	AW	186	LEU
1	AW	192	THR
1	AW	196	ASN
1	AW	208	SER
1	AW	211	SER
1	AW	225	GLN
1	AW	236	ASN
1	AW	264	SER
1	AW	271	THR
1	AW	312	VAL
1	AW	317	ASP
1	CW	35	THR
1	CW	43	SER
1	CW	54	ASP
1	CW	63	ILE
1	CW	72	THR
1	CW	74	THR
1	CW	75	ASP
1	CW	87	ASP

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Mol	Chain	Res	Type
1	CW	101	ARG
1	CW	106	THR
1	CW	112	GLN
1	CW	114	MET
1	CW	137	THR
1	CW	141	LEU
1	CW	151	LYS
1	CW	173	LYS
1	CW	175	GLN
1	CW	176	ARG
1	CW	177	LEU
1	CW	185	LEU
1	CW	186	LEU
1	CW	198	SER
1	CW	204	SER
1	CW	208	SER
1	CW	217	GLU
1	CW	288	ASN
1	CW	316	SER
1	CW	337	GLU
1	BX	57	LEU
1	BX	58	SER
1	BX	63	ILE
1	BX	67	VAL
1	BX	68	LEU
1	BX	78	VAL
1	BX	79	VAL
1	BX	80	VAL
1	BX	86	PRO
1	BX	88	LEU
1	BX	92	LEU
1	BX	100	GLN
1	BX	101	ARG
1	BX	104	VAL
1	BX	105	GLU
1	BX	111	ILE
1	BX	128	LEU
1	BX	134	ASN
1	BX	145	ARG
1	BX	156	ARG
1	BX	165	THR
1	BX	167	LEU

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Mol	Chain	Res	Type
1	BX	173	LYS
1	BX	176	ARG
1	BX	183	LEU
1	BX	184	ILE
1	BX	185	LEU
1	BX	191	ASN
1	BX	196	ASN
1	BX	198	SER
1	BX	202	ARG
1	BX	207	LEU
1	BX	212	LEU
1	BX	271	THR
1	BX	319	GLN
1	AX	58	SER
1	AX	62	ARG
1	AX	67	VAL
1	AX	72	THR
1	AX	74	THR
1	AX	75	ASP
1	AX	87	ASP
1	AX	111	ILE
1	AX	118	ASN
1	AX	124	VAL
1	AX	128	LEU
1	AX	137	THR
1	AX	141	LEU
1	AX	142	GLN
1	AX	144	THR
1	AX	149	VAL
1	AX	156	ARG
1	AX	159	ARG
1	AX	162	TYR
1	AX	163	THR
1	AX	165	THR
1	AX	167	LEU
1	AX	170	SER
1	AX	176	ARG
1	AX	183	LEU
1	AX	186	LEU
1	AX	196	ASN
1	AX	208	SER
1	AX	211	SER

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Mol	Chain	Res	Type
1	AX	225	GLN
1	AX	236	ASN
1	AX	253	ASP
1	AX	264	SER
1	AX	271	THR
1	AX	312	VAL
1	AX	317	ASP
1	CX	35	THR
1	CX	43	SER
1	CX	54	ASP
1	CX	72	THR
1	CX	74	THR
1	CX	75	ASP
1	CX	87	ASP
1	CX	101	ARG
1	CX	106	THR
1	CX	112	GLN
1	CX	114	MET
1	CX	137	THR
1	CX	141	LEU
1	CX	151	LYS
1	CX	173	LYS
1	CX	175	GLN
1	CX	176	ARG
1	CX	177	LEU
1	CX	185	LEU
1	CX	186	LEU
1	CX	190	ASN
1	CX	198	SER
1	CX	204	SER
1	CX	208	SER
1	CX	217	GLU
1	CX	246	THR
1	CX	288	ASN
1	CX	316	SER
1	CX	337	GLU
1	BY	57	LEU
1	BY	58	SER
1	BY	63	ILE
1	BY	67	VAL
1	BY	68	LEU
1	BY	78	VAL

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Mol	Chain	Res	Type
1	BY	79	VAL
1	BY	80	VAL
1	BY	85	VAL
1	BY	88	LEU
1	BY	92	LEU
1	BY	100	GLN
1	BY	101	ARG
1	BY	104	VAL
1	BY	105	GLU
1	BY	111	ILE
1	BY	128	LEU
1	BY	134	ASN
1	BY	145	ARG
1	BY	156	ARG
1	BY	165	THR
1	BY	167	LEU
1	BY	173	LYS
1	BY	183	LEU
1	BY	184	ILE
1	BY	185	LEU
1	BY	191	ASN
1	BY	196	ASN
1	BY	198	SER
1	BY	207	LEU
1	BY	212	LEU
1	BY	271	THR
1	BY	319	GLN
1	AY	55	VAL
1	AY	58	SER
1	AY	62	ARG
1	AY	67	VAL
1	AY	72	THR
1	AY	74	THR
1	AY	75	ASP
1	AY	87	ASP
1	AY	111	ILE
1	AY	118	ASN
1	AY	119	THR
1	AY	124	VAL
1	AY	128	LEU
1	AY	137	THR
1	AY	141	LEU

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Mol	Chain	Res	Type
1	AY	142	GLN
1	AY	149	VAL
1	AY	156	ARG
1	AY	157	THR
1	AY	159	ARG
1	AY	162	TYR
1	AY	163	THR
1	AY	165	THR
1	AY	167	LEU
1	AY	170	SER
1	AY	176	ARG
1	AY	183	LEU
1	AY	186	LEU
1	AY	192	THR
1	AY	196	ASN
1	AY	208	SER
1	AY	211	SER
1	AY	225	GLN
1	AY	236	ASN
1	AY	253	ASP
1	AY	264	SER
1	AY	271	THR
1	AY	312	VAL
1	AY	317	ASP
1	CY	35	THR
1	CY	43	SER
1	CY	54	ASP
1	CY	63	ILE
1	CY	72	THR
1	CY	74	THR
1	CY	75	ASP
1	CY	87	ASP
1	CY	101	ARG
1	CY	106	THR
1	CY	112	GLN
1	CY	114	MET
1	CY	137	THR
1	CY	141	LEU
1	CY	151	LYS
1	CY	173	LYS
1	CY	175	GLN
1	CY	176	ARG

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Mol	Chain	Res	Type
1	CY	177	LEU
1	CY	185	LEU
1	CY	186	LEU
1	CY	198	SER
1	CY	204	SER
1	CY	208	SER
1	CY	217	GLU
1	CY	288	ASN
1	CY	316	SER
1	CY	337	GLU
1	BZ	57	LEU
1	BZ	58	SER
1	BZ	63	ILE
1	BZ	67	VAL
1	BZ	68	LEU
1	BZ	78	VAL
1	BZ	79	VAL
1	BZ	80	VAL
1	BZ	85	VAL
1	BZ	88	LEU
1	BZ	92	LEU
1	BZ	100	GLN
1	BZ	101	ARG
1	BZ	104	VAL
1	BZ	105	GLU
1	BZ	111	ILE
1	BZ	134	ASN
1	BZ	145	ARG
1	BZ	156	ARG
1	BZ	165	THR
1	BZ	167	LEU
1	BZ	173	LYS
1	BZ	183	LEU
1	BZ	184	ILE
1	BZ	185	LEU
1	BZ	196	ASN
1	BZ	198	SER
1	BZ	202	ARG
1	BZ	207	LEU
1	BZ	212	LEU
1	BZ	271	THR
1	BZ	319	GLN

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Mol	Chain	Res	Type
1	AZ	55	VAL
1	AZ	58	SER
1	AZ	62	ARG
1	AZ	67	VAL
1	AZ	72	THR
1	AZ	74	THR
1	AZ	75	ASP
1	AZ	87	ASP
1	AZ	111	ILE
1	AZ	118	ASN
1	AZ	124	VAL
1	AZ	128	LEU
1	AZ	137	THR
1	AZ	141	LEU
1	AZ	142	GLN
1	AZ	144	THR
1	AZ	149	VAL
1	AZ	159	ARG
1	AZ	163	THR
1	AZ	165	THR
1	AZ	167	LEU
1	AZ	170	SER
1	AZ	176	ARG
1	AZ	183	LEU
1	AZ	186	LEU
1	AZ	196	ASN
1	AZ	208	SER
1	AZ	211	SER
1	AZ	225	GLN
1	AZ	236	ASN
1	AZ	264	SER
1	AZ	271	THR
1	AZ	312	VAL
1	AZ	315	TYR
1	AZ	317	ASP
1	CZ	35	THR
1	CZ	43	SER
1	CZ	54	ASP
1	CZ	63	ILE
1	CZ	72	THR
1	CZ	74	THR
1	CZ	75	ASP

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Mol	Chain	Res	Type
1	CZ	87	ASP
1	CZ	101	ARG
1	CZ	112	GLN
1	CZ	114	MET
1	CZ	137	THR
1	CZ	141	LEU
1	CZ	151	LYS
1	CZ	173	LYS
1	CZ	175	GLN
1	CZ	176	ARG
1	CZ	177	LEU
1	CZ	185	LEU
1	CZ	186	LEU
1	CZ	190	ASN
1	CZ	198	SER
1	CZ	204	SER
1	CZ	208	SER
1	CZ	217	GLU
1	CZ	288	ASN
1	CZ	316	SER
1	CZ	337	GLU
1	Ba	57	LEU
1	Ba	58	SER
1	Ba	63	ILE
1	Ba	67	VAL
1	Ba	68	LEU
1	Ba	78	VAL
1	Ba	79	VAL
1	Ba	80	VAL
1	Ba	85	VAL
1	Ba	88	LEU
1	Ba	92	LEU
1	Ba	100	GLN
1	Ba	101	ARG
1	Ba	104	VAL
1	Ba	105	GLU
1	Ba	111	ILE
1	Ba	128	LEU
1	Ba	134	ASN
1	Ba	145	ARG
1	Ba	156	ARG
1	Ba	165	THR

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Mol	Chain	Res	Type
1	Ba	167	LEU
1	Ba	173	LYS
1	Ba	176	ARG
1	Ba	183	LEU
1	Ba	184	ILE
1	Ba	191	ASN
1	Ba	196	ASN
1	Ba	198	SER
1	Ba	202	ARG
1	Ba	207	LEU
1	Ba	212	LEU
1	Ba	271	THR
1	Ba	319	GLN
1	Aa	55	VAL
1	Aa	58	SER
1	Aa	62	ARG
1	Aa	67	VAL
1	Aa	72	THR
1	Aa	74	THR
1	Aa	75	ASP
1	Aa	83	THR
1	Aa	87	ASP
1	Aa	111	ILE
1	Aa	114	MET
1	Aa	119	THR
1	Aa	124	VAL
1	Aa	128	LEU
1	Aa	137	THR
1	Aa	141	LEU
1	Aa	142	GLN
1	Aa	149	VAL
1	Aa	156	ARG
1	Aa	157	THR
1	Aa	159	ARG
1	Aa	162	TYR
1	Aa	163	THR
1	Aa	165	THR
1	Aa	167	LEU
1	Aa	170	SER
1	Aa	176	ARG
1	Aa	183	LEU
1	Aa	186	LEU

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Mol	Chain	Res	Type
1	Aa	192	THR
1	Aa	196	ASN
1	Aa	208	SER
1	Aa	211	SER
1	Aa	212	LEU
1	Aa	225	GLN
1	Aa	236	ASN
1	Aa	253	ASP
1	Aa	264	SER
1	Aa	271	THR
1	Aa	312	VAL
1	Aa	315	TYR
1	Aa	317	ASP
1	Ca	35	THR
1	Ca	43	SER
1	Ca	54	ASP
1	Ca	72	THR
1	Ca	74	THR
1	Ca	75	ASP
1	Ca	87	ASP
1	Ca	101	ARG
1	Ca	106	THR
1	Ca	112	GLN
1	Ca	114	MET
1	Ca	137	THR
1	Ca	141	LEU
1	Ca	151	LYS
1	Ca	173	LYS
1	Ca	175	GLN
1	Ca	176	ARG
1	Ca	177	LEU
1	Ca	185	LEU
1	Ca	186	LEU
1	Ca	198	SER
1	Ca	204	SER
1	Ca	208	SER
1	Ca	217	GLU
1	Ca	288	ASN
1	Ca	316	SER
1	Ca	337	GLU
1	Bb	57	LEU
1	Bb	58	SER

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Mol	Chain	Res	Type
1	Bb	63	ILE
1	Bb	67	VAL
1	Bb	68	LEU
1	Bb	78	VAL
1	Bb	79	VAL
1	Bb	80	VAL
1	Bb	85	VAL
1	Bb	88	LEU
1	Bb	92	LEU
1	Bb	100	GLN
1	Bb	101	ARG
1	Bb	104	VAL
1	Bb	105	GLU
1	Bb	111	ILE
1	Bb	128	LEU
1	Bb	134	ASN
1	Bb	145	ARG
1	Bb	156	ARG
1	Bb	165	THR
1	Bb	167	LEU
1	Bb	173	LYS
1	Bb	183	LEU
1	Bb	184	ILE
1	Bb	185	LEU
1	Bb	191	ASN
1	Bb	196	ASN
1	Bb	198	SER
1	Bb	202	ARG
1	Bb	207	LEU
1	Bb	212	LEU
1	Bb	271	THR
1	Bb	319	GLN
1	Ab	55	VAL
1	Ab	58	SER
1	Ab	62	ARG
1	Ab	67	VAL
1	Ab	72	THR
1	Ab	74	THR
1	Ab	75	ASP
1	Ab	83	THR
1	Ab	87	ASP
1	Ab	111	ILE

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Mol	Chain	Res	Type
1	Ab	118	ASN
1	Ab	119	THR
1	Ab	124	VAL
1	Ab	128	LEU
1	Ab	137	THR
1	Ab	141	LEU
1	Ab	142	GLN
1	Ab	144	THR
1	Ab	149	VAL
1	Ab	156	ARG
1	Ab	157	THR
1	Ab	159	ARG
1	Ab	162	TYR
1	Ab	163	THR
1	Ab	165	THR
1	Ab	167	LEU
1	Ab	170	SER
1	Ab	176	ARG
1	Ab	183	LEU
1	Ab	186	LEU
1	Ab	192	THR
1	Ab	196	ASN
1	Ab	208	SER
1	Ab	211	SER
1	Ab	212	LEU
1	Ab	225	GLN
1	Ab	236	ASN
1	Ab	253	ASP
1	Ab	264	SER
1	Ab	271	THR
1	Ab	312	VAL
1	Ab	315	TYR
1	Ab	317	ASP
1	Cb	35	THR
1	Cb	43	SER
1	Cb	54	ASP
1	Cb	63	ILE
1	Cb	72	THR
1	Cb	74	THR
1	Cb	75	ASP
1	Cb	87	ASP
1	Cb	101	ARG

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Mol	Chain	Res	Type
1	Cb	112	GLN
1	Cb	114	MET
1	Cb	137	THR
1	Cb	141	LEU
1	Cb	151	LYS
1	Cb	173	LYS
1	Cb	175	GLN
1	Cb	176	ARG
1	Cb	177	LEU
1	Cb	185	LEU
1	Cb	186	LEU
1	Cb	190	ASN
1	Cb	198	SER
1	Cb	204	SER
1	Cb	208	SER
1	Cb	217	GLU
1	Cb	246	THR
1	Cb	288	ASN
1	Cb	316	SER
1	Cb	337	GLU
1	Bc	57	LEU
1	Bc	58	SER
1	Bc	63	ILE
1	Bc	67	VAL
1	Bc	68	LEU
1	Bc	78	VAL
1	Bc	79	VAL
1	Bc	80	VAL
1	Bc	85	VAL
1	Bc	88	LEU
1	Bc	92	LEU
1	Bc	100	GLN
1	Bc	101	ARG
1	Bc	104	VAL
1	Bc	105	GLU
1	Bc	111	ILE
1	Bc	128	LEU
1	Bc	134	ASN
1	Bc	145	ARG
1	Bc	156	ARG
1	Bc	165	THR
1	Bc	167	LEU

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Mol	Chain	Res	Type
1	Bc	173	LYS
1	Bc	176	ARG
1	Bc	183	LEU
1	Bc	184	ILE
1	Bc	185	LEU
1	Bc	191	ASN
1	Bc	196	ASN
1	Bc	198	SER
1	Bc	202	ARG
1	Bc	207	LEU
1	Bc	212	LEU
1	Bc	271	THR
1	Bc	319	GLN
1	Ac	55	VAL
1	Ac	58	SER
1	Ac	62	ARG
1	Ac	67	VAL
1	Ac	72	THR
1	Ac	74	THR
1	Ac	75	ASP
1	Ac	87	ASP
1	Ac	111	ILE
1	Ac	114	MET
1	Ac	118	ASN
1	Ac	119	THR
1	Ac	124	VAL
1	Ac	128	LEU
1	Ac	137	THR
1	Ac	141	LEU
1	Ac	142	GLN
1	Ac	149	VAL
1	Ac	156	ARG
1	Ac	159	ARG
1	Ac	162	TYR
1	Ac	163	THR
1	Ac	165	THR
1	Ac	167	LEU
1	Ac	170	SER
1	Ac	176	ARG
1	Ac	183	LEU
1	Ac	186	LEU
1	Ac	192	THR

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Mol	Chain	Res	Type
1	Ac	196	ASN
1	Ac	208	SER
1	Ac	211	SER
1	Ac	225	GLN
1	Ac	236	ASN
1	Ac	253	ASP
1	Ac	264	SER
1	Ac	271	THR
1	Ac	312	VAL
1	Ac	315	TYR
1	Ac	317	ASP
1	Cc	35	THR
1	Cc	43	SER
1	Cc	54	ASP
1	Cc	63	ILE
1	Cc	72	THR
1	Cc	74	THR
1	Cc	75	ASP
1	Cc	87	ASP
1	Cc	101	ARG
1	Cc	106	THR
1	Cc	112	GLN
1	Cc	114	MET
1	Cc	137	THR
1	Cc	141	LEU
1	Cc	151	LYS
1	Cc	173	LYS
1	Cc	175	GLN
1	Cc	176	ARG
1	Cc	177	LEU
1	Cc	185	LEU
1	Cc	186	LEU
1	Cc	190	ASN
1	Cc	198	SER
1	Cc	204	SER
1	Cc	208	SER
1	Cc	217	GLU
1	Cc	288	ASN
1	Cc	316	SER
1	Cc	337	GLU
1	Bd	57	LEU
1	Bd	58	SER

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Mol	Chain	Res	Type
1	Bd	63	ILE
1	Bd	67	VAL
1	Bd	68	LEU
1	Bd	78	VAL
1	Bd	79	VAL
1	Bd	80	VAL
1	Bd	85	VAL
1	Bd	88	LEU
1	Bd	92	LEU
1	Bd	100	GLN
1	Bd	101	ARG
1	Bd	104	VAL
1	Bd	105	GLU
1	Bd	111	ILE
1	Bd	128	LEU
1	Bd	134	ASN
1	Bd	145	ARG
1	Bd	156	ARG
1	Bd	165	THR
1	Bd	167	LEU
1	Bd	173	LYS
1	Bd	183	LEU
1	Bd	184	ILE
1	Bd	185	LEU
1	Bd	191	ASN
1	Bd	196	ASN
1	Bd	198	SER
1	Bd	202	ARG
1	Bd	207	LEU
1	Bd	212	LEU
1	Bd	271	THR
1	Bd	319	GLN
1	Ad	55	VAL
1	Ad	58	SER
1	Ad	62	ARG
1	Ad	67	VAL
1	Ad	72	THR
1	Ad	74	THR
1	Ad	75	ASP
1	Ad	87	ASP
1	Ad	111	ILE
1	Ad	118	ASN

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Mol	Chain	Res	Type
1	Ad	124	VAL
1	Ad	128	LEU
1	Ad	137	THR
1	Ad	141	LEU
1	Ad	142	GLN
1	Ad	149	VAL
1	Ad	156	ARG
1	Ad	159	ARG
1	Ad	162	TYR
1	Ad	163	THR
1	Ad	165	THR
1	Ad	167	LEU
1	Ad	170	SER
1	Ad	176	ARG
1	Ad	183	LEU
1	Ad	186	LEU
1	Ad	196	ASN
1	Ad	208	SER
1	Ad	211	SER
1	Ad	225	GLN
1	Ad	236	ASN
1	Ad	264	SER
1	Ad	271	THR
1	Ad	312	VAL
1	Ad	317	ASP
1	Cd	35	THR
1	Cd	43	SER
1	Cd	54	ASP
1	Cd	63	ILE
1	Cd	72	THR
1	Cd	74	THR
1	Cd	75	ASP
1	Cd	87	ASP
1	Cd	101	ARG
1	Cd	112	GLN
1	Cd	114	MET
1	Cd	137	THR
1	Cd	141	LEU
1	Cd	151	LYS
1	Cd	173	LYS
1	Cd	175	GLN
1	Cd	176	ARG

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Mol	Chain	Res	Type
1	Cd	177	LEU
1	Cd	185	LEU
1	Cd	186	LEU
1	Cd	190	ASN
1	Cd	198	SER
1	Cd	204	SER
1	Cd	208	SER
1	Cd	217	GLU
1	Cd	246	THR
1	Cd	288	ASN
1	Cd	316	SER
1	Cd	337	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (631) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	100	GLN
1	BA	134	ASN
1	BA	136	HIS
1	BA	142	GLN
1	BA	190	ASN
1	BA	191	ASN
1	BA	196	ASN
1	BA	214	ASN
1	BA	225	GLN
1	BA	236	ASN
1	AA	65	GLN
1	AA	94	HIS
1	AA	134	ASN
1	AA	142	GLN
1	AA	196	ASN
1	AA	225	GLN
1	AA	258	GLN
1	AA	319	GLN
1	CA	56	HIS
1	CA	94	HIS
1	CA	112	GLN
1	CA	175	GLN
1	CA	190	ASN
1	CA	230	ASN
1	BB	100	GLN
1	BB	134	ASN

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Mol	Chain	Res	Type
1	BB	142	GLN
1	BB	190	ASN
1	BB	191	ASN
1	BB	214	ASN
1	BB	236	ASN
1	AB	65	GLN
1	AB	134	ASN
1	AB	142	GLN
1	AB	196	ASN
1	AB	319	GLN
1	CB	56	HIS
1	CB	94	HIS
1	CB	112	GLN
1	CB	175	GLN
1	CB	190	ASN
1	CB	258	GLN
1	CB	281	HIS
1	BC	100	GLN
1	BC	112	GLN
1	BC	142	GLN
1	BC	190	ASN
1	BC	191	ASN
1	BC	196	ASN
1	BC	225	GLN
1	BC	236	ASN
1	AC	65	GLN
1	AC	134	ASN
1	AC	142	GLN
1	AC	196	ASN
1	AC	225	GLN
1	AC	258	GLN
1	AC	319	GLN
1	CC	56	HIS
1	CC	94	HIS
1	CC	112	GLN
1	CC	175	GLN
1	CC	190	ASN
1	CC	230	ASN
1	BD	65	GLN
1	BD	100	GLN
1	BD	134	ASN
1	BD	136	HIS

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Mol	Chain	Res	Type
1	BD	142	GLN
1	BD	190	ASN
1	BD	191	ASN
1	BD	196	ASN
1	BD	214	ASN
1	BD	225	GLN
1	BD	236	ASN
1	AD	94	HIS
1	AD	134	ASN
1	AD	142	GLN
1	AD	196	ASN
1	AD	225	GLN
1	AD	319	GLN
1	CD	56	HIS
1	CD	94	HIS
1	CD	112	GLN
1	CD	175	GLN
1	CD	190	ASN
1	CD	230	ASN
1	BE	100	GLN
1	BE	112	GLN
1	BE	136	HIS
1	BE	142	GLN
1	BE	190	ASN
1	BE	191	ASN
1	BE	196	ASN
1	BE	225	GLN
1	AE	65	GLN
1	AE	94	HIS
1	AE	134	ASN
1	AE	142	GLN
1	AE	196	ASN
1	AE	225	GLN
1	AE	319	GLN
1	AE	322	GLN
1	CE	56	HIS
1	CE	112	GLN
1	CE	175	GLN
1	CE	190	ASN
1	CE	230	ASN
1	BF	100	GLN
1	BF	142	GLN

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Mol	Chain	Res	Type
1	BF	190	ASN
1	BF	191	ASN
1	BF	196	ASN
1	BF	225	GLN
1	BF	236	ASN
1	AF	65	GLN
1	AF	94	HIS
1	AF	134	ASN
1	AF	142	GLN
1	AF	196	ASN
1	AF	225	GLN
1	AF	319	GLN
1	CF	56	HIS
1	CF	112	GLN
1	CF	175	GLN
1	CF	190	ASN
1	CF	230	ASN
1	BG	65	GLN
1	BG	100	GLN
1	BG	134	ASN
1	BG	136	HIS
1	BG	142	GLN
1	BG	190	ASN
1	BG	191	ASN
1	BG	196	ASN
1	BG	225	GLN
1	BG	236	ASN
1	AG	65	GLN
1	AG	94	HIS
1	AG	118	ASN
1	AG	134	ASN
1	AG	196	ASN
1	AG	225	GLN
1	AG	319	GLN
1	CG	56	HIS
1	CG	94	HIS
1	CG	112	GLN
1	CG	175	GLN
1	CG	190	ASN
1	CG	230	ASN
1	BH	94	HIS
1	BH	100	GLN

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Mol	Chain	Res	Type
1	BH	112	GLN
1	BH	134	ASN
1	BH	136	HIS
1	BH	142	GLN
1	BH	190	ASN
1	BH	191	ASN
1	BH	196	ASN
1	BH	225	GLN
1	BH	236	ASN
1	AH	65	GLN
1	AH	94	HIS
1	AH	118	ASN
1	AH	134	ASN
1	AH	142	GLN
1	AH	196	ASN
1	AH	225	GLN
1	AH	319	GLN
1	CH	56	HIS
1	CH	94	HIS
1	CH	112	GLN
1	CH	175	GLN
1	CH	190	ASN
1	CH	230	ASN
1	CH	258	GLN
1	CH	281	HIS
1	BI	65	GLN
1	BI	100	GLN
1	BI	112	GLN
1	BI	134	ASN
1	BI	142	GLN
1	BI	190	ASN
1	BI	191	ASN
1	BI	196	ASN
1	BI	214	ASN
1	BI	225	GLN
1	BI	236	ASN
1	AI	65	GLN
1	AI	94	HIS
1	AI	134	ASN
1	AI	142	GLN
1	AI	196	ASN
1	AI	225	GLN

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Mol	Chain	Res	Type
1	AI	319	GLN
1	CI	56	HIS
1	CI	94	HIS
1	CI	112	GLN
1	CI	175	GLN
1	CI	190	ASN
1	CI	230	ASN
1	BJ	65	GLN
1	BJ	100	GLN
1	BJ	112	GLN
1	BJ	134	ASN
1	BJ	142	GLN
1	BJ	190	ASN
1	BJ	191	ASN
1	BJ	196	ASN
1	BJ	225	GLN
1	AJ	65	GLN
1	AJ	94	HIS
1	AJ	134	ASN
1	AJ	142	GLN
1	AJ	196	ASN
1	AJ	225	GLN
1	AJ	319	GLN
1	CJ	56	HIS
1	CJ	94	HIS
1	CJ	112	GLN
1	CJ	175	GLN
1	CJ	190	ASN
1	CJ	230	ASN
1	CJ	258	GLN
1	CJ	281	HIS
1	BK	100	GLN
1	BK	112	GLN
1	BK	134	ASN
1	BK	190	ASN
1	BK	191	ASN
1	BK	225	GLN
1	BK	236	ASN
1	AK	65	GLN
1	AK	94	HIS
1	AK	134	ASN
1	AK	196	ASN

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Mol	Chain	Res	Type
1	AK	225	GLN
1	CK	56	HIS
1	CK	112	GLN
1	CK	175	GLN
1	CK	190	ASN
1	CK	230	ASN
1	BL	100	GLN
1	BL	134	ASN
1	BL	190	ASN
1	BL	191	ASN
1	BL	196	ASN
1	BL	214	ASN
1	BL	225	GLN
1	BL	236	ASN
1	AL	94	HIS
1	AL	134	ASN
1	AL	142	GLN
1	AL	196	ASN
1	AL	225	GLN
1	AL	319	GLN
1	CL	56	HIS
1	CL	112	GLN
1	CL	175	GLN
1	CL	190	ASN
1	CL	230	ASN
1	BM	100	GLN
1	BM	142	GLN
1	BM	190	ASN
1	BM	191	ASN
1	BM	196	ASN
1	BM	214	ASN
1	BM	236	ASN
1	AM	134	ASN
1	AM	196	ASN
1	AM	225	GLN
1	AM	319	GLN
1	CM	56	HIS
1	CM	94	HIS
1	CM	112	GLN
1	CM	175	GLN
1	CM	190	ASN
1	CM	230	ASN

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Mol	Chain	Res	Type
1	BN	100	GLN
1	BN	134	ASN
1	BN	190	ASN
1	BN	191	ASN
1	BN	214	ASN
1	BN	225	GLN
1	BN	236	ASN
1	AN	65	GLN
1	AN	94	HIS
1	AN	134	ASN
1	AN	142	GLN
1	AN	196	ASN
1	AN	225	GLN
1	AN	319	GLN
1	CN	56	HIS
1	CN	112	GLN
1	CN	175	GLN
1	CN	190	ASN
1	CN	230	ASN
1	BO	65	GLN
1	BO	100	GLN
1	BO	112	GLN
1	BO	134	ASN
1	BO	142	GLN
1	BO	190	ASN
1	BO	191	ASN
1	BO	196	ASN
1	BO	225	GLN
1	BO	236	ASN
1	AO	65	GLN
1	AO	94	HIS
1	AO	134	ASN
1	AO	196	ASN
1	AO	225	GLN
1	AO	319	GLN
1	CO	56	HIS
1	CO	94	HIS
1	CO	112	GLN
1	CO	175	GLN
1	CO	190	ASN
1	CO	230	ASN
1	BP	100	GLN

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Mol	Chain	Res	Type
1	BP	134	ASN
1	BP	142	GLN
1	BP	190	ASN
1	BP	191	ASN
1	BP	196	ASN
1	BP	225	GLN
1	BP	236	ASN
1	AP	65	GLN
1	AP	94	HIS
1	AP	134	ASN
1	AP	142	GLN
1	AP	196	ASN
1	AP	319	GLN
1	CP	56	HIS
1	CP	94	HIS
1	CP	112	GLN
1	CP	175	GLN
1	CP	190	ASN
1	CP	230	ASN
1	BQ	65	GLN
1	BQ	100	GLN
1	BQ	142	GLN
1	BQ	190	ASN
1	BQ	191	ASN
1	BQ	196	ASN
1	BQ	214	ASN
1	BQ	225	GLN
1	AQ	94	HIS
1	AQ	134	ASN
1	AQ	142	GLN
1	AQ	196	ASN
1	AQ	225	GLN
1	AQ	258	GLN
1	AQ	319	GLN
1	CQ	56	HIS
1	CQ	94	HIS
1	CQ	112	GLN
1	CQ	175	GLN
1	CQ	190	ASN
1	CQ	230	ASN
1	CQ	281	HIS
1	BR	100	GLN

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Mol	Chain	Res	Type
1	BR	134	ASN
1	BR	136	HIS
1	BR	142	GLN
1	BR	190	ASN
1	BR	191	ASN
1	BR	196	ASN
1	BR	214	ASN
1	BR	225	GLN
1	AR	94	HIS
1	AR	134	ASN
1	AR	142	GLN
1	AR	196	ASN
1	AR	225	GLN
1	AR	319	GLN
1	CR	56	HIS
1	CR	112	GLN
1	CR	175	GLN
1	CR	190	ASN
1	CR	196	ASN
1	CR	230	ASN
1	BS	65	GLN
1	BS	100	GLN
1	BS	134	ASN
1	BS	136	HIS
1	BS	190	ASN
1	BS	191	ASN
1	BS	196	ASN
1	BS	225	GLN
1	BS	236	ASN
1	AS	65	GLN
1	AS	94	HIS
1	AS	134	ASN
1	AS	196	ASN
1	AS	225	GLN
1	AS	319	GLN
1	CS	56	HIS
1	CS	112	GLN
1	CS	118	ASN
1	CS	175	GLN
1	CS	190	ASN
1	CS	230	ASN
1	BT	100	GLN

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Mol	Chain	Res	Type
1	BT	112	GLN
1	BT	134	ASN
1	BT	142	GLN
1	BT	190	ASN
1	BT	191	ASN
1	BT	196	ASN
1	BT	214	ASN
1	BT	225	GLN
1	BT	236	ASN
1	AT	65	GLN
1	AT	134	ASN
1	AT	142	GLN
1	AT	196	ASN
1	AT	225	GLN
1	AT	319	GLN
1	CT	56	HIS
1	CT	112	GLN
1	CT	175	GLN
1	CT	190	ASN
1	CT	196	ASN
1	CT	230	ASN
1	BU	100	GLN
1	BU	112	GLN
1	BU	134	ASN
1	BU	136	HIS
1	BU	142	GLN
1	BU	190	ASN
1	BU	191	ASN
1	BU	196	ASN
1	BU	236	ASN
1	AU	65	GLN
1	AU	94	HIS
1	AU	134	ASN
1	AU	196	ASN
1	AU	225	GLN
1	AU	319	GLN
1	CU	56	HIS
1	CU	112	GLN
1	CU	175	GLN
1	CU	190	ASN
1	CU	230	ASN
1	BV	65	GLN

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Mol	Chain	Res	Type
1	BV	100	GLN
1	BV	134	ASN
1	BV	136	HIS
1	BV	142	GLN
1	BV	190	ASN
1	BV	191	ASN
1	BV	196	ASN
1	BV	214	ASN
1	BV	225	GLN
1	BV	236	ASN
1	AV	65	GLN
1	AV	94	HIS
1	AV	134	ASN
1	AV	142	GLN
1	AV	196	ASN
1	AV	225	GLN
1	AV	319	GLN
1	CV	56	HIS
1	CV	94	HIS
1	CV	112	GLN
1	CV	175	GLN
1	CV	190	ASN
1	CV	230	ASN
1	BW	100	GLN
1	BW	190	ASN
1	BW	191	ASN
1	BW	196	ASN
1	BW	214	ASN
1	BW	225	GLN
1	BW	236	ASN
1	AW	65	GLN
1	AW	134	ASN
1	AW	142	GLN
1	AW	196	ASN
1	AW	225	GLN
1	AW	319	GLN
1	CW	56	HIS
1	CW	112	GLN
1	CW	175	GLN
1	CW	190	ASN
1	CW	230	ASN
1	BX	100	GLN

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Mol	Chain	Res	Type
1	BX	112	GLN
1	BX	134	ASN
1	BX	142	GLN
1	BX	190	ASN
1	BX	191	ASN
1	BX	196	ASN
1	BX	236	ASN
1	AX	65	GLN
1	AX	94	HIS
1	AX	134	ASN
1	AX	142	GLN
1	AX	196	ASN
1	AX	225	GLN
1	AX	319	GLN
1	CX	56	HIS
1	CX	94	HIS
1	CX	112	GLN
1	CX	175	GLN
1	CX	190	ASN
1	CX	230	ASN
1	BY	65	GLN
1	BY	100	GLN
1	BY	118	ASN
1	BY	134	ASN
1	BY	142	GLN
1	BY	190	ASN
1	BY	191	ASN
1	BY	196	ASN
1	BY	214	ASN
1	BY	225	GLN
1	BY	236	ASN
1	AY	65	GLN
1	AY	94	HIS
1	AY	134	ASN
1	AY	142	GLN
1	AY	196	ASN
1	AY	225	GLN
1	AY	319	GLN
1	CY	56	HIS
1	CY	94	HIS
1	CY	112	GLN
1	CY	175	GLN

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Mol	Chain	Res	Type
1	CY	190	ASN
1	CY	230	ASN
1	BZ	100	GLN
1	BZ	112	GLN
1	BZ	134	ASN
1	BZ	136	HIS
1	BZ	142	GLN
1	BZ	190	ASN
1	BZ	191	ASN
1	BZ	196	ASN
1	BZ	214	ASN
1	AZ	65	GLN
1	AZ	134	ASN
1	AZ	142	GLN
1	AZ	196	ASN
1	AZ	225	GLN
1	AZ	319	GLN
1	CZ	56	HIS
1	CZ	94	HIS
1	CZ	112	GLN
1	CZ	175	GLN
1	CZ	190	ASN
1	CZ	230	ASN
1	Ba	65	GLN
1	Ba	100	GLN
1	Ba	134	ASN
1	Ba	142	GLN
1	Ba	190	ASN
1	Ba	191	ASN
1	Ba	196	ASN
1	Ba	225	GLN
1	Ba	236	ASN
1	Aa	65	GLN
1	Aa	94	HIS
1	Aa	134	ASN
1	Aa	142	GLN
1	Aa	196	ASN
1	Aa	225	GLN
1	Aa	319	GLN
1	Ca	56	HIS
1	Ca	94	HIS
1	Ca	112	GLN

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Mol	Chain	Res	Type
1	Ca	175	GLN
1	Ca	230	ASN
1	Bb	100	GLN
1	Bb	112	GLN
1	Bb	142	GLN
1	Bb	190	ASN
1	Bb	191	ASN
1	Bb	196	ASN
1	Bb	225	GLN
1	Ab	94	HIS
1	Ab	134	ASN
1	Ab	196	ASN
1	Ab	225	GLN
1	Ab	319	GLN
1	Ab	322	GLN
1	Cb	56	HIS
1	Cb	94	HIS
1	Cb	112	GLN
1	Cb	175	GLN
1	Cb	190	ASN
1	Cb	230	ASN
1	Cb	319	GLN
1	Bc	100	GLN
1	Bc	134	ASN
1	Bc	142	GLN
1	Bc	190	ASN
1	Bc	191	ASN
1	Bc	196	ASN
1	Bc	225	GLN
1	Bc	236	ASN
1	Ac	94	HIS
1	Ac	134	ASN
1	Ac	142	GLN
1	Ac	196	ASN
1	Ac	225	GLN
1	Ac	319	GLN
1	Cc	56	HIS
1	Cc	94	HIS
1	Cc	112	GLN
1	Cc	175	GLN
1	Cc	190	ASN
1	Cc	230	ASN

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Mol	Chain	Res	Type
1	Bd	100	GLN
1	Bd	134	ASN
1	Bd	190	ASN
1	Bd	191	ASN
1	Bd	196	ASN
1	Bd	225	GLN
1	Ad	134	ASN
1	Ad	142	GLN
1	Ad	196	ASN
1	Ad	225	GLN
1	Ad	258	GLN
1	Ad	319	GLN
1	Cd	56	HIS
1	Cd	112	GLN
1	Cd	175	GLN
1	Cd	190	ASN
1	Cd	230	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

Of 90 ligands modelled in this entry, 90 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AA	287/338 (84%)	0.64	26 (9%) 15 11	44, 93, 184, 235	0
1	AB	287/338 (84%)	0.85	43 (14%) 5 5	31, 79, 239, 363	0
1	AC	287/338 (84%)	1.03	65 (22%) 2 2	32, 75, 244, 339	0
1	AD	287/338 (84%)	0.51	18 (6%) 26 16	40, 82, 155, 215	0
1	AE	287/338 (84%)	0.73	26 (9%) 15 11	44, 88, 179, 251	0
1	AF	287/338 (84%)	0.56	19 (6%) 24 15	37, 80, 176, 225	0
1	AG	287/338 (84%)	0.73	28 (9%) 13 10	42, 89, 208, 293	0
1	AH	287/338 (84%)	0.94	48 (16%) 4 5	39, 86, 244, 334	0
1	AI	287/338 (84%)	1.09	61 (21%) 2 3	38, 93, 255, 333	0
1	AJ	287/338 (84%)	0.52	18 (6%) 26 16	36, 75, 146, 223	0
1	AK	287/338 (84%)	0.60	16 (5%) 30 18	31, 63, 120, 191	0
1	AL	287/338 (84%)	0.51	16 (5%) 30 18	32, 69, 138, 194	0
1	AM	287/338 (84%)	1.06	49 (17%) 4 4	41, 91, 249, 306	0
1	AN	287/338 (84%)	0.71	27 (9%) 14 10	41, 85, 200, 285	0
1	AO	287/338 (84%)	0.65	26 (9%) 15 11	36, 83, 203, 294	0
1	AP	287/338 (84%)	0.80	27 (9%) 14 10	41, 81, 187, 253	0
1	AQ	287/338 (84%)	0.57	26 (9%) 15 11	46, 83, 172, 212	0
1	AR	287/338 (84%)	0.47	13 (4%) 38 21	40, 77, 141, 197	0
1	AS	287/338 (84%)	0.54	21 (7%) 21 14	28, 78, 171, 271	0
1	AT	287/338 (84%)	0.50	16 (5%) 30 18	46, 89, 169, 226	0
1	AU	287/338 (84%)	0.81	35 (12%) 8 7	32, 86, 200, 301	0
1	AV	287/338 (84%)	0.75	34 (11%) 9 8	45, 90, 183, 234	0
1	AW	287/338 (84%)	0.47	14 (4%) 35 20	37, 72, 129, 194	0
1	AX	287/338 (84%)	0.71	31 (10%) 11 9	37, 79, 185, 294	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AY	287/338 (84%)	0.40	12 (4%) 40 22	37, 77, 153, 206	0
1	AZ	287/338 (84%)	0.60	14 (4%) 35 20	39, 84, 178, 279	0
1	Aa	287/338 (84%)	0.67	23 (8%) 18 13	41, 90, 182, 222	0
1	Ab	287/338 (84%)	0.90	55 (19%) 3 3	38, 81, 245, 357	0
1	Ac	287/338 (84%)	0.79	42 (14%) 6 6	45, 82, 169, 236	0
1	Ad	287/338 (84%)	0.76	24 (8%) 17 12	43, 77, 141, 218	0
1	BA	286/338 (84%)	0.80	33 (11%) 9 8	37, 88, 199, 239	0
1	BB	286/338 (84%)	1.16	80 (27%) 1 1	25, 71, 229, 336	0
1	BC	286/338 (84%)	0.86	47 (16%) 4 5	30, 79, 265, 341	0
1	BD	286/338 (84%)	0.68	23 (8%) 18 13	34, 79, 172, 283	0
1	BE	286/338 (84%)	0.77	37 (12%) 7 7	40, 81, 198, 285	0
1	BF	286/338 (84%)	0.79	42 (14%) 6 5	32, 75, 188, 271	0
1	BG	286/338 (84%)	1.00	59 (20%) 2 3	39, 81, 214, 307	0
1	BH	286/338 (84%)	1.30	84 (29%) 1 1	36, 78, 245, 329	0
1	BI	286/338 (84%)	1.21	81 (28%) 1 1	35, 82, 280, 360	0
1	BJ	286/338 (84%)	0.54	24 (8%) 17 12	24, 67, 162, 275	0
1	BK	286/338 (84%)	0.63	23 (8%) 18 13	27, 62, 144, 203	0
1	BL	286/338 (84%)	0.60	18 (6%) 26 16	29, 66, 129, 190	0
1	BM	286/338 (84%)	1.31	88 (30%) 1 1	32, 79, 256, 365	0
1	BN	286/338 (84%)	0.85	43 (15%) 5 5	37, 80, 201, 324	0
1	BO	286/338 (84%)	1.24	78 (27%) 1 2	29, 76, 223, 315	0
1	BP	286/338 (84%)	1.01	54 (18%) 3 3	37, 81, 198, 270	0
1	BQ	286/338 (84%)	0.84	30 (10%) 11 9	35, 78, 180, 295	0
1	BR	286/338 (84%)	0.54	11 (3%) 44 25	37, 80, 149, 225	0
1	BS	286/338 (84%)	0.70	40 (13%) 6 6	27, 67, 180, 308	0
1	BT	286/338 (84%)	0.76	19 (6%) 24 15	38, 84, 176, 270	0
1	BU	286/338 (84%)	1.23	80 (27%) 1 1	32, 75, 209, 323	0
1	BV	286/338 (84%)	0.75	26 (9%) 15 11	38, 86, 183, 243	0
1	BW	286/338 (84%)	0.48	10 (3%) 47 27	33, 66, 123, 203	0
1	BX	286/338 (84%)	0.79	42 (14%) 6 5	35, 80, 198, 263	0
1	BY	286/338 (84%)	0.44	15 (5%) 33 19	35, 78, 150, 213	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	BZ	286/338 (84%)	0.56	15 (5%) 33 19	38, 83, 195, 246	0
1	Ba	286/338 (84%)	0.70	23 (8%) 18 13	34, 81, 197, 330	0
1	Bb	286/338 (84%)	1.26	87 (30%) 1 1	30, 69, 249, 342	0
1	Bc	286/338 (84%)	1.38	87 (30%) 1 1	33, 79, 214, 279	0
1	Bd	286/338 (84%)	0.83	35 (12%) 8 7	37, 79, 168, 230	0
1	CA	304/338 (89%)	0.68	42 (13%) 6 6	40, 78, 206, 252	0
1	CB	304/338 (89%)	1.13	74 (24%) 2 2	29, 75, 282, 357	0
1	CC	304/338 (89%)	1.17	76 (25%) 2 2	28, 72, 269, 370	0
1	CD	304/338 (89%)	0.70	28 (9%) 14 11	38, 76, 190, 273	0
1	CE	304/338 (89%)	0.88	49 (16%) 4 5	34, 76, 239, 323	0
1	CF	304/338 (89%)	0.87	55 (18%) 3 4	34, 72, 234, 326	0
1	CG	304/338 (89%)	1.02	67 (22%) 2 2	39, 83, 269, 342	0
1	CH	304/338 (89%)	1.10	74 (24%) 2 2	37, 79, 323, 403	0
1	CI	304/338 (89%)	1.11	66 (21%) 2 2	34, 81, 284, 396	0
1	CJ	304/338 (89%)	0.90	49 (16%) 4 5	26, 70, 200, 287	0
1	CK	304/338 (89%)	0.71	32 (10%) 11 9	28, 64, 113, 174	0
1	CL	304/338 (89%)	0.42	10 (3%) 49 28	26, 66, 129, 190	0
1	CM	304/338 (89%)	1.26	79 (25%) 1 2	33, 75, 306, 389	0
1	CN	304/338 (89%)	0.81	50 (16%) 4 5	39, 77, 229, 320	0
1	CO	304/338 (89%)	1.02	60 (19%) 3 3	30, 74, 258, 396	0
1	CP	304/338 (89%)	0.75	32 (10%) 11 9	33, 81, 201, 288	0
1	CQ	304/338 (89%)	0.77	35 (11%) 9 8	39, 80, 187, 294	0
1	CR	304/338 (89%)	0.42	11 (3%) 46 26	34, 79, 153, 209	0
1	CS	304/338 (89%)	0.74	49 (16%) 4 5	28, 66, 226, 306	0
1	CT	304/338 (89%)	0.59	25 (8%) 17 12	37, 76, 186, 299	0
1	CU	304/338 (89%)	1.06	74 (24%) 2 2	31, 70, 249, 303	0
1	CV	304/338 (89%)	0.70	25 (8%) 17 12	41, 80, 196, 237	0
1	CW	304/338 (89%)	0.51	15 (4%) 35 20	30, 75, 137, 176	0
1	CX	304/338 (89%)	0.82	37 (12%) 8 7	39, 78, 244, 302	0
1	CY	304/338 (89%)	0.75	38 (12%) 8 7	33, 73, 176, 256	0
1	CZ	304/338 (89%)	0.64	23 (7%) 20 13	43, 82, 187, 293	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	Ca	304/338 (89%)	0.84	51 (16%) 4 5	35, 78, 209, 267	0
1	Cb	304/338 (89%)	1.32	87 (28%) 1 1	30, 73, 298, 419	0
1	Cc	304/338 (89%)	1.14	74 (24%) 2 2	38, 80, 263, 325	0
1	Cd	304/338 (89%)	0.84	36 (11%) 9 8	35, 75, 137, 221	0
All	All	26310/30420 (86%)	0.81	3630 (13%) 6 6	24, 78, 223, 419	0

All (3630) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	CI	279	TYR	8.7
1	Cb	232	SER	8.6
1	CI	265	ILE	8.5
1	CI	263	LEU	8.5
1	BI	296	PHE	8.1
1	CB	262	PRO	8.0
1	CM	328	GLY	7.7
1	CH	262	PRO	7.7
1	BB	262	PRO	7.6
1	CM	244	GLY	7.4
1	Cb	279	TYR	7.3
1	BB	264	SER	7.3
1	BC	263	LEU	7.2
1	AK	105	GLU	7.1
1	Cb	265	ILE	7.1
1	Cb	227	SER	7.0
1	BM	238	PHE	7.0
1	CU	328	GLY	7.0
1	CC	105	GLU	7.0
1	CC	325	LEU	6.9
1	AH	164	ARG	6.9
1	BI	228	LEU	6.8
1	CF	257	PHE	6.7
1	CH	257	PHE	6.7
1	CI	277	ALA	6.7
1	Bb	298	TRP	6.7
1	CM	257	PHE	6.7
1	AA	164	ARG	6.6
1	CB	257	PHE	6.6
1	Cb	262	PRO	6.6
1	AK	164	ARG	6.5
1	CM	279	TYR	6.5

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Mol	Chain	Res	Type	RSRZ
1	BO	296	PHE	6.5
1	BM	264	SER	6.4
1	BB	328	GLY	6.4
1	BB	228	LEU	6.4
1	CE	265	ILE	6.4
1	CC	282	LEU	6.4
1	AA	105	GLU	6.3
1	BC	264	SER	6.3
1	CH	282	LEU	6.3
1	BB	296	PHE	6.3
1	Cc	246	THR	6.3
1	BO	298	TRP	6.3
1	CM	246	THR	6.3
1	CI	278	VAL	6.3
1	Bb	228	LEU	6.3
1	AI	262	PRO	6.2
1	BI	263	LEU	6.2
1	CF	265	ILE	6.2
1	Cc	264	SER	6.2
1	CC	332	THR	6.1
1	BM	298	TRP	6.1
1	AU	105	GLU	6.1
1	Cb	257	PHE	6.1
1	BC	278	VAL	6.1
1	BH	281	HIS	6.1
1	BO	309	THR	6.1
1	BH	264	SER	6.1
1	CM	245	SER	6.1
1	Bc	309	THR	6.0
1	Cb	231	ASP	6.0
1	BI	281	HIS	6.0
1	CI	325	LEU	6.0
1	BC	262	PRO	6.0
1	CM	282	LEU	6.0
1	BH	296	PHE	6.0
1	Bc	318	GLU	6.0
1	Bb	325	LEU	6.0
1	BH	278	VAL	6.0
1	BI	298	TRP	6.0
1	BG	298	TRP	5.9
1	CG	265	ILE	5.9
1	CU	325	LEU	5.9

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Mol	Chain	Res	Type	RSRZ
1	BB	327	VAL	5.9
1	CM	265	ILE	5.9
1	Cb	221	PRO	5.9
1	Aa	105	GLU	5.9
1	Bc	312	VAL	5.9
1	CU	231	ASP	5.9
1	CX	279	TYR	5.9
1	CB	221	PRO	5.8
1	BM	254	GLY	5.8
1	BM	296	PHE	5.8
1	CH	265	ILE	5.8
1	BU	238	PHE	5.8
1	CI	262	PRO	5.8
1	CX	265	ILE	5.8
1	CC	259	LEU	5.8
1	BI	262	PRO	5.7
1	CI	282	LEU	5.7
1	CI	220	ALA	5.7
1	CO	279	TYR	5.7
1	CC	263	LEU	5.7
1	BH	238	PHE	5.7
1	CU	262	PRO	5.7
1	Bb	262	PRO	5.7
1	CB	263	LEU	5.7
1	BU	296	PHE	5.7
1	BB	298	TRP	5.7
1	CO	265	ILE	5.7
1	Cc	265	ILE	5.6
1	CO	257	PHE	5.6
1	Cc	279	TYR	5.6
1	BH	228	LEU	5.6
1	BI	325	LEU	5.6
1	CC	279	TYR	5.6
1	BH	298	TRP	5.6
1	Cb	239	LYS	5.6
1	CP	278	VAL	5.6
1	CT	54	ASP	5.6
1	CI	264	SER	5.6
1	CG	253	ASP	5.6
1	Cb	247	PRO	5.5
1	CH	263	LEU	5.5
1	AO	324	LEU	5.5

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Mol	Chain	Res	Type	RSRZ
1	BU	328	GLY	5.5
1	BM	278	VAL	5.5
1	Bb	281	HIS	5.5
1	BH	262	PRO	5.5
1	Cb	263	LEU	5.5
1	CM	248	LEU	5.5
1	AH	262	PRO	5.5
1	CC	258	GLN	5.5
1	CI	228	LEU	5.5
1	BB	281	HIS	5.5
1	Bb	296	PHE	5.5
1	BR	331	CYS	5.5
1	BO	239	LYS	5.4
1	BB	278	VAL	5.4
1	BG	296	PHE	5.4
1	Bc	54	ASP	5.4
1	CS	255	ALA	5.4
1	CM	262	PRO	5.4
1	BH	327	VAL	5.4
1	CB	318	GLU	5.4
1	BP	262	PRO	5.4
1	AC	257	PHE	5.4
1	BH	325	LEU	5.4
1	BI	238	PHE	5.4
1	CH	243	LEU	5.3
1	BI	282	LEU	5.3
1	AI	228	LEU	5.3
1	Bc	255	ALA	5.3
1	AI	164	ARG	5.3
1	Bb	280	TRP	5.3
1	CC	248	LEU	5.3
1	CF	255	ALA	5.3
1	CO	255	ALA	5.3
1	BH	328	GLY	5.3
1	BM	325	LEU	5.3
1	CI	300	ILE	5.3
1	BP	105	GLU	5.3
1	CB	291	THR	5.3
1	Ac	268	SER	5.3
1	BO	262	PRO	5.2
1	CG	279	TYR	5.2
1	Bc	317	ASP	5.2

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Mol	Chain	Res	Type	RSRZ
1	Cb	243	LEU	5.2
1	AB	262	PRO	5.2
1	Ab	218	THR	5.2
1	Cd	254	GLY	5.2
1	Bb	238	PHE	5.2
1	CM	263	LEU	5.2
1	CM	325	LEU	5.2
1	Bb	312	VAL	5.2
1	CH	279	TYR	5.2
1	CU	243	LEU	5.2
1	CU	265	ILE	5.2
1	CP	265	ILE	5.2
1	CC	228	LEU	5.2
1	Cc	247	PRO	5.1
1	Ac	264	SER	5.1
1	AC	282	LEU	5.1
1	CN	243	LEU	5.1
1	Cb	291	THR	5.1
1	Cb	282	LEU	5.1
1	BO	291	THR	5.1
1	CC	264	SER	5.1
1	AH	260	ASP	5.1
1	CU	248	LEU	5.1
1	Bc	302	ASP	5.1
1	BO	255	ALA	5.1
1	Cb	228	LEU	5.1
1	BT	323	ILE	5.1
1	BH	326	PRO	5.1
1	AC	243	LEU	5.1
1	CU	228	LEU	5.1
1	BX	264	SER	5.0
1	BB	263	LEU	5.0
1	BN	228	LEU	5.0
1	BO	228	LEU	5.0
1	CE	253	ASP	5.0
1	Cc	253	ASP	5.0
1	CM	247	PRO	5.0
1	AC	298	TRP	5.0
1	BO	278	VAL	5.0
1	AM	262	PRO	5.0
1	Ca	250	ILE	5.0
1	CJ	56	HIS	5.0

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Mol	Chain	Res	Type	RSRZ
1	Cb	325	LEU	5.0
1	BH	255	ALA	5.0
1	BI	255	ALA	5.0
1	AD	105	GLU	5.0
1	CJ	105	GLU	5.0
1	BO	327	VAL	5.0
1	CH	221	PRO	5.0
1	AJ	105	GLU	5.0
1	CY	264	SER	5.0
1	Ca	253	ASP	5.0
1	CS	247	PRO	4.9
1	Aa	164	ARG	4.9
1	CM	253	ASP	4.9
1	Bb	326	PRO	4.9
1	BM	228	LEU	4.9
1	Bc	53	ASN	4.9
1	Bc	296	PHE	4.9
1	BQ	56	HIS	4.9
1	Cb	321	ARG	4.9
1	BQ	52	THR	4.9
1	BT	52	THR	4.9
1	Ca	257	PHE	4.9
1	CY	232	SER	4.9
1	Bb	264	SER	4.9
1	CG	252	PRO	4.9
1	BI	317	ASP	4.9
1	Cb	248	LEU	4.9
1	BB	309	THR	4.9
1	AI	218	THR	4.9
1	AB	218	THR	4.9
1	CB	265	ILE	4.9
1	AC	324	LEU	4.8
1	CI	243	LEU	4.8
1	AP	105	GLU	4.8
1	CN	265	ILE	4.8
1	AF	288	ASN	4.8
1	AH	105	GLU	4.8
1	BO	238	PHE	4.8
1	AI	230	ASN	4.8
1	CB	282	LEU	4.8
1	BI	264	SER	4.8
1	BB	237	ASP	4.8

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Mol	Chain	Res	Type	RSRZ
1	CO	253	ASP	4.8
1	CM	228	LEU	4.8
1	Cc	231	ASP	4.8
1	AC	255	ALA	4.8
1	AE	218	THR	4.8
1	BM	255	ALA	4.8
1	Cb	281	HIS	4.8
1	CB	279	TYR	4.7
1	Bb	255	ALA	4.7
1	BU	242	LEU	4.7
1	CU	257	PHE	4.7
1	BH	237	ASP	4.7
1	BX	325	LEU	4.7
1	CB	232	SER	4.7
1	CF	279	TYR	4.7
1	AP	164	ARG	4.7
1	AP	262	PRO	4.7
1	AD	164	ARG	4.7
1	CF	333	ARG	4.7
1	Bb	318	GLU	4.7
1	Ad	164	ARG	4.7
1	AC	228	LEU	4.7
1	Cb	246	THR	4.7
1	Cb	244	GLY	4.7
1	CC	164	ARG	4.7
1	CA	256	VAL	4.7
1	BX	309	THR	4.7
1	CC	262	PRO	4.6
1	BM	328	GLY	4.7
1	Bc	237	ASP	4.6
1	Ac	265	ILE	4.6
1	AU	262	PRO	4.6
1	AC	264	SER	4.6
1	CF	282	LEU	4.6
1	BI	297	ARG	4.6
1	Bc	249	ASP	4.6
1	Bb	327	VAL	4.6
1	Aa	108	GLU	4.6
1	CI	257	PHE	4.6
1	BC	277	ALA	4.6
1	AV	289	ALA	4.6
1	AC	281	HIS	4.6

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Mol	Chain	Res	Type	RSRZ
1	CO	252	PRO	4.6
1	BH	263	LEU	4.6
1	CM	243	LEU	4.6
1	BJ	323	ILE	4.6
1	AN	105	GLU	4.6
1	CU	279	TYR	4.6
1	Ac	218	THR	4.6
1	Ab	228	LEU	4.6
1	CS	257	PHE	4.6
1	CI	218	THR	4.6
1	CD	221	PRO	4.6
1	CM	221	PRO	4.6
1	BE	239	LYS	4.5
1	BF	262	PRO	4.5
1	Ab	262	PRO	4.5
1	CO	251	ALA	4.5
1	CR	289	ALA	4.5
1	AC	262	PRO	4.5
1	CP	279	TYR	4.5
1	AG	218	THR	4.5
1	CO	291	THR	4.5
1	CU	232	SER	4.5
1	CG	250	ILE	4.5
1	Cb	294	GLY	4.5
1	AN	262	PRO	4.5
1	CI	238	PHE	4.5
1	BP	277	ALA	4.5
1	Cb	251	ALA	4.5
1	BN	264	SER	4.5
1	CQ	279	TYR	4.5
1	BG	317	ASP	4.5
1	AM	260	ASP	4.5
1	AC	248	LEU	4.5
1	CG	257	PHE	4.5
1	CI	254	GLY	4.5
1	BM	309	THR	4.5
1	Cb	278	VAL	4.5
1	CA	307	THR	4.4
1	Bb	254	GLY	4.4
1	Bb	309	THR	4.4
1	Ab	306	LYS	4.4
1	BT	105	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
1	AT	105	GLU	4.4
1	BX	298	TRP	4.4
1	CS	250	ILE	4.4
1	Cb	255	ALA	4.4
1	BI	252	PRO	4.4
1	Ab	308	PHE	4.4
1	BQ	323	ILE	4.4
1	CU	312	VAL	4.4
1	CB	317	ASP	4.4
1	CC	260	ASP	4.4
1	CU	253	ASP	4.4
1	CE	282	LEU	4.4
1	AH	263	LEU	4.4
1	BU	263	LEU	4.4
1	CM	313	ALA	4.4
1	AQ	164	ARG	4.4
1	CU	251	ALA	4.4
1	CQ	56	HIS	4.4
1	CH	218	THR	4.4
1	CH	224	THR	4.4
1	AH	230	ASN	4.4
1	BM	327	VAL	4.4
1	AV	228	LEU	4.4
1	Ca	255	ALA	4.4
1	BO	237	ASP	4.4
1	BW	136	HIS	4.4
1	BW	287	GLY	4.4
1	CU	278	VAL	4.4
1	CC	257	PHE	4.4
1	BO	257	PHE	4.4
1	AI	266	ASP	4.4
1	BY	136	HIS	4.4
1	CI	267	TYR	4.3
1	BM	312	VAL	4.3
1	BB	301	TRP	4.3
1	BA	52	THR	4.3
1	BB	325	LEU	4.3
1	CI	221	PRO	4.3
1	Bb	278	VAL	4.3
1	BB	238	PHE	4.3
1	BV	323	ILE	4.3
1	Cb	226	GLY	4.3

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Mol	Chain	Res	Type	RSRZ
1	Ac	269	LEU	4.3
1	CQ	278	VAL	4.3
1	BU	298	TRP	4.3
1	Bc	323	ILE	4.3
1	BN	52	THR	4.3
1	BO	292	PRO	4.3
1	BU	262	PRO	4.3
1	Bc	298	TRP	4.3
1	Ac	278	VAL	4.3
1	BI	239	LYS	4.3
1	Bc	315	TYR	4.3
1	CB	243	LEU	4.3
1	CO	325	LEU	4.3
1	BX	228	LEU	4.3
1	Cb	300	ILE	4.3
1	CE	250	ILE	4.3
1	CJ	54	ASP	4.3
1	AH	324	LEU	4.3
1	Cc	250	ILE	4.3
1	CY	242	LEU	4.2
1	BB	317	ASP	4.2
1	BF	298	TRP	4.2
1	CB	278	VAL	4.2
1	CN	257	PHE	4.2
1	Cb	312	VAL	4.2
1	CE	221	PRO	4.2
1	CG	247	PRO	4.2
1	CE	243	LEU	4.2
1	BU	228	LEU	4.2
1	AU	264	SER	4.2
1	CI	281	HIS	4.2
1	Bb	224	THR	4.2
1	Bd	189	GLY	4.2
1	BU	330	VAL	4.2
1	CD	250	ILE	4.2
1	CC	238	PHE	4.2
1	BM	280	TRP	4.2
1	AQ	262	PRO	4.2
1	CH	248	LEU	4.2
1	BM	237	ASP	4.2
1	BB	300	ILE	4.2
1	Cc	300	ILE	4.2

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Mol	Chain	Res	Type	RSRZ
1	BH	280	TRP	4.2
1	CH	280	TRP	4.2
1	BO	264	SER	4.2
1	Ad	322	GLN	4.2
1	BB	282	LEU	4.2
1	BP	296	PHE	4.2
1	CM	312	VAL	4.1
1	CS	312	VAL	4.1
1	Ca	293	ALA	4.1
1	BM	263	LEU	4.1
1	BS	315	TYR	4.1
1	Bc	238	PHE	4.1
1	CG	278	VAL	4.1
1	Bc	307	THR	4.1
1	BI	237	ASP	4.1
1	AI	227	SER	4.1
1	Cb	280	TRP	4.1
1	AB	322	GLN	4.1
1	BB	326	PRO	4.1
1	CE	247	PRO	4.1
1	CO	247	PRO	4.1
1	BN	325	LEU	4.1
1	Ac	267	TYR	4.1
1	AM	218	THR	4.1
1	Ab	281	HIS	4.1
1	AA	206	ARG	4.1
1	AG	262	PRO	4.1
1	CV	279	TYR	4.1
1	CM	278	VAL	4.1
1	CC	240	SER	4.1
1	CF	243	LEU	4.1
1	BM	282	LEU	4.1
1	BY	321	ARG	4.1
1	Cc	232	SER	4.1
1	CB	247	PRO	4.1
1	Ac	320	PRO	4.1
1	BO	242	LEU	4.1
1	CJ	264	SER	4.1
1	Aa	161	GLN	4.0
1	CA	282	LEU	4.0
1	CK	315	TYR	4.0
1	AS	105	GLU	4.0

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Mol	Chain	Res	Type	RSRZ
1	BU	325	LEU	4.0
1	CI	309	THR	4.0
1	BO	311	GLY	4.0
1	CN	250	ILE	4.0
1	AH	281	HIS	4.0
1	Ad	320	PRO	4.0
1	CB	280	TRP	4.0
1	CN	300	ILE	4.0
1	CO	250	ILE	4.0
1	Cb	313	ALA	4.0
1	CH	281	HIS	4.0
1	Bb	237	ASP	4.0
1	BF	315	TYR	4.0
1	BG	315	TYR	4.0
1	AN	218	THR	4.0
1	AA	262	PRO	4.0
1	BB	280	TRP	4.0
1	AI	105	GLU	4.0
1	BM	251	ALA	4.0
1	Cc	293	ALA	4.0
1	CG	262	PRO	4.0
1	CU	252	PRO	4.0
1	Bc	228	LEU	4.0
1	BP	322	GLN	4.0
1	CC	229	TYR	4.0
1	CM	224	THR	4.0
1	CO	328	GLY	4.0
1	Cc	270	GLY	4.0
1	Cb	277	ALA	4.0
1	Bd	303	ASN	4.0
1	AP	336	SER	3.9
1	Cb	240	SER	3.9
1	AI	324	LEU	3.9
1	CI	248	LEU	3.9
1	BB	255	ALA	3.9
1	CK	313	ALA	3.9
1	Cc	274	VAL	3.9
1	CX	257	PHE	3.9
1	AF	264	SER	3.9
1	CF	264	SER	3.9
1	CO	263	LEU	3.9
1	Bb	315	TYR	3.9

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Mol	Chain	Res	Type	RSRZ
1	CF	293	ALA	3.9
1	AL	313	ALA	3.9
1	CE	266	ASP	3.9
1	BO	280	TRP	3.9
1	CA	262	PRO	3.9
1	AM	180	PRO	3.9
1	Ca	247	PRO	3.9
1	CC	243	LEU	3.9
1	CH	325	LEU	3.9
1	CC	226	GLY	3.9
1	BD	52	THR	3.9
1	Bb	229	TYR	3.9
1	BH	282	LEU	3.9
1	Cc	243	LEU	3.9
1	AI	318	GLU	3.9
1	Bb	293	ALA	3.9
1	CG	300	ILE	3.9
1	CM	261	ARG	3.9
1	CB	325	LEU	3.9
1	BE	303	ASN	3.9
1	BF	296	PHE	3.9
1	BH	53	ASN	3.9
1	BM	257	PHE	3.9
1	BM	305	ASN	3.9
1	BW	231	ASP	3.9
1	Bb	317	ASP	3.9
1	Ac	263	LEU	3.9
1	CB	256	VAL	3.9
1	AG	264	SER	3.9
1	BH	227	SER	3.9
1	BV	163	THR	3.9
1	Bc	291	THR	3.9
1	BG	229	TYR	3.9
1	BH	318	GLU	3.9
1	BP	279	TYR	3.9
1	Cc	289	ALA	3.9
1	BB	239	LYS	3.9
1	CQ	323	ILE	3.9
1	AC	280	TRP	3.9
1	CH	228	LEU	3.9
1	BV	262	PRO	3.9
1	Cc	257	PHE	3.9

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Mol	Chain	Res	Type	RSRZ
1	BI	278	VAL	3.9
1	Ab	305	ASN	3.9
1	Bc	322	GLN	3.9
1	BL	136	HIS	3.9
1	AT	164	ARG	3.8
1	Ca	323	ILE	3.8
1	CJ	296	PHE	3.8
1	AC	322	GLN	3.8
1	Bc	227	SER	3.8
1	CE	323	ILE	3.8
1	BU	281	HIS	3.8
1	AA	162	TYR	3.8
1	AH	325	LEU	3.8
1	BM	243	LEU	3.8
1	CN	282	LEU	3.8
1	CO	248	LEU	3.8
1	Bb	263	LEU	3.8
1	BX	262	PRO	3.8
1	BG	278	VAL	3.8
1	Ba	322	GLN	3.8
1	Cd	319	GLN	3.8
1	CA	305	ASN	3.8
1	AL	232	SER	3.8
1	AB	310	ASP	3.8
1	AC	263	LEU	3.8
1	CF	248	LEU	3.8
1	AH	218	THR	3.8
1	CM	329	THR	3.8
1	AV	235	THR	3.8
1	Ca	282	LEU	3.8
1	Ca	290	GLY	3.8
1	CU	221	PRO	3.8
1	CB	312	VAL	3.8
1	BG	312	VAL	3.8
1	BP	278	VAL	3.8
1	BI	227	SER	3.8
1	CM	227	SER	3.8
1	Cb	264	SER	3.8
1	Bc	214	ASN	3.8
1	CU	282	LEU	3.8
1	Cb	249	ASP	3.8
1	CM	294	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
1	CE	257	PHE	3.8
1	BF	228	LEU	3.8
1	CG	282	LEU	3.8
1	CN	325	LEU	3.8
1	CX	248	LEU	3.8
1	BY	323	ILE	3.8
1	CG	255	ALA	3.8
1	CA	281	HIS	3.8
1	CJ	278	VAL	3.8
1	CQ	312	VAL	3.8
1	Bb	322	GLN	3.8
1	Ab	324	LEU	3.8
1	Cc	245	SER	3.8
1	BB	297	ARG	3.8
1	BH	297	ARG	3.8
1	BH	329	THR	3.8
1	CK	235	THR	3.8
1	BO	178	THR	3.8
1	CC	54	ASP	3.8
1	CQ	54	ASP	3.8
1	Cd	249	ASP	3.8
1	BO	279	TYR	3.8
1	CH	247	PRO	3.8
1	BM	281	HIS	3.8
1	CG	263	LEU	3.7
1	BH	300	ILE	3.7
1	CO	243	LEU	3.7
1	BS	228	LEU	3.7
1	CS	248	LEU	3.7
1	CU	263	LEU	3.7
1	Cb	301	TRP	3.7
1	Ad	277	ALA	3.7
1	BO	284	LYS	3.7
1	CB	250	ILE	3.7
1	CG	243	LEU	3.7
1	CU	330	VAL	3.7
1	Cc	278	VAL	3.7
1	Cc	282	LEU	3.7
1	Cd	279	TYR	3.7
1	AN	56	HIS	3.7
1	CM	264	SER	3.7
1	AM	164	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
1	AN	206	ARG	3.7
1	Bc	297	ARG	3.7
1	BO	251	ALA	3.7
1	Bb	329	THR	3.7
1	AA	324	LEU	3.7
1	BO	282	LEU	3.7
1	CX	263	LEU	3.7
1	BO	300	ILE	3.7
1	BP	317	ASP	3.7
1	AT	323	ILE	3.7
1	CU	327	VAL	3.7
1	AC	252	PRO	3.7
1	CC	326	PRO	3.7
1	CB	281	HIS	3.7
1	CC	227	SER	3.7
1	BJ	159	ARG	3.7
1	CM	281	HIS	3.7
1	CC	296	PHE	3.7
1	CB	288	ASN	3.7
1	CI	255	ALA	3.7
1	Bb	311	GLY	3.7
1	AM	325	LEU	3.7
1	AV	324	LEU	3.7
1	BI	300	ILE	3.7
1	CJ	265	ILE	3.7
1	CU	300	ILE	3.7
1	BO	312	VAL	3.7
1	BM	315	TYR	3.7
1	CB	264	SER	3.7
1	AO	262	PRO	3.7
1	AB	324	LEU	3.7
1	CM	303	ASN	3.7
1	BG	291	THR	3.7
1	BI	309	THR	3.7
1	Bc	52	THR	3.7
1	CU	250	ILE	3.7
1	AV	323	ILE	3.7
1	BB	315	TYR	3.7
1	CH	264	SER	3.7
1	CO	262	PRO	3.7
1	CQ	164	ARG	3.7
1	Bc	279	TYR	3.7

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Mol	Chain	Res	Type	RSRZ
1	Bc	320	PRO	3.7
1	BS	317	ASP	3.7
1	CS	228	LEU	3.7
1	CM	277	ALA	3.7
1	BI	329	THR	3.7
1	BO	189	GLY	3.7
1	Bb	323	ILE	3.7
1	Cb	224	THR	3.7
1	BS	327	VAL	3.7
1	BI	257	PHE	3.7
1	CS	279	TYR	3.7
1	CV	257	PHE	3.7
1	CC	239	LYS	3.7
1	BU	239	LYS	3.7
1	CE	325	LEU	3.7
1	Cb	233	LEU	3.7
1	AJ	56	HIS	3.7
1	Bc	94	HIS	3.7
1	BC	265	ILE	3.6
1	CV	250	ILE	3.6
1	CX	115	CYS	3.6
1	Bb	241	ILE	3.6
1	BO	254	GLY	3.6
1	BU	52	THR	3.6
1	Bc	305	ASN	3.6
1	CS	264	SER	3.6
1	CJ	279	TYR	3.6
1	Ab	263	LEU	3.6
1	CC	323	ILE	3.6
1	BE	323	ILE	3.6
1	AH	310	ASP	3.6
1	CB	218	THR	3.6
1	Cc	309	THR	3.6
1	Ad	299	GLY	3.6
1	CM	327	VAL	3.6
1	AC	238	PHE	3.6
1	CG	325	LEU	3.6
1	CP	54	ASP	3.6
1	BM	224	THR	3.6
1	AM	181	GLY	3.6
1	Bc	189	GLY	3.6
1	Cc	287	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	Bb	297	ARG	3.6
1	AG	324	LEU	3.6
1	BI	243	LEU	3.6
1	Ab	325	LEU	3.6
1	BB	322	GLN	3.6
1	BM	262	PRO	3.6
1	CB	300	ILE	3.6
1	BM	229	TYR	3.6
1	CN	279	TYR	3.6
1	Bd	267	TYR	3.6
1	BF	239	LYS	3.6
1	CI	253	ASP	3.6
1	CM	226	GLY	3.6
1	CO	332	THR	3.6
1	BS	328	GLY	3.6
1	Cb	290	GLY	3.6
1	BG	238	PHE	3.6
1	Cd	235	THR	3.6
1	CG	330	VAL	3.6
1	CN	228	LEU	3.6
1	CO	256	VAL	3.6
1	AS	324	LEU	3.6
1	CF	262	PRO	3.6
1	Ca	292	PRO	3.6
1	AP	279	TYR	3.6
1	Ca	105	GLU	3.6
1	Bc	151	LYS	3.6
1	BB	287	GLY	3.6
1	CE	248	LEU	3.6
1	AI	233	LEU	3.6
1	Bc	254	GLY	3.6
1	Bb	253	ASP	3.6
1	Cc	263	LEU	3.6
1	CG	264	SER	3.6
1	BB	323	ILE	3.6
1	AC	250	ILE	3.6
1	CS	265	ILE	3.6
1	BT	322	GLN	3.6
1	Ac	279	TYR	3.6
1	CC	293	ALA	3.6
1	CC	242	LEU	3.6
1	CP	228	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	BU	233	LEU	3.6
1	Bb	242	LEU	3.6
1	Cb	324	LEU	3.6
1	CC	244	GLY	3.6
1	BM	256	VAL	3.6
1	BM	307	THR	3.6
1	AO	218	THR	3.6
1	CU	224	THR	3.6
1	BS	231	ASP	3.6
1	BU	240	SER	3.6
1	Ac	310	ASP	3.6
1	CU	247	PRO	3.5
1	CX	247	PRO	3.5
1	Bc	283	LYS	3.5
1	CI	324	LEU	3.5
1	BH	287	GLY	3.5
1	BX	278	VAL	3.5
1	Ba	52	THR	3.5
1	Bc	270	GLY	3.5
1	Bc	299	GLY	3.5
1	CN	312	VAL	3.5
1	CO	264	SER	3.5
1	AQ	264	SER	3.5
1	AC	283	LYS	3.5
1	CM	283	LYS	3.5
1	BC	221	PRO	3.5
1	CG	221	PRO	3.5
1	BI	261	ARG	3.5
1	CM	280	TRP	3.5
1	BN	269	LEU	3.5
1	BU	248	LEU	3.5
1	BV	324	LEU	3.5
1	AV	162	TYR	3.5
1	Bb	243	LEU	3.5
1	CB	321	ARG	3.5
1	AE	164	ARG	3.5
1	CM	220	ALA	3.5
1	Cc	296	PHE	3.5
1	Ab	336	SER	3.5
1	BO	249	ASP	3.5
1	CY	253	ASP	3.5
1	CB	248	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	BI	248	LEU	3.5
1	BC	276	ARG	3.5
1	Ba	318	GLU	3.5
1	Aa	162	TYR	3.5
1	BO	293	ALA	3.5
1	CE	287	GLY	3.5
1	CV	312	VAL	3.5
1	Bc	300	ILE	3.5
1	CC	232	SER	3.5
1	CG	246	THR	3.5
1	BC	324	LEU	3.5
1	AI	263	LEU	3.5
1	CX	282	LEU	3.5
1	Bb	282	LEU	3.5
1	CI	266	ASP	3.5
1	BU	54	ASP	3.5
1	Bc	285	PHE	3.5
1	CB	220	ALA	3.5
1	BP	229	TYR	3.5
1	BU	255	ALA	3.5
1	AG	51	GLY	3.5
1	CM	218	THR	3.5
1	BC	282	LEU	3.5
1	CO	282	LEU	3.5
1	BI	322	GLN	3.5
1	AI	56	HIS	3.5
1	Aa	56	HIS	3.5
1	Bc	236	ASN	3.5
1	Cc	310	ASP	3.5
1	Cb	250	ILE	3.5
1	Ad	105	GLU	3.5
1	BU	278	VAL	3.5
1	Ca	278	VAL	3.5
1	CI	290	GLY	3.5
1	BO	120	GLY	3.5
1	AM	163	THR	3.5
1	CP	263	LEU	3.5
1	AH	257	PHE	3.5
1	BO	236	ASN	3.5
1	CN	262	PRO	3.5
1	CU	281	HIS	3.5
1	Bb	292	PRO	3.5

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Mol	Chain	Res	Type	RSRZ
1	BA	300	ILE	3.4
1	BX	249	ASP	3.4
1	Cd	313	ALA	3.4
1	BH	279	TYR	3.4
1	AC	105	GLU	3.4
1	BS	318	GLU	3.4
1	Cd	318	GLU	3.4
1	BF	312	VAL	3.4
1	CJ	312	VAL	3.4
1	BO	263	LEU	3.4
1	BU	208	SER	3.4
1	CU	227	SER	3.4
1	Cc	240	SER	3.4
1	CA	309	THR	3.4
1	BH	224	THR	3.4
1	BI	52	THR	3.4
1	Cc	218	THR	3.4
1	BA	281	HIS	3.4
1	CJ	250	ILE	3.4
1	CO	281	HIS	3.4
1	BU	323	ILE	3.4
1	BC	325	LEU	3.4
1	CC	327	VAL	3.4
1	AF	324	LEU	3.4
1	BG	228	LEU	3.4
1	CH	278	VAL	3.4
1	BM	248	LEU	3.4
1	CO	312	VAL	3.4
1	CQ	166	LEU	3.4
1	Bc	229	TYR	3.4
1	Bc	324	LEU	3.4
1	AB	264	SER	3.4
1	BG	264	SER	3.4
1	BN	234	SER	3.4
1	BE	309	THR	3.4
1	CF	280	TRP	3.4
1	BN	298	TRP	3.4
1	BS	298	TRP	3.4
1	Ab	280	TRP	3.4
1	Cb	287	GLY	3.4
1	Cd	295	TRP	3.4
1	CE	300	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	BM	288	ASN	3.4
1	AM	239	LYS	3.4
1	CX	221	PRO	3.4
1	Ca	251	ALA	3.4
1	AC	256	VAL	3.4
1	BZ	327	VAL	3.4
1	CZ	278	VAL	3.4
1	BA	227	SER	3.4
1	CG	331	CYS	3.4
1	AM	264	SER	3.4
1	BO	302	ASP	3.4
1	CV	87	ASP	3.4
1	Cb	115	CYS	3.4
1	Bc	208	SER	3.4
1	Cd	317	ASP	3.4
1	CC	291	THR	3.4
1	BF	178	THR	3.4
1	CJ	301	TRP	3.4
1	BO	224	THR	3.4
1	AI	206	ARG	3.4
1	BB	236	ASN	3.4
1	AB	230	ASN	3.4
1	CC	233	LEU	3.4
1	BM	303	ASN	3.4
1	CG	251	ALA	3.4
1	Bb	227	SER	3.4
1	BH	317	ASP	3.4
1	BI	310	ASP	3.4
1	CI	329	THR	3.4
1	Ca	249	ASP	3.4
1	Bb	291	THR	3.4
1	Ab	335	ASP	3.4
1	Cc	298	TRP	3.4
1	AM	265	ILE	3.4
1	BQ	322	GLN	3.4
1	BB	248	LEU	3.4
1	AB	325	LEU	3.4
1	CC	324	LEU	3.4
1	CE	293	ALA	3.4
1	BO	303	ASN	3.4
1	Cb	220	ALA	3.4
1	BB	312	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
1	AQ	278	VAL	3.4
1	BV	278	VAL	3.4
1	Cd	256	VAL	3.4
1	CA	279	TYR	3.4
1	CE	279	TYR	3.4
1	BI	105	GLU	3.4
1	CI	294	GLY	3.4
1	CK	254	GLY	3.4
1	AC	218	THR	3.4
1	BM	283	LYS	3.4
1	Ac	178	THR	3.4
1	CH	115	CYS	3.4
1	AP	324	LEU	3.4
1	AZ	324	LEU	3.4
1	Cb	223	MET	3.4
1	CE	262	PRO	3.4
1	AS	262	PRO	3.4
1	CE	255	ALA	3.4
1	CF	256	VAL	3.4
1	AI	278	VAL	3.4
1	BU	227	SER	3.4
1	BN	296	PHE	3.4
1	AV	164	ARG	3.4
1	Ca	279	TYR	3.4
1	Ab	239	LYS	3.4
1	CC	241	ILE	3.3
1	AF	271	THR	3.3
1	CG	218	THR	3.3
1	AU	323	ILE	3.3
1	BM	324	LEU	3.3
1	AM	228	LEU	3.3
1	BO	325	LEU	3.3
1	CX	228	LEU	3.3
1	BE	249	ASP	3.3
1	CI	249	ASP	3.3
1	BU	237	ASP	3.3
1	BI	331	CYS	3.3
1	CJ	331	CYS	3.3
1	BU	95	ALA	3.3
1	Cc	286	ALA	3.3
1	BC	268	SER	3.3
1	CM	240	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	CX	264	SER	3.3
1	AC	164	ARG	3.3
1	BG	297	ARG	3.3
1	AI	281	HIS	3.3
1	CN	56	HIS	3.3
1	BB	224	THR	3.3
1	BI	224	THR	3.3
1	Aa	163	THR	3.3
1	AR	320	PRO	3.3
1	Bc	293	ALA	3.3
1	Ac	262	PRO	3.3
1	CM	330	VAL	3.3
1	Ac	274	VAL	3.3
1	AT	206	ARG	3.3
1	CA	325	LEU	3.3
1	BF	323	ILE	3.3
1	BI	324	LEU	3.3
1	CL	269	LEU	3.3
1	Ca	324	LEU	3.3
1	CQ	108	GLU	3.3
1	Ab	217	GLU	3.3
1	BI	280	TRP	3.3
1	BK	275	ASP	3.3
1	AH	239	LYS	3.3
1	Ca	252	PRO	3.3
1	Cb	252	PRO	3.3
1	BB	240	SER	3.3
1	CJ	206	ARG	3.3
1	BO	285	PHE	3.3
1	CT	278	VAL	3.3
1	CF	263	LEU	3.3
1	BX	241	ILE	3.3
1	CI	224	THR	3.3
1	BL	235	THR	3.3
1	BP	52	THR	3.3
1	BS	229	TYR	3.3
1	BN	105	GLU	3.3
1	BU	224	THR	3.3
1	CZ	105	GLU	3.3
1	AB	281	HIS	3.3
1	AT	56	HIS	3.3
1	BG	280	TRP	3.3

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Mol	Chain	Res	Type	RSRZ
1	AI	220	ALA	3.3
1	BS	255	ALA	3.3
1	BT	54	ASP	3.3
1	CV	278	VAL	3.3
1	CX	250	ILE	3.3
1	BB	329	THR	3.3
1	AH	163	THR	3.3
1	BU	229	TYR	3.3
1	AU	163	THR	3.3
1	AE	105	GLU	3.3
1	BP	281	HIS	3.3
1	AC	233	LEU	3.3
1	AA	278	VAL	3.3
1	CC	265	ILE	3.3
1	CH	327	VAL	3.3
1	CJ	221	PRO	3.3
1	CN	263	LEU	3.3
1	BP	323	ILE	3.3
1	BU	243	LEU	3.3
1	AZ	228	LEU	3.3
1	CZ	263	LEU	3.3
1	Bb	248	LEU	3.3
1	Cc	321	ARG	3.3
1	CC	208	SER	3.3
1	BU	260	ASP	3.3
1	AG	189	GLY	3.3
1	BP	328	GLY	3.3
1	BB	267	TYR	3.3
1	BH	229	TYR	3.3
1	BQ	309	THR	3.3
1	Ab	337	GLU	3.3
1	AI	243	LEU	3.2
1	AM	324	LEU	3.2
1	CP	282	LEU	3.2
1	Ac	324	LEU	3.2
1	AG	323	ILE	3.2
1	CM	300	ILE	3.2
1	CC	278	VAL	3.2
1	Cd	231	ASP	3.2
1	CB	224	THR	3.2
1	BH	332	THR	3.2
1	CK	267	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	BV	52	THR	3.2
1	CZ	279	TYR	3.2
1	AQ	105	GLU	3.2
1	AV	105	GLU	3.2
1	AB	228	LEU	3.2
1	BC	248	LEU	3.2
1	CG	248	LEU	3.2
1	BC	323	ILE	3.2
1	BD	300	ILE	3.2
1	BH	241	ILE	3.2
1	CQ	265	ILE	3.2
1	Ab	323	ILE	3.2
1	CN	255	ALA	3.2
1	AB	278	VAL	3.2
1	Ab	320	PRO	3.2
1	CA	54	ASP	3.2
1	AI	239	LYS	3.2
1	Ac	273	ASP	3.2
1	BI	226	GLY	3.2
1	CI	219	THR	3.2
1	Cb	218	THR	3.2
1	BH	324	LEU	3.2
1	CF	337	GLU	3.2
1	Bb	300	ILE	3.2
1	BF	136	HIS	3.2
1	BM	293	ALA	3.2
1	AP	278	VAL	3.2
1	AW	313	ALA	3.2
1	CB	115	CYS	3.2
1	BG	262	PRO	3.2
1	AX	262	PRO	3.2
1	CE	228	LEU	3.2
1	CC	235	THR	3.2
1	CF	253	ASP	3.2
1	BG	299	GLY	3.2
1	AI	325	LEU	3.2
1	CJ	282	LEU	3.2
1	BM	236	ASN	3.2
1	AC	276	ARG	3.2
1	BI	318	GLU	3.2
1	CV	105	GLU	3.2
1	Ab	277	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	AI	264	SER	3.2
1	BG	326	PRO	3.2
1	CI	269	LEU	3.2
1	AM	280	TRP	3.2
1	Bd	120	GLY	3.2
1	BI	332	THR	3.2
1	CO	303	ASN	3.2
1	Bd	52	THR	3.2
1	CB	335	ASP	3.2
1	CK	231	ASP	3.2
1	BG	279	TYR	3.2
1	AI	314	TYR	3.2
1	CM	258	GLN	3.2
1	BQ	206	ARG	3.2
1	Bc	335	ASP	3.2
1	Cc	275	ASP	3.2
1	Ac	105	GLU	3.2
1	BH	289	ALA	3.2
1	CA	264	SER	3.2
1	CM	256	VAL	3.2
1	CO	278	VAL	3.2
1	AI	326	PRO	3.2
1	CB	324	LEU	3.2
1	BG	325	LEU	3.2
1	BS	269	LEU	3.2
1	AU	324	LEU	3.2
1	Ba	269	LEU	3.2
1	AM	250	ILE	3.2
1	CO	300	ILE	3.2
1	CW	115	CYS	3.2
1	Bd	331	CYS	3.2
1	CB	329	THR	3.2
1	BD	53	ASN	3.2
1	CI	305	ASN	3.2
1	BU	332	THR	3.2
1	BB	260	ASP	3.2
1	BC	266	ASP	3.2
1	BI	54	ASP	3.2
1	CK	253	ASP	3.2
1	BO	253	ASP	3.2
1	CM	223	MET	3.2
1	AZ	336	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	Bc	251	ALA	3.2
1	BB	252	PRO	3.2
1	BC	243	LEU	3.2
1	Bb	269	LEU	3.2
1	CA	250	ILE	3.1
1	AC	323	ILE	3.1
1	BH	323	ILE	3.1
1	CH	323	ILE	3.1
1	AM	299	GLY	3.1
1	BZ	328	GLY	3.1
1	Cb	254	GLY	3.1
1	BK	52	THR	3.1
1	CS	332	THR	3.1
1	Cc	332	THR	3.1
1	CL	337	GLU	3.1
1	BM	302	ASP	3.1
1	AH	228	LEU	3.1
1	CE	252	PRO	3.1
1	BI	326	PRO	3.1
1	BJ	241	ILE	3.1
1	CN	241	ILE	3.1
1	Bd	136	HIS	3.1
1	BM	297	ARG	3.1
1	BO	121	GLY	3.1
1	BO	297	ARG	3.1
1	Aa	159	ARG	3.1
1	BE	178	THR	3.1
1	BH	178	THR	3.1
1	BD	161	GLN	3.1
1	CB	289	ALA	3.1
1	CD	255	ALA	3.1
1	BG	327	VAL	3.1
1	CG	220	ALA	3.1
1	BN	278	VAL	3.1
1	AO	264	SER	3.1
1	AU	263	LEU	3.1
1	Bb	234	SER	3.1
1	Bb	324	LEU	3.1
1	Bc	269	LEU	3.1
1	CO	249	ASP	3.1
1	BV	54	ASP	3.1
1	CO	323	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	Ac	308	PHE	3.1
1	BN	239	LYS	3.1
1	AD	218	THR	3.1
1	CO	329	THR	3.1
1	CS	246	THR	3.1
1	BX	322	GLN	3.1
1	BI	242	LEU	3.1
1	CM	324	LEU	3.1
1	AL	293	ALA	3.1
1	BS	312	VAL	3.1
1	BU	327	VAL	3.1
1	AI	331	CYS	3.1
1	BM	253	ASP	3.1
1	CY	250	ILE	3.1
1	AB	257	PHE	3.1
1	AK	320	PRO	3.1
1	BM	252	PRO	3.1
1	BX	238	PHE	3.1
1	BB	261	ARG	3.1
1	CB	239	LYS	3.1
1	CC	294	GLY	3.1
1	BP	299	GLY	3.1
1	BI	235	THR	3.1
1	BM	332	THR	3.1
1	CO	228	LEU	3.1
1	Ac	322	GLN	3.1
1	BB	334	VAL	3.1
1	CB	277	ALA	3.1
1	CD	256	VAL	3.1
1	CH	312	VAL	3.1
1	BI	327	VAL	3.1
1	CN	278	VAL	3.1
1	BX	277	ALA	3.1
1	CC	253	ASP	3.1
1	AF	262	PRO	3.1
1	BO	252	PRO	3.1
1	CP	262	PRO	3.1
1	CX	266	ASP	3.1
1	Bb	252	PRO	3.1
1	Ab	310	ASP	3.1
1	Bc	252	PRO	3.1
1	BP	261	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
1	BB	242	LEU	3.1
1	AI	242	LEU	3.1
1	CJ	228	LEU	3.1
1	BW	189	GLY	3.1
1	BZ	269	LEU	3.1
1	Ab	233	LEU	3.1
1	BC	235	THR	3.1
1	CA	277	ALA	3.1
1	BS	227	SER	3.1
1	BU	53	ASN	3.1
1	Cb	241	ILE	3.1
1	BG	318	GLU	3.1
1	CL	105	GLU	3.1
1	AO	308	PHE	3.1
1	CP	105	GLU	3.1
1	BV	108	GLU	3.1
1	AX	105	GLU	3.1
1	CF	283	LYS	3.1
1	CN	247	PRO	3.1
1	CD	248	LEU	3.1
1	AF	263	LEU	3.1
1	BQ	54	ASP	3.1
1	BB	226	GLY	3.1
1	BH	322	GLN	3.0
1	BK	136	HIS	3.1
1	BL	52	THR	3.1
1	CO	246	THR	3.1
1	Bc	178	THR	3.1
1	AC	278	VAL	3.0
1	CH	300	ILE	3.0
1	AI	232	SER	3.0
1	CK	250	ILE	3.0
1	CM	232	SER	3.0
1	BO	256	VAL	3.0
1	Ab	232	SER	3.0
1	Cc	312	VAL	3.0
1	CG	286	ALA	3.0
1	CG	293	ALA	3.0
1	AC	230	ASN	3.0
1	BF	238	PHE	3.0
1	BS	296	PHE	3.0
1	Bb	236	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	Cd	230	ASN	3.0
1	AM	105	GLU	3.0
1	CT	337	GLU	3.0
1	BM	320	PRO	3.0
1	CQ	252	PRO	3.0
1	Bc	292	PRO	3.0
1	BH	260	ASP	3.0
1	BM	335	ASP	3.0
1	CI	299	GLY	3.0
1	BM	311	GLY	3.0
1	Bd	287	GLY	3.0
1	AC	224	THR	3.0
1	CH	246	THR	3.0
1	BU	309	THR	3.0
1	AZ	323	ILE	3.0
1	Ab	264	SER	3.0
1	Cb	256	VAL	3.0
1	AB	239	LYS	3.0
1	BB	303	ASN	3.0
1	AH	162	TYR	3.0
1	BI	236	ASN	3.0
1	BS	321	ARG	3.0
1	Cb	297	ARG	3.0
1	CB	231	ASP	3.0
1	BH	310	ASP	3.0
1	BM	310	ASP	3.0
1	Ab	266	ASP	3.0
1	Cd	121	GLY	3.0
1	AU	161	GLN	3.0
1	CE	264	SER	3.0
1	CG	281	HIS	3.0
1	CH	251	ALA	3.0
1	AM	281	HIS	3.0
1	BR	136	HIS	3.0
1	CU	293	ALA	3.0
1	AJ	164	ARG	3.0
1	AN	324	LEU	3.0
1	AO	325	LEU	3.0
1	CO	324	LEU	3.0
1	BU	97	ARG	3.0
1	AS	53	ASN	3.0
1	CC	298	TRP	3.0

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Mol	Chain	Res	Type	RSRZ
1	BQ	105	GLU	3.0
1	CD	262	PRO	3.0
1	BI	292	PRO	3.0
1	BO	320	PRO	3.0
1	CG	335	ASP	3.0
1	CM	266	ASP	3.0
1	CO	237	ASP	3.0
1	CU	329	THR	3.0
1	Bb	332	THR	3.0
1	BB	227	SER	3.0
1	CE	278	VAL	3.0
1	AH	264	SER	3.0
1	CH	304	PHE	3.0
1	AI	274	VAL	3.0
1	AX	227	SER	3.0
1	AX	232	SER	3.0
1	BA	269	LEU	3.0
1	AC	325	LEU	3.0
1	AK	313	ALA	3.0
1	CN	293	ALA	3.0
1	BO	286	ALA	3.0
1	AR	313	ALA	3.0
1	BH	236	ASN	3.0
1	CK	115	CYS	3.0
1	BO	229	TYR	3.0
1	Bc	267	TYR	3.0
1	CI	318	GLU	3.0
1	CU	292	PRO	3.0
1	CC	245	SER	3.0
1	BD	332	THR	3.0
1	BS	52	THR	3.0
1	Cb	245	SER	3.0
1	Cc	291	THR	3.0
1	Ad	312	VAL	3.0
1	AD	206	ARG	3.0
1	CG	277	ALA	3.0
1	CJ	255	ALA	3.0
1	CP	231	ASP	3.0
1	CC	56	HIS	3.0
1	BI	315	TYR	3.0
1	CT	279	TYR	3.0
1	BU	303	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	Aa	53	ASN	3.0
1	AA	108	GLU	3.0
1	CM	115	CYS	3.0
1	AH	265	ILE	3.0
1	CO	280	TRP	3.0
1	Bc	280	TRP	3.0
1	BC	189	GLY	3.0
1	CK	294	GLY	3.0
1	AM	166	LEU	3.0
1	BO	332	THR	3.0
1	CP	325	LEU	3.0
1	BQ	228	LEU	3.0
1	CQ	282	LEU	3.0
1	BS	242	LEU	3.0
1	BU	269	LEU	3.0
1	CU	324	LEU	3.0
1	AX	228	LEU	3.0
1	CK	316	SER	3.0
1	Cb	329	THR	3.0
1	BU	297	ARG	3.0
1	CD	220	ALA	3.0
1	CH	293	ALA	3.0
1	CU	220	ALA	3.0
1	CU	317	ASP	3.0
1	Ac	275	ASP	3.0
1	Bd	275	ASP	3.0
1	CE	56	HIS	2.9
1	BD	303	ASN	2.9
1	BO	315	TYR	2.9
1	BZ	315	TYR	2.9
1	Cc	288	ASN	2.9
1	BH	252	PRO	2.9
1	BJ	105	GLU	2.9
1	CK	337	GLU	2.9
1	BO	323	ILE	2.9
1	CW	337	GLU	2.9
1	CG	280	TRP	2.9
1	BU	280	TRP	2.9
1	AB	233	LEU	2.9
1	CB	228	LEU	2.9
1	CE	324	LEU	2.9
1	CY	331	CYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	CA	254	GLY	2.9
1	BG	328	GLY	2.9
1	BI	299	GLY	2.9
1	CJ	224	THR	2.9
1	CO	232	SER	2.9
1	AS	164	ARG	2.9
1	AU	274	VAL	2.9
1	CU	264	SER	2.9
1	CW	264	SER	2.9
1	CY	307	THR	2.9
1	Bb	235	THR	2.9
1	Ac	312	VAL	2.9
1	Ca	289	ALA	2.9
1	Cb	289	ALA	2.9
1	Bc	286	ALA	2.9
1	BA	139	ASP	2.9
1	AB	260	ASP	2.9
1	AC	310	ASP	2.9
1	CN	253	ASP	2.9
1	BF	241	ILE	2.9
1	BG	239	LYS	2.9
1	AD	236	ASN	2.9
1	BI	230	ASN	2.9
1	AI	315	TYR	2.9
1	CS	300	ILE	2.9
1	BP	252	PRO	2.9
1	BR	252	PRO	2.9
1	BU	292	PRO	2.9
1	Cd	320	PRO	2.9
1	BE	238	PHE	2.9
1	BG	263	LEU	2.9
1	AI	238	PHE	2.9
1	BP	228	LEU	2.9
1	BP	257	PHE	2.9
1	Ca	228	LEU	2.9
1	CN	264	SER	2.9
1	CO	297	ARG	2.9
1	Cc	120	GLY	2.9
1	BC	218	THR	2.9
1	AE	278	VAL	2.9
1	AG	307	THR	2.9
1	AW	312	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	AY	336	SER	2.9
1	BZ	278	VAL	2.9
1	AB	220	ALA	2.9
1	BP	289	ALA	2.9
1	CS	283	LYS	2.9
1	AC	241	ILE	2.9
1	AE	253	ASP	2.9
1	CH	317	ASP	2.9
1	CA	228	LEU	2.9
1	BD	136	HIS	2.9
1	CG	242	LEU	2.9
1	CM	267	TYR	2.9
1	AS	236	ASN	2.9
1	BV	263	LEU	2.9
1	BA	292	PRO	2.9
1	AB	238	PHE	2.9
1	CB	292	PRO	2.9
1	CJ	298	TRP	2.9
1	AI	330	VAL	2.9
1	BL	274	VAL	2.9
1	BM	226	GLY	2.9
1	BM	301	TRP	2.9
1	CM	297	ARG	2.9
1	AO	322	GLN	2.9
1	CT	208	SER	2.9
1	CX	270	GLY	2.9
1	CZ	333	ARG	2.9
1	AC	312	VAL	2.9
1	BM	322	GLN	2.9
1	BH	235	THR	2.9
1	AX	178	THR	2.9
1	CE	115	CYS	2.9
1	CH	331	CYS	2.9
1	CO	289	ALA	2.9
1	Cc	255	ALA	2.9
1	Ad	313	ALA	2.9
1	BM	239	LYS	2.9
1	AL	323	ILE	2.9
1	CM	323	ILE	2.9
1	CG	324	LEU	2.9
1	CN	248	LEU	2.9
1	CC	314	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	CJ	257	PHE	2.9
1	CM	135	ASP	2.9
1	CM	249	ASP	2.9
1	AX	238	PHE	2.9
1	BE	262	PRO	2.9
1	AI	53	ASN	2.9
1	BM	223	MET	2.9
1	BN	223	MET	2.9
1	BO	281	HIS	2.9
1	AO	320	PRO	2.9
1	CO	320	PRO	2.9
1	Bc	303	ASN	2.9
1	BS	297	ARG	2.9
1	AV	145	ARG	2.9
1	BC	322	GLN	2.9
1	AE	264	SER	2.9
1	BP	280	TRP	2.9
1	Ca	322	GLN	2.9
1	Cb	328	GLY	2.9
1	Bd	256	VAL	2.9
1	CV	332	THR	2.9
1	Cb	283	LYS	2.9
1	CJ	243	LEU	2.9
1	CQ	324	LEU	2.9
1	BB	229	TYR	2.9
1	AB	320	PRO	2.9
1	AH	320	PRO	2.9
1	Ac	314	TYR	2.9
1	CJ	164	ARG	2.9
1	BM	321	ARG	2.9
1	BR	305	ASN	2.9
1	Bb	231	ASP	2.9
1	CA	278	VAL	2.9
1	BB	254	GLY	2.9
1	CH	294	GLY	2.9
1	BP	264	SER	2.9
1	AW	208	SER	2.9
1	CX	328	GLY	2.9
1	Bc	284	LYS	2.9
1	BH	309	THR	2.9
1	CC	277	ALA	2.9
1	CG	323	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
1	BQ	300	ILE	2.9
1	Ca	325	LEU	2.9
1	CJ	238	PHE	2.9
1	CJ	262	PRO	2.9
1	Ac	164	ARG	2.9
1	CA	275	ASP	2.8
1	BM	275	ASP	2.8
1	BN	237	ASP	2.8
1	BY	318	GLU	2.9
1	AF	278	VAL	2.8
1	AY	264	SER	2.8
1	CG	254	GLY	2.8
1	CH	225	GLN	2.8
1	BO	322	GLN	2.8
1	Ca	254	GLY	2.8
1	Ab	322	GLN	2.8
1	CD	228	LEU	2.8
1	BI	295	TRP	2.8
1	BS	289	ALA	2.8
1	BZ	248	LEU	2.8
1	CG	285	PHE	2.8
1	BA	276	ARG	2.8
1	BB	279	TYR	2.8
1	AC	314	TYR	2.8
1	AE	279	TYR	2.8
1	AI	229	TYR	2.8
1	CI	320	PRO	2.8
1	Bb	320	PRO	2.8
1	Ac	151	LYS	2.8
1	CO	288	ASN	2.8
1	BQ	136	HIS	2.8
1	BX	136	HIS	2.8
1	Cd	274	VAL	2.8
1	AI	282	LEU	2.8
1	CT	249	ASP	2.8
1	BU	226	GLY	2.8
1	Bb	328	GLY	2.8
1	Bc	294	GLY	2.8
1	Cd	323	ILE	2.8
1	CH	220	ALA	2.8
1	BS	332	THR	2.8
1	BV	178	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	Ca	286	ALA	2.8
1	AH	280	TRP	2.8
1	BO	295	TRP	2.8
1	BE	296	PHE	2.8
1	CM	285	PHE	2.8
1	CY	296	PHE	2.8
1	CB	261	ARG	2.8
1	BA	262	PRO	2.8
1	CS	262	PRO	2.8
1	BC	105	GLU	2.8
1	CF	250	ILE	2.8
1	BG	269	LEU	2.8
1	CH	250	ILE	2.8
1	CL	264	SER	2.8
1	AM	263	LEU	2.8
1	BO	227	SER	2.8
1	CN	108	GLU	2.8
1	AU	265	ILE	2.8
1	CU	233	LEU	2.8
1	BX	85	VAL	2.8
1	Bb	233	LEU	2.8
1	BD	120	GLY	2.8
1	AK	56	HIS	2.8
1	Bc	136	HIS	2.8
1	BB	335	ASP	2.8
1	CC	255	ALA	2.8
1	CK	317	ASP	2.8
1	AR	293	ALA	2.8
1	AS	106	THR	2.8
1	AU	289	ALA	2.8
1	AY	266	ASP	2.8
1	Bb	178	THR	2.8
1	Bb	302	ASP	2.8
1	Cc	313	ALA	2.8
1	BP	159	ARG	2.8
1	BS	239	LYS	2.8
1	AB	263	LEU	2.8
1	AC	265	ILE	2.8
1	AE	263	LEU	2.8
1	CF	247	PRO	2.8
1	BN	300	ILE	2.8
1	CN	221	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	CO	292	PRO	2.8
1	CQ	221	PRO	2.8
1	AH	274	VAL	2.8
1	AH	278	VAL	2.8
1	BU	334	VAL	2.8
1	BY	229	TYR	2.8
1	BB	288	ASN	2.8
1	AG	322	GLN	2.8
1	BH	254	GLY	2.8
1	BK	236	ASN	2.8
1	BO	328	GLY	2.8
1	BR	189	GLY	2.8
1	AC	313	ALA	2.8
1	AI	163	THR	2.8
1	CM	332	THR	2.8
1	BU	251	ALA	2.8
1	BU	293	ALA	2.8
1	Aa	165	THR	2.8
1	Bb	313	ALA	2.8
1	Bd	289	ALA	2.8
1	BC	317	ASP	2.8
1	CC	249	ASP	2.8
1	AH	266	ASP	2.8
1	CY	310	ASP	2.8
1	Bb	310	ASP	2.8
1	BH	239	LYS	2.8
1	AH	206	ARG	2.8
1	BO	301	TRP	2.8
1	BO	321	ARG	2.8
1	AM	233	LEU	2.8
1	CY	243	LEU	2.8
1	Bc	325	LEU	2.8
1	Ad	300	ILE	2.8
1	AB	252	PRO	2.8
1	BE	292	PRO	2.8
1	CE	292	PRO	2.8
1	BF	264	SER	2.8
1	CP	256	VAL	2.8
1	Cb	327	VAL	2.8
1	BN	108	GLU	2.8
1	CU	290	GLY	2.8
1	BX	290	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	Cb	288	ASN	2.8
1	Ad	118	ASN	2.8
1	Cd	226	GLY	2.8
1	AV	106	THR	2.8
1	BX	178	THR	2.8
1	AG	151	LYS	2.8
1	CN	281	HIS	2.8
1	AC	260	ASP	2.8
1	CF	335	ASP	2.8
1	BI	253	ASP	2.8
1	CI	275	ASP	2.8
1	CO	333	ARG	2.8
1	CS	253	ASP	2.8
1	CU	54	ASP	2.8
1	AV	206	ARG	2.8
1	Ca	260	ASP	2.8
1	CE	331	CYS	2.8
1	BE	324	LEU	2.8
1	CX	243	LEU	2.8
1	AI	323	ILE	2.8
1	AO	300	ILE	2.8
1	CB	320	PRO	2.8
1	BC	330	VAL	2.8
1	CG	292	PRO	2.8
1	CO	221	PRO	2.8
1	Ca	330	VAL	2.8
1	Bc	256	VAL	2.8
1	Bd	315	TYR	2.8
1	Cd	267	TYR	2.8
1	BA	290	GLY	2.8
1	BG	254	GLY	2.8
1	AH	322	GLN	2.8
1	CH	296	PHE	2.8
1	CO	218	THR	2.8
1	CO	286	ALA	2.8
1	CU	283	LYS	2.8
1	CX	220	ALA	2.8
1	CZ	218	THR	2.8
1	Ad	293	ALA	2.8
1	Bb	261	ARG	2.7
1	Cc	276	ARG	2.7
1	BH	269	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	CJ	248	LEU	2.7
1	AP	269	LEU	2.7
1	AQ	263	LEU	2.7
1	AC	266	ASP	2.7
1	CC	231	ASP	2.7
1	BG	323	ILE	2.7
1	BH	253	ASP	2.7
1	AI	54	ASP	2.7
1	CM	241	ILE	2.7
1	BN	317	ASP	2.7
1	BQ	87	ASP	2.7
1	AQ	300	ILE	2.7
1	CQ	249	ASP	2.7
1	BU	317	ASP	2.7
1	Cd	253	ASP	2.7
1	BK	295	TRP	2.7
1	AV	331	CYS	2.7
1	Cd	115	CYS	2.7
1	BH	234	SER	2.7
1	BV	274	VAL	2.7
1	Ab	227	SER	2.7
1	Bc	234	SER	2.7
1	BC	320	PRO	2.7
1	BH	319	GLN	2.7
1	AJ	313	ALA	2.7
1	CU	255	ALA	2.7
1	CC	218	THR	2.7
1	CQ	332	THR	2.7
1	CU	218	THR	2.7
1	Ac	235	THR	2.7
1	BF	233	LEU	2.7
1	AG	263	LEU	2.7
1	BM	242	LEU	2.7
1	BM	269	LEU	2.7
1	AR	164	ARG	2.7
1	Bc	276	ARG	2.7
1	BC	300	ILE	2.7
1	AQ	265	ILE	2.7
1	CU	323	ILE	2.7
1	Ab	250	ILE	2.7
1	AC	302	ASP	2.7
1	CF	266	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	CH	260	ASP	2.7
1	CI	280	TRP	2.7
1	Cb	295	TRP	2.7
1	AB	274	VAL	2.7
1	CB	327	VAL	2.7
1	AE	274	VAL	2.7
1	AG	278	VAL	2.7
1	CI	256	VAL	2.7
1	AS	58	SER	2.7
1	Ab	278	VAL	2.7
1	CC	320	PRO	2.7
1	AO	239	LYS	2.7
1	CU	296	PHE	2.7
1	CU	320	PRO	2.7
1	CX	262	PRO	2.7
1	Ab	304	PHE	2.7
1	Cb	238	PHE	2.7
1	Cb	285	PHE	2.7
1	CX	267	TYR	2.7
1	BA	325	LEU	2.7
1	AC	289	ALA	2.7
1	BD	309	THR	2.7
1	AM	217	GLU	2.7
1	CN	233	LEU	2.7
1	BP	263	LEU	2.7
1	CQ	105	GLU	2.7
1	AX	337	GLU	2.7
1	AY	313	ALA	2.7
1	BG	236	ASN	2.7
1	BN	178	THR	2.7
1	CS	224	THR	2.7
1	Ba	178	THR	2.7
1	BM	300	ILE	2.7
1	CT	250	ILE	2.7
1	BI	136	HIS	2.7
1	BT	136	HIS	2.7
1	BH	334	VAL	2.7
1	CK	295	TRP	2.7
1	BN	302	ASP	2.7
1	CN	232	SER	2.7
1	AP	280	TRP	2.7
1	CQ	264	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	CU	249	ASP	2.7
1	CA	257	PHE	2.7
1	CB	238	PHE	2.7
1	CE	256	VAL	2.7
1	Cc	283	LYS	2.7
1	CU	238	PHE	2.7
1	AI	221	PRO	2.7
1	CS	221	PRO	2.7
1	BX	252	PRO	2.7
1	CG	228	LEU	2.7
1	BB	289	ALA	2.7
1	CB	290	GLY	2.7
1	CC	267	TYR	2.7
1	AI	270	GLY	2.7
1	CI	258	GLN	2.7
1	CW	315	TYR	2.7
1	Cb	242	LEU	2.7
1	CB	337	GLU	2.7
1	CC	206	ARG	2.7
1	BN	297	ARG	2.7
1	CU	297	ARG	2.7
1	BV	164	ARG	2.7
1	CX	261	ARG	2.7
1	CG	332	THR	2.7
1	CH	291	THR	2.7
1	BA	190	ASN	2.7
1	BN	323	ILE	2.7
1	AN	323	ILE	2.7
1	CP	300	ILE	2.7
1	Cb	222	ILE	2.7
1	Ad	309	THR	2.7
1	CE	281	HIS	2.7
1	CW	151	LYS	2.7
1	AC	232	SER	2.7
1	AN	232	SER	2.7
1	AN	264	SER	2.7
1	AQ	232	SER	2.7
1	AW	336	SER	2.7
1	CW	257	PHE	2.7
1	BX	296	PHE	2.7
1	CY	308	PHE	2.7
1	CZ	264	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	AL	312	VAL	2.7
1	Cc	308	PHE	2.7
1	BA	298	TRP	2.7
1	BC	310	ASP	2.7
1	CK	275	ASP	2.7
1	CP	249	ASP	2.7
1	AS	260	ASP	2.7
1	BI	320	PRO	2.7
1	Aa	269	LEU	2.7
1	BK	319	GLN	2.7
1	CM	225	GLN	2.7
1	BP	319	GLN	2.7
1	CD	279	TYR	2.7
1	BH	277	ALA	2.7
1	BI	289	ALA	2.7
1	BO	122	GLY	2.7
1	AV	293	ALA	2.7
1	Cb	229	TYR	2.7
1	BG	300	ILE	2.7
1	CC	108	GLU	2.7
1	AI	271	THR	2.7
1	CU	291	THR	2.7
1	Bb	307	THR	2.7
1	Bd	105	GLU	2.7
1	BU	151	LYS	2.7
1	BF	240	SER	2.7
1	CG	232	SER	2.7
1	BH	240	SER	2.7
1	AH	238	PHE	2.7
1	CH	336	SER	2.7
1	CO	227	SER	2.7
1	BC	269	LEU	2.7
1	BH	312	VAL	2.7
1	BJ	269	LEU	2.7
1	CV	256	VAL	2.7
1	Ab	274	VAL	2.7
1	Cc	228	LEU	2.7
1	CF	298	TRP	2.7
1	BG	231	ASP	2.7
1	AH	298	TRP	2.7
1	CL	87	ASP	2.7
1	BM	292	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	BN	262	PRO	2.7
1	Bb	275	ASP	2.7
1	Ad	266	ASP	2.7
1	BG	226	GLY	2.7
1	CM	250	ILE	2.7
1	BP	300	ILE	2.7
1	BX	255	ALA	2.7
1	BY	328	GLY	2.7
1	AY	51	GLY	2.7
1	BZ	323	ILE	2.7
1	Ba	250	ILE	2.7
1	BI	229	TYR	2.7
1	Bb	226	GLY	2.7
1	BK	318	GLU	2.7
1	BO	216	GLU	2.7
1	BO	329	THR	2.7
1	CO	224	THR	2.7
1	AW	52	THR	2.7
1	BX	318	GLU	2.7
1	CX	246	THR	2.7
1	CA	53	ASN	2.7
1	AE	288	ASN	2.7
1	AX	236	ASN	2.7
1	Aa	239	LYS	2.7
1	CD	257	PHE	2.7
1	AM	127	PHE	2.7
1	Ab	257	PHE	2.7
1	BE	228	LEU	2.7
1	CF	316	SER	2.7
1	AG	325	LEU	2.7
1	CG	227	SER	2.7
1	AN	228	LEU	2.7
1	Ca	263	LEU	2.7
1	Ca	264	SER	2.7
1	Ac	316	SER	2.7
1	CC	281	HIS	2.6
1	BI	330	VAL	2.6
1	AX	281	HIS	2.6
1	CX	281	HIS	2.6
1	Ba	56	HIS	2.6
1	BC	247	PRO	2.6
1	AO	321	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	BX	323	ILE	2.6
1	CX	298	TRP	2.6
1	Cb	323	ILE	2.6
1	Ac	323	ILE	2.6
1	CB	293	ALA	2.6
1	CB	313	ALA	2.6
1	CJ	310	ASP	2.6
1	AP	311	GLY	2.6
1	BS	237	ASP	2.6
1	AC	235	THR	2.6
1	BJ	163	THR	2.6
1	BM	235	THR	2.6
1	BU	235	THR	2.6
1	AU	239	LYS	2.6
1	AQ	337	GLU	2.6
1	BB	324	LEU	2.6
1	Ab	238	PHE	2.6
1	BO	240	SER	2.6
1	CT	264	SER	2.6
1	Ca	64	SER	2.6
1	BN	312	VAL	2.6
1	Cb	330	VAL	2.6
1	AI	241	ILE	2.6
1	Ca	333	ARG	2.6
1	CF	221	PRO	2.6
1	BU	252	PRO	2.6
1	AU	180	PRO	2.6
1	AV	262	PRO	2.6
1	BB	293	ALA	2.6
1	AC	311	GLY	2.6
1	AD	220	ALA	2.6
1	CD	290	GLY	2.6
1	CF	311	GLY	2.6
1	BG	251	ALA	2.6
1	CM	298	TRP	2.6
1	CM	301	TRP	2.6
1	Bc	226	GLY	2.6
1	Bc	287	GLY	2.6
1	Cc	280	TRP	2.6
1	Cc	290	GLY	2.6
1	AA	163	THR	2.6
1	CB	246	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	CF	249	ASP	2.6
1	BK	291	THR	2.6
1	AK	162	TYR	2.6
1	AQ	279	TYR	2.6
1	AT	52	THR	2.6
1	CT	253	ASP	2.6
1	Cb	332	THR	2.6
1	Bc	253	ASP	2.6
1	CS	324	LEU	2.6
1	CY	233	LEU	2.6
1	BU	236	ASN	2.6
1	CZ	257	PHE	2.6
1	BA	234	SER	2.6
1	BF	227	SER	2.6
1	CI	240	SER	2.6
1	BM	227	SER	2.6
1	CC	312	VAL	2.6
1	BH	330	VAL	2.6
1	AO	274	VAL	2.6
1	CO	330	VAL	2.6
1	CA	265	ILE	2.6
1	AE	206	ARG	2.6
1	AL	164	ARG	2.6
1	CT	323	ILE	2.6
1	BW	145	ARG	2.6
1	BY	331	CYS	2.6
1	Bc	321	ARG	2.6
1	CD	292	PRO	2.6
1	CJ	247	PRO	2.6
1	BB	311	GLY	2.6
1	CC	286	ALA	2.6
1	CG	289	ALA	2.6
1	CG	290	GLY	2.6
1	CG	294	GLY	2.6
1	BI	313	ALA	2.6
1	AI	51	GLY	2.6
1	BN	254	GLY	2.6
1	CN	290	GLY	2.6
1	CU	286	ALA	2.6
1	BB	310	ASP	2.6
1	AC	269	LEU	2.6
1	BD	269	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	CK	269	LEU	2.6
1	BL	178	THR	2.6
1	AN	235	THR	2.6
1	BO	248	LEU	2.6
1	BP	178	THR	2.6
1	AP	263	LEU	2.6
1	BQ	324	LEU	2.6
1	AQ	106	THR	2.6
1	BX	291	THR	2.6
1	BX	315	TYR	2.6
1	Ca	243	LEU	2.6
1	Bb	267	TYR	2.6
1	Cc	324	LEU	2.6
1	Cd	315	TYR	2.6
1	BF	237	ASP	2.6
1	CG	249	ASP	2.6
1	Bb	249	ASP	2.6
1	AD	337	GLU	2.6
1	AI	217	GLU	2.6
1	CX	217	GLU	2.6
1	AE	236	ASN	2.6
1	BF	234	SER	2.6
1	CT	53	ASN	2.6
1	CY	303	ASN	2.6
1	BB	241	ILE	2.6
1	BB	250	ILE	2.6
1	AC	297	ARG	2.6
1	CG	241	ILE	2.6
1	CH	330	VAL	2.6
1	AU	164	ARG	2.6
1	AV	250	ILE	2.6
1	Bb	321	ARG	2.6
1	Bb	239	LYS	2.6
1	AU	281	HIS	2.6
1	BW	331	CYS	2.6
1	Ba	136	HIS	2.6
1	Bd	322	GLN	2.6
1	CF	120	GLY	2.6
1	BM	233	LEU	2.6
1	BN	263	LEU	2.6
1	CS	254	GLY	2.6
1	AC	279	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	AD	315	TYR	2.6
1	CE	224	THR	2.6
1	BG	332	THR	2.6
1	CU	280	TRP	2.6
1	Ac	52	THR	2.6
1	Cc	314	TYR	2.6
1	Bd	295	TRP	2.6
1	Bd	332	THR	2.6
1	CD	266	ASP	2.6
1	CE	54	ASP	2.6
1	BG	237	ASP	2.6
1	AL	217	GLU	2.6
1	BU	249	ASP	2.6
1	AV	260	ASP	2.6
1	AP	264	SER	2.6
1	Bc	268	SER	2.6
1	Cc	227	SER	2.6
1	CU	256	VAL	2.6
1	CU	261	ARG	2.6
1	AX	278	VAL	2.6
1	Bd	274	VAL	2.6
1	Ad	278	VAL	2.6
1	CO	283	LYS	2.6
1	AS	306	LYS	2.6
1	BA	322	GLN	2.6
1	AD	269	LEU	2.6
1	BI	233	LEU	2.6
1	CT	293	ALA	2.6
1	Ca	320	PRO	2.6
1	Cc	233	LEU	2.6
1	AE	254	GLY	2.6
1	AX	56	HIS	2.6
1	BN	238	PHE	2.6
1	CO	238	PHE	2.6
1	BE	291	THR	2.6
1	CI	246	THR	2.6
1	AI	280	TRP	2.6
1	BL	315	TYR	2.6
1	BN	309	THR	2.6
1	Cb	307	THR	2.6
1	BN	318	GLU	2.6
1	BU	337	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	CG	310	ASP	2.6
1	BI	234	SER	2.6
1	BM	240	SER	2.6
1	BX	227	SER	2.6
1	AX	265	ILE	2.6
1	BZ	300	ILE	2.6
1	Cc	222	ILE	2.6
1	CF	236	ASN	2.6
1	CI	276	ARG	2.6
1	CK	236	ASN	2.6
1	BM	330	VAL	2.6
1	BV	53	ASN	2.6
1	Ab	230	ASN	2.6
1	Cd	288	ASN	2.6
1	AH	233	LEU	2.6
1	AB	258	GLN	2.6
1	BG	255	ALA	2.6
1	BH	286	ALA	2.6
1	CI	293	ALA	2.6
1	BM	313	ALA	2.6
1	BM	326	PRO	2.6
1	AM	220	ALA	2.6
1	BN	255	ALA	2.6
1	AQ	322	GLN	2.6
1	CQ	247	PRO	2.6
1	CE	285	PHE	2.6
1	BS	238	PHE	2.6
1	AZ	254	GLY	2.6
1	Ba	328	GLY	2.6
1	Bc	121	GLY	2.6
1	CD	115	CYS	2.5
1	CO	331	CYS	2.5
1	BA	108	GLU	2.5
1	AB	318	GLU	2.5
1	CS	217	GLU	2.5
1	BU	261	ARG	2.5
1	AW	227	SER	2.5
1	CZ	239	LYS	2.5
1	BI	334	VAL	2.5
1	CC	53	ASN	2.5
1	BH	243	LEU	2.5
1	Bd	263	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	BE	322	GLN	2.5
1	AG	304	PHE	2.5
1	AL	322	GLN	2.5
1	AM	326	PRO	2.5
1	BP	238	PHE	2.5
1	Cc	292	PRO	2.5
1	CE	270	GLY	2.5
1	BH	226	GLY	2.5
1	CW	270	GLY	2.5
1	AA	218	THR	2.5
1	BG	281	HIS	2.5
1	BG	329	THR	2.5
1	AH	300	ILE	2.5
1	CH	329	THR	2.5
1	AJ	52	THR	2.5
1	CJ	332	THR	2.5
1	BP	291	THR	2.5
1	BS	291	THR	2.5
1	AS	323	ILE	2.5
1	BU	241	ILE	2.5
1	AW	178	THR	2.5
1	BX	281	HIS	2.5
1	AW	314	TYR	2.5
1	BZ	229	TYR	2.5
1	Bb	279	TYR	2.5
1	BC	280	TRP	2.5
1	CC	295	TRP	2.5
1	BE	297	ARG	2.5
1	CP	295	TRP	2.5
1	BU	321	ARG	2.5
1	AV	336	SER	2.5
1	BX	276	ARG	2.5
1	AY	316	SER	2.5
1	Bb	301	TRP	2.5
1	AO	278	VAL	2.5
1	Cd	337	GLU	2.5
1	AR	228	LEU	2.5
1	CS	282	LEU	2.5
1	BU	282	LEU	2.5
1	Bd	282	LEU	2.5
1	CF	275	ASP	2.5
1	CG	288	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	CI	288	ASN	2.5
1	AN	230	ASN	2.5
1	CO	310	ASP	2.5
1	BY	317	ASP	2.5
1	Aa	236	ASN	2.5
1	CF	252	PRO	2.5
1	CF	320	PRO	2.5
1	BG	252	PRO	2.5
1	CI	289	ALA	2.5
1	AK	319	GLN	2.5
1	AM	129	PRO	2.5
1	CN	220	ALA	2.5
1	AP	322	GLN	2.5
1	CS	313	ALA	2.5
1	AD	51	GLY	2.5
1	CH	328	GLY	2.5
1	BM	250	ILE	2.5
1	AM	323	ILE	2.5
1	CX	283	LYS	2.5
1	AC	106	THR	2.5
1	AF	235	THR	2.5
1	CU	246	THR	2.5
1	Ab	307	THR	2.5
1	Bd	178	THR	2.5
1	BC	136	HIS	2.5
1	BF	281	HIS	2.5
1	BT	206	ARG	2.5
1	CX	34	ARG	2.5
1	AF	336	SER	2.5
1	CH	268	SER	2.5
1	BV	208	SER	2.5
1	Aa	208	SER	2.5
1	CF	318	GLU	2.5
1	AJ	278	VAL	2.5
1	AN	263	LEU	2.5
1	BP	324	LEU	2.5
1	CS	256	VAL	2.5
1	Aa	324	LEU	2.5
1	AB	331	CYS	2.5
1	CA	253	ASP	2.5
1	CB	260	ASP	2.5
1	CB	296	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	CE	275	ASP	2.5
1	BX	317	ASP	2.5
1	Bc	257	PHE	2.5
1	BU	322	GLN	2.5
1	CU	313	ALA	2.5
1	CV	313	ALA	2.5
1	BL	247	PRO	2.5
1	Bb	258	GLN	2.5
1	CB	323	ILE	2.5
1	AE	265	ILE	2.5
1	BG	283	LYS	2.5
1	CI	250	ILE	2.5
1	BP	250	ILE	2.5
1	CQ	250	ILE	2.5
1	BS	300	ILE	2.5
1	BU	189	GLY	2.5
1	AU	181	GLY	2.5
1	CC	321	ARG	2.5
1	CG	224	THR	2.5
1	CG	309	THR	2.5
1	Aa	206	ARG	2.5
1	Bc	271	THR	2.5
1	CA	242	LEU	2.5
1	BH	248	LEU	2.5
1	AO	263	LEU	2.5
1	BP	325	LEU	2.5
1	AQ	324	LEU	2.5
1	CQ	208	SER	2.5
1	CR	56	HIS	2.5
1	BU	234	SER	2.5
1	CU	269	LEU	2.5
1	BV	56	HIS	2.5
1	Bb	240	SER	2.5
1	CH	256	VAL	2.5
1	AP	104	VAL	2.5
1	AU	280	TRP	2.5
1	CX	280	TRP	2.5
1	BA	53	ASN	2.5
1	BE	236	ASN	2.5
1	BF	236	ASN	2.5
1	CS	303	ASN	2.5
1	AC	320	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	BE	320	PRO	2.5
1	AE	250	ILE	2.5
1	AF	265	ILE	2.5
1	CH	253	ASP	2.5
1	CH	275	ASP	2.5
1	AJ	54	ASP	2.5
1	BM	249	ASP	2.5
1	AM	266	ASP	2.5
1	BP	161	GLN	2.5
1	BQ	161	GLN	2.5
1	CQ	286	ALA	2.5
1	AR	201	CYS	2.5
1	CU	277	ALA	2.5
1	BY	239	LYS	2.5
1	Ca	266	ASP	2.5
1	Cc	241	ILE	2.5
1	Bd	277	ALA	2.5
1	AT	262	PRO	2.5
1	BB	189	GLY	2.5
1	AV	51	GLY	2.5
1	AF	164	ARG	2.5
1	BG	324	LEU	2.5
1	AH	321	ARG	2.5
1	CM	233	LEU	2.5
1	BR	269	LEU	2.5
1	BY	269	LEU	2.5
1	Ba	206	ARG	2.5
1	AB	232	SER	2.5
1	AA	56	HIS	2.5
1	BE	315	TYR	2.5
1	CE	274	VAL	2.5
1	CF	278	VAL	2.5
1	BG	136	HIS	2.5
1	CG	223	MET	2.5
1	BQ	279	TYR	2.5
1	Bc	281	HIS	2.5
1	AY	217	GLU	2.5
1	AZ	105	GLU	2.5
1	BE	298	TRP	2.5
1	BB	283	LYS	2.5
1	CC	236	ASN	2.5
1	BN	303	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	CB	251	ALA	2.5
1	BE	293	ALA	2.5
1	BU	320	PRO	2.5
1	Bc	262	PRO	2.5
1	CA	302	ASP	2.5
1	BC	260	ASP	2.5
1	AH	331	CYS	2.5
1	CH	266	ASP	2.5
1	BN	321	ARG	2.5
1	AN	164	ARG	2.5
1	BU	331	CYS	2.5
1	CW	269	LEU	2.5
1	CX	324	LEU	2.5
1	CN	224	THR	2.5
1	BS	178	THR	2.5
1	Ab	332	THR	2.5
1	Cb	309	THR	2.5
1	BB	223	MET	2.5
1	BC	234	SER	2.5
1	CC	330	VAL	2.5
1	AF	274	VAL	2.5
1	AH	279	TYR	2.5
1	BK	267	TYR	2.5
1	AS	279	TYR	2.5
1	AE	281	HIS	2.4
1	AJ	337	GLU	2.4
1	BP	318	GLU	2.4
1	BV	105	GLU	2.4
1	Cb	296	PHE	2.4
1	Ba	151	LYS	2.4
1	AE	300	ILE	2.4
1	BF	250	ILE	2.4
1	AF	323	ILE	2.4
1	AH	323	ILE	2.4
1	BU	300	ILE	2.4
1	Bc	241	ILE	2.4
1	AB	118	ASN	2.4
1	AJ	53	ASN	2.4
1	CJ	289	ALA	2.4
1	CP	53	ASN	2.4
1	AT	289	ALA	2.4
1	AW	293	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	BY	288	ASN	2.4
1	Bc	277	ALA	2.4
1	BF	324	LEU	2.4
1	BQ	166	LEU	2.4
1	Cc	319	GLN	2.4
1	BG	276	ARG	2.4
1	BH	321	ARG	2.4
1	CJ	34	ARG	2.4
1	CS	292	PRO	2.4
1	CY	262	PRO	2.4
1	CF	290	GLY	2.4
1	CA	249	ASP	2.4
1	CU	266	ASP	2.4
1	Ba	54	ASP	2.4
1	Bd	317	ASP	2.4
1	AA	336	SER	2.4
1	BB	235	THR	2.4
1	AB	227	SER	2.4
1	AD	178	THR	2.4
1	AL	227	SER	2.4
1	CR	264	SER	2.4
1	BU	329	THR	2.4
1	Ba	208	SER	2.4
1	BU	312	VAL	2.4
1	CB	304	PHE	2.4
1	Bd	279	TYR	2.4
1	BC	250	ILE	2.4
1	CK	323	ILE	2.4
1	CL	323	ILE	2.4
1	AQ	217	GLU	2.4
1	Ac	318	GLU	2.4
1	Cc	281	HIS	2.4
1	AA	57	LEU	2.4
1	CJ	242	LEU	2.4
1	CN	324	LEU	2.4
1	BP	243	LEU	2.4
1	AF	236	ASN	2.4
1	AG	230	ASN	2.4
1	AI	322	GLN	2.4
1	CK	164	ARG	2.4
1	BL	303	ASN	2.4
1	BW	319	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	CX	321	ARG	2.4
1	Bb	303	ASN	2.4
1	CJ	292	PRO	2.4
1	BA	299	GLY	2.4
1	CB	287	GLY	2.4
1	BI	254	GLY	2.4
1	CS	290	GLY	2.4
1	Ab	189	GLY	2.4
1	CD	291	THR	2.4
1	BE	275	ASP	2.4
1	CE	310	ASP	2.4
1	BF	275	ASP	2.4
1	AH	307	THR	2.4
1	BM	317	ASP	2.4
1	BO	310	ASP	2.4
1	AP	268	SER	2.4
1	AP	271	THR	2.4
1	CQ	227	SER	2.4
1	CR	87	ASP	2.4
1	BS	275	ASP	2.4
1	CS	54	ASP	2.4
1	BU	275	ASP	2.4
1	BV	332	THR	2.4
1	BA	278	VAL	2.4
1	CF	285	PHE	2.4
1	CG	238	PHE	2.4
1	AU	300	ILE	2.4
1	CZ	323	ILE	2.4
1	CA	217	GLU	2.4
1	AB	105	GLU	2.4
1	BC	228	LEU	2.4
1	AH	282	LEU	2.4
1	BJ	56	HIS	2.4
1	BM	216	GLU	2.4
1	CM	242	LEU	2.4
1	BU	94	HIS	2.4
1	CX	325	LEU	2.4
1	CZ	242	LEU	2.4
1	AB	280	TRP	2.4
1	CB	255	ALA	2.4
1	BE	255	ALA	2.4
1	CG	295	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	BH	301	TRP	2.4
1	AJ	206	ARG	2.4
1	AK	206	ARG	2.4
1	AN	322	GLN	2.4
1	AO	277	ALA	2.4
1	BP	276	ARG	2.4
1	BP	293	ALA	2.4
1	BS	261	ARG	2.4
1	BV	277	ALA	2.4
1	Bd	333	ARG	2.4
1	AA	53	ASN	2.4
1	BB	305	ASN	2.4
1	CB	230	ASN	2.4
1	BE	288	ASN	2.4
1	CJ	303	ASN	2.4
1	BK	247	PRO	2.4
1	BN	320	PRO	2.4
1	BS	320	PRO	2.4
1	CI	270	GLY	2.4
1	BK	189	GLY	2.4
1	BA	178	THR	2.4
1	AA	239	LYS	2.4
1	BG	224	THR	2.4
1	BG	227	SER	2.4
1	BM	329	THR	2.4
1	CQ	106	THR	2.4
1	AS	264	SER	2.4
1	CU	316	SER	2.4
1	AX	235	THR	2.4
1	CI	330	VAL	2.4
1	BP	312	VAL	2.4
1	Ca	256	VAL	2.4
1	Ca	312	VAL	2.4
1	Cc	285	PHE	2.4
1	BD	260	ASP	2.4
1	BQ	249	ASP	2.4
1	Cb	275	ASP	2.4
1	BM	241	ILE	2.4
1	BQ	241	ILE	2.4
1	BS	323	ILE	2.4
1	Bb	250	ILE	2.4
1	Ab	265	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	CB	242	LEU	2.4
1	CD	282	LEU	2.4
1	BH	242	LEU	2.4
1	AI	248	LEU	2.4
1	AV	269	LEU	2.4
1	AD	217	GLU	2.4
1	BH	105	GLU	2.4
1	BN	281	HIS	2.4
1	CO	261	ARG	2.4
1	AQ	97	ARG	2.4
1	BS	159	ARG	2.4
1	BT	56	HIS	2.4
1	AX	217	GLU	2.4
1	BB	286	ALA	2.4
1	AK	286	ALA	2.4
1	Cb	286	ALA	2.4
1	BI	288	ASN	2.4
1	BP	320	PRO	2.4
1	BQ	236	ASN	2.4
1	CN	283	LYS	2.4
1	AP	189	GLY	2.4
1	CW	290	GLY	2.4
1	Cc	316	SER	2.4
1	BA	238	PHE	2.4
1	BC	178	THR	2.4
1	CK	334	VAL	2.4
1	BN	235	THR	2.4
1	BW	235	THR	2.4
1	Ca	291	THR	2.4
1	AS	265	ILE	2.4
1	AW	323	ILE	2.4
1	CF	242	LEU	2.4
1	CG	233	LEU	2.4
1	BI	269	LEU	2.4
1	AX	324	LEU	2.4
1	CZ	282	LEU	2.4
1	Ca	166	LEU	2.4
1	BA	54	ASP	2.4
1	CD	249	ASP	2.4
1	BH	302	ASP	2.4
1	CO	54	ASP	2.4
1	BP	253	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	Ba	317	ASP	2.4
1	BF	279	TYR	2.4
1	BI	276	ARG	2.4
1	CJ	297	ARG	2.4
1	CP	318	GLU	2.4
1	Ca	337	GLU	2.4
1	Ad	318	GLU	2.4
1	BB	277	ALA	2.4
1	BE	281	HIS	2.4
1	CG	313	ALA	2.4
1	BH	293	ALA	2.4
1	CM	251	ALA	2.4
1	CO	220	ALA	2.4
1	AP	95	ALA	2.4
1	CP	56	HIS	2.4
1	CY	115	CYS	2.4
1	Cb	293	ALA	2.4
1	AC	301	TRP	2.4
1	CC	280	TRP	2.4
1	AE	262	PRO	2.4
1	BK	239	LYS	2.4
1	CJ	288	ASN	2.4
1	BO	326	PRO	2.4
1	AO	189	GLY	2.4
1	CP	320	PRO	2.4
1	AQ	236	ASN	2.4
1	CR	287	GLY	2.4
1	AY	236	ASN	2.4
1	CY	288	ASN	2.4
1	CD	264	SER	2.4
1	BH	308	PHE	2.4
1	CJ	208	SER	2.4
1	CM	296	PHE	2.4
1	BQ	296	PHE	2.4
1	CA	269	LEU	2.4
1	AB	323	ILE	2.4
1	CF	327	VAL	2.4
1	BG	309	THR	2.4
1	CG	256	VAL	2.4
1	CG	312	VAL	2.4
1	BI	178	THR	2.4
1	CI	271	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	CJ	246	THR	2.4
1	CM	307	THR	2.4
1	BR	274	VAL	2.4
1	BX	263	LEU	2.4
1	Ba	327	VAL	2.4
1	CB	275	ASP	2.4
1	CG	266	ASP	2.4
1	AM	206	ARG	2.4
1	BP	315	TYR	2.4
1	Ab	333	ARG	2.4
1	Cd	275	ASP	2.4
1	AE	108	GLU	2.4
1	BF	255	ALA	2.4
1	CF	286	ALA	2.4
1	AI	108	GLU	2.4
1	BJ	108	GLU	2.4
1	AR	105	GLU	2.4
1	Cc	251	ALA	2.4
1	CG	239	LYS	2.4
1	BU	173	LYS	2.4
1	Bd	281	HIS	2.3
1	AD	190	ASN	2.3
1	AF	272	GLY	2.3
1	BH	299	GLY	2.3
1	BI	287	GLY	2.3
1	AJ	51	GLY	2.3
1	BK	292	PRO	2.3
1	AL	320	PRO	2.3
1	BM	299	GLY	2.3
1	BN	247	PRO	2.3
1	BN	299	GLY	2.3
1	AO	323	ILE	2.3
1	BP	227	SER	2.3
1	CQ	300	ILE	2.3
1	CS	208	SER	2.3
1	AU	336	SER	2.3
1	Ac	272	GLY	2.3
1	BG	242	LEU	2.3
1	BH	233	LEU	2.3
1	AI	259	LEU	2.3
1	CI	323	ILE	2.3
1	CJ	222	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	BN	241	ILE	2.3
1	Ab	300	ILE	2.3
1	Cb	269	LEU	2.3
1	Bc	250	ILE	2.3
1	BA	327	VAL	2.3
1	CK	274	VAL	2.3
1	AN	52	THR	2.3
1	CP	274	VAL	2.3
1	AS	278	VAL	2.3
1	BJ	297	ARG	2.3
1	Ba	276	ARG	2.3
1	CH	223	MET	2.3
1	AT	279	TYR	2.3
1	CE	249	ASP	2.3
1	CF	310	ASP	2.3
1	CI	317	ASP	2.3
1	BO	151	LYS	2.3
1	BT	135	ASP	2.3
1	CT	239	LYS	2.3
1	Ac	266	ASP	2.3
1	Cc	249	ASP	2.3
1	BB	251	ALA	2.3
1	AE	286	ALA	2.3
1	BG	293	ALA	2.3
1	AG	277	ALA	2.3
1	CM	255	ALA	2.3
1	CN	277	ALA	2.3
1	CO	277	ALA	2.3
1	Aa	217	GLU	2.3
1	AA	281	HIS	2.3
1	AB	240	SER	2.3
1	CB	234	SER	2.3
1	CF	324	LEU	2.3
1	AG	265	ILE	2.3
1	BH	292	PRO	2.3
1	BI	250	ILE	2.3
1	AI	316	SER	2.3
1	AJ	300	ILE	2.3
1	BN	242	LEU	2.3
1	BS	240	SER	2.3
1	CS	243	LEU	2.3
1	BU	122	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	CU	208	SER	2.3
1	CV	248	LEU	2.3
1	Ca	308	PHE	2.3
1	Ab	254	GLY	2.3
1	Bc	243	LEU	2.3
1	Bc	263	LEU	2.3
1	Cd	263	LEU	2.3
1	Cd	264	SER	2.3
1	AC	303	ASN	2.3
1	BY	295	TRP	2.3
1	Bb	288	ASN	2.3
1	CI	331	CYS	2.3
1	BM	291	THR	2.3
1	AM	274	VAL	2.3
1	CZ	165	THR	2.3
1	Bb	256	VAL	2.3
1	Bc	295	TRP	2.3
1	Ab	52	THR	2.3
1	BF	297	ARG	2.3
1	BF	321	ARG	2.3
1	CG	333	ARG	2.3
1	BH	223	MET	2.3
1	BN	145	ARG	2.3
1	Bb	223	MET	2.3
1	Cc	297	ARG	2.3
1	CV	239	LYS	2.3
1	AJ	279	TYR	2.3
1	CD	289	ALA	2.3
1	CH	277	ALA	2.3
1	CM	289	ALA	2.3
1	CQ	277	ALA	2.3
1	Bc	289	ALA	2.3
1	BB	231	ASP	2.3
1	BG	253	ASP	2.3
1	CH	322	GLN	2.3
1	AI	273	ASP	2.3
1	CK	54	ASP	2.3
1	AN	54	ASP	2.3
1	CN	249	ASP	2.3
1	CP	317	ASP	2.3
1	BT	317	ASP	2.3
1	CU	275	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	Ab	237	ASP	2.3
1	BG	285	PHE	2.3
1	CH	242	LEU	2.3
1	BP	248	LEU	2.3
1	AP	323	ILE	2.3
1	CR	250	ILE	2.3
1	AV	242	LEU	2.3
1	BA	136	HIS	2.3
1	BC	252	PRO	2.3
1	BE	264	SER	2.3
1	BF	311	GLY	2.3
1	AH	56	HIS	2.3
1	CK	56	HIS	2.3
1	CP	264	SER	2.3
1	CS	245	SER	2.3
1	BU	264	SER	2.3
1	BX	234	SER	2.3
1	Aa	336	SER	2.3
1	Bb	287	GLY	2.3
1	Cc	262	PRO	2.3
1	Bd	299	GLY	2.3
1	Cd	294	GLY	2.3
1	Cd	316	SER	2.3
1	AB	330	VAL	2.3
1	AD	278	VAL	2.3
1	AJ	236	ASN	2.3
1	BK	53	ASN	2.3
1	AU	278	VAL	2.3
1	BX	288	ASN	2.3
1	Ca	274	VAL	2.3
1	CF	329	THR	2.3
1	CH	295	TRP	2.3
1	CI	298	TRP	2.3
1	Ca	246	THR	2.3
1	CB	276	ARG	2.3
1	CF	115	CYS	2.3
1	BK	333	ARG	2.3
1	CS	297	ARG	2.3
1	AX	164	ARG	2.3
1	AJ	314	TYR	2.3
1	BM	289	ALA	2.3
1	BM	314	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	BB	243	LEU	2.3
1	BE	269	LEU	2.3
1	AE	324	LEU	2.3
1	AM	277	ALA	2.3
1	BU	279	TYR	2.3
1	BO	233	LEU	2.3
1	BO	269	LEU	2.3
1	BP	255	ALA	2.3
1	BH	285	PHE	2.3
1	AI	296	PHE	2.3
1	CS	325	LEU	2.3
1	CU	242	LEU	2.3
1	AX	296	PHE	2.3
1	CC	266	ASP	2.3
1	BD	317	ASP	2.3
1	CH	337	GLU	2.3
1	BJ	231	ASP	2.3
1	CJ	253	ASP	2.3
1	CJ	275	ASP	2.3
1	AP	266	ASP	2.3
1	CS	302	ASP	2.3
1	BC	208	SER	2.3
1	BG	240	SER	2.3
1	CH	232	SER	2.3
1	AM	234	SER	2.3
1	AX	268	SER	2.3
1	Bc	240	SER	2.3
1	Ab	272	GLY	2.3
1	AR	312	VAL	2.3
1	BZ	281	HIS	2.3
1	AZ	56	HIS	2.3
1	Ad	56	HIS	2.3
1	AC	219	THR	2.3
1	CD	246	THR	2.3
1	AH	303	ASN	2.3
1	AI	235	THR	2.3
1	CP	52	THR	2.3
1	CY	246	THR	2.3
1	BZ	332	THR	2.3
1	CI	283	LYS	2.3
1	BM	261	ARG	2.3
1	AT	239	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	BB	233	LEU	2.3
1	AB	282	LEU	2.3
1	CB	233	LEU	2.3
1	BF	269	LEU	2.3
1	AO	269	LEU	2.3
1	CP	248	LEU	2.3
1	CS	331	CYS	2.3
1	AX	263	LEU	2.3
1	Cc	242	LEU	2.3
1	AA	279	TYR	2.3
1	BC	220	ALA	2.3
1	AC	229	TYR	2.3
1	CF	300	ILE	2.3
1	AG	257	PHE	2.3
1	BI	314	TYR	2.3
1	CI	251	ALA	2.3
1	CM	238	PHE	2.3
1	CN	222	ILE	2.3
1	CT	257	PHE	2.3
1	CA	337	GLU	2.3
1	BB	318	GLU	2.3
1	BO	337	GLU	2.3
1	AY	337	GLU	2.3
1	Bc	216	GLU	2.3
1	AX	264	SER	2.3
1	CB	226	GLY	2.3
1	CB	249	ASP	2.3
1	CL	249	ASP	2.3
1	CN	266	ASP	2.3
1	CN	287	GLY	2.3
1	BQ	237	ASP	2.3
1	BU	121	GLY	2.3
1	AW	85	VAL	2.3
1	CY	252	PRO	2.3
1	CY	290	GLY	2.3
1	Cc	320	PRO	2.3
1	BB	321	ARG	2.3
1	AE	56	HIS	2.3
1	CE	239	LYS	2.3
1	BX	283	LYS	2.3
1	Bc	239	LYS	2.3
1	CF	246	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	CF	321	ARG	2.3
1	BJ	164	ARG	2.3
1	AM	230	ASN	2.3
1	CN	218	THR	2.3
1	BP	332	THR	2.3
1	Bc	288	ASN	2.3
1	Ad	230	ASN	2.3
1	Ab	298	TRP	2.3
1	BE	325	LEU	2.3
1	BS	325	LEU	2.3
1	CL	250	ILE	2.3
1	BR	257	PHE	2.3
1	CY	323	ILE	2.3
1	BA	161	GLN	2.3
1	BA	229	TYR	2.3
1	BA	289	ALA	2.3
1	BG	161	GLN	2.3
1	AH	161	GLN	2.3
1	BL	279	TYR	2.3
1	CN	251	ALA	2.3
1	CX	251	ALA	2.3
1	Cb	225	GLN	2.3
1	CL	318	GLU	2.3
1	AC	292	PRO	2.3
1	BG	151	LYS	2.3
1	BG	306	LYS	2.3
1	BI	306	LYS	2.3
1	AM	104	VAL	2.3
1	AN	278	VAL	2.3
1	CN	330	VAL	2.3
1	CO	254	GLY	2.3
1	CY	274	VAL	2.3
1	Ca	327	VAL	2.3
1	Ac	270	GLY	2.3
1	CC	237	ASP	2.3
1	CG	135	ASP	2.3
1	CM	335	ASP	2.3
1	BU	223	MET	2.3
1	BU	253	ASP	2.3
1	CU	276	ARG	2.3
1	AV	54	ASP	2.3
1	Cb	253	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	BF	303	ASN	2.2
1	CM	230	ASN	2.2
1	CM	309	THR	2.2
1	AN	53	ASN	2.2
1	CP	281	HIS	2.2
1	AQ	53	ASN	2.2
1	Aa	218	THR	2.2
1	Aa	235	THR	2.2
1	Ca	288	ASN	2.2
1	Ad	281	HIS	2.2
1	CF	325	LEU	2.2
1	Cb	298	TRP	2.2
1	BO	241	ILE	2.2
1	AQ	238	PHE	2.2
1	CX	323	ILE	2.2
1	Ac	238	PHE	2.2
1	Cc	323	ILE	2.2
1	AM	286	ALA	2.2
1	BO	289	ALA	2.2
1	AG	279	TYR	2.2
1	AG	314	TYR	2.2
1	CI	322	GLN	2.2
1	BJ	161	GLN	2.2
1	BJ	229	TYR	2.2
1	AP	267	TYR	2.2
1	BV	322	GLN	2.2
1	AX	229	TYR	2.2
1	Bd	319	GLN	2.2
1	BB	234	SER	2.2
1	BB	331	CYS	2.2
1	CC	331	CYS	2.2
1	CE	283	LYS	2.2
1	CE	316	SER	2.2
1	CJ	245	SER	2.2
1	CT	227	SER	2.2
1	BG	108	GLU	2.2
1	CM	331	CYS	2.2
1	CV	337	GLU	2.2
1	CF	270	GLY	2.2
1	AH	330	VAL	2.2
1	AO	272	GLY	2.2
1	AP	206	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	Cb	276	ARG	2.2
1	Cc	256	VAL	2.2
1	Cd	278	VAL	2.2
1	BB	253	ASP	2.2
1	CB	302	ASP	2.2
1	BF	309	THR	2.2
1	CH	335	ASP	2.2
1	BI	275	ASP	2.2
1	AK	275	ASP	2.2
1	BM	178	THR	2.2
1	BP	310	ASP	2.2
1	AP	218	THR	2.2
1	CR	228	LEU	2.2
1	CT	52	THR	2.2
1	BU	302	ASP	2.2
1	AV	275	ASP	2.2
1	BX	237	ASP	2.2
1	AZ	310	ASP	2.2
1	BJ	136	HIS	2.2
1	CK	288	ASN	2.2
1	CP	230	ASN	2.2
1	AQ	281	HIS	2.2
1	CW	288	ASN	2.2
1	AA	323	ILE	2.2
1	CH	238	PHE	2.2
1	BL	250	ILE	2.2
1	AO	238	PHE	2.2
1	AU	308	PHE	2.2
1	Ba	323	ILE	2.2
1	AV	298	TRP	2.2
1	CC	313	ALA	2.2
1	BG	277	ALA	2.2
1	AQ	277	ALA	2.2
1	CS	220	ALA	2.2
1	CT	286	ALA	2.2
1	Bb	251	ALA	2.2
1	Ac	313	ALA	2.2
1	CB	240	SER	2.2
1	BC	229	TYR	2.2
1	BC	279	TYR	2.2
1	BH	315	TYR	2.2
1	AM	322	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	AN	239	LYS	2.2
1	AP	162	TYR	2.2
1	CS	239	LYS	2.2
1	AU	151	LYS	2.2
1	Cb	322	GLN	2.2
1	BE	240	SER	2.2
1	CS	232	SER	2.2
1	Cd	314	TYR	2.2
1	Cb	114	MET	2.2
1	BB	256	VAL	2.2
1	CG	327	VAL	2.2
1	BH	261	ARG	2.2
1	CI	105	GLU	2.2
1	BM	274	VAL	2.2
1	BP	326	PRO	2.2
1	CP	243	LEU	2.2
1	CQ	228	LEU	2.2
1	CS	263	LEU	2.2
1	AT	324	LEU	2.2
1	CU	226	GLY	2.2
1	CW	121	GLY	2.2
1	Bc	97	ARG	2.2
1	Ac	276	ARG	2.2
1	CC	292	PRO	2.2
1	AD	262	PRO	2.2
1	AI	252	PRO	2.2
1	CI	252	PRO	2.2
1	BM	247	PRO	2.2
1	Ca	115	CYS	2.2
1	Ca	248	LEU	2.2
1	Cc	328	GLY	2.2
1	AC	331	CYS	2.2
1	AG	332	THR	2.2
1	CP	307	THR	2.2
1	AU	218	THR	2.2
1	CU	235	THR	2.2
1	BC	275	ASP	2.2
1	AD	323	ILE	2.2
1	BO	87	ASP	2.2
1	CQ	253	ASP	2.2
1	BR	275	ASP	2.2
1	AV	53	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	BX	236	ASN	2.2
1	Ca	310	ASP	2.2
1	Cb	310	ASP	2.2
1	Cc	317	ASP	2.2
1	BB	306	LYS	2.2
1	AE	306	LYS	2.2
1	CE	280	TRP	2.2
1	BF	151	LYS	2.2
1	CH	283	LYS	2.2
1	CY	283	LYS	2.2
1	BC	258	GLN	2.2
1	Cd	322	GLN	2.2
1	BF	229	TYR	2.2
1	BI	279	TYR	2.2
1	BK	232	SER	2.2
1	AL	314	TYR	2.2
1	AZ	232	SER	2.2
1	CH	269	LEU	2.2
1	AL	228	LEU	2.2
1	AL	233	LEU	2.2
1	BV	55	VAL	2.2
1	CY	321	ARG	2.2
1	AW	318	GLU	2.2
1	AZ	274	VAL	2.2
1	Bd	278	VAL	2.2
1	CC	290	GLY	2.2
1	BH	320	PRO	2.2
1	AH	326	PRO	2.2
1	CK	290	GLY	2.2
1	AM	272	GLY	2.2
1	CM	252	PRO	2.2
1	AR	189	GLY	2.2
1	Ab	121	GLY	2.2
1	CE	329	THR	2.2
1	BH	250	ILE	2.2
1	CH	332	THR	2.2
1	BI	241	ILE	2.2
1	BI	323	ILE	2.2
1	BJ	52	THR	2.2
1	BS	241	ILE	2.2
1	AT	218	THR	2.2
1	BV	250	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	CW	291	THR	2.2
1	CA	115	CYS	2.2
1	CD	331	CYS	2.2
1	CI	304	PHE	2.2
1	CQ	257	PHE	2.2
1	BU	257	PHE	2.2
1	CU	331	CYS	2.2
1	CZ	238	PHE	2.2
1	Bd	257	PHE	2.2
1	BJ	305	ASN	2.2
1	CC	283	LYS	2.2
1	BD	239	LYS	2.2
1	CJ	283	LYS	2.2
1	BK	317	ASP	2.2
1	CK	249	ASP	2.2
1	AT	54	ASP	2.2
1	Ab	260	ASP	2.2
1	Cb	230	ASN	2.2
1	Cc	81	ASP	2.2
1	Ad	134	ASN	2.2
1	CM	151	LYS	2.2
1	CY	151	LYS	2.2
1	Bc	56	HIS	2.2
1	Bd	239	LYS	2.2
1	AA	95	ALA	2.2
1	BI	251	ALA	2.2
1	CB	223	MET	2.2
1	CK	322	GLN	2.2
1	AA	159	ARG	2.2
1	CA	263	LEU	2.2
1	BE	233	LEU	2.2
1	CF	228	LEU	2.2
1	BM	234	SER	2.2
1	Ab	258	GLN	2.2
1	BJ	321	ARG	2.2
1	BM	279	TYR	2.2
1	BQ	269	LEU	2.2
1	BT	229	TYR	2.2
1	Cb	261	ARG	2.2
1	AV	312	VAL	2.2
1	Ab	334	VAL	2.2
1	CG	318	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	BH	210	PRO	2.2
1	CH	105	GLU	2.2
1	CH	122	GLY	2.2
1	AM	51	GLY	2.2
1	BO	287	GLY	2.2
1	AP	217	GLU	2.2
1	BT	108	GLU	2.2
1	BT	189	GLY	2.2
1	BU	254	GLY	2.2
1	AU	272	GLY	2.2
1	BF	300	ILE	2.2
1	AH	250	ILE	2.2
1	CV	262	PRO	2.2
1	Cb	292	PRO	2.2
1	BC	332	THR	2.2
1	AE	52	THR	2.2
1	CH	271	THR	2.2
1	BJ	332	THR	2.2
1	CJ	99	PHE	2.2
1	BK	235	THR	2.2
1	AM	238	PHE	2.2
1	CN	291	THR	2.2
1	CS	307	THR	2.2
1	Ca	224	THR	2.2
1	CG	151	LYS	2.2
1	BM	284	LYS	2.2
1	AZ	230	ASN	2.2
1	BB	136	HIS	2.2
1	BF	293	ALA	2.2
1	AI	293	ALA	2.2
1	BM	136	HIS	2.2
1	AM	237	ASP	2.2
1	BP	136	HIS	2.2
1	AV	281	HIS	2.2
1	BX	286	ALA	2.2
1	BY	275	ASP	2.2
1	Bb	289	ALA	2.2
1	BC	242	LEU	2.2
1	BG	248	LEU	2.2
1	CA	276	ARG	2.2
1	CB	297	ARG	2.2
1	AC	295	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
1	BH	164	ARG	2.2
1	AK	208	SER	2.2
1	CK	268	SER	2.2
1	BM	145	ARG	2.2
1	AM	208	SER	2.2
1	BO	243	LEU	2.2
1	BV	269	LEU	2.2
1	Bc	301	TRP	2.2
1	CA	334	VAL	2.2
1	CE	267	TYR	2.2
1	CS	278	VAL	2.2
1	AV	274	VAL	2.2
1	CY	312	VAL	2.2
1	Ab	279	TYR	2.2
1	CA	292	PRO	2.2
1	BD	189	GLY	2.2
1	BE	189	GLY	2.2
1	BE	299	GLY	2.2
1	BF	254	GLY	2.2
1	AN	241	ILE	2.2
1	AR	121	GLY	2.2
1	CR	290	GLY	2.2
1	CU	241	ILE	2.2
1	BF	318	GLU	2.2
1	AG	320	PRO	2.2
1	CG	320	PRO	2.2
1	CH	285	PHE	2.2
1	BJ	320	PRO	2.2
1	CN	285	PHE	2.2
1	CS	296	PHE	2.2
1	AU	238	PHE	2.2
1	CV	221	PRO	2.2
1	CX	116	PRO	2.2
1	CY	247	PRO	2.2
1	CY	337	GLU	2.2
1	Cc	252	PRO	2.2
1	BA	235	THR	2.2
1	CA	219	THR	2.2
1	AF	52	THR	2.2
1	AI	224	THR	2.2
1	CK	283	LYS	2.2
1	AX	239	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	CY	239	LYS	2.2
1	Bd	306	LYS	2.2
1	Ad	52	THR	2.2
1	Ad	178	THR	2.2
1	AO	230	ASN	2.2
1	CR	288	ASN	2.2
1	AB	277	ALA	2.1
1	CD	286	ALA	2.1
1	BK	263	LEU	2.2
1	BX	324	LEU	2.2
1	AX	95	ALA	2.1
1	CZ	248	LEU	2.2
1	CZ	277	ALA	2.1
1	Cc	248	LEU	2.2
1	AB	237	ASP	2.1
1	CC	261	ARG	2.1
1	CG	275	ASP	2.1
1	BI	321	ARG	2.1
1	AI	317	ASP	2.1
1	CI	261	ARG	2.1
1	BK	54	ASP	2.1
1	BL	317	ASP	2.1
1	BN	275	ASP	2.1
1	CO	260	ASP	2.1
1	BV	136	HIS	2.1
1	CV	54	ASP	2.1
1	CV	281	HIS	2.1
1	BX	253	ASP	2.1
1	AX	336	SER	2.1
1	Bb	335	ASP	2.1
1	Ac	145	ARG	2.1
1	Ac	193	ASP	2.1
1	Ba	161	GLN	2.1
1	Ac	319	GLN	2.1
1	CS	301	TRP	2.1
1	AB	162	TYR	2.1
1	BE	229	TYR	2.1
1	CF	323	ILE	2.1
1	CH	229	TYR	2.1
1	CH	241	ILE	2.1
1	AI	279	TYR	2.1
1	AJ	312	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	AM	278	VAL	2.1
1	AQ	274	VAL	2.1
1	CX	312	VAL	2.1
1	CY	265	ILE	2.1
1	CZ	312	VAL	2.1
1	Cb	267	TYR	2.1
1	AB	51	GLY	2.1
1	CH	270	GLY	2.1
1	BI	328	GLY	2.1
1	CI	326	PRO	2.1
1	CJ	285	PHE	2.1
1	BK	252	PRO	2.1
1	BL	120	GLY	2.1
1	CS	238	PHE	2.1
1	AP	151	LYS	2.1
1	BQ	93	GLY	2.1
1	BU	93	GLY	2.1
1	CY	116	PRO	2.1
1	Bb	257	PHE	2.1
1	Cc	299	GLY	2.1
1	AO	105	GLU	2.1
1	CR	217	GLU	2.1
1	CC	224	THR	2.1
1	BI	291	THR	2.1
1	CS	291	THR	2.1
1	AV	52	THR	2.1
1	BZ	178	THR	2.1
1	Ac	309	THR	2.1
1	AC	242	LEU	2.1
1	CJ	233	LEU	2.1
1	Bc	212	LEU	2.1
1	BD	289	ALA	2.1
1	CF	251	ALA	2.1
1	BK	286	ALA	2.1
1	CN	286	ALA	2.1
1	BP	134	ASN	2.1
1	BQ	286	ALA	2.1
1	BT	313	ALA	2.1
1	BU	277	ALA	2.1
1	Ab	236	ASN	2.1
1	Cd	255	ALA	2.1
1	BP	164	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	AZ	206	ARG	2.1
1	BH	208	SER	2.1
1	AH	268	SER	2.1
1	BS	208	SER	2.1
1	BD	56	HIS	2.1
1	AW	322	GLN	2.1
1	CA	323	ILE	2.1
1	CA	335	ASP	2.1
1	AB	265	ILE	2.1
1	CB	273	ASP	2.1
1	AC	231	ASP	2.1
1	AF	237	ASP	2.1
1	BL	275	ASP	2.1
1	BO	250	ILE	2.1
1	BO	275	ASP	2.1
1	AU	266	ASP	2.1
1	CW	250	ILE	2.1
1	AY	317	ASP	2.1
1	CY	231	ASP	2.1
1	CZ	56	HIS	2.1
1	CZ	281	HIS	2.1
1	Bc	310	ASP	2.1
1	CN	280	TRP	2.1
1	BX	280	TRP	2.1
1	CZ	331	CYS	2.1
1	BD	296	PHE	2.1
1	CD	296	PHE	2.1
1	AK	314	TYR	2.1
1	BO	306	LYS	2.1
1	CU	267	TYR	2.1
1	CU	285	PHE	2.1
1	AC	254	GLY	2.1
1	BL	121	GLY	2.1
1	AN	86	PRO	2.1
1	BZ	120	GLY	2.1
1	Ca	294	GLY	2.1
1	Bb	290	GLY	2.1
1	AO	217	GLU	2.1
1	Bd	216	GLU	2.1
1	BH	291	THR	2.1
1	BN	329	THR	2.1
1	AQ	271	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	AS	235	THR	2.1
1	AX	332	THR	2.1
1	BJ	233	LEU	2.1
1	CK	282	LEU	2.1
1	CM	259	LEU	2.1
1	BO	324	LEU	2.1
1	CP	242	LEU	2.1
1	CT	242	LEU	2.1
1	Bc	282	LEU	2.1
1	AB	236	ASN	2.1
1	BJ	236	ASN	2.1
1	BP	313	ALA	2.1
1	AT	53	ASN	2.1
1	BU	206	ARG	2.1
1	CY	305	ASN	2.1
1	Bb	305	ASN	2.1
1	Cb	303	ASN	2.1
1	Cd	236	ASN	2.1
1	CB	227	SER	2.1
1	CN	240	SER	2.1
1	BS	264	SER	2.1
1	CU	245	SER	2.1
1	BW	208	SER	2.1
1	CB	319	GLN	2.1
1	CO	258	GLN	2.1
1	Aa	323	ILE	2.1
1	Ca	65	GLN	2.1
1	AN	281	HIS	2.1
1	BO	283	LYS	2.1
1	CO	304	PHE	2.1
1	BR	278	VAL	2.1
1	AX	310	ASP	2.1
1	Bb	285	PHE	2.1
1	Ad	275	ASP	2.1
1	BB	295	TRP	2.1
1	AM	298	TRP	2.1
1	CU	301	TRP	2.1
1	AC	290	GLY	2.1
1	BI	290	GLY	2.1
1	CS	226	GLY	2.1
1	Bb	299	GLY	2.1
1	CH	292	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	AO	326	PRO	2.1
1	CT	320	PRO	2.1
1	AV	292	PRO	2.1
1	Cc	331	CYS	2.1
1	CA	324	LEU	2.1
1	CB	217	GLU	2.1
1	BE	318	GLU	2.1
1	CE	318	GLU	2.1
1	CI	217	GLU	2.1
1	AN	325	LEU	2.1
1	CN	105	GLU	2.1
1	CN	269	LEU	2.1
1	AT	337	GLU	2.1
1	CV	282	LEU	2.1
1	AY	269	LEU	2.1
1	BA	332	THR	2.1
1	CD	218	THR	2.1
1	CE	246	THR	2.1
1	BF	291	THR	2.1
1	BM	246	THR	2.1
1	CN	178	THR	2.1
1	CN	329	THR	2.1
1	AV	329	THR	2.1
1	BY	291	THR	2.1
1	CZ	219	THR	2.1
1	AC	145	ARG	2.1
1	AC	321	ARG	2.1
1	BD	276	ARG	2.1
1	BV	206	ARG	2.1
1	BA	286	ALA	2.1
1	CQ	255	ALA	2.1
1	CV	277	ALA	2.1
1	AA	230	ASN	2.1
1	CC	250	ILE	2.1
1	BD	305	ASN	2.1
1	BJ	208	SER	2.1
1	CK	303	ASN	2.1
1	BN	240	SER	2.1
1	BP	236	ASN	2.1
1	AV	230	ASN	2.1
1	BB	258	GLN	2.1
1	BB	319	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	CD	151	LYS	2.1
1	Bb	283	LYS	2.1
1	CC	256	VAL	2.1
1	BI	304	PHE	2.1
1	CN	256	VAL	2.1
1	CP	312	VAL	2.1
1	CR	304	PHE	2.1
1	AQ	136	HIS	2.1
1	CA	295	TRP	2.1
1	BD	301	TRP	2.1
1	BE	135	ASP	2.1
1	BH	189	GLY	2.1
1	AK	315	TYR	2.1
1	AO	228	LEU	2.1
1	BS	279	TYR	2.1
1	BU	311	GLY	2.1
1	CU	298	TRP	2.1
1	AV	325	LEU	2.1
1	AW	228	LEU	2.1
1	CW	317	ASP	2.1
1	AX	315	TYR	2.1
1	CX	233	LEU	2.1
1	Bb	135	ASP	2.1
1	CV	290	GLY	2.1
1	CZ	254	GLY	2.1
1	AB	221	PRO	2.1
1	CH	326	PRO	2.1
1	AC	291	THR	2.1
1	CC	271	THR	2.1
1	AG	217	GLU	2.1
1	AK	106	THR	2.1
1	BW	291	THR	2.1
1	Ac	307	THR	2.1
1	BM	276	ARG	2.1
1	CM	333	ARG	2.1
1	BX	321	ARG	2.1
1	BD	255	ALA	2.1
1	CD	323	ILE	2.1
1	AF	300	ILE	2.1
1	CJ	323	ILE	2.1
1	BM	323	ILE	2.1
1	AM	300	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	AA	227	SER	2.1
1	CB	283	LYS	2.1
1	BQ	103	ALA	2.1
1	BU	286	ALA	2.1
1	CV	289	ALA	2.1
1	BJ	240	SER	2.1
1	CP	208	SER	2.1
1	CS	316	SER	2.1
1	CV	245	SER	2.1
1	CY	240	SER	2.1
1	Ca	284	LYS	2.1
1	Ab	268	SER	2.1
1	CA	308	PHE	2.1
1	BG	322	GLN	2.1
1	BH	288	ASN	2.1
1	BM	285	PHE	2.1
1	CO	322	GLN	2.1
1	AU	236	ASN	2.1
1	CB	330	VAL	2.1
1	BC	334	VAL	2.1
1	BH	256	VAL	2.1
1	AM	85	VAL	2.1
1	BT	274	VAL	2.1
1	AT	278	VAL	2.1
1	AA	228	LEU	2.1
1	AA	233	LEU	2.1
1	CP	269	LEU	2.1
1	BX	248	LEU	2.1
1	AG	281	HIS	2.1
1	BS	281	HIS	2.1
1	CT	56	HIS	2.1
1	Aa	281	HIS	2.1
1	BH	311	GLY	2.1
1	BH	314	TYR	2.1
1	AA	320	PRO	2.1
1	AB	266	ASP	2.1
1	BD	54	ASP	2.1
1	BE	237	ASP	2.1
1	BG	249	ASP	2.1
1	AH	299	GLY	2.1
1	CU	223	MET	2.1
1	CU	229	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	CW	226	GLY	2.1
1	BX	229	TYR	2.1
1	AX	162	TYR	2.1
1	BH	221	PRO	2.1
1	BI	301	TRP	2.1
1	AJ	275	ASP	2.1
1	BL	249	ASP	2.1
1	BP	275	ASP	2.1
1	AS	237	ASP	2.1
1	BT	247	PRO	2.1
1	AU	237	ASP	2.1
1	CA	105	GLU	2.1
1	CF	332	THR	2.1
1	CG	35	THR	2.1
1	AQ	318	GLU	2.1
1	AR	217	GLU	2.1
1	AS	337	GLU	2.1
1	AU	106	THR	2.1
1	AU	337	GLU	2.1
1	BY	178	THR	2.1
1	CY	318	GLU	2.1
1	Bc	235	THR	2.1
1	CA	333	ARG	2.1
1	Ba	321	ARG	2.1
1	CH	151	LYS	2.1
1	CN	331	CYS	2.1
1	BT	300	ILE	2.1
1	CV	63	ILE	2.1
1	AY	306	LYS	2.1
1	Cc	239	LYS	2.1
1	CC	268	SER	2.1
1	AG	268	SER	2.1
1	AG	316	SER	2.1
1	CH	313	ALA	2.1
1	BI	286	ALA	2.1
1	CJ	286	ALA	2.1
1	BM	277	ALA	2.1
1	CM	293	ALA	2.1
1	AN	234	SER	2.1
1	CQ	232	SER	2.1
1	Bb	232	SER	2.1
1	Ab	234	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	Ac	293	ALA	2.1
1	BI	308	PHE	2.1
1	Ab	296	PHE	2.1
1	CA	312	VAL	2.1
1	AG	190	ASN	2.1
1	CG	274	VAL	2.1
1	AM	330	VAL	2.1
1	BO	305	ASN	2.1
1	CM	269	LEU	2.1
1	BN	243	LEU	2.1
1	AO	85	VAL	2.1
1	CQ	243	LEU	2.1
1	CQ	256	VAL	2.1
1	CT	312	VAL	2.1
1	BX	312	VAL	2.1
1	CZ	269	LEU	2.1
1	Ba	228	LEU	2.1
1	Cb	195	VAL	2.1
1	Cc	330	VAL	2.1
1	CF	294	GLY	2.0
1	BG	311	GLY	2.0
1	CH	120	GLY	2.0
1	BT	281	HIS	2.0
1	CY	244	GLY	2.0
1	Ca	281	HIS	2.0
1	AE	335	ASP	2.0
1	CE	298	TRP	2.0
1	CH	116	PRO	2.0
1	AU	221	PRO	2.0
1	CV	203	TRP	2.0
1	CV	295	TRP	2.0
1	Ab	326	PRO	2.0
1	CE	178	THR	2.0
1	CF	291	THR	2.0
1	AI	260	ASP	2.0
1	CI	335	ASP	2.0
1	BK	178	THR	2.0
1	AL	144	THR	2.0
1	AM	321	ARG	2.0
1	BO	235	THR	2.0
1	AS	52	THR	2.0
1	Bb	276	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
1	Bc	266	ASP	2.0
1	CT	217	GLU	2.0
1	Ad	108	GLU	2.0
1	Ad	206	ARG	2.0
1	AA	300	ILE	2.0
1	AG	300	ILE	2.0
1	CJ	241	ILE	2.0
1	BL	300	ILE	2.0
1	AX	300	ILE	2.0
1	Cd	105	GLU	2.0
1	CD	293	ALA	2.0
1	CD	313	ALA	2.0
1	BF	313	ALA	2.0
1	BI	293	ALA	2.0
1	AP	232	SER	2.0
1	CQ	293	ALA	2.0
1	CY	277	ALA	2.0
1	CF	296	PHE	2.0
1	CA	243	LEU	2.0
1	BB	269	LEU	2.0
1	CE	242	LEU	2.0
1	AI	269	LEU	2.0
1	BJ	324	LEU	2.0
1	CK	319	GLN	2.0
1	CL	115	CYS	2.0
1	BS	322	GLN	2.0
1	AV	243	LEU	2.0
1	AX	322	GLN	2.0
1	Bd	233	LEU	2.0
1	BL	278	VAL	2.0
1	AS	274	VAL	2.0
1	CY	330	VAL	2.0
1	BA	236	ASN	2.0
1	AH	118	ASN	2.0
1	Bd	236	ASN	2.0
1	CB	294	GLY	2.0
1	AC	299	GLY	2.0
1	BF	121	GLY	2.0
1	BM	287	GLY	2.0
1	CM	287	GLY	2.0
1	BS	226	GLY	2.0
1	CU	254	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	BB	292	PRO	2.0
1	AB	326	PRO	2.0
1	AD	314	TYR	2.0
1	BC	261	ARG	2.0
1	AE	252	PRO	2.0
1	BF	267	TYR	2.0
1	CH	267	TYR	2.0
1	AF	206	ARG	2.0
1	BI	56	HIS	2.0
1	AN	229	TYR	2.0
1	BQ	320	PRO	2.0
1	AS	281	HIS	2.0
1	BU	326	PRO	2.0
1	BV	320	PRO	2.0
1	BX	314	TYR	2.0
1	Bb	136	HIS	2.0
1	Cb	320	PRO	2.0
1	Ac	56	HIS	2.0
1	Cc	210	PRO	2.0
1	BB	52	THR	2.0
1	BE	329	THR	2.0
1	CH	301	TRP	2.0
1	CI	332	THR	2.0
1	BM	271	THR	2.0
1	BQ	218	THR	2.0
1	BR	178	THR	2.0
1	AR	163	THR	2.0
1	CT	241	ILE	2.0
1	CX	300	ILE	2.0
1	CY	298	TRP	2.0
1	Cc	224	THR	2.0
1	AC	337	GLU	2.0
1	BD	335	ASP	2.0
1	AH	302	ASP	2.0
1	AJ	217	GLU	2.0
1	CX	317	ASP	2.0
1	BZ	317	ASP	2.0
1	Ba	105	GLU	2.0
1	Cd	87	ASP	2.0
1	AC	296	PHE	2.0
1	AH	232	SER	2.0
1	AH	242	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	CH	240	SER	2.0
1	AL	336	SER	2.0
1	AM	232	SER	2.0
1	CM	304	PHE	2.0
1	CO	285	PHE	2.0
1	BA	228	LEU	2.0
1	BF	325	LEU	2.0
1	AN	233	LEU	2.0
1	BQ	242	LEU	2.0
1	BQ	293	ALA	2.0
1	AR	177	LEU	2.0
1	BT	324	LEU	2.0
1	BV	289	ALA	2.0
1	AZ	264	SER	2.0
1	Ba	324	LEU	2.0
1	Aa	289	ALA	2.0
1	Cd	220	ALA	2.0
1	CS	258	GLN	2.0
1	Cc	45	VAL	2.0
1	AC	236	ASN	2.0
1	CE	288	ASN	2.0
1	Bd	288	ASN	2.0
1	AB	151	LYS	2.0
1	BE	254	GLY	2.0
1	BP	145	ARG	2.0
1	BP	311	GLY	2.0
1	CT	51	GLY	2.0
1	BU	287	GLY	2.0
1	AU	121	GLY	2.0
1	CU	41	LYS	2.0
1	Bb	121	GLY	2.0
1	BA	162	TYR	2.0
1	AD	162	TYR	2.0
1	AH	241	ILE	2.0
1	AI	320	PRO	2.0
1	AU	279	TYR	2.0
1	Ba	300	ILE	2.0
1	Ca	300	ILE	2.0
1	Ab	321	ARG	2.0
1	BH	163	THR	2.0
1	AK	52	THR	2.0
1	BN	56	HIS	2.0

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Mol	Chain	Res	Type	RSRZ
1	AQ	235	THR	2.0
1	CS	218	THR	2.0
1	BZ	291	THR	2.0
1	BB	308	PHE	2.0
1	CB	269	LEU	2.0
1	BC	238	PHE	2.0
1	CJ	337	GLU	2.0
1	AK	217	GLU	2.0
1	AL	337	GLU	2.0
1	CM	295	TRP	2.0
1	BG	233	LEU	2.0
1	CF	313	ALA	2.0
1	BH	275	ASP	2.0
1	CH	193	ASP	2.0
1	AI	268	SER	2.0
1	BL	253	ASP	2.0
1	AM	227	SER	2.0
1	CM	237	ASP	2.0
1	CQ	296	PHE	2.0
1	CT	228	LEU	2.0
1	AU	257	PHE	2.0
1	AZ	88	LEU	2.0
1	Bc	242	LEU	2.0
1	AU	82	ALA	2.0
1	AV	264	SER	2.0
1	Bb	286	ALA	2.0
1	AI	327	VAL	2.0
1	BQ	104	VAL	2.0

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

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

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CA	AE	401	1/1	0.97	0.05	38,38,38,38	0
2	CA	AF	401	1/1	0.97	0.05	50,50,50,50	0
2	CA	BN	402	1/1	0.97	0.05	50,50,50,50	0
2	CA	Ba	401	1/1	0.97	0.07	53,53,53,53	0
2	CA	BJ	401	1/1	0.98	0.06	27,27,27,27	0
2	CA	BN	401	1/1	0.98	0.06	39,39,39,39	0
2	CA	BI	401	1/1	0.98	0.05	43,43,43,43	0
2	CA	BO	401	1/1	0.98	0.06	34,34,34,34	0
2	CA	BO	402	1/1	0.98	0.05	52,52,52,52	0
2	CA	BP	401	1/1	0.98	0.06	33,33,33,33	0
2	CA	AP	401	1/1	0.98	0.04	42,42,42,42	0
2	CA	BZ	401	1/1	0.98	0.03	36,36,36,36	0
2	CA	AZ	401	1/1	0.98	0.06	36,36,36,36	0
2	CA	BI	402	1/1	0.98	0.03	54,54,54,54	0
2	CA	Aa	401	1/1	0.98	0.05	45,45,45,45	0
2	CA	Ac	401	1/1	0.98	0.07	48,48,48,48	0
2	CA	BH	401	1/1	0.99	0.03	34,34,34,34	0
2	CA	BH	402	1/1	0.99	0.03	41,41,41,41	0
2	CA	AH	401	1/1	0.99	0.04	34,34,34,34	0
2	CA	AA	401	1/1	0.99	0.03	57,57,57,57	0
2	CA	BB	402	1/1	0.99	0.04	35,35,35,35	0
2	CA	AI	401	1/1	0.99	0.04	43,43,43,43	0
2	CA	AB	401	1/1	0.99	0.04	40,40,40,40	0
2	CA	BJ	402	1/1	0.99	0.04	29,29,29,29	0
2	CA	AJ	401	1/1	0.99	0.04	38,38,38,38	0
2	CA	BK	401	1/1	0.99	0.03	22,22,22,22	0
2	CA	AK	401	1/1	0.99	0.04	36,36,36,36	0
2	CA	BL	401	1/1	0.99	0.03	24,24,24,24	0
2	CA	AL	401	1/1	0.99	0.03	41,41,41,41	0
2	CA	BM	401	1/1	0.99	0.05	39,39,39,39	0
2	CA	BM	402	1/1	0.99	0.03	33,33,33,33	0
2	CA	BC	401	1/1	0.99	0.03	22,22,22,22	0
2	CA	BC	402	1/1	0.99	0.03	38,38,38,38	0
2	CA	AN	401	1/1	0.99	0.04	42,42,42,42	0
2	CA	AC	401	1/1	0.99	0.03	28,28,28,28	0
2	CA	BD	401	1/1	0.99	0.03	36,36,36,36	0
2	CA	AO	401	1/1	0.99	0.04	47,47,47,47	0
2	CA	AD	401	1/1	0.99	0.03	36,36,36,36	0
2	CA	BP	402	1/1	0.99	0.03	35,35,35,35	0
2	CA	BE	401	1/1	0.99	0.03	35,35,35,35	0
2	CA	BQ	401	1/1	0.99	0.03	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CA	BQ	402	1/1	0.99	0.05	43,43,43,43	0
2	CA	AQ	401	1/1	0.99	0.03	57,57,57,57	0
2	CA	BR	401	1/1	0.99	0.02	26,26,26,26	0
2	CA	BR	402	1/1	0.99	0.03	53,53,53,53	0
2	CA	BS	401	1/1	0.99	0.05	23,23,23,23	0
2	CA	BS	402	1/1	0.99	0.02	36,36,36,36	0
2	CA	AS	401	1/1	0.99	0.03	27,27,27,27	0
2	CA	AT	401	1/1	0.99	0.03	36,36,36,36	0
2	CA	BU	401	1/1	0.99	0.02	32,32,32,32	0
2	CA	AU	401	1/1	0.99	0.03	30,30,30,30	0
2	CA	BV	401	1/1	0.99	0.03	36,36,36,36	0
2	CA	BV	402	1/1	0.99	0.04	57,57,57,57	0
2	CA	AV	401	1/1	0.99	0.04	39,39,39,39	0
2	CA	BW	401	1/1	0.99	0.02	25,25,25,25	0
2	CA	BW	402	1/1	0.99	0.04	42,42,42,42	0
2	CA	AW	401	1/1	0.99	0.04	39,39,39,39	0
2	CA	BX	401	1/1	0.99	0.04	35,35,35,35	0
2	CA	AX	401	1/1	0.99	0.03	38,38,38,38	0
2	CA	BY	401	1/1	0.99	0.03	31,31,31,31	0
2	CA	BY	402	1/1	0.99	0.04	33,33,33,33	0
2	CA	AY	401	1/1	0.99	0.03	30,30,30,30	0
2	CA	BA	401	1/1	0.99	0.03	35,35,35,35	0
2	CA	BZ	402	1/1	0.99	0.04	57,57,57,57	0
2	CA	BF	402	1/1	0.99	0.03	36,36,36,36	0
2	CA	BA	402	1/1	0.99	0.02	41,41,41,41	0
2	CA	Ba	402	1/1	0.99	0.04	42,42,42,42	0
2	CA	BG	401	1/1	0.99	0.03	38,38,38,38	0
2	CA	Bb	402	1/1	0.99	0.02	33,33,33,33	0
2	CA	Ab	401	1/1	0.99	0.03	38,38,38,38	0
2	CA	Bc	401	1/1	0.99	0.03	29,29,29,29	0
2	CA	Bc	402	1/1	0.99	0.06	43,43,43,43	0
2	CA	BG	402	1/1	0.99	0.04	54,54,54,54	0
2	CA	Bd	401	1/1	0.99	0.02	37,37,37,37	0
2	CA	Bd	402	1/1	0.99	0.02	48,48,48,48	0
2	CA	Ad	401	1/1	0.99	0.03	42,42,42,42	0
2	CA	BB	401	1/1	1.00	0.02	26,26,26,26	0
2	CA	BF	401	1/1	1.00	0.02	27,27,27,27	0
2	CA	AR	401	1/1	1.00	0.02	40,40,40,40	0
2	CA	AG	401	1/1	1.00	0.03	44,44,44,44	0
2	CA	AM	401	1/1	1.00	0.03	45,45,45,45	0
2	CA	Bb	401	1/1	1.00	0.03	24,24,24,24	0
2	CA	BK	402	1/1	1.00	0.03	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CA	BT	401	1/1	1.00	0.02	19,19,19,19	0
2	CA	BX	402	1/1	1.00	0.02	31,31,31,31	0
2	CA	BT	402	1/1	1.00	0.02	42,42,42,42	0
2	CA	BD	402	1/1	1.00	0.02	44,44,44,44	0
2	CA	BE	402	1/1	1.00	0.02	33,33,33,33	0
2	CA	BU	402	1/1	1.00	0.02	29,29,29,29	0
2	CA	BL	402	1/1	1.00	0.03	34,34,34,34	0

6.5 Other polymers

There are no such residues in this entry.